





# Experimental Design and Investigation of How Cosmetic Proteins Affect Bacteria Found on the Skin

Вy

Hannah E. Salvage

A thesis submitted to Cardiff University for the degree of Doctor of Philosophy

March 2022

Cardiff School of Biosciences Sir Martin Evans Building Museum Avenue Cardiff CF10 3AX

# Abstract

Skin care companies have started to invest in products which are microbe friendly or promote and support 'good' microbes. Cosmetic proteins are proteolysates used in cosmetic formulations for their hydration and moisturization properties. This thesis investigates how cosmetic proteins could affect skin bacteria and the steps required to take the research from in vitro to in vivo. The preservatives in the cosmetic proteins had varied inhibitory effects on the three chosen species, Staphylococcus aureus, Staphylococcus epidermidis and Corynebacterium jeikeium. The three species were also able to utilize the peptides and amino acids found in the cosmetic proteins to aid in both planktonic growth and formation of biofilms. The low pH of the cosmetic proteins controlled S. aureus from dominating when in a mixed biofilm culture model. Once skin cells were included in the experiments, it was clear how *S. aureus* elicited an immune response, significantly greater than any of the cosmetic protein were able to elicit. S. epidermidis however, was able to reduce the amount of inflammation and stop over proliferation of S. aureus. Planning future experiments in vivo required investigations of different swab types and buffers for collection of the skin microbiota, as well as choosing suitable swab sites for bacterial studies. The research also found that past cosmetic skin study protocols may not be appropriate for microbial investigations, as the differences in bacterial communities and mass across different skin sites had not been previously considered. In conclusion, in vitro, cosmetic proteins are ingredients which can both promote and harm the bacteria that live on our skin. The amino acids can provide nutrients, while the preservatives have a bacteriostatic or bactericidal effects. Using dry cosmetic proteins would remove the need for preservatives, however this has the potential to cause over-proliferation of undesirable species. Further work using skin panel testing, launching from the final chapters of this thesis, would help conclude whether the answers from the *in vitro* work would be repeated in the in vivo experiments.

# Contents

Abstr	act	ii
1 I	ntroduction to The Skin, Skin Inhabitants and Cosmetics	1
1.1	Human Skin	2
1.2	pH and Temperature	2
1.3	Skin Layers and Structure	2
1.4	Pores and Glands	3
1.5	Skin Immunity	6
1.6	Repairing Skin Damage	6
1.7	Dealing with Skin Cancer	6
1.8	Defence against Microbes	6
1.9	Skin Microbial Transplants and Bacteriotherapy	7
1.1	0 The Skin and Microbes	11
1.1	1 Mites	11
1.1	2 Viruses	
1.1	3 Fungal Residents of the Skin	
1.1	4 Dominant Skin Bacteria - Phyla and Genera	
1.1	5 Commensal and Pathogenic Staphylococcus spp	14
1.1	6 Skin Dwelling Coryneform	
1.1	7 New Classification for the old <i>Propionibacterium</i> spp	
1.1	8 Splitting of the <i>Micrococcus</i> Genus	20
1.1	9 Do Gram-negative skin commensals exist?	21
1.2	0 Commensal or Pathogen? It Isn't Straightforward	21
1.2	1 Changes in Skin Bacteria from Birth	22
1.2	2 Skin Microbial Diversity of the Western World	23
1.2	3 Battle of the Sexes	23
1.2	4 Cosmetics	24
1.2	5 Probiotics	24
1.2	6 Emulsifiers and Surfactants	25
1.2	7 Preserving Measures	25
1.2	8 Cosmetic Proteins	
1.2	9 Reasons for Research	
1.3	0 Hypothesis	32
1.3	1 Aims	32
2 F	Production of a Minimal Medium to Reflect the Skin's Harsh Environment	
2.1	Growth Requirements	34
2.2	Growth Kinetics	

	2.3	Null Hypothesis	37
	2.4	Aims	37
	2.5	Materials	38
	2.6	Bacteria	38
	2.7	Media	38
	2.8	Minimal Medium	38
	2.9	Methods	39
	2.10	Media Growth Curves	39
	2.11	Statistics	39
	2.12	Results	40
	2.13	Growth Curves with TSB, Mueller-Hinton and Minimal Medium	40
	2.14	Discussion	44
	2.15	Why are Nutrient Rich Media not useful for Skin experiments?	44
	2.16	Nutrient Rich Media can Provide both Metabolic Advantages and Disadvantages	44
	2.17	Conclusion	45
		ting Experimental Conditions to Determine whether Bacterial Skin Species Can Util	
		c Proteins as a Peptide and Amino Acid Source and if Preserving Measures are Effec	
1	3.1	Introduction	
	3.2	Uptake of Amino Acids	
	3.3	Preservatives	
	3.4	Studying Growth Kinetics When Switching Nutritional Sources	
	3.5	Biofilms	
	3.6	Null Hypothesis	_
	3.7	Aims	
	3.8	Materials	
	3.9	Bacteria	
	3.10	Cosmetic Proteins	
	3.11	Media	
	3.12	Methods	
	3.13	Calculating Minimum Inhibitory Concentration	
	3.14	Lactose-free Skimmed Milk Agar Protease Test	
	3.15	Growth Curve Kinetics Experiment	
	3.16	Counting the CFU/ml of The Growth Curves	
	3.17	Biofilm Formations	
	3.18	Statistics	
	3.19	Results	

	ng Lactose Free Skimmed-Milk Agar to Assess Whether the Bacteria Possess ar Proteases
	the Preservatives found in the Proteins reach the Minimum Inhibitory Concentration
	cterial Growth?
3.21.1 Skin Bac	Do the Preservatives found in Crosilk Lpc inhibit Visible Growth of Three Common teria?
3.21.2 Commoi	Do the Preservatives found in Hydroavena HPO inhibit Visible Growth of Three n Skin Bacteria?56
3.21.3 Commoi	Do the Preservatives found in Hydrolactin Liquid PE inhibit Visible Growth of Three n Skin Bacteria?57
3.21.4 Commoi	Do the Preservatives found in Hydrosativum P inhibit Visible Growth of Three n Skin Bacteria?57
3.21.5 Commoi	Do the Preservatives found in Hydrosolanum PE inhibit Visible Growth of Three n Skin Bacteria?57
3.21.6 Skin Bac	Do the Preservatives found in Prolevium inhibit Visible Growth of Three Common teria?58
	ng Growth Curves to Determine Whether Cosmetic Proteins Can Supplement rowth62
3.22.1	Growth Curves of Three Skin Bacteria Supplemented with Crosilk Lpc62
3.22.2	Growth Curves of Three Skin Bacteria Supplemented with Hydroavena HPO64
3.22.3	Growth Curves of Three Skin Bacteria Supplemented with Hydrolactin Liquid PE67
3.22.4	Growth Curves of Three Skin Bacteria Supplemented with Hydrosativum P70
3.22.5	Growth Curves of Three Skin Bacteria Supplemented with Hydrosolanum PE73
3.22.6	Growth Curves of Three Skin Bacteria Supplemented with Prolevium75
	ne Addition of Cosmetic Proteins Did Not Result in Visible Growth, Are the Cosmetic acteriostatic or Bactericidal Towards the Three Skin Species?
3.23.1	Was the addition of any Active Level of Crosilk Lpc Bacteriostatic or Bactericidal? 77
3.23.2 Bacteric	Was the addition of any Active Level of Hydroavena HPO Bacteriostatic or idal?77
3.23.3 Bacteric	Was the addition of any Active Level of Hydrolactin Liquid PE Bacteriostatic or idal?77
3.23.4 Bacteric	Was the addition of any Active Level of Hydrosativum P Bacteriostatic or idal?77
3.23.5 Bacteric	Was the addition of any Active Level of Hydrosolanum PE Bacteriostatic or idal?78
3.23.6	Was the addition of any Active Level of Prolevium Bacteriostatic or Bactericidal?.78
3.24 Car	Cosmetic Proteins Provide Enough Sustenance for the Bacteria to Form Biofilms78
3.24.1 Commoi	The Effect of Different Active Levels of Crosilk Lpc on Biofilm Formation in the 3 n Skin Bacteria79
3.24.2 the 3 Co	The Effect of Different Active Levels of Hydroavena HPO on Biofilm Formation in mmon Skin Bacteria79

3.24 in tl	1.3 The Effect of Different Active Levels of Hydrolactin Liquid PE On Biofilm Formation the 3 Common Skin Bacteria	
3.24 3 Co	4.4 The Effect of Different Active Levels of Hydrosativum P On Biofilm Formation in th mmon Skin Bacteria8	
3.24 the	<ul> <li>The Effect of Different Active Levels of Hydrosolanum PE on Biofilm Formation in</li> <li>Common Skin Bacteria8</li> </ul>	1
3.24 Con	1.6 The Effect of Different Active Levels of Prolevium on Biofilm Formation in the 3 amon Skin Bacteria	1
3.25	Discussion	3
3.26	Identifying Bacteria with Extracellular Proteases	3
3.27	Are Preservatives found in Cosmetic Proteins Effective Against the Three Skin Species? 85	
3.28	What do the Protease assay, MIC tests and Growth Experiments reveal?	9
	ktonic Growth and Biofilm Formation of Co-Cultured Staphylococcus spp. with	
	Proteins	
4.1	Introduction	
4.2	Aims	
4.3	Null Hypothesis	
4.4	Methods	
4.5	Bacteria	
4.6	Media	
4.7	Preparation for Planktonic Growth	
4.8	Preparation for Sessile Growth	
4.9	Statistics	
4.10		5
4.11 Anoth	Does Incubation with Cosmetic Proteins Promote One <i>Staphylococcus</i> spp. Over er in a Planktonic Growth Co-Culture?	5
4.11 a Pl	1 Does Incubation with Crosilk Lpc Promote One <i>Staphylococcus</i> spp. Over Another anktonic Growth Co-Culture?	
4.11 Ano	2 Does Incubation with Hydroavena HPO Promote One <i>Staphylococcus</i> spp. Over ther in a Planktonic Growth Co-Culture?	5
4.11 Anc	3 Does Incubation with Hydrolactin Liquid PE Promote One <i>Staphylococcus</i> spp. Ove ther in a Planktonic Growth Co-Culture?	
4.11 Ano	4 Does Incubation with Hydrosativum P Promote One <i>Staphylococcus</i> spp. Over ther in a Planktonic Growth Co-Culture?	6
4.11 Anc	5 Does Incubation with Hydrosolanum PE Promote One <i>Staphylococcus</i> spp. Over ther in a Planktonic Growth Co-Culture?	6
4.11 a Pl	6 Does Incubation with Prolevium Promote One <i>Staphylococcus</i> spp. Over Another i anktonic Growth Co-Culture?	
4.12 Anoth	Does Incubation with Cosmetic Proteins Promote One <i>Staphylococcus</i> spp. Over er in a Sessile Growth Co-Culture?	8

	12.1 Does Incubation with Crosilk Lpc Promote One <i>Staphylococcus</i> spp. Over A Sessile Growth Co-Culture?	
	12.2 Does Incubation with Hydroavena HPO Promote One <i>Staphylococcus</i> spp. other in a Sessile Growth Co-Culture?	
	12.3 Does Incubation with Hydrolactin Liquid PE Promote One <i>Staphylococcus</i> other in a Sessile Growth Co-Culture?	• •
	12.4 Does Incubation with Hydrosativum P Promote One <i>Staphylococcus</i> spp. ( other in a Sessile Growth Co-Culture?	
	12.5 Does Incubation with Hydrosolanum PE Promote One <i>Staphylococcus</i> spp other in a Sessile Growth Co-Culture?	
	12.6 Does Incubation with Prolevium Promote One <i>Staphylococcus</i> spp. Over A Sessile Growth Co-Culture?	
4.13	Discussion	101
4.14	Planktonic Mixed Species Growth Reflects Individual Species Growth	101
4.15	Staphylococcus species May Tolerate the Presence of Each Other	101
4.16	The Lower pH favours S. epidermidis in Biofilm Domination	101
4.17	Planktonic Growth and Sessile Growths are Dominated by Different Bacteria	102
	<i>Vitro</i> Stimulation of Immune Response Biomarkers of an Immortal Keratinocyte ition of <i>Staphylococcus</i> spp. and Cosmetic Proteins	
5.1	Immune Response to Commensal Microbes	
5.2	HaCaT Cells in Skin Studies	
5.3	Immune Response Biomarkers	105
IL-8	8	105
TN	ΙΕ-α	105
IFN	N-Y	106
5.4	Null Hypothesis	106
5.5	Aims	106
5.6	Materials	108
5.7	Proteins	
5.8	Bacteria	
5.9	HaCaT Cells	
5.10	Methods	109
5.11	Tissue Experiment	
5.12	Microscope Images	
5.13	Biomarker Assays	
5.14	Measurement of Adhered Bacteria	
5.15	Statistics	110
5.16	Results	110
5.17	24 Hours After Seeding HaCaT Cells	110

5.18	48 Hours After Incubation with Bacteria111
	Microscope Images of HaCaT Cells After 48 hours, Incubation with and without
Staphyl	ococcus spp113
5.19.	1 How did the HaCaT Cells Look without Bacteria?113
5.19.	2 How did the HaCaT cells look when Grown with <i>Staphylococcus epidermidis</i> ?113
5.19.	How did the HaCaT cells look when Grown with <i>Staphylococcus aureus</i> ?113
5.19. spp.?	
	Does Exposure to Hydrosativum P Affect Interactions Between the <i>Staphylococcus</i> spp. CaT Immune Marker Concentration?115
5.20. HaCa	1 How did exposure to Hydrosativum P alone Affect the Concentration of IL-8 from T cells?
5.20. cells	2 How did exposure to Hydrosativum P Affect the Concentration of IL-8 from HaCaT incubated with <i>S. epidermidis</i> ?115
5.20. cells	3 How did exposure to Hydrosativum P Affect the Concentration of IL-8 from HaCaT incubated with S. aureus?115
	4 How did exposure to Hydrosativum P Affect the Concentration of IL-8 from HaCaT incubated with <i>Staphylococcus</i> spp. Co-culture?116 
5.20.	
5.20. cells	6 How did exposure to Hydrosativum P Affect the Concentration of IFN-Y from HaCaT ncubated with <i>S. epidermidis</i> ?118
5.20. cells	7 How did exposure to Hydrosativum P Affect the Concentration of IFN-Y from HaCaT ncubated with <i>S. aureus</i> ?118
	8 How did exposure to Hydrosativum P Affect the Concentration of IFN-Y from HaCaT Incubated with <i>Staphylococcus</i> spp. Co-culture?118
5.20. HaCa	$9$ How did exposure to Hydrosativum P alone Affect the Concentration of TNF- $\alpha$ from T cells?
5.20. HaCa	10 How did exposure to Hydrosativum P Affect the Concentration of TNF-α from T cells incubated with <i>S. epidermidis</i> ?121
5.20. HaCa	How did exposure to Hydrosativum P Affect the Concentration of TNF-α from T cells incubated with <i>S. aureus</i> ?121
5.20. HaCa	How did exposure to Hydrosativum P Affect the Concentration of TNF-α from T cells incubated with <i>Staphylococcus</i> spp. Co-culture?121
5.20. grow	13 How did exposure to Hydrosativum P Affect the Final CFU/ml of <i>S. epidermidis</i> n with HaCaT cells?
5.20. with	14 How did exposure to Hydrosativum P Affect the Final CFU/ml of <i>S. aureus</i> grown HaCaT cells?
5.20. spp. (	How did exposure to Hydrosativum P Affect the Final CFU/ml of <i>Staphylococcus</i> Co-culture grown with HaCaT cells?

5.21 Does Exposure to Hydrosolanum PE Affect In spp. and HaCaT Immune Marker Concentration?	
5.21.1 How did exposure to Hydrosolanum PE HaCaT cells?	alone Affect the Concentration of IL-8 from
5.21.2 How did exposure to Hydrosolanum PE cells incubated with <i>S. epidermidis</i> ?	Affect the Concentration of IL-8 from HaCaT 127
5.21.3 How did exposure to Hydrosolanum PE cells incubated with <i>S. aureus</i> ?	Affect the Concentration of IL-8 from HaCaT 127
5.21.4 How did exposure to Hydrosolanum PE cells incubated with <i>Staphylococcus</i> spp. Co-cultu	
5.21.5 How did exposure to Hydrosolanum PE from HaCaT cells?	alone Affect the Concentration of IFN-X
5.21.6 How did exposure to Hydrosolanum PE HaCaT cells incubated with <i>S. epidermidis</i> ?	
5.21.7 How did exposure to Hydrosolanum PE HaCaT cells incubated with <i>S. aureus</i> ?	
5.21.8 How did exposure to Hydrosolanum PE HaCaT cells incubated with <i>Staphylococcus</i> spp. C	o-culture?131
	alone Affect the Concentration of TNF- $\alpha$
5.21.10 How did exposure to Hydrosolanum I HaCaT cells incubated with <i>S. epidermidis</i> ?	PE Affect the Concentration of TNF-α from 133
5.21.11 How did exposure to Hydrosolanum I HaCaT cells incubated with <i>S. aureus</i> ?	PE Affect the Concentration of TNF-α from 133
5.21.12 How did exposure to Hydrosolanum HaCaT cells incubated with <i>Staphylococcus</i> spp. C	
5.21.13 How did exposure to Hydrosolanum I grown with HaCaT cells?	PE Affect the Final CFU/ml of <i>S. epidermidis</i> 136
5.21.14 How did exposure to Hydrosolanum I grown with HaCaT cells?	PE Affect the Final CFU/ml of <i>S. aureus</i> 136
5.21.15 How did exposure to Hydrosolanum I Staphylococcus spp. Co-culture grown with HaCa	
5.22 Discussion	
5.23 Microscopic Observation of HaCaT cells show Monolayer	
5.24 Detection of Immune Biomarkers	
5.24.1 Immune Markers are Expressed withou	t Stimulation139
5.24.2 Addition of either Cosmetic Protein did increase Concentration of other Immune Markers	not Increase Concentration of IL-8 but did

5.2	25	The	Presence of Staphylococcus epidermidis Alone Reduces the Immune Response	.140
	5.25	.1	S. epidermidis Possess Many TNF-α Reducing Techniques	.140
	5.25	.2	Modulation of IL-8 Can be Direct and Indirect	.141
	5.25 epid		IFN-Y Concentration May have Increased due to Irritation as well as Reduced S.	.141
	5.25 Incre		Adhered <i>S. epidermidis</i> Cells were Reduced as the Active Level of Proteins d141	
	5.25 Path		Future Investigation into Whether <i>S. epidermidis</i> being a Commensal or a n?	.142
5.2	26	Stap	ohylococcus aureus Increases Concentration of Immune Markers by HaCaT Cells	.143
	5.26 Alon		<i>S. aureus</i> increased IL-8 Concentration at least 10-Fold More Than HaCaT cells 143	
	5.26	.2	Could EDTA Induce a Stress Response in <i>S. aureus</i> ?	.144
	Adh	ered	S. aureus Cells were not Reduced by Preservatives	.144
5.2	27	The	Co-culture of Staphylococcus spp. Increased the Immune Marker Concentration	.145
	5.27	.1	Staphylococcus aureus Was More Likely to Dominate a Sample	.145
	5.27	.2	Staphylococcus epidermidis alerts the Immune System to Staphylococcus aureus 145	s
	5.27	.3	Conclusion	.146
	5.27	.4	Future Work to Enhance the Experiment to be More Akin to the Habitat of Skin.	.146
		-	ating the Effect of Swab Head Type and Buffer Composition on Bacterial Collectine Skin Model	
6.2			oduction	
6.2			Microbe Research is Lagging	
6.3			ecting Skin Microbiota	
6.4			) Models	
6.5			S	
6.0			Hypothesis	
6.3			terials	
6.8			teria	
6.9			dia	
6.:			cine Skin	
6.1			b and Buffer Types	
6.:			thods	
6.1			terial Suspension Preparation	
6.1			cine Skin Preparation	
6.:			culation of Porcine Skin	
÷				
6.3	16	Stat	istics	.153

6.18	Collecting Individual Species from Porcine Skin	155
6.19	Collection of the Mixed Staphylococcus spp. from Porcine Skin	159
6.20	Discussion	
6.21	Moistening the Tip of the Swab Improves Recovery of Bacterial Biomass fro 162	m the Skin
6.22	Importance of Buffer Composition When Collecting Bacterial Biomass from	the Skin162
6.23	The influence of Swab Head Types on Viable Bacterial Cells Collection	
6.24	Conclusion	164
	oosing a Suitable Swab Site for Skin Microbiome Experiments to Limit Backg ination Interference	
7.1	Introduction	
7.2	Microbial Inhabitants Differ from Person-to-Person	
7.3	Cosmetic Testing on Skin	
7.4	Background Contamination of Microbial Samples	
7.5	16S rRNA gene Sequencing to Identify Microbial Communities	
7.6	Sequencing reads and Operational Taxononomic Units (OTUs)	
7.7	Diversity Indices	
7.7	1 Alpha Diversity Indices	
7.7	2 Beta Diversity	
7.8	Null Hypothesis	
7.9	Aims	
7.10	Materials	
7.11	Swab type and Buffer	
7.12	Swabbing Participants	
7.13	Methods	
7.14	Swabbing Technique	
7.15	Extraction of Bacterial DNA from Swabs	
7.16	16S rRNA Amplification and Sequencing	
7.17	Statistics	
7.18	Results	
7.19	Sequencing reads Recovered from Samples	
7.1 and	9.1 Male Participant's Results for Total, Usable, Percentage, Unique Seque I OTUs172	encing reads
7.1		-
	ds and OTUs	
7.20	T-tests and One-way ANOVA of OTU abundance	

	7.21	Diversity Indices Results	174
	7.21	.1 Alpha Diversity of Samples	174
	7.22	8.1 Beta Diversity Between Samples	177
			179
	7.23	Top 10 Isolated Genera from the Samples	180
	7.23	.1 Male Samples Genera Abundance	180
	7.23	2.2 Female Samples Genera Abundance	180
	7.23	3.3 The Unnamed Genera Group	180
	7.24	Percentage of Background Contamination and Likely Contaminants	183
	7.24	.1 The Sample from the Female Forehead was not Highly Contaminated	183
	7.24	.2 The Sample from the Female Volar Forearm had Higher Contamination Levels	184
	7.25	Discussion	189
	7.26	Ideal Number of Volunteers	189
	7.27	Likely Background Contaminants	189
	7.28	Were Transient Bacteria Present?	190
	7.29	Contaminants influenced the Diversity Indices	190
	7.30	Removal of Controls May Not Be So Easy	192
	7.31	Microbial Communities and Biomass at Different Swab Sites	192
	7.32	What about Shotgun Metagenomic Sequencing?	193
	7.33	Conclusion	194
8	Con	clusions of Sections 2-7	195
	8.1	Introduction	196
	8.2	Laboratory-based Studies	196
	8.3	Tissue Culture	197
	8.4	Designing a Human Panel Study	198
	8.5	What Have all the Sections from this Thesis achieved?	199
9	Refe	erences	200
1	0 A	ppendix	xiv
	10.1	MIC Tables	xv
	10.2	Consent Forms	xvi
	10.3	Taxonomic Trees	xviii
	10.4	OTUs Abundance of All Samples	xxx

#### Acknowledgements

I would like to thank the following individuals and groups who helped me undertake this project, without these people I would not have started, let alone finished this project.

Firstly, thank you to my funding bodies, Cardiff University, BBSRC and Croda Europe Ltd.

Thank you to my supervisors, who supported me throughout, even if it was just a friendly chat to keep me going when working through the pandemic. Thank you, Julian, Rhian, Neil, and Andy.

To my colleagues at the Cardiff University MMI lab and the PIs who helped me through the tough times when I was not their responsibility. Specifically, I would like to mention Laura, Alex and Gordon, their expertise in microbiology was useful in the lab, and their coffee and tea consumption meant for great company in the break room.

To my family who have always supported me and given me the confidence to achieve whatever I set out to do. My Nan and Bampy have always been my absolute rocks and my Dad, who could distract me from the stress with some extended lunch breaks. Thank you especially to my Mum, who was my first female STEM role model and the person who I always aspired to be.

And finally, thank you to Dan, my husband-to-be, who tried to warn me, but knew my stubbornness would prevail. You encouraged me through the toughest of times, whether that be an ear to listen, or a hug to comfort, without saying the all-important 'I told you so'.

# 1 Introduction to The Skin, Skin Inhabitants and Cosmetics

#### 1.1 Human Skin

Adult human skin has an average weight of 3.6 kg and covers an area of up to 2 m<sup>2</sup>, making skin, not the largest (Sontheimer 2014), but one of the largest organs of the human body (Gravitz 2018). The skin is not only a barrier to physical trauma, but is the first line of defence against pathogenic microorganisms, UV damage and exogenous toxins (Proksch 2008). Other roles that the skin provides are osmotic and temperature regulation, waste disposal and vitamin D synthesis (Tanowitz et al. 1990).

#### 1.2 pH and Temperature

The average pH for skin is around 5 (Lambers et al. 2006), however, the skin is made up of dry, moist or oily regions which causes the skin pH to vary dependent on location (Blank 1938). The most acidic regions of the skin are the scalp and face, these oily areas can have a pH range of 4.2-5.9 (Ali and Yosipov 2013). Moist areas of the skin, including perineal and axilla, are often found to have a pH at the upper end of the scale of around pH 6-8. The dry areas of skin, including the arms, hands, legs and buttocks, tend to stay within the pH range of 5-5.5 (Boer et al. 2016). The varied figures are also reflected in the range of temperatures found on human skin, exposed regions can be as low as 29.5°C, while covered areas and genitals can reach approximately 36°C. On a whole the average temperature of human skin is around 34°C, 3 degrees lower than internal organs (Figure 1) (Wilson 2004).

#### 1.3 Skin Layers and Structure

The three main layers of skin are the top level epidermis, the middle dermis and the lower subcutaneous fatty hypodermis (Figure 2) (Yousef et al. 2020). While these three skin layers are always present, the thickness of skin varies at different locations. The thickest part of the skin is found at the palms of hands, buttocks and at the soles of the feet where the epidermis can reach up to 4 mm thick. The thinnest parts are located on the scrotum and eyelids, where the epidermis is a very thin 0.4 mm (Betts et al. 2016).

The hypodermis is the adipose fat layer which insulates the body, it is also home to large blood vessels and nerves (Wong et al. 2015). The thickness of this fatty layer is mostly dependent on a person's nutritional and fitness levels, once carbohydrate produced energy is used up, the body metabolises into the adipose layer (Lumen 2020). Gender also influences the thickness of these fat layers, with men having a thicker fat level around the stomach and shoulders, while women having the thickest fat layers at the hips, thighs and buttocks (Karastergiou et al. 2012). As an individual ages, this hypodermal layer loses fat which reduces the support of the skin causing drooping. This loss of fat also means that the elderly find it harder to stay warm in the cold, and reduces the ability to sweat so it is also more difficult to stay cool in the warmer weather (Caso et al. 2013).

The dermis lies above the subcutaneous level and is split into two layers, the reticular and

papillary dermis. The lower reticular dermis forms most of the dermis. This layer contains a thicker meshwork of elastic fibres and collagen wads allowing for the flexibility and strength of the skin. Damage to the reticular dermis would cause deeper and longer scarring (Rippa et al. 2019). The papillary is the thinner layer of the dermis, its structure is similar to that of the reticular, but is less bulky and is used structurally to connect to the bottom of the epidermal layer above (Vapniarsky et al. 2015). These two layers are connected throughout by intertwined elastin and collagen created by fibroblasts. This dermal layer also is home to capillaries, smaller nerves, hair follicles and sweat glands (Nafisi and Maibach 2018).

The epidermis itself has four layers; the stratum basale, stratum spinosule, stratum granulosum and stratum corneum (Figure 2) (Kennedy and Wendelschafer-Crabb 1993). Thicker areas of skin have an extra layer below the stratum corneum; the stratum lucidum (Tuomanen 2005). The stratum basale is the bottom layer of the epidermis, to which the dermis is attached. The single layer is made up of basal cells, the precursor to the keratin producing keratinocytes. These migrate upwards and form 90% of the cells of the epidermal layers. The stratum basale is also home to Merkel cells, which are the touch sensory receptors, and melanocytes, the cell which produce the black/brown pigment melanin. Melanin absorbs UV light and protects the skin from sun exposure (Mo et al. 2019). The stratum spinosum is the next layer of the epidermis and is also referred to as the prickle cell layer. Desmosomes connect keratinocytes and these tight bridges appear 'prickly'. Langerhans cells are also present at this level, they only make up 5% of the epidermis, but they stretch and cover 25%. Involved in the immunology of the skin, they obtain antigens which are transported to the local lymph nodes and presented to lymphocytes (Mauldin et al. 2016). At the stratum granulosum keratinocytes begin to lose cell structures and organelles, ready to be released as squames at the stratum corneum. In thicker areas of the skin, the stratum lucidum is a layer which helps reduce friction. The final epidermal layer, the stratum corneum, is largely made up of interconnecting dead cells, the final differentiation of keratinocytes, called corneocytes or squames (Tuomanen 2005). These hardy cells are less permeable than their previous form and have a range of uses. They act as an extra layer to protect DNA below the skin from being damaged by UV light. Sebum production at this site is reduced and while many commensals can survive on the minimal nutrients provided by the stratum corneum, oil-loving microbes would not survive for long (van der Krieken et al. 2016). This uppermost layer is shed almost daily, this stops pathogens from successfully attaching, replicating, invading and causing infection (Egelrud 1995).

#### 1.4 Pores and Glands

The surface of the epidermis is scattered with pilosebaceous units. Also known as hair follicles, one of their functions is to produce hair and anchor them deep into the dermal layer (Treister and

Lio 2018). Mammalian hairs are used for thermal regulation, when the body is too cold, hairs trap air against the skin creating an insulating layer (Arens and Zhang 2006). More specialised hair such as eyelashes and eyebrows protect the eyes from dust fragments. Growth of hairs on the human body is an indication of the beginning of sexual maturity (Yu et al. 2014). Many of these hair follicles contain sebaceous glands, which are common across the body, especially concentrated on the scalp and forehead, only absent from palms and the soles of the feet. Sebaceous glands secrete sebum, this lipid rich substance prevents excess moisture loss from both the skin and scalp (Picardo et al. 2009).

The other pores found on the skin are the sudoriferous glands which release sweat. The two types of sudoriferous glands are the abundant eccrine and less common apocrine. The eccrine glands open directly onto the skin through the sweat pore (Tanowitz et al. 1990). The apocrine glands are attached to hair follicles through a duct and are inactive until puberty, it is thought they release sex-related steroids and pheromones. They are only found in the axillae and perineal regions. The hypotonic solution sweat regulates body temperature, disposes of waste and carries mediators of the immune response (Patel et al. 2019).

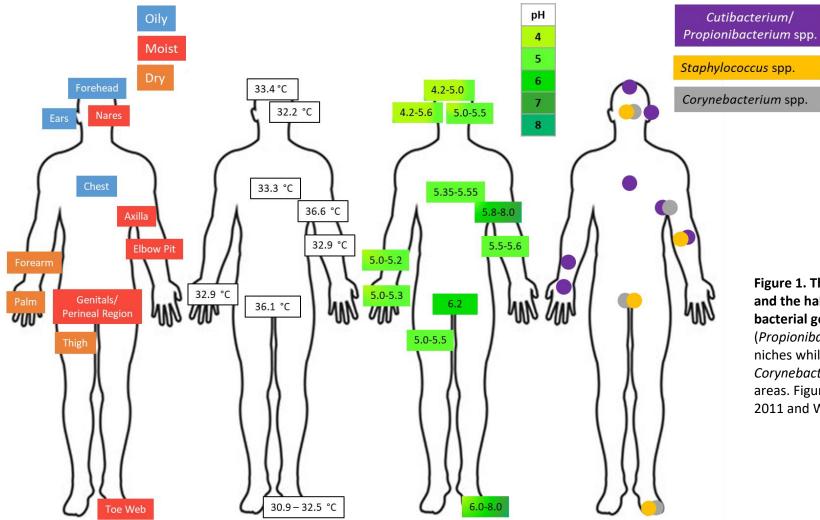


Figure 1. The skin type, temperature, pH, and the habitats of three common bacterial genera. *Cutibacterium* (*Propionibacterium*) occupy the most niches while both *Staphylococcus* spp. and *Corynebacterium* spp. inhabit mostly moist areas. Figure adapted from Grice and Segre, 2011 and Wilson, 2005.

#### 1.5 Skin Immunity

As the first barrier for the body, the skin can suffer serious traumas including wounds, cancers, and pathogenic invasion. Only in the last 30 years has research uncovered that the skin has its own line of defence to handle these stresses (Matejuk 2018). For any type of stress, skin immunity acts in three steps, firstly detection of the problem, secondly destruction of said problem and thirdly, remembering how to handle the problem should it arise again (Pandya et al. 2016).

### 1.6 Repairing Skin Damage

Wound healing is the regeneration of tissue resulting from an action which has torn the physical skin barrier. The process itself involves many immune factors working together and overlapping phases to ensure that the tissue is repaired, if this is unsuccessful it can lead to potentially fatal infections (Gonzalez et al. 2016).

Macrophages are involved in wound healing; these phagocytic cells release cytokines which start the inflammatory response. To halt the inflammatory stage, these cells activate apoptosis and remove the dead cells (Guo and DiPietro 2010). Peptides such as LL-37, which proliferate at the margins of wounds, activate keratinocytes and their subsequent growth factors to start the wound closure. LL-37 also is involved in angiogenesis and the restoration of blood vessels to the wound (Ramos et al. 2011).

#### 1.7 Dealing with Skin Cancer

White skin is highly vulnerable to both basal and squamous skin cancer and is 50 times more likely to develop these types of cancers than darker skinned ethnicities. Ozone depletion and the subsequent exposure to ultraviolet light is one of the many reasons for the sharp increase in incidences (Diepgen and Mahler 2002). However, without the immune system, the prevalence of these cancers would be even higher (Pandya et al. 2016).

Precancerous cells are often dealt with before being able to proliferate (Pandya et al. 2016), the elimination stage. This stage relies heavily on T-cells being able to identity tumour antigens. If these antigens are not detected then the cancerous cells grow and the immune system can enter the equilibrium state in which harsher measures are needed to rid these cells (Mittal et al. 2014). However, if this stage is bypassed, the cancer can evade the immune system and in fact become tolerated by it (Pandya et al. 2016).

#### 1.8 Defence against Microbes

Immune system specialised cells live throughout the dermal layers. Keratinocytes, which make up 90% of the epidermis, are key to the skin's immunity. These cells have the ability to differentiate between non-pathogenic or pathogenic microbes (Albanesi et al. 2005). Pathogenic microorganisms have numerous infection molecules which come under the umbrella term 'pathogen associated molecular patterns' or PAMPS (Richmond and Harris 2014). Pattern recognition receptors such as Toll-like receptors (TLR) attach to PAMPS, and this step creates an immune response to the invading pathogen. These receptors work by triggering T-helper cells, which in turn activate lymphocytes. Keratinocytes possess numerous TLRs on their surface, including TLR7 which targets double stranded RNA viruses by stimulating interferons which upregulate the anti-viral cellular defences (Novak et al. 2008). These cells can also produce numerous antimicrobial peptides (AMPs) including cathelicidin, which is effective against a broad number of pathogens (Schittek et al. 2008).

## 1.9 Skin Microbial Transplants and Bacteriotherapy

Bacteriotherapy treatments are the transference of bacteria from a healthy individual to a patient in the hopes that the microbial composition becomes more akin to a healthy person (Huovinen 2001). This differs from probiotics as these often introduce bacteria which are not normally localised to the original habitat (Shi et al. 2016). Faecal transplants are used commonly to treat recurring antibiotic resistant infections caused by *Clostridiodes difficile* (Mullish et al. 2018). Faecal matter removed from a healthy donor patient can be transferred either via the nasoduodenal route, colonoscopy or ingested in a freeze-dried capsule (Borody et al. 2013; Hecker et al. 2016). Repairing the microbial gut community restores healthy immune-bacterial interactions (Huus et al. 2020). Future potential for this method could be used in the treatment of vastly different diseases, including Type II diabetes (Mullish et al. 2019) and dementia symptoms (Hazan 2020).

The principle behind faecal transplants could therefore be repeated with regards to skin diseases. However, bacterial abundance on the skin is significantly less than that of the gut (Quigley 2013; Coates et al. 2019), and culture methods would be needed to increase the organic material. Adjustment from nutrient rich media to the unnourishing skin environment may prove the transplant to be unsuccessful (Callewaert et al. 2021). When (Perin et al. 2019) attempted to transfer skin from the arm to the back, many of the species that were identified via 16S rRNA gene analysis could not be cultured and therefore were not successfully transferred.

Movement of skin bacteria could cause detrimental results, accidental transferring of pathogenic or unwelcome bacteria. Bacteria originating from the armpit were successfully transferred to the forearm, however the malodour associated with the armpits were now also produced on the arm (Leyden et al. 1981). The reverse of this transfer has also been carried out, where non-smell producing siblings have donated bacteria to the armpits of malodourous siblings and a significant odour reduction did occur (Callewaert et al. 2021).

Like bacteriotherapy, probiotics have been used to introduce 'good' bacteria to skin areas populated by pathogenic species. Applications *in vitro* of the lysates of *Vitreoscilia filiformis* (Hendricks et al. 2019) and *Lactobacillus plantarum* (Kim et al. 2015a) to combat atopic dermatitis have been shown to reduce the symptoms of the diseased areas, although in clinical practice the route is changed to oral administration.

Disease	Symptoms	Microbes Involved
		Bacteria
Impetigo	Yellow crusty lesions on the skin, very contagious.	<sup>1</sup> Staphylococcus aureus, Streptococcus pyogenes (Aly 1996)
Erythrasma	Patches of skin discolouration in areas such as arm pit, groin, and toe webs. Patches turn from red to brown. Skin may be itchy or uncomfortable.	Corynebacterium minitissium (Forouzan and Cohen 2020)
Acne Vulgaris	Blocked pilosebaceous units causing inflamed comedones and cysts	Cutibacterium acnes, <sup>2</sup> Staphylococcus epidermidis (Claudel et al. 2019)
Rosacea	Redness around the cheeks and nose. Little pink or red bumps may appear. Visible Blood Vessels.	Bacillus oleronius (Jarmuda et al.)
		Fungi
Seborrheic dermatitis	Scaly patches of dandruff on scalp. Red flaky patches in oily areas of the skin.	Malessezia furfur
Tinea Pedis (Athlete's foot)	Scaly, itchy, and burning rash between the toes and on the soles of feet.	Trichophyton rubrum, Trichophyton tonsurans
Candidiasis	Redness and intense itching at site. Commonly causes infections in the mouth, vagina and on the skin.	Candida albicans (White et al. 2014)
		Viruses
Herpes Labialis (cold sores)	Red blistering around the mouth	<sup>3</sup> Human alphaherpesvirus 1
Varicella zoster (Chicken pox and shingles)	Chickenpox – Mainly a childhood disease. Small itchy blisters which start from the trunk and face which then spread to the rest of the body	Human alphaherpesvirus 3 (Wu et al. 2020a)
	Shingles – Disease usually found in adults who have previously suffered from chickenpox. A rash of blisters is usually localised to one side of the face or body.	
Hand, foot, and mouth disease	Discoloured spots and bumps which may open into sores and blister – Common in children	Enterovirus A (Guerra et al. 2022)

<sup>&</sup>lt;sup>1</sup> Both *S. aureus* and *S. pyogenes* can cause impetigo. Bullous impetigo, which is characterised by large pusfilled blisters is caused by *S. aureus* alone.

 $<sup>^{2}</sup>$  S. epidermidis has been found in the pores of acne lesions, however little is known about their involvement

<sup>&</sup>lt;sup>3</sup> While Herpes labialis can be caused by *Human alphaherpesvirus 2*, this species mostly causes genital herpes

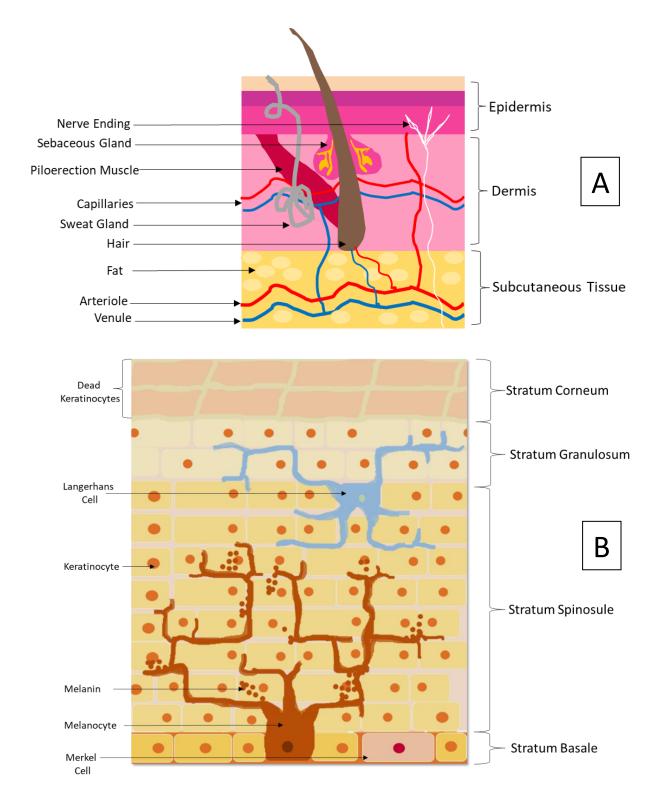


Figure 2. 2A) Layers of the Skin. The skin is made of many layers and components. The subcutaneous tissue layer contains the insulating fat and the blood vessels that supply the capillaries of the skin. The dermis is home to the capillaries and the bottom of the pores, including the hair follicle and sweat gland. The upper most layer is the epidermis which is divided into more layers as seen in 2B. **2B)** Layers of the Epidermis. Keratinocytes migrate upwards through the layers of the epidermis. Starting at the stratum basale where Merkel cells also reside. Merkel cells lay close to nerves and are involved in relaying touch stimuli. Melanocytes start here and entwine through the upper layers. In the stratum spinosule melanocytes release the pigment melanin. Langerhans cells mostly reside here and outstretch through the epidermal layers. These cells are involved in immune presentation of antimicrobial agents. As keratinocytes move through the stratum granulosum, they lose their nuclei and organelles, ready to be shed at the stratum corneum.

#### 1.10 The Skin and Microbes

While the skin has numerous mechanisms to aid the immune system in evading microbial pathogens from occupying and invading the body, the epidermis is home to many microbes who simply reside commensally (Coates et al. 2018). The skin is an ecosystem inhabited by a diverse range of organisms, inclusive of bacteria, viruses, fungi and mites (Grice and Segre 2011). These microbes reside mainly on the surface of the skin and the upper portion of the follicles, but some do extend into the deeper skin layers and sebaceous glands (Zeeuwen et al. 2012). Many of these organisms are classed as commensal species; they reside on our skin with potentially beneficial attributes and only become pathogenic when opportunity presents (Cogen et al. 2008). Colonisation is dependent on various aspects including pH, topography, exogenous and endogenous factors and the immune system response (Grice et al. 2008).

#### 1.11 Mites

Humans are the only mammalian host for two ectoparasitic mites from the genus *Demodex*. The larger of these two species, *D. folliculorum*, are approximately 0.3-0.4 mm long and reside in the base of lashes. The smaller, around 0.15-0.2 mm long, *D. brevis*, in the pilosebaceous unit (Rather and Hassan 2014). These mites feed off dead skin cells and can be problematic when found in high numbers or the immune system is weakened. Facial demodicosis is an uncommon infection that is caused by these parasites. The infection can present with many different symptoms including red skin, raised spots and an itchy rash (Kaur et al. 2012). While there are many speculations as to how these organisms cause such infections such as pore blocking, skin shedding and faecal droppings, the inconsistency in affected individuals suggests that these mites may act as a vector for the rosacea causing bacteria, *Bacillus oleronius* (Gunn and Pitt 2012; Zhu et al. 2018). However, the majority of people living with these parasites on their skin do not have any problems and do not even realise they share their skin with them (Fromstein et al. 2018).

#### 1.12 Viruses

Viruses are not as easy as other microbes to detect on our skin. Microbiological techniques, both culture and culture independent, used to isolate bacteria from the skin are unable to isolate viruses with ease (Kong and Segre 2012). To identify viruses on the skin, transcriptomics and metagenomics sequencing are used as well as imaging of viral-like particles by EM.

However, due to the ever-increasing problem of antibiotic resistant bacterial species, more research is emerging into bacteriophages (bacteria infecting viruses) (Bragg et al. 2014). Bacteriophages work by entering a host cell and using the bacteria's own DNA and RNA replication system to create more virus instead. The replicated viruses then diffuse out of the host cell, causing lysis and death to the bacteria (Clokie et al. 2011). The virus can also integrate into the chromosome of the cell and become a lysogenic phage. Replicating and passing on to

daughter cells without destroying the host (Kasman and Porter 2020). Many of these species which are becoming less sensitive to antibiotics are skin commensals (Chabi and Momtaz 2019), and therefore bacteriophages which target these species are also likely to be found on skin. Prior work, 'bacteriophage mining' on skin, have revealed that there are virus families present, Siphoviridae, Podoviridae and Myoviridae, which target *Staphylococcus* spp. (Valente et al. 2021). Other bacteriophages identified on skin are known to target *Samonella* spp., *Rhodoferax* spp. and *Mycobacterium* spp. (Wang et al. 2020). However, bacteriophages may collect host genetic material, including any resistance genes, and may aid in transfer of these genes into the next bacterial host. Therefore, these viruses also have the potential to spread antibiotic resistance throughout a community (Principi et al. 2019)

Byrd (et al., 2018) identified four viruses found on human skin, human papillomavirus (HPV), Merkel cell polyomavirus, Polyomavirus HPvV7 and RD-114 retrovirus. HPV is a common human virus as it is associated with cervical cancers. This double-stranded DNA virus is passed through skin-to-skin contact, with around 50% of individuals having contracted the virus at some point in their lives. However, it is often asymptomatic and most immune systems are able to clear the virus (Brianti et al. 2017). Merkel cell polyomavirus is a double-stranded DNA virus that has only come into prominence in the last decade. Humans are commonly infected with the virus where it is most likely to reside on the skin. This type of virus has associations with a rare neuroendocrine cancer (Spurgeon and Lambert 2013). HPvV7 is another common double-stranded DNA virus which is part of the skin microbiota on healthy individuals. This virus is mostly asymptomatic but individuals who have undergone organ transplants have been found to have itchy rashes in which the virus was discovered (Ho et al. 2015). While RD-114 is a feline endogenous retrovirus (Miyazawa et al. 2016), the microbes found on human skin can be influenced by the animals that we live with (Song et al. 2013; Trinh et al. 2018).

#### 1.13 Fungal Residents of the Skin

The slightly acidic pH of the skin allows colonisation by fungal species (Vylkova 2017). The hair and scalp are regions with more genus diversity, but distinct differences exist between healthy individuals and those with skin ailments. In a group of healthy individuals, genera such as *Cryptococcus, Acermonium* and *Didymella* were present in high numbers (Findley et al. 2013). However, in scalps which are affected by dandruff, significant quantities of the genera *Penicillium*, *Eupenicillium* and *Filobasidium* were seen (Park et al. 2012).

Fungal infections of the feet are common, one of the most prevalent being Tinea Pedis (Athlete's Foot). This highly infectious fungal disease causes itchy, flaky rashes on the top, soles and toe webs of the feet, but the infection can spread to other areas of the body (Crawford 2009). Three

species of dermatophytes are thought to be involved in the infection, *Trichophyton rubrum, Trichophyton mentagrophytes,* and *Epidermophyton floccosum* (Gupta et al. 2018). However, the feet have some of the greatest fungal diversity with over 11 different genera having been isolated from healthy skin (Findley et al. 2013).

While moist or oily areas have the most varied fungal diversity, the dry and core areas are dominated by one genus (Byrd et al. 2018). Malassezia spp. constitute up to 80% of the adult skin fungal species in both culture and culture independent methods (Grice and Segre 2011; Findley et al. 2013). Malassezia is a genus of dimorphic fungi, with more than 90% of the species being lipophilic (Inamadar and Palit 2003). Lipophilic species feed from the fatty acids on the skin and therefore are mostly found in the seborrheic regions of the upper core, hair and face (Grice and Segre 2011). This genus is mostly commensal but can cause superficial skin problems if sebum levels get too high and the organism is allowed to proliferate. The only disease, in which the genus has been conclusively linked to, is Pityriasis versicolor (PV). M. furfur is the main pathogen responsible (Young et al. 2015), but other *Malassezia* spp. have been isolated from the infection sites. PV is an infection which discolour patches of skin on the upper core (Inamadar and Palit 2003). Individuals effected mostly live in humid or tropical countries and are typically younger adults who may have excessive sebum or do not wear breathable clothes (Karray and McKinney 2020). Other infections associated with the genus include seborrheic dermatitis and Malassezia folliculitis (Thayikkannu et al. 2015). While this genus can cause nasty skin infections, the commensal microbe has some potential benefits. Pityriacitrin is a tryptophan induced alkaloid which reduces the sensitivity of the yeast formations to ultraviolet. While the yeasts can cause PV, (Saunte et al. 2020) and reduce melanin production, these skin sites were also shown to have reduced susceptibility to UV damage (Mayser et al. 2002). Suggesting that pityriacitrin is protecting the skin, not just the organism. (Limon et al. 2017)

#### 1.14 Dominant Skin Bacteria - Phyla and Genera

The most abundant kingdom found on skin is Bacteria (Byrd et al. 2018). The majority of the resident bacteria found on the skin are Gram-positive species, while most Gram-negative bacteria are only present transiently and rarely become part of the resident microbiota (Roth and James 1988). Phyla diversity is low, the three most abundant being Actinobacteria, Firmicutes and Proteobacteria. Contrariwise, the species diversity found at specific skin locations is very high (Grice and Segre 2011). As with any ecosystem, when these bacterial species cohabit peacefully, the skin is healthy. However, if any of the species proliferate and an imbalance occurs, ecosystems become susceptible to bacterial infections (Sanford and Gallo 2013).

Each species of bacteria found on skin occupies a niche and therefore the make-up of the community is dependent on the habitat; these include dry, moist and sebaceous areas of the skin

(Schommer and Gallo 2013). High species diversity is found at the dry areas of the skin, while moist areas are habituated by more specific species such as *Staphylococcus aureus*, *Corynebacterium jeikeium* (Costello et al. 2009). While most of the residents on the skin are relatively benign, some have beneficial attributes. The production of AMPs and antibiotics limit the adhesion and colonisation of pathogens (Gallo 2015). Some bacteria also have the ability to interact with the host immune system, especially regarding inflammation and expression of AMPs and lymphocytes (Cogen et al. 2008). The most prominent species that reside on the skin typically belong to three genera, *Staphylococcus, Corynebacterium* and *Cutibacterium* (*Propionibacterium*) (Figure 1)(Dréno et al. 2018).

#### 1.15 Commensal and Pathogenic *Staphylococcus* spp.

Numerous *Staphylococcus* species are found to reside on the skin as part of the natural microbiota (Foster 1996). *Staphylococcus* spp. are Gram-positive, non-motile, facultative anaerobes that form grape-like clusters (Figure 3). Pigmentation is dependent on species, but are most notably yellow or white (Madigan et al. 2014). The two most common species found on skin include the commensal, *Staphylococcus epidermidis* and the pathogenic *Staphylococcus aureus*. *S. epidermidis* can be isolated from almost all body sites, while *S. aureus* resides mainly in and around the nose (Otto 2010), axillae and perineum (Wertheim et al. 2005). Other well-known skin commensal *Staphylococcus* spp. include the 'honeymoon cystitis' causing *S. saprophyticus* (Hovelius and Mardh 1984) and the body odour producing *S. hominis* (Lam et al. 2018).

The golden pigmented *Staphylococcus aureus* (Lowy 1998) is one of the only two species of *Staphylococcus* which produces the extracellular protein coagulase (Foster 1996). The other being *S. intermedius*, an animal facial skin microbe which very rarely infects humans (Kelesidis and Tsiodras 2010). *S. aureus* is carried by approximately 50% of the population; 20% carry the microbe constantly while the other 30% are inhabited transiently (Wertheim et al. 2005). The organism is an opportunist pathogen and resides peacefully with the commensal species when an individually is healthy (Krismer et al. 2017). However, in the immunosuppressed, *S. aureus* can cause several skin ailments (Kobayashi et al. 2015). Individuals can be colonised by both methicillin-susceptible *Staphylococcus aureus* (MSSA) and methicillin-resistant (MRSA). MRSA strains are mostly found on oily or moist skin sites, infected wounds and up the nose (Albrecht et al. 2015; Sakr et al. 2018). *S. aureus* is still classed mostly on the side of pathogenic rather than commensal, due to its array of virulence factors which can cause diseases in otherwise healthy individuals (Newstead et al. 2020).

To colonise the skin, *S. aureus* uses fibronectin-binding proteins to adhere to the stratum corneum (Cho et al. 2001). The pathogen also can create pores by binding to the lipid layers in skin and expressing exotoxins (Bhakdi and Tranum-Jensen 1991). Once adhered, *S. aureus* must

avoid the host defence mechanisms. Protein A is a cell wall surface protein which aides *S. aureus* in evading the immune system by binding to the FC region of antibodies, this stops the bacteria being marked for phagocytosis (Kobayashi and DeLeo 2013). Other factors that hinder the immune response include  $\gamma$ -toxin and leucocidin, separate toxins which work together to impair host membranes.  $\gamma$ -toxin produces weak leukotoxins, while leucocidins produce a much more potent form (Foster et al. 2014).

Infections caused by *S. aureus* can be mild and treatable, these include common skin ailments such as impetigo, atopic dermatitis, and abscesses (Leyden et al. 1974; Foster 1996; Ghazvini P et al. 2017). However, complications arising from these can lead to life threatening diseases (Corey 2009). When causing as infection, *S. aureus* produces  $\alpha$ -haemolysin, an extremely aggressive toxin which, through mechanisms unknown, can cause sepsis induced organ failure (Bhakdi and Tranum-Jensen 1991; Surewaard et al. 2018). However, *S. aureus* can have beneficial attributes, some produce bacteriocins which are effective against other pathogenic Gram-positives (Gagliano and Hinsdill 1970).

*Staphylococcus epidermidis* is the non-pigmented (Madigan et al. 2014), commensal cousin of *Staphylococcus aureus* (Otto 2009). It is part of the collective coagulase negative *Staphylococcus* spp. (Otto 2009). *S. epidermidis* is a highly resilient organism which can tolerate environments with both low water activity and high salt concentrations. This bacterium can also grow in a wide range of temperatures,  $10^{\circ}C - 45^{\circ}C$ , and at pHs of between 4 - 9 (Wilson 2004). These qualities aide in the colonisation of the skin, *S. epidermidis* is actually the most commonly isolated bacterium from the stratum corneum (Cogen et al. 2008)

Beneficial attributes of *S. epidermidis* include the production of antimicrobials which reduce competition from and colonisation of pathogenic Gram-positive species; these lantibiotics include epidermin and Pep5 (Otto 2010). The lantibiotics primarily work against Gram-positive bacteria, but some activity has been noted against Gram negative bacteria too. These antimicrobial agents work by producing openings in the cytoplasmic membrane, which disrupts the proton motive force (McAuliffe et al. 2001). This disruption prevents adenosine triphosphate (ATP) synthesis (Divakaruni et al. 2014) and therefore reduces the target bacteria's ability to produce energy (McAuliffe et al. 2001).

*S. epidermidis* is often referred to as a beneficial skin microbe (Nakatsuji et al. 2018), however, the common commensal can cause a plethora of nosocomial infections (Otto 2009). This opportunistic pathogen can cause ailments in the immunocompromised, the microbes low virulence, antibiotic resistance and ability to form biofilms on implanted medical devices make it hard to treat (Blum and Rodvold 1987; Ziebuhr et al. 2006) Planktonic *S. epidermidis* adhere to hydrophobic surfaces, facilitated by adhesins such as AtlE and biofilm-associated pili Ebp. The size

of the biofilm increases through aggregation of cells and becomes three-dimensional as it undergoes maturation (Otto 2009). It is unclear the processes in which *S. epidermidis* biofilm go through maturation, but as with other bacteria it is highly likely quorum sensing is involved (Trautner and Darouiche 2004; Kostakioti et al. 2013). Catheterisation often results in a bacterial infection possible by a range of organisms (Ziebuhr et al. 2006). *Staphylococcus epidermidis* releases urease enzymes which break down urea to ammonium hydroxide and increases the pH of urine. The increased pH causes the release of minerals which crystallise and cause a blockage (Nickel and Costerton 1992). While non-motile itself, *S. epidermidis* can migrate through to the bladder with motile species capable of swarming, such as *Proteus mirabilis* (Sabbuba et al. 2008).

# Gram Stain TSA MSA Figure 3. The Gram-Stain of S. aureus and S. epidermidis, plus **Colonies of each on Mannitol Salt** Agar and Tryptone Soy Agar. As Staphylococcus spp. are grampositive, they stain purple. They both form clustered groups made up of individual round colonies. While near impossible to tell apart when stained under the microscope, they appear very different when grown on different media types. Both species grow on the mannitol salt agar surface, but only S. aureus utilises mannitol, so yellow halos appear around S. aureus alone. When grown on TSA, S. aureus displays its namesakes colouring of large gold colonies. While S. epidermidis colonies are smaller and white.

S. aureus

S. epidermidis

#### 1.16 Skin Dwelling Coryneform

Coryneform is a term which encompasses non-acid fast, non-spore forming, non-branching, Gram-positive, bacillus-shaped bacteria (Funke et al. 1997; Wilson 2004). They also have pleomorphic abilities (Brabb et al. 2012) which allows them to change their shape or size in response to their habitat (Wainwright 1997). However, the genus Corynebacterium, covers bacteria with the aforementioned morphological properties along with other attributes such as being non-motile, catalase-positive (Brabb et al. 2012), arabinogalactan containing cell walls and having a guanine-cytosine content of 46-74 mol% (Wilson 2004). There are over 80 known species of Corynebacterium, although only a small few are part of the skin commensals including Corynebacterium amycolatum, Corynebacterium jeikeium and a group of cutaneous lipophilic Corynebacterium spp. (Bernard 2012). These skin species are all halophiles, except C. jeikeium, and can be facultative or obligate aerobes (Riegel 1998; Ventosa et al. 1998; Wilson 2004). *Corynebacterium* spp. occupy the moist areas of the body and are thought to be involved in breaking down sweat and releasing the subsequent odour (Grice and Segre 2011; Troccaz et al. 2015). Corynebacterium spp. require amino acids as a nitrogen and energy source but lack extracellular proteases necessary to hydrolyse proteins. It is likely that these bacteria utilise the by-products from other skin bacteria breaking down larger proteins (Kwaszewska et al. 2014).

While not part of the skin microbiota, the pathogen *Corynebacterium diphtheriae* releases an exotoxin which causes the respiratory and skin disease Diphtheria. It is often isolated from abscesses formed on alcoholics, intravenous drug users and individuals who live in poor areas with limited access to hygiene (Murphy 1996). A vaccine has successfully reduced outbreaks in first world countries, but the disease is still prevalent in the developing world (Cogen et al. 2008).

*Corynebacterium jeikeium* is a species which is commonly isolated from the skin (Cartwright et al. 1993; Cogen et al. 2008). Unlike other *Corynebacterium* spp., *C. jeikeium* is an obligate aerobe and is unlikely to be found in pores or follicles due to the competition for the reduced oxygen (Ifantidou et al. 2010). It is a species that is lipophilic and requires a fat source to grow, when the organism is cultured, a lipid substitute is added to the media, Tween 80 is commonly used between 0.1 and 1% v/v (Kim et al. 2015b). *C. jeikeium* is another well-known opportunistic pathogen that often infects the immunocompromised. Like *Staphylococcus epidermidis, Corynebacterium jeikeium* can be highly problematic in a clinical setting and can form antibiotic resistant biofilms, often on medically implanted devices (Soriano et al. 1993; Ziebuhr et al. 2006). Complications arising from these biofilms can lead to sepsis and endocarditis (vanderLelie et al. 1995). *C. jeikeium* also has some beneficial attributes; the bacterium acquires manganese to protect itself from superoxide free radicals and in the process may protect the host from them too (Tauch et al. 2005; Balamurugan 2019). Although under-researched, *Corynebacterium* 

*jeikeium* release compounds which are not too dissimilar from known bacteriocins to which pathogens are susceptible (Tauch et al. 2005; Cogen et al. 2008).

#### 1.17 New Classification for the old *Propionibacterium* spp.

*Propionibacterium* was a genus in which four species were commonly found on the skin, *P. acnes, P. granulosum, P. avidum* and *P. propionicum* (Gharamti and Kanafani 2017; Corvec 2018; Suzuki et al. 2019). However, whole genome sequencing highlighted the inaccuracies of the previous 16S rRNA gene sequencing and thus three of the species were placed into the new genus, *Cutibacterium* and the fourth into another new genus *Pseudopropionibacterium* (Scholz and Kilian 2016).

The *Cutibacterium* gen. are a group of non-motile, non-sporing, fermentative, Gram-positive rods. These species range from obligate and facultative anaerobes to microaerophilic; explaining why they can be found both on the surface and within pores of the skin (Wilson 2004). Both *Cutibacterium granulosum* and *Cutibacterium acnes* are follicle dwellers, while *Cutibacterium avidum* is found in the axillary regions, where sweat is abundantly produced (Corvec 2018). While commonly found on adult skin *Cutibacterium* spp. are rarely seen on prepubescent children (Chomnawang et al. 2005). The *Cutibacterium* genus adapt to living on the skin by growing at a range of pHs, optimally between 5.5 and 6. They also produce numerous lipases which release fatty acids from lipids to use as carbon and energy sources (Brzuszkiewicz et al. 2011).

The most well-studied species, *Cutibacterium acnes*, was isolated from an acne vulgaris region over 100 years ago and has been associated with disease ever since (Bojar and Holland 2004). Acne vulgaris is a very common skin ailment and a large proportion of the population will have had it in their teenage years (Bhate and Williams 2013). The condition results in numerous closed (whiteheads) and open (blackheads) comedones caused from blockages of the pilosebaceous units (Izumi et al. 1970). While this ailment is not life threatening, it can make sufferers feels embarrassed and self-conscious (Kellett and Gawkrodger 1999) and extreme cases can lead to facial scarring (Fabbrocini et al. 2010). The cause is still not clear, but it is thought that as puberty onsets, an influx of sebum in the follicles causes a proliferation of *C. acnes*. The immune system responds to the proliferation and the pores inflame and fill with white blood cells (Vary 2015). It is disputed that *C. acnes* is not the sole cause and that other species which co-occupy acne lesions, including antibiotic resistant strains of *S. epidermidis*, may be involved (Nishijima et al. 2000).

Although *C. acnes* has pathogenic potential, and has been the target of antibiotics for acne treatment (Leyden and Del Rosso 2011), it is in fact a commensal and has a range of advantageous properties. The species stimulates the sebaceous glands into releasing sebum, *C. acnes* then break down the sebum which releases free fatty acids onto the skin thus lowering the pH of the skin

(McLaughlin et al. 2019). This lower pH stops colonisation from pathogenic species which often prefer more neutral pHs (Grice and Segre 2011).

Multiple strains of *C. acnes* also release an enzyme which converts linoleic acid into conjugated linoleic acid (CLA) (Liavonchanka et al. 2006). These isomers have been shown to have some capabilities in reducing tumour formation by triggering apoptosis (Lee et al. 2005). Many *C. acnes* strains also release bactericidal chemicals such as acnecin which inhibits other species and strains of *C. acnes* without the acnecin producing gene (Fujimura and Nakamura 1978).

#### 1.18 Splitting of the *Micrococcus* Genus

Micrococcus is a Gram-positive genus that is associated with the human skin, these catalasepositive, non-sporing, cocci are not unalike in appearance to Staphylococcus spp., but are genetically dissimilar (Becker et al. 2015) and unlike Staphylococcus spp., Micrococcus spp. are resistant to the bacterial enzyme lysostaphin (Geary and Stevens 1986). Micrococcus luteus is the most clinically important of the species and has been isolated from the head, legs, and arms (Kloos and Musselwhite 1975). The small, bright, yellow colonies are a frequent contamination from the skin and surroundings when aseptic techniques are poor (Hall and Lyman 2006; Hetem et al. 2017). The species is tolerant to a range of temperatures and high salt concentrations (Chan and Leung 1979), this tolerance and their ability to create nutrients from bacterial metabolic waste, make them ideal skin dwellers (Wilson 2004). While not an issue for healthy people, Micrococcus luteus can cause problems in the immunocompromised and is often the source of cutaneous infections in HIV infected individuals (Smith et al. 1999). Teichuronic acids found in the cell walls of M. luteus are involved in activating immune responses, including tumour necrosis factors (Yang et al. 2001) which assign cell death (Chu 2013). In 1995, Micrococcus was split into five separate genera after 16S rRNA gene analysis and chemotaxonomic tests highlighted differences (Ekkelenkamp et al. 2010).

Three previous *Micrococcus* spp. have now been placed into the genus *Kocuria* (Stackebrandt et al. 1995). *Kocuria rosea* (formally *M. rosea*) is another classic species which resides peacefully on the skin until given an opportunity to become pathogenic (Altuntas et al. 2004) As with other commensal Gram-positives, this *K. rosea* can cause serious illness in individuals with underlying health problems or people who have had implanted medical devices (Dunn et al. 2011). Although unlike other opportunistic skin pathogens, *K. rosea* has not been noted with the ability to produce biofilms and therefore it is suggested that this species causes illness by entering the bloodstream and causing chronic bacteraemia (Purty et al. 2013). *Kocuria varians* is the most frequented skin isolate from this genus and have been noted to be able to cause relapsing infections deep into the tissue (Dotis et al. 2015). Two strains, isolated from meat in a salami factory, have been shown to produce heat and pH resistant antimicrobial chemicals which are effective against a broad range

of Gram-positives (Gálvez et al. 2007). Although not skin isolates, it is likely that they will produce similar bacteriocins to protect themselves.

#### 1.19 Do Gram-negative skin commensals exist?

The debate as to whether Gram-negative bacteria are skin commensals or transient visitors is ongoing, but their numbers are significantly less than Gram-positive species (Evans et al. 1950; Wilson 2004; Grice and Segre 2011; Myles et al. 2016). Resident Gram-negative bacteria are only found in the moist, more pH neutral areas such as the toe web or axillae (Davis 1996). The combination of dry and acidic proves the skin too harsh of an environment for the majority of Gram-negative bacteria (Chiller et al. 2001). However, culture-independent techniques have revealed that skin dwelling Gram-negative species may be more prevalent than originally proposed (Conlan et al. 2012). More thoroughly developed culturing methods for these species have been established for future works (Myles et al. 2016). The prevalent skin genera are the enteric, *Enterobacter, Klebsiella, Escherichia, Proteus* and soil dwelling, *Acinetobacter* (Davis 1996). The common gut residents are also regularly found around the anal regions, where there is a possible a lingering faecal veneer (Ki and Rotstein 2008). However, Gram-negative bacteria can be highly prevalent on people with poor hygiene or skin infections (Wassilew 1989; WHO 2009; Tang et al. 2020). Over treatment of chronic skin infections may also lead to over-growth by Gram-negative bacteria and the prevalence of harsher skin ailments (Böni and Nehrhoff 2003)

## 1.20 Commensal or Pathogen? It Isn't Straightforward

Bacteria that reside on the skin can be placed into beneficial, commensal, or pathogenic categories. In reality the beneficial or commensal species have the potential to cause skin infections when given the opportunity (Grice and Segre 2011). Equally, species which are classed as problematic can live harmlessly on the skin with other microbes and can alert the immune system to invasion from more pathogenic organisms (Krismer et al. 2017).

#### 1.21 Changes in Skin Bacteria from Birth

Initial colonisation starts pre-birth. Microbes originally thought to be from the uterus, placenta, umbilical cord, and amniotic fluids have been isolated from new-borns. However, the mass colonisation starts with delivery and is dependent on both method and whether the baby has reached term (Dunn et al. 2017). Immediately after birth, babies delivered by vaginal delivery are covered by *Lactobacillus* spp., the genera responsible for maintaining a healthy vagina (Zapata and Quagliarello 2015). C-Section babies, however, are dominated by *Staphylococcus* and *Corynebacterium* spp., as would be common on their mother's skin and in hospital settings (Neu and Rushing 2011). The difference in skin microbiota, aided with an under-developed immune system (Shao et al. 2019), may explain why C-Section babies are more likely to acquire nosocomial infections (Miller et al. 2020). Preterm babies differ from full term babies, they possess large abundancies of *Staphylococcus* spp. and gut associated Gram-negative bacteria (Younge et al. 2018). At around three months of age, birthing route differences in skin microbiota begin to dissipate, skin species are no longer present all over the body, but start to become site-specific (Zhu et al. 2019; Skowron et al. 2021).

The skin microbiome of children is vastly different to those of adults, with the most significant difference being around oily areas like the nose (Oh et al. 2012). However, Zhu (et al., 2019) found that both the mode of delivery and the mother's own bacterial community do have an influence on the facial microbes in children even as old as ten. *Streptococcus mitis* and *Streptococcus pseudopneumoniae* are two species found on children's skin which are not commonly part of the adult commensal microbiota (Oh et al. 2012) Once the body starts to undergo puberty however, the increased production in sweat and sebum causes a proliferation in more adult skin organisms, such as *Cutibacterium* spp. (Bhatia et al. 2004; Ellis et al. 2019). This increase in sebum aides in pH reduction of the skin, thus inhibiting neutral pH loving staphylococcal and streptococcal spp., genera which are found more abundantly on children (Oh et al. 2012).

When adulthood is reached, the microbes on the skin reach an equilibrium tailored to that individual (Oh et al. 2012), although hormonal changes and lifestyle choices like smoking or drinking alcohol, can disrupt the equilibrium and cause microbial imbalances (Oh et al. 2012; Wallen Russell 2018; Bagatin et al. 2019; Dimitriu et al. 2019). For instance, cigarette smoke may even be able to promote and increase antibiotic resistance in MRSA by stressing *S. aureus* into more frequent mutations (Lacoma et al. 2019). While *Corynebacterium* spp. could be used as a biomarker for obesity related diseases (Brandwein et al. 2019).

Like children, the elderly produce less oil and sweat than adults (Wu et al. 2020b) and their lack of microbial diversity reflects this (Rodrigues Hoffmann 2017). The microbial skin colonisation of elderly people is dependent on numerous factors including home residence (Grice and Segre

2011). Many of the older society live in care homes, where full showers are less frequent and bed baths are a common way of washing. (Groven et al. 2017). Therefore the skin of people residing in nursing homes are more likely to harbour gut residing Gram-negative bacteria, drug resistant microbes and an abundance of bacteria responsible for nosocomial infections (Roghmann et al. 2017).

#### 1.22 Skin Microbial Diversity of the Western World

In the modern Western world there has been an increase in cases of skin diseases, which had been much less prevalent in the previous centuries (Chu et al. 2017). Antibiotics have been the saviour of humans and cured a multitude of infectious diseases, and allowed many surgical procedures to be performed, including bone marrow and solid organ transplants (Adedeji 2016). Preservatives have been very useful in preventing products in both the food and cosmetic industry from spoiling (Parke and Lewis 1992; Halla et al. 2018). However, compliant use and the broad range of these antibiotics and preservatives could have reduced the number of helpful bacteria that reside on our skin (Llor and Bjerrum 2014; Langdon et al. 2016). Another possibility includes changes in the way westerners go about their daily lives. Sedentary jobs in the cities are now more common than physical jobs in agriculture or the fishing industry (Uhlig 2003; Seafarers 2018; Harrison 2019; Trussler 2019).

This theory that our western lifestyles have contributed to a change of residential skin microbiota is highlighted by studies in which the skin community of isolated rural human populations was analysed. Communities in which hunting and gathering are still the means to collect food and whose bodies have been untouched by modern day antibiotics, possess skin bacterial species unseen on urbanised populations (Blaser et al. 2013). Societies in which agriculture is still a key part of life also, unsurprisingly, have been found to harbour higher levels of soil dwelling associated bacteria on their hands. Even in western communities, individuals exposed to a farming or rural lifestyle possess differing microbial skin communities than those brought up in a more urban existence (Parajuli et al. 2018; Steiman et al. 2018)

All of these studies tie in with the 'hygiene hypothesis', in which our extra clean lifestyles may have abetted changing the microbes which reside on, and in our bodies (Okada et al. 2010).

#### 1.23 Battle of the Sexes

Women and Men have differences between the topographical, physiological, hormonal and the pH of their skin (Giacomoni et al. 2009) and the differences in their skin microbiota reflect this. However, many studies are contradictory as to which gender has the most microbial skin diversity (Fierer et al. 2008; Song et al. 2013; Ma and Li 2019). Women have been found to harbour less bacterial diversity than men in several studies. The most significant difference being around the thighs, groin, and axilla (Marples 1982; Ma and Li 2019). Fierer (et al., 2008) found that women's hands had a more diverse microbial content than men. This study stated that women's higher pH may allow for more species colonisation. While genera on the hands of males and females are not significantly different, the abundance of these genera is. Women tend to have a higher proportion of gram-negative bacteria associated with their genitalia, while men have more 'classic' skin genera like *Corynebacterium* and *Cutibacterium*. Song (et al., 2013) echoed Fierer, and found that women have a higher microbial diversity. They also found that cohabiting couples of different sexes have similar microbiota and that the couples could be correctly identified by simply examining their microbial communities. Any differences between men and women could be down to numerous causes (Giacomoni et al. 2009; Wallen Russell 2018). The way that individuals of the same gender have significantly different microbial skin communities (Leung et al. 2015) ensures that it is near impossible to pinpoint one reason alone (Grice and Segre 2011).

#### 1.24 Cosmetics

Cosmetics have been used in many cultures throughout the ages. The ancient Egyptians used cosmetics to satisfy their extremely hygienic ethos and wore cosmetic make-up at celebrations (Hardy and Rollinson 2012). Until relatively recently, cosmetics were a luxury that the upper classes could afford. Modern day cosmetics are mostly used for hair removal, personal hygiene, improvement of skin health and appearance, inhibiting the signs of aging and enhancing or diminishing features. These products include, but are not limited to, deodorants, moisturisers, hair washing and styling, body washes, make-up and perfumes (Draelos 2014). As these products are designed to be used on or near the body, so the formulations and ingredients are vigorously tested to ensure that they are not harmful or damaging to the skin (Walker et al. 1996). However, only recently have cosmetics been tested on how they interact with skin microbiota. Many ingredients found in cosmetic products have the potential to either enrich or cause stress to the microbes (Dobler et al. 2019).

#### 1.25 Probiotics

Past studies of cosmetics and microbes have focused on the use of probiotics and prebiotics. Probiotics are used to introduce helpful microorganisms into an environment, while prebiotics are used to promote 'good' microbes which already reside (Kechagia et al. 2013). Products which claim to possess probiotic and/or prebiotic properties are mostly 'leave-on' formulations targeting the face (Warming et al. 2018), although skin probiotics are also often ingested (Kober and Bowe 2015). These kinds of products have been met with scepticism in the past (Reid 2005). For example, *Lactobacillus* is a genus which is often endorsed as an excellent all round body probiotic (Rossi et al. 2019). Research into *L. rhamnosus* lysates usage have reported that tight junction proteins are further expressed and that skin sensitivity to surfactants have been reduced (Jung et al. 2019). However the additional promotion of phagocytes, in turn, could actually induce skin

diseases (Ouwehand et al. 2010). However, there has been studies into compounds commonly found in cosmetics and their interactions with a range of microbes.

#### 1.26 Emulsifiers and Surfactants

Emulsifiers are used as stabilisers in cosmetic formulations to stop separation of oil and water. Polysorbates, or Tween are a derivative of ethoxylated sorbitan. They are common emulsifiers and act as non-ionic surfactants in formulations as they are mild on skin. Previous studies have shown how polysorbates affect a range of bacterial species. Polysorbate 80 and 20 have been show to disperse in vitro biofilms of common gut bacteria (Sloup et al. 2016). However, the opposite is true for S. aureus, in which the addition of Tween 80 to the growth media causes increased biomass for biofilm formation (Nielsen et al. 2016). These polysorbate groups are a common addition to growth media to allow lipid loving bacteria to have a fat source, including common skin species Cutibacterium acnes and Corynebacterium jeikeium (Ray and Kellum 1970; Chevalier et al. 1987). Another widely used emulsifier/surfactant used in cosmetics is lecithin (Figure 4) and hydrogenated lecithin (Fiume 2001). The amphiphile is found in all living organisms, but plant-sourced lecithin is in higher demand, mostly due to the diminished role of animal derivatives in cosmetic formulations (Kabene and Baadel 2019; Partridge et al. 2019). The stabilising agent can form viscous gels which can easily deliver formulations onto the skin (Attar Nasseri et al. 2010; Zhou et al. 2010; Raut et al. 2012). However, previous in vitro studies have noted that using 2% purified bovine lecithin in media can support the growth of *Cutibacterium* acnes, while showing inhibitory effects to Staphylococcus aureus (Kabongo et al. 1982).

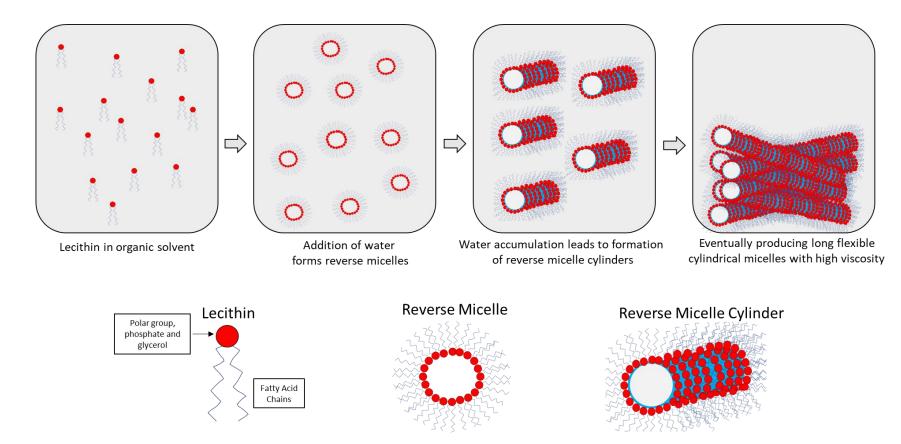
#### 1.27 Preserving Measures

Liquid ingredients or formulations, require protection from microbial spoilage to increase the lifespan of the cosmetics (Panico et al. 2019). Preservatives are used throughout the cosmetic and food industry to prevent contamination without causing unpleasant tastes or harm to the consumer or user (Halla et al. 2018). Many of the organisms that cause bacterial spoilage are also bacteria that are naturally found on skin, thus simply lowering the pH of the formulation is not always sufficient (Varvaresou et al. 2009; Halla et al. 2018).

Other tactics include reducing the water activity (aw) by the addition of sugars, salts, or proteolysates (Hahn-Hägerdal 1986). Most organisms require a water activity of 0.9 or above to be able to grow, reducing the water activity limits the bacterial spoilage (Table 2) (FDA 1984-2014). However, the addition of too many sugars or salts will affect the taste of food, and water activity is key component in cosmetic products. This type of preservation also opens up contamination by halophilic or osmophilic microorganisms (Todar 2015). Another common way of preserving foods or cosmetics is the addition of either natural or synthetic compounds which have specific antimicrobial properties (Juhász and Marmur 2014; Pandey et al. 2016). Synthetic

preservatives cover a range of chemical types including, but not limited to, organic acids, formaldehyde releasers and aromatic alcohols (Halla et al. 2018) (See Table 3 for examples and mechanisms). Although all possess antimicrobial activity, using two or more together increases the spectrum of spoilage targets. Many preservatives are also often paired with the chelating agent Ethylenediaminetetraacetic acid (EDTA) (Izzat and Bennett 1979). EDTA is used to improve the efficacy of preservatives by reducing the integrity of the cell membrane (Finnegan and Percival 2015).

Societal pressures are now causing cosmetic companies to step away from synthetically produced preservatives and be replaced with naturally derived antimicrobial ingredients (Vergis et al. 2015). Essential oils are secondary metabolites produced by aromatic plants (Guerriero et al. 2018). Originally used for cosmetic properties, these oils are packed full of antimicrobial terpenes, hydrocarbons, lipids and phenyls (Swamy et al. 2016). Although they are antimicrobial, studies have shown that essential oils' preserving properties are only comparable to synthetic compounds when used in high concentrations (Dreger and Wielgus 2013).



**Figure 4. Formation of Lecithin Gel**. The addition of water to free lecithin in organic solvent causes the formation of reverse micelles. Further addition of water leads to cylindrical reverse micelles, eventually leading to long flexible cylinders forming a compound trapping gel.

#### 1.28 Cosmetic Proteins

Highly adept at binding water to the skin, cosmetic proteins are used for their moisturising properties and often marketed for their 'regenerating' and 'rejuvenating' qualities (Prokopowicz and Różycki 2017). Acid hydrolysis is commonly used to split the insoluble native protein into mixture of soluble amino acids and peptides (Secchi and Teglia 1999). This type of hydrolysis, however, can cause the loss of amino acids cysteine and tryptophan as well as increasing the chances of racemisation (Burnett et al. 2014). An alkaline process for hydrolysis utilises hydroxide variants at high temperatures to split the protein, however this method can cause a high percentage loss of amino acid return can be poor. Enzymatic hydrolysis can use individual or mixed enzymes to cleave proteins into peptides and amino acids, thermal denaturation of the enzymes are often required to limit further cleavage and damage of the desired product (Verzeaux 2021). Powdered cosmetic proteins have negligible water activity, but liquid protein complexes (lpcs) are vulnerable to spoilage and therefore are preserved with synthetic preservatives (Scibisz et al. 2008).

The hydrolysed proteins can come from numerous animal or plant sources, and less commonly algae or fungi (Secchi 2008). Cosmetic proteins originating from animal sources include collagen, keratin, elastin and silk derivatives (Secchi and Teglia 1999). These can provide amino acids, such as proline, which is often marketed to aid in the healing of skin (Trookman et al. 2009; Szpak 2011). However, many cosmetic companies are moving away from using animal products and so the use of animal derived proteolysates are running out of favour (Secchi 2008). Plant proteins are concentrated in the seeds (Nehete et al. 2013). The amino acid make-up of plant proteins differs significantly from animal proteins. Therefore, these hydrolysed proteins can deliver exogenous amino acids which humans cannot synthesize, but can lack other useful amino acids, such as proline (Scibisz et al. 2008).

As the composition of these cosmetic proteins include amino acids and/or peptides, the use of cosmetic proteins could both benefit or hinder the natural microbiota found on skin (Holland and Bojar 2002). Amino acids are used by bacteria as a nutritional source of nitrogen and for protein synthesis. The addition of amino acids may go further than simply providing sustenance. Introduction of proline onto the skin could be valuable to bacteria undergoing osmotic or saline imbalances, the stocking of this amino acid protects cells from these physical stresses (Liang et al. 2013). The uptake of amino acids by *Staphylococcus aureus* and subsequent synthesis of ammonia offsets any pH decreases, thus allowing formation and sustaining of biofilms (Ammons et al. 2014). Bacteria enveloped by keratinocytes may have the potential to steal and uptake essential amino acids to extend their life before apoptosis occurs. While beneficial for the bacteria, the

amino acids now unavailable to skin cells could cause disruption to the host cell's metabolism pathways (Chi et al. 2013; Arimoto et al. 2017)

In contrast, the use of cosmetic proteins could negatively affect the resident bacteria and their virulence factors. Several D-amino acids, have been shown to be able to reduce the attachment and biofilm formation of bacteria, including *S. aureus* (Kolodkin-Gal et al. 2010; Hochbaum et al. 2011; Ampornaramveth et al. 2018). Proteolysates reduce the water activity of a formulation, therefore it is possible that this could lower the water activity of skin (lbèr et al. 2014). This could potentially disrupt the balance of the skin microbiota as different species require different water activity levels (FDA 1984-2014; Rahman 2009; Ijabadeniyi and Pillay 2017).

Table 2. The Lowest Water Activity  $(a_w)^4$  Level in which Select Bacteria Species can Grow.

Lowest Water Activity (a <sub>w</sub> ) for Growth	Bacteria Species		
0.97	Pseudomonas fluorescens		
0.94	Clostridium botulinum A		
0.93	Bacillus cereus		
0.91	Bacillus subtilis		
0.90	Staphylococcus epidermidis		
0.87	Staphylococcus aureus		
0.85	No Bacterial Growth		

<sup>&</sup>lt;sup>4</sup> Water activity (aw) is defined as the ratio of the partial pressure of water in the atmosphere in equilibrium with the substrate to that of the atmosphere in equilibrium with pure water at the same temperature and is expressed on a scale of 0 to 1 where 1 is pure water. Most bacteria require a water activity level of above 0.9 to be able to grow.

### Table 3. Molecular Structure, Susceptible Species and Mechanisms of Synthetic Preservatives<sup>5</sup>

Preservative and Molecular Structure	Some Known Susceptible Species	Mechanisms		
Organic Acids				
Sodium Benzoate O Na <sup>+</sup>	Gram Positive Staphylococcus aureus Bacillus subtilis Bacillus mycoides	Sodium benzoate is bacteriostatic rather than bactericidal. At pH 5 and below benzoic acid is formed.		
	Gram Negative Escherichia coli Pseudomonas aeruginosa	This impedes with the permeability of the cell membrane and energy formed from the electron		
	Fungi Aspergillus spp. Pencillium citrinum	transport chain. The acid also inhibits the uptake of amino acids and thus restricting access to a nitrogen source.		
Potassium Sorbate	Gram Positive Staphylococcus aureus Bacillus cereus Clostridium botulinum	When in solution, sorbic acid can infiltrate the cell wall of an organism and effect the osmotic balance. The ability		
о. к <sup>+</sup>	Gram Negative Vibrio parahaemolyticus Salmononella spp.	to form covalent bonds with thiol groups, this hinders a range of enzymatic processes including carbohydrate uptake		
	Fungi Aspergillus flavus Aspergillus parasiticus Penicillium cyclopium	and energy release. Amino acid uptake is also reduced.		
Aromatic Alcohols	Gram Positive Staphylococcus spp.	Phenoxyethanol interrupts the cell membrane and allows		
Phenoxyethanol	Micrococcus spp.	potassium ions to pass through, disrupting osmotic		
Он	<b>Gram Negative</b> Pseudomonas aeruginosa Proteus mirabilis Escherichia coli	balance. The preservative also inhibits the coupling of the electron transport and phosphorylation and stops the synthesis of ATP. It also is		
	Fungi Candida albicans Aspergillus niger	involved in stopping both DNA and RNA synthesis. Pairing with a chelating agent improves efficacy.		
Phenyl Alcohol	Gram Positive Streptococcus spp.	Aromatic alcohols inactivate cell membrane proteins in bacteria. The change in the		
ОН	Gram Negative Shigella spp. Escherichia coli Pseudomonas aeruginosa Salmonella spp.	cell membrane causes some bacteria to go into a 'cold shock response' in which enzyme productivity decreases and there is a		
	Fungi Candida albicans Candida Africana	reduction in transcription and translation.		
Formaldehyde Releasers	Gram Positive Staphylococcus spp.			
Diazolidinyl urea	<b>Gram Negative</b> Klebsiella pneumoniae Pseudomonas spp. Escherichia coli	These type of preservatives release formaldehyde in solution. Formaldehyde stops		
N N N OH HO	<b>Fungi</b> Aspergillus niger Candida albicans	the production of the essential amino acid methionine. This in turn halts		
Quarternium - 15	Gram Positive Staphylococcus aureus Bacillus spp.	messenger RNA being translated into proteins. Formaldehyde also has coagulating properties which		
	<b>Gram Negative</b> Escherichia coli Pseudomonas aeruginosa	dehydrates the membranes and dries out the cytoplasm inside the cell.		
	<b>Fungi</b> Aspergillus niger Candida albicans			

<sup>5</sup> Common synthetic cosmetic preservatives

Essential Oil and Antimicrobial Compounds		Susceptible Species	Mechanisms of Antimicrobial Compounds	
			Citrone	ila Oil
Citronellal $CH_3$ CHO $H_3C$ CHO $H_3C$ CHO			Gram Positive Staphylococcus aureus Cutibacterium acnes Streptococcus spp. Gram Negative Pseudomonas aeruginosa Salmonella spp. Campylobacter spp. Fungi Candida albicans Aspergillus niger	Citronellal, linalool and myrcene are all types of terpenes. The mechanism is not well known but it is believed that these compounds work by disrupting the integrity of the bacterial cell membrane and disrupting it's functions. Linalool not only disrupts the cell membrane of bacteria but the electron transport chain is targeted and damaged. Citronellal disturbs the stability of electron donor components and causes changes to the electrophoretic separation. Myrcene has been shown to increase the antimicrobial effects compounds through limiting microbial resistance mechanisms.
			Clove	
Oleic Acid	Eugenol	Linoleic Acid	Gram Positive Streptococcus pyogenes Corynebacterium spp. Staphylococcus spp. Gram Negative Salmonella enteritidis Escherichia coli Bacteroides fragilis Fungi Candida albicans Trichophyton rubrum	Linoleic acid and oleic acid are both antimicrobial fatty acids. These are most efficient at penetrating gram-positive cytoplasmic membrane. Gram-negative bacteria posses lipopolysaccharides in the cell membrane which prevent permeation from fatty acids. The disruption the cell membrane eventually causes the cell to lyse. Eugenol is an allylbenzene and has antimicrobial activity due to its hydroxyl group. Eugenol causes an increase in bacterial cell membrane and causes an influx of potassium ions which upsets the osmotic balance. Eugenol also produces excess reactive oxygen species resulting in the inability of cell growth and causes DNA damage. Eugenol also causes similar problems for fungi, bypassing the envelope disrupts cell morphology and permeability, while also disabling the ability for fungi to attach to a host.
			Sandalw	rood Oil
$\begin{array}{c} \alpha \text{-Santalol} \\ & & \\ & \\ & \\ & \\ & \\ & \\ & \\ & \\ & $		antalol	Gram Positive Staphylococcus aureus Bacillus subtilis Gram Negative Helicobacter pylori Klebsiella pneumoniae Fungi Candida spp. Microsporum spp.	Santalol is a sesquiterpene found in sandalwood oil. $\alpha$ -Santalol is more abundant than $\beta$ -Santalol. The ratio of alpha and beta- Santalol, as well as sensitive microbial species, changes dependent on sandalwood species. Along with other essential oil antimicrobial compounds, the mechanisms of sesquiterpenes are faily unknown. However, they have been shown to disrupt the bacterial membranes and reduce biofilm formation of <i>Staphylococcus</i> spp $\beta$ -Santalol has been shown to interrupt replication of influenza viruses.

### Table 4. Essential oils and their Antimicrobial Compounds <sup>6</sup>

<sup>&</sup>lt;sup>6</sup> Essential oils are packed with chemicals which have antimicrobial properties

#### 1.29 Reasons for Research

With the rise of urban skin ailments, it is important to note how cosmetics, or their ingredients interact with natural microbiota that reside on our skin. Cosmetic companies are now starting to move away from the once popular antimicrobial tag line in their formulations to making products with claims of promoting the 'good bacteria' that reside on our skin. However, these 'good' bacteria, include species which are common sources of nosocomial infections. These are opportunistic pathogens, which may not be as harmful as other more pathogenic species, can cause nasty infections in the immunocompromised. Even what companies would class as 'bad bacteria' often live peacefully on our skin and cause no problems day-to-day, as well as potentially stopping other pathogens from living on our skin.

#### 1.30 Hypothesis

Cosmetic proteins have the potential to be utilised by the bacteria found on skin, to help with their growth. While the preservatives found in cosmetic proteins are likely to have inhibitory effect against the same bacteria.

#### 1.31 Aims

- Design a minimal medium to produce growth conditions more akin to skin (Section 2)
- To use minimal inhibitory concentration methods to understand the inhibitory effect of the preservatives found in cosmetic proteins (Section 3)
- To use growth kinetics and biofilm formation techniques to identify whether the cosmetic proteins can be utilised by skin bacteria (Section 3)
- To co-culture Staphylococcus aureus and Staphylococcus epidermidis (Section 4)
- Expose co-cultured *Staphylococcus* spp. to the cosmetic proteins and investigate dominance of species in both planktonic conditions and for biofilm formation (Section 4)
- Use tissue culture to understand the bigger picture by incorporating skin cells and their interactions with cosmetic proteins and skin bacteria (Section 5)
- Start to move this study from the *in vitro* phase to *in vivo*, by investigating retrieval of bacteria from skin using different swab head types and buffer compositions (Section 6)
- Investigate whether current cosmetic protocols for skin tests can be used when incorporating a microbial element (Section 7)
- Find a body site with the highest bacterial return to limit relative background contamination (Section 7)

2 Production of a Minimal Medium to Reflect the Skin's Harsh Environment

#### 2.1 Growth Requirements

To successfully grow microorganisms, the growth medium must reflect the need of the species and the environment in which they naturally live (Boundless 2017). Bacterial respiration occurs when the organism is in contact with the correct balance of gases (Rogers and Kadner 2020). Aerobes, facultative anaerobes, and micro-aerobes, require access to varying levels of oxygen to grow (Morris and Schmidt 2013; Singh 2016). Many aerobic species can grow in micro-aerobic conditions when there is competition for, or low levels of oxygen present (Partridge et al. 2007). While facultative anaerobes can switch between aerobic and anaerobic respiration, when oxygen is reduced or not present (Sanz 2011). Obligate anaerobes, however, can be negatively affected or harmed by the presence of oxygen (Hentges 1996). Cultivations *in vitro* involve atmospheres of either a hydrogen/nitrogen or nitrogen/carbon dioxide combination (Cox and Mangels 1976; Behbehani et al. 1982).

Correct pH is also important for the growth of bacteria. Acidophilic bacteria prefer growing in a pH of between 3-5 (Jin and Kirk 2018), while alkaliphilic species grow at the higher end of the scale between 9 and 11 (Horikoshi 1999; Rampelotto 2013). Neutrophiles are unlikely to proliferate in a pH which is more than two units away from neutral (Keenleyside 2019), but often can adapt to survive at the edges of acidic and alkaline conditions (Pradeep and Sarika 2008).

The cultivation of bacteria requires the ambient temperature to be within the species' range for growth. While most mesophilic bacteria can endure harsher temperatures than larger organisms, they are not adapted to proliferate below 10°C and above 50°C (Bendia et al. 2018). The ideal temperature for these bacteria is between 20-45°C (Schiraldi and De Rosa 2016). At low temperatures, the cell membrane of mesophiles becomes rigid which interferes with transport of ions and waste. Protein production slows and leads to inaccurate folding of the nascent molecules, leading to lack of function. Cell division ceases and the bacteria enter a stasis (D'Amico et al. 2006). While at high temperatures the thermo-sensitive proteins denature, and fluidity of structural lipids cause cell membranes damage (Kumar et al. 2000; Siliakus et al. 2017).

Bacteria utilise compounds in the environment to fuel growth and anabolic (energy required) and catabolic (energy produced) metabolisms (Jurtshuk 1996). The speed of growth, or cell division is dependent on the richness of the nutrient source (Monahan et al. 2014). In ideal conditions, some bacterial species' cells can double in minutes, while in severely depleted environments, it may take decades or more (Berry et al. 2010; Allen and Waclaw 2019). The minimal nutritional requirements for bacterial growth include water, mineral salts, a carbon source, a nitrogen source, phosphorus for adenosine triphosphate (ATP) and sulphur for cysteine and methionine (Fagerbakke et al. 1996). However, some more niche species may also need more specific

supplements (Atlas 2010). Selenium supplements, for example, have been shown to help *Lactobacillus* spp. inhibit the growth of pathogenic bacteria (Kousha et al. 2017).

Bacteria are around 70% water, which means it is vital for their survival (Hobot et al. 2015; Boundless 2021). Bacteria also require access to unbound water to allow for the transference of nutrients into the bacteria and waste products to be removed (Bonnet et al. 2019). Water activity (aw) measures the amount of unbound water of a solution. With the highest water activity of 1, distilled water is the most ideal source of water for the base of growth media as there is no additional salts or chemicals and the composition is therefore consistent (Schultz 2016; Allen 2018). Gram-negative bacteria require more than 0.96 aw to grow, while Gram-positive bacteria require upwards of 0.9 aw (Beuchat 1981; Sperber 1983). Only halophilic bacteria, yeasts and fungi can generally survive below 0.89 aw (Stevenson et al. 2015).

Mineral salts supply trace elements which are vital for synthesis of essential cellular components, nutrition, and cell metabolism. Phosphates are required to produce nucleic acids (Lodish et al. 2000), sulphates in methionine and cysteine production (Kushkevych et al. 2020), while magnesium ions are divalent cations involved in catalysation of ATP decomposition (Ebashi et al. 1973; Matevosyan et al. 2019). The reduction and reoxidation of Copper II ions on the isoenzyme superoxide dismutase are integral to the conversion of oxygen radicals into hydrogen peroxide (Nóbrega et al. 2019) and potassium is a counterion used to maintain cell homeostasis through preserving neutrality (Epstein 2003).

Carbon sources are broken down into smaller molecules such as amino acids or sugars through catabolic metabolism. These are used in various metabolic pathways which can generate proteins, nucleic acids and energy (Cooper 2000a). Autotrophic bacteria can utilise carbon dioxide to produce energy (Baas-Becking and Parks 1927), while heterotrophs rely on carbon sources available in the environment (Kirchman 1994). These carbon sources include various monosaccharides and disaccharides (Wawrik et al. 2005), while polysaccharides require extra enzymatic steps to reduce them to lower molecular weight molecules which will be small enough to enter the cell (Inman 2011). Carbohydrates enter the cellular respiration pathways in which the energy-carrying molecule ATP is produced. In the most ideal conditions, using the carbon source of glucose (Bren et al. 2016), a maximum of 38 molecules of ATP can be produced, two from glycolysis and the Kreb's cycle and upwards of 34 from the electron transport chain (Jurtshuk 1996). In the less efficient anaerobic respiration, ATP production count stands at two (Stojan and Christopher-Stine 2015; Melkonian and Schury 2020)

A source of nitrogen is required to produce nucleic acids and proteins. Organic nitrogen sources, such as amino acids, are more commonly utilised by bacteria than inorganic sources such as ammonium salts. While some bacteria possess extracellular enzymes, which can hydrolyse large

proteins (Wandersman 1989; Dalbey et al. 2012; Garai et al. 2017) and carbohydrates (Rivière et al. 2016), most Gram-negative bacteria prefer smaller peptides, which are easier to transfer through into the cell (Walker and Altman 2005).

Most standard recipes for non-selective media are very nutrient rich and contain abundant amounts of the minimum requirements to try and achieve maximum growth of bacteria. Tryptone soy broth or agar (TSB and TSA respectively) is a commonly used medium, which can grow numerous bacteria species. The composition of TSB includes nitrogen rich casein and soya peptones, the latter which also supplies natural sugars, a carbon source of glucose and an osmotic balancer of sodium chloride and with a suggested neutral pH to finish (SigmaAldrich 2018). Mueller-Hinton (MH) is a medium used for studying the antimicrobial effects of antibiotics and preservatives on bacteria (Lenczewski et al. 1996). It contains beef extract, casein hydrolysates and starch. While still nutrient rich, there is a lack of an additional sugar source as found in TSB. The addition of starch absorbs the bacterial waste products and stop them interfering with the antibiotics (Mueller and Hinton 1941).

Both media have been designed for a purpose, whether that be optimising growth conditions or testing susceptibility of a species. However, neither reflect the environment in which most bacterial species are found. For example, the human skin is a nutrient depleted niche (Moskovicz et al. 2020) and too acidic for many Gram-negative species to permanently settle (Grice and Segre 2011).

Previous research into bacteria which originated in low nutritional habitats had simply diluted nutritionally rich media. Dilution of the medium enabled the slower growing species to be cultivated. In media of high nutrients, fast growing bacteria use up the nutrients far too quickly and out-compete other, slower growing species (Medina et al. 2017; Chaudhary et al. 2019; Sun et al. 2019). If one wanted to carry out experiments on skin bacteria *in vitro*, using a nutrient rich medium such as TSB would not reflect the conditions which many of the skin dwelling bacteria find themselves and are adapted to overcome.

#### 2.2 Growth Kinetics

The growth pattern of a microorganism is dependent on the environment they are grown in and their access to nutrition. In a batch culture, most go through a recognised staged process (Figure 5). The collective phases of this process are known as the growth curve (Zwietering et al. 1990; Rolfe et al. 2012). These stages of the growth curve start with the adaption of the organism to the medium source and growth space. At this lag phase, while metabolically active, little or no growth is seen (Rolfe et al. 2012). If the medium is complex, with different sugar sources available, there can be multiple lag phases. This is called diauxic growth (Chu and Barnes 2016). The log phase begins as the organism utilises the nutrients available and multiply exponentially (Bruslind 2017). As nutrients and space available decrease or toxins accumulate, growth decelerates, and the

curve enters the stationary phase (Stanbury et al. 2017). If left long enough, the bacteria will enter the final decline or death phase. In a closed batch system, this is where the competition for lack of space or nutrients finally causes the bacteria to die off (Prado Barragán et al. 2016).

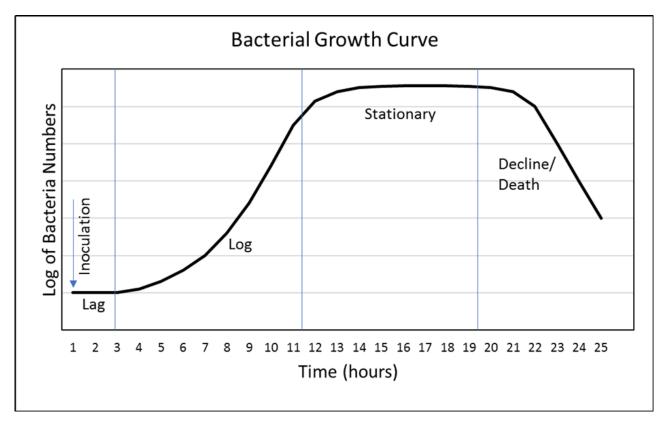
Growth curves and kinetics are a way of measuring how successful a species of bacteria is at utilising components of a given medium source (Budd and Spencer 1968). They can also be used to compare the behaviour of bacteria when grown at different temperatures, pH and when given different substrates (Zwietering et al. 1990). Observations can be made from the length of the lag period, growth rate and total growth yield, among others (Kneifel 2009).

### 2.3 Null Hypothesis

There would be no difference in growth between the conventional, high nutrition media in comparison to the low nutritional minimal medium.

#### 2.4 Aims

• To produce a medium which reflects the low nutrition and low pH of the skin



• To show that conventional, high nutritional media are unsuitable for skin bacteria

#### experiments

**Figure 5. The Four Phases of a Bacterial Growth Curve in a Closed Batch System**. The stages include the lag, log, stationary and decline/death.

#### 2.5 Materials

#### 2.6 Bacteria

The three bacteria species used in this study were all from two common skin genera (Dréno et al. 2018). *Staphylococcus epidermidis* (DSMZ-20044), *Corynebacterium jeikeium* (DSMZ-7171) and a clinical isolate, *Staphylococcus aureus*, taken from the perineal region of a patient. The three species were confirmed using 16S rRNA gene sequencing. These three skin species were chosen as all can grow aerobically and in similar media conditions. Previous works have often compared the pathogenic *S. aureus* with its commensal cousin *S. epidermidis*. However, it was decided to also use a slower growing *Corynebacterium* spp., to compare to the fast-growing *Staphylococcus* spp..

#### 2.7 Media

Dehydrated tryptone soy broth and dehydrated Mueller-Hinton broth were both purchased from Thermofisher Scientific (Waltham). The media were made as per instructions located on the packaging provided.

#### 2.8 Minimal Medium

To reproduce conditions more akin to skin, a minimal medium was required. The Davis minimal broth is a medium which is a mixture of salts and a low concentration of glucose as a single energy source, it was designed to isolate *Escherichia coli* (Atlas 2010). The medium was chosen as it was low nutritional but contained the bare minimum required for microbial growth. A modified version of this minimal medium was created to carry out experiments. Modified Davis medium composition as stated below (Table 5). HCl (1 M) was added to the medium until pH 5 ± 0.2. The medium was autoclaved at 121°C, 15 psi for 15 minutes. Supplements could be added separately as required. A 1-2% w/v agar version of the minimal medium was attempted, but there was either no growth or very small and unusable colonies.

Minimal Medium Composition					
Component	Per Litre				
Dipotassium phosphate	7.0 g				
Potassium phosphate	2.0 g				
Ammonium citrate	0.5 g				
Ammonium chloride	1.0 g				
Magnesium sulphate	0.1 g				
Glucose	1.0 g				
Supplements					
Casamino acids	0.6% w/v				
Tween 80	0.2% v/v				

**Table 5.** Recipe for Modified Davismedium.

#### 2.9 Methods

#### 2.10 Media Growth Curves

The three bacterial species were grown overnight in TSB for 18 hours. The suspension was placed into a 1 ml cuvette and optical density (OD) was measured at 600 nm using a Jenway 6300 spectrophotometer (Cole-Palmer Ltd., Cheshire). The cell suspensions were diluted in either the TSB, Mueller-Hinton or the Minimal Medium, to approximately 1x10<sup>5</sup> cfu/ml. The cfu/ml was confirmed by serial dilution, incubation and by colony count method of Miles and Misra (Miles et al. 1938) the following day. Growth assessments were carried out by producing growth curves using an Infinite<sup>®</sup> 200 PRO microplate reader (Tecan, Zurich). An aliquot (100 µl) was plated into a MicroWell<sup>™</sup> 96-Well Microplate (Corning, New York) well and placed into the 200 PRO multimode reader platform. Programme specifications were temperature 37 °C and absorbance reading 600 nm. The plates were orbitally shaken at 30-minute intervals before each read at a frequency of 218 rpm for 10 seconds.

#### 2.11 Statistics

Growth curves were illustrated, and kinetics analysed using GraphPad (San Diego) Prism (Version 9.1.2). Comparisons between a group of growth curves were analysed using One-way ANOVA, while comparisons between individual growth curves were analysed using a t-test. Total yield (total OD) was calculated using descriptive statistics of the curve. Growth rate and doubling time were calculated using non-linear regression fit of the curve analysis. Lag and log phase time were taken from observations straight from the growth curves, as there were no analysis options for these.

#### 2.12 Results

#### 2.13 Growth Curves with TSB, Mueller-Hinton and Minimal Medium

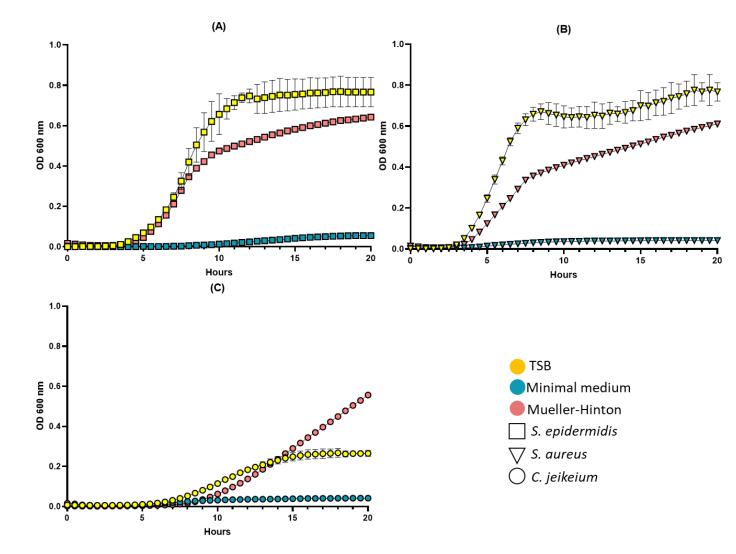
All three species were grown in TSB, Mueller-Hinton, and the minimal medium for 20 hours at 37  $^{\circ}$ C, however, a Tween 20 supplement of 0.2 % v/v, was required for *C. jeikeium* to utilise as a lipid source. In the main, sigmoid growth curves were observed with clearly defined stages of lag, log, and stationery. However, when the two *Staphylococcus* spp. were grown in Mueller-Hinton, the stationary phase did not follow the traditional pattern. *S. aureus* continued growth never led to a stationary plateau, while *S. epidermidis* did reach a plateau, but at around 20 hours, also following some extra, non-exponential growth. *C. jeikeium* did not reach stationary phase in 20 hours, when grown in Mueller-Hinton (Figure 6, Figure 7). However, there were significant (P<0.001) differences between the growth kinetics of each of the species when grown in the three media.

The lag phase of *S. epidermidis* totalled six hours when grown in the minimal medium, while only four hours when grown in TSB or Mueller-Hinton. Exponential growth of *S. epidermidis* lasted 11.5 hours in TSB, 9 hours in Mueller-Hinton and 7 hours in the Minimal medium. *S. epidermidis* had the slowest exponential growth rate when grown in TSB at 0.087 OD/hour compared to 0.092 OD/hour in Mueller-Hinton and 0.149 OD/hour in the Minimal medium. Doubling times were longer for *S. epidermidis* when grown in TSB, 7.9 hours, and MH broth, 7.5 hours, than in the minimal medium, 4.7 hours. The total yield for *S. epidermidis* when grown in TSB, with an optical density of 0.769. The final total OD when grown in Mueller-Hinton is slightly less at 0.642, and significantly lower (P<0.05). when grown in the minimal medium, only having reached 0.055.

The total lag phase time of *S. aureus*, when grown in all three media was approximately 3 - 3.5 hours. The exponential growth rate is also similar across the board, 0.070 OD/hour in TSB, slightly higher at 0.086 OD/hour in Minimal medium and 0.070 OD/hour in Mueller-Hinton. Doubling time was similar when *S. aureus* was grown in all three media but longer than *S. epidermidis*. Doubling time in TSB was 9.9 hours, in MH broth was 8.0 hours and 9.9 hours in the minimal medium. The log phase of *S. aureus'* growth lasted 5 hours in TSB, 4.5 in Mueller-Hinton and 7.5 hours in the Minimal medium. Again, as seen in *S. epidermidis*, while the exponential growth stopped, non-exponential growth was still observed during what would be the stationary phase in Mueller-Hinton broth. The final OD reached in TSB was 0.780, 0.610 in Mueller-Hinton and, again, the significantly lower (P<0.05) 0.041 in the minimal medium.

*C. jeikeium* had the longest lag phase in two out of the three media lasting approximately 6.7 hours in TSB and 10 hours in Mueller Hinton (Figure 6). The lag phase in minimal medium lasted approximately 3.5 hours, the same length of time as *S. aureus* (Figure 7). Once the exponential

growth had started, both the growth rate was faster than that of the *Staphylococcus* spp. The exponential growth rate of *C. jeikeium* had the most rapid in both TSB (0.118 OD/hour) and Mueller-Hinton Broth (0.190 OD/hour) and slowest in minimal medium at 0.082 OD/hour, slightly quicker than the growth rate of *S. aureus*. The final OD of *C. jeikeium* is less when grown in all three media, though the total yield had not yet been reached after 20 hours in Mueller Hinton. The final OD of *C. jeikeium* in TSB is 0.268, 0.042 in the Minimal medium and, although the growth had not reached stationary phase, 0.557 in Mueller Hinton. Again, doubling time of *C. jeikeium* in all media were shorter than *S. epidermidis* and *S. aureus*. When grown in TSB, the doubling time was 5.9 hours, 3.7 hours in MH, and the slowest in the minimal medium at 8.5 hours.



**Figure 6. Growth Curves of the Three Skin Bacteria with all Three Media Types.** This experiment was performed with three technical replicates and three biological replicates. (A) *Staphylococcus epidermidis* grown with TSB and Mueller-Hinton Broth at pH 7 and the Minimal medium at pH 5. (B) *Staphylococcus aureus* grown with TSB and Mueller-Hinton broth at pH 7 and the Minimal medium at pH 5. (C) *Corynebacterium jeikeium* grown with TSB

and Mueller-Hinton broth at pH 7 and the Minimal medium at pH 5. Figure 7 shows more clearly the growth curve of all three bacteria and the minimal medium.

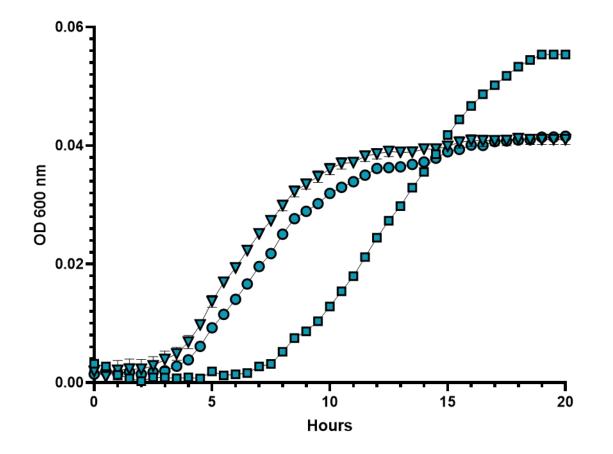


Figure 7. Growth Curves of the Three Skin Species Grown in the Minimal Medium. This experiment was performed with three technical replicates and three biological replicates. Growth curves of *S. epidermidis* ( $\Box$ ), *S. aureus* ( $\nabla$ ) and *C. jeikeium* (O) when grown for 20 hours with the Minimal Medium at pH 5. While exponential growth starts later for *S. epidermidis* than the other two species, total yield is far greater. There was no significant difference between the growth curves of *S. aureus* and *C. jeikeium* (P>0.05).

#### 2.14 Discussion

We can reject the null hypothesis that the three bacteria have the same growth pattern when grown with any of the chosen media.

#### 2.15 Why are Nutrient Rich Media not useful for Skin experiments?

Previous research has highlighted the disadvantages of using high nutritional media when investigating bacteria from low nutritional environments. Using high nutritional medium has meant that many species isolated from non-equivalent conditions have not been accurately represented (Davis et al. 2005). Disproportionate species growth can be seen in the growth curves from Figure 6. Both Staphylococcus spp. started the exponential phase sooner, had faster growth rates and higher final OD than *C. jeikeium* when grown in TSB. Using a depleted medium more akin to the natural environment has previously conveyed a more accurate species representation (Janssen et al. 2002; Davis et al. 2005). Once grown in minimal medium the growth curves patterns were much more alike between the three species, with no significance noted between *S. aureus* and *C. jeikeium*. Therefore, using growth medium designed for optimum growth kinetics would not be representative of the harsh conditions that organisms face while living on skin, it could also give faster growing organisms an advantage when grown in a culture of multiple species. While using a minimal medium can 'level the playing field'.

# 2.16 Nutrient Rich Media can Provide both Metabolic Advantages and Disadvantages

Using a complex nutrient rich medium could provide metabolic advantages to bacteria which would not be present in their natural surroundings. *S. aureus*, for example, when grown in Mueller-Hinton broth has enhanced membrane integrity compared to other media. The membrane improvement comes from an increased production of the carotenoid virulence factor, staphyloxanthin (Jaśkiewicz et al. 2017). Free amino acids from the casein digest induce higher production of branched-fatty acids composition and staphyloxanthin levels are also subsequently increased (Sen et al. 2016). The improved membrane integrity gives *S. aureus* better coping mechanisms with both oxidative stress and host immune responses (Clauditz et al. 2006). Mueller-Hinton broth also contains starch, which soaks up toxins produced by bacteria into the surrounding medium (Olsen and Scott 1946). Advantages caused by medium composition could be why there is no clear stationary phase when *S. aureus* is grown with MH (Figure 6) the management of oxidative stress or lack of toxin build up could increase the total yield of the bacteria over time.

The growth of *S. epidermidis*, however, produced a more traditional looking growth curve with MH than *S. aureus*, but still exhibited some non-logarithmic growth before finally plateauing at 20 hours. When *S. epidermidis* has previously been grown with Mueller-Hinton broth, the effect on membrane integrity is the opposite to that of *S. aureus*. Staphyloxanthin is not present in the cell membranes of *S. epidermidis*, so that when branched chain fatty acids are increased, the

membrane becomes more flexible. This decreased membrane integrity made *S. epidermidis* more susceptible to surrounding stresses (Tiwari et al. 2020). This may be why there was an eventual stationary phase, the starch removed the toxins which allowed for longer period of growth, but the decreased membrane integrity did eventually mean that *S. epidermidis* could succumb to other growth stresses.

When grown in TSB, *C. jeikeium* reaches stationary phase in 15 hours, with a poor growth rate and low yield to show for it. *C. jeikeium* does not possess extracellular proteases (Kwaszewska et al. 2014), which would mean that when grown in a peptide rich medium such as TSB (Moss and Speck 1966), *C jeikeium* may not be able to uptake enough of a nitrogen source for successful growth. When grown in MH, *C. jeikeium* started the log phase of growth slightly later than when grown in TSB. However, total yield when grown in MH surpassed that of TSB, and, within 20 hours, a stationary phase was never achieved. Mueller-Hinton broth contains a lot of free amino acids, due to the casein digest. This medium therefore suited *C. jeikeium* better, as the free amino acids were utilised without the extra hydrolysis steps.

#### 2.17 Conclusion

Once the resources of these high nutritional media are used up, competition increases and waste accumulates, the initial surge of logarithmic growth and high cell yield can negatively affect the long-term cell survival (Kram and Finkel 2015). In a normal skin environment, there is some competition, but many of the niche organisms simply reside with each other, some even offering other species vital compounds through their by-products or protection against antimicrobials (Kwaszewska et al. 2014).

Unlike the high nutritional media, the minimal medium only provides small quantities, or the bare minimum of the nutritional compounds needed for bacterial growth. The pH was changed to reflect the acidic conditions found on skin. The complex media are designed to have the optimum pH for most culturable bacteria, while the skin has a mostly acidic pH range. While pH can easily be rectified, the compositions of these media are also designed to provide optimum nutrition for metabolic pathways. The complex media are not without their experimental uses. The fast growth and high yield when all three bacteria were grown in TSB means the medium is useful for quickly setting up bacterial experiments. While the addition of starch in MH allows for unaltered sensitivity testing of antimicrobial compounds. However, a medium with an acidic pH and the addition of nutritional compounds that only provide the bare minimum for survival and not provide a metabolic advantage for faster growing organism, would be more reflective to how species survive on skin.

3 Testing Experimental Conditions to Determine whether Bacterial Skin Species Can Utilise Cosmetic Proteins as a Peptide and Amino Acid Source and if Preserving Measures are Effective Against Them

#### 3.1 Introduction

Hydrolysed proteins are a common ingredient in cosmetics to add moisturising and hydrating qualities to the final formulation (Aguirre-Cruz et al. 2020). Cosmetic proteins are used in formulations at a range of desired active levels. The active level signifies the percentage of organic material in the final product. Formulations with cosmetic proteins can deliver amino acids to the surface which claim to benefit the skin health (Sethi et al. 2016). However, there is little research into how this ingredient group interacts with the microorganisms which live there.

#### 3.2 Uptake of Amino Acids

Most bacteria possess genes which enable production of 20 amino acids used in protein synthesis (Amorim Franco and Blanchard 2017; Price et al. 2018; Sanchez et al. 2018). However, exogenous peptides and amino acids are brought into the cell to be used in further metabolic pathways, and can make up to 50% of the amino nitrogen needed by bacteria (Coffin 1989). Only some genera possess extracellular proteases which can break down large protein molecules (Wistreich and Lechtman 1988), which is why protein digests are often added as a nutritional supplement in media (Robinson and Rettger 1918). Lactose-free skimmed milk media can be used to identify bacteria which possess these extracellular proteases able to break down proteins or large peptides (Morris et al. 2012).

Due to differences in their chemical make-up, there are many different routes by which bacteria assimilate amino acids (Gale 1947). Membrane bound proteins are involved in many of these different methods in moving amino acids across the cell membrane (Alberts et al. 2002). Facilitated diffusion uses channel proteins to bypass the phospholipid membrane. There is no energy required, the amino acids move across into the cell by the electrical potential differences between the outside and inside the cytoplasm (Cooper 2000b). ATP-Binding Cassettes (ABCs) are made up of ATP enzymes and membrane bound proteins. The amino acids attach to the outer-membrane, ABCs then use the energy from ATP hydrolysis to alter their shape, which moves the amino acids (Schneider and Hunke 1998). Ion-coupled transport is another way to bring amino acids into the cell. Ions are released from the cell, so the gradient of ions is shifted (Jacquez). Amino acids can enter the cytoplasm as the ions return into the cytoplasm through protein channels (Wilson and Ding 2001). These are mostly hydrogen ions although sodium ions are also commonly used (Heyne et al. 1991).

Individual bacterial species select amino acids to utilise, based on their specific needs (Jiang et al. 2020). These needs include changes in the environment, such as fluctuating salt concentrations (Alreshidi et al. 2019) and surrounding/dissolved gas composition (Sun et al. 2012). There have also been noted differences amino acid usage dependent on whether the bacterial growth is planktonic or sessile (Zhu et al. 2007; Ammons et al. 2014).

#### 3.3 Preservatives

All six cosmetic proteins, manufactured by Croda Europe Ltd., were liquid and therefore had preservatives added to stop microbial spoilage. These preservative measures are found in the product description found on the Croda Europe Ltd. personal care website (Croda 2022). While these preservatives would be diluted in the final formulation, their presence could influence the microbiota that reside on the skin (Pinto et al. 2021). A lot of what would be classed as formulation contaminants, also happen to be species of bacteria found on skin (Flores et al. 1997), so cosmetic preservatives are knowingly effective against them (Campana et al. 2006). Recent research has shown that while these common preservatives are effective against skin species *in vitro*, *in vivo* this is less so (Murphy et al. 2021).

#### 3.4 Studying Growth Kinetics When Switching Nutritional Sources

To examine whether bacteria utilise certain compounds in a media, previous work had switched out the source of nutrition with the test compounds (Fallah et al. 2015; Liu et al. 2020b). Experiments have also used a minimal media with only the bare minimum growth requirements so as not to introduce exogenous interference (Collins and Thune 1996) and to not favour the faster growing organisms. Analysis of growth kinetics have been used to investigate and compare microbial utilisation of various compounds (Meletiadis et al. 2001).

#### 3.5 Biofilms

Many bacteria can have a different form of growth than planktonic; biofilm formations are a type of growth which are especially prevalent in hospital settings (Dincer et al. 2020). While biofilms do not occur on healthy skin, many of the bacteria which reside there are opportunistic pathogens and under the correct circumstances could form one. A simple cut would cause a break in the skin barrier, which could allow opportunistic bacteria to enter and form a biofilm (Percival et al. 2014). A biofilm is a collection of microbials cells, from one or more species, which significantly adhere to a surface (Brandwein et al. 2016). These cells are surrounded by extracellular polymeric substances, which make it difficult to remove either physically or chemically (Donlan 2002; Sharma et al. 2019). Therefore, supplying bacteria with enough nutrition or suitable conditions to be able to create a biofilm could be detrimental for the health of the skin. While no sure links have been found between skin conditions and biofilm formation of skin microbiota, biofilms have long been associated with antibiotic resistant and deadly diseases (Vaishnavi et al. 2019).

#### 3.6 Null Hypothesis

Cosmetic proteins do no provide sufficient nutrition to aid or support bacterial growth of any kind.

#### 3.7 Aims

- To undertake experiments as to whether cosmetic proteins can deliver nutrition to skin bacteria for a) successful growth b) biofilm formation
- To investigate whether the addition of preservatives could have a detrimental effect on skin microbiota

#### 3.8 Materials

#### 3.9 Bacteria

The three bacterial species used were as described in Section 2.6.

#### 3.10 Cosmetic Proteins

The cosmetic proteins were all produced by Croda Europe Ltd., Hydrolysis of the proteins were carried out either by blended acid/alkali or enzymatically. The proteins were all sent at various active levels. All were diluted to 10% active in deionised water and measured to ensure that the pH was 5  $\pm$  0.2. Preservative content can be viewed in Table 6 and the amino acid content of the proteins in Table 7

#### 3.11 Media

The media used were TSB for overnight cultures, pH adjusted Mueller-Hinton broth for MIC and pH adjusted minimal media described in Section 2.9. Both Mueller-Hinton broth and the minimal medium were adjusted to pH 5 using 1 M HCl solution.

#### 3.12 Methods

#### 3.13 Calculating Minimum Inhibitory Concentration

The three bacteria were grown overnight in tryptone soy broth in conditions as stated in Section 2.9 and diluted to OD 1. The bacteria were centrifuged at 4000 g for 10 minutes, and the media removed. The bacterial pellet was resuspended in 2 x Mueller Hinton broth and diluted further to approximately  $1 \times 10^5$  cfu/ml. The preservative combinations (Table 6) were made up to their stated concentrations in pH 5 dH<sub>2</sub>O. These were diluted further in pH 5 dH<sub>2</sub>O to the concentration at which would be found if the protein was used at 8% active. 200 µl of this '8%' preservative mix were added to three wells on the first line of a 96-Well microplate (Nunc, Denmark) and 100 µl of pH 5 dH<sub>2</sub>O was added to the wells proceeding these. 100 µl of the preservatives from the first line were then added to the 100 µl of dH<sub>2</sub>O of the second. 100 µl of this mixture was added to the 100 µl of dH<sub>2</sub>O below and continued until the sixth row when after mixing 100 µl was discarded to keep consistent volumes. The seventh row was kept as 100 µl of dH<sub>2</sub>O. 100 µl of bacterial suspension was added to all the wells apart from the empty eighth row and media controls. The preservative concentrations were at the active levels as seen in Figure 8. To ensure that stationary phase was achieved, a growth curve of each bacterium in Mueller-Hinton broth at pH 5 was also performed (data not shown).

#### 3.14 Lactose-free Skimmed Milk Agar Protease Test

Lactose-free-skimmed milk (LFSM) agar was prepared as according to (Morris et al. 2012). The three species were grown overnight in tryptone soy broth as in Section 2.10. The bacteria were serial diluted in 1xPBS. Each dilution was spread onto the LFSM agar using the spread-plating method (Sanders 2012). The plates were incubated overnight at 37 °C. Dilution plates with clear, individual colonies were then examined for protease activity zones surrounding the colonies.

#### 3.15 Growth Curve Kinetics Experiment

Minimal media from previous work was used as a way of producing some conditions which reflect the skin environment. However, to test whether bacteria can utilise the cosmetic proteins, the casamino acid growth supplement was removed from the recipe. Instead, the media was supplemented with the cosmetic protein at active levels in which they may be used in the final formulation 0, 0.125, 0.25, 0.5, 0.75, 1 and 2%.

Bacteria were grown into single colonies on TSA. A single colony was removed and place into 4 ml of TSB, which were then grown for 18 hours at 37 °C on a shaker. The optical density (OD) was measured at 600 nm and the cell suspensions were diluted 1x10<sup>5</sup> cfu/ml in minimal media containing the cosmetic protein. 100 µl was plated into a MicroWell<sup>™</sup> 96-Well Microplate well plate (Nunc, Denmark) and placed into the 200 PRO multimode reader platform (Tecan, USA). For the programme specifications, the temperature was set to 37 °C and absorbance was read at 600 nm every 30 minutes, over 21 hours.

#### 3.16 Counting the CFU/ml of The Growth Curves

After incubation for the growth curve data, the cells were diluted and plated onto tryptone soy agar plates and counted using the Miles and Misra method (Miles et al. 1938). If no growth was recorded on the plate reader, the number of colonies would determine as to whether the addition of the cosmetic proteins was bacteriostatic or bactericidal. The use of a neutraliser was decided as unnecessary, as the concentration of preservatives were already low and would be further diluted using this method.

#### 3.17 Biofilm Formations

Bacteria were grown overnight, as stated above, and diluted to 1x10<sup>5</sup> cfu/ml in minimal media. The media was supplemented with the cosmetic protein at active levels in which they may be used in the final formulation 0, 0.125, 0.25, 0.5, 1, 2% and 4%. 200 µl of bacteria and supplemented minimal media were placed into a flat bottom MicroWell<sup>™</sup> 96-Well Microplate well plate (Nunc, Denmark). Flat bottom plates were chosen due to the non-motile nature of the three organisms (O'Toole 2011). The method chosen to quantify biofilm formation was the crystal violet staining method, which measures the bacterial cells and extracellular matrix which forms the biofilm as a whole (Welch et al. 2012). These plates were placed into a 37 °C incubator for 24 hours. The biofilms were stained and quantified using the protocol stated by O'Toole (2011). This involved quickly expelling out the cells from the plate and submerging in dH<sub>2</sub>O twice, before adding 125  $\mu$ l of 0.1% w/v crystal violet to each well and incubating at room temperature. After staining the wells were then submerged in dH<sub>2</sub>O again and dried overnight. The following day 125  $\mu$ l of 30% v/v acetic acid was added to the wells to remove the adhered crystal violet, incubated, and transferred to a clean 96 well plate. Measurements were carried out using the 200 PRO multimode reader platform (Tecan, USA) at 550 nm. This process was previously completed using TSB and MH as the media source to confirm that the three species were able to produce biofilms.

#### 3.18 Statistics

All statistics were analysed using GraphPad Prism (Version 9.1.2). Growth curves were illustrated, and kinetics analysed using GraphPad Prism (Version 9.1.2). Comparisons between a group of growth curves were analysed using One-way ANOVA, while comparisons between individual growth curves were analysed using a t-test. Total yield (total OD) was calculated using descriptive statistics of the curve. Growth rate was calculated using non-linear regression fit of the curve analysis. Lag and log phase time were taken from observations straight from the growth curves, as there were no analysis options for these. Both Biofilm and MIC values were both comparison of mean values and were also analysed using t-tests.

Cosmetic Protein	Active Level Supplied	Preservatives	Source	Hydrolysis Method	Molecular Weight (Da)
Crosilk Lpc	12.7	0.5% w/w sodium benzoate + w/w 0.01% disodium EDTA	Silk Noils	Acid/Alkaline	200
Hydroavena HPO	22.4	0.5% w/w sodium Oat Enzymatic benzoate + w/w 0.3% potassium sorbate		1000	
Hydrolactin Liquid PE	18.3	1% w/w phenoxyethanol + w/w 0.2% disodium EDTA	Milk - Casein	Enzymatic	1800
Hydrosativum P	20.3	1% w/w phenoxyethanol + w/w 0.3% potassium sorbate	Реа	Enzymatic	1500
Hydrosolanum PE	20.8	1% w/w phenoxyethanol + 0.3% w/w potassium sorbate + 0.2% w/w disodium EDTA	Potato	Enzymatic	750
Prolevium	21.3	1% w/w phenoxyethanol + 0.3% w/w potassium sorbate + 0.2% w/w disodium EDTA	Cottonseed	Enzymatic	800

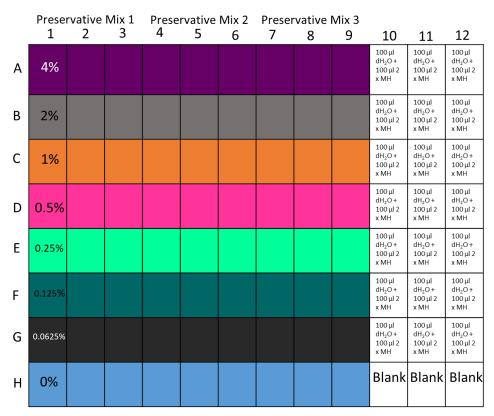
### Table 6. Table of Information Regarding the Cosmetic Proteins.

w/w %	Crosilk Liquid Protein Complex (LPC)	Hydroavena HPO	Hydrolactin Liquid PE	Hydrosativum P	Hydrosolanum PE	Prolevium
Alanine	28.4	5.1	2.9	4.74	5.0	4.1
Arginine	1.5	5.3	3.6	8.36	5.2	12.2
Aspartic Acid	4.7	7.4	6.5	12.37	12.1	10.3
Cys <sup>7</sup>	0.1	2.5	0.4	1.75	0.6	1.2
Glutamic Acid	4.1	25.8	20.5	18.82	13.6	22.7
Glycine	34.7	5.3	1.8	3.92	4.3	4.2
Histidine	0.8	2.4	2.7	2.88	2.7	5.0
Isoleucine	0.8	3.5	5.8	4.2	4.3	3.1
Leucine	1.2	7.8	8.8	7.91	9.6	5.9
Lysine	1.4	4.4	7	8.52	7.7	4.0
Methionine	0.2	2	2.7	0.98	2.2	1.4
Phenylalanine	0.9	5.4	4.7	3.72	4.7	5.5
Proline	1.2	6.6	10.4	4.31	5.4	3.7
Serine	15.4	6	5.9	6.18	6.1	5.4
Threonine	1.9	4.1	3.8	4.14	6.1	4.0
Tyrosine	0.6	1.2	5.1	2.41	4.9	2.9
Valine <sup>8</sup>	2	5.4	6.5	4.8	5.5	4.5

#### Table 7. Amino Acid Content of the Cosmetic Proteins

<sup>&</sup>lt;sup>7</sup> May be in form of cystine, cysteine, cysteic acid or lanthionine

<sup>&</sup>lt;sup>8</sup> Tryptophan content was only available for Hydrolactin Liquid PE- found at 1.2%. It is likely that similar tryptophan levels would be found in the enzymatically digested proteins but not found in the acid hydrolysed proteins

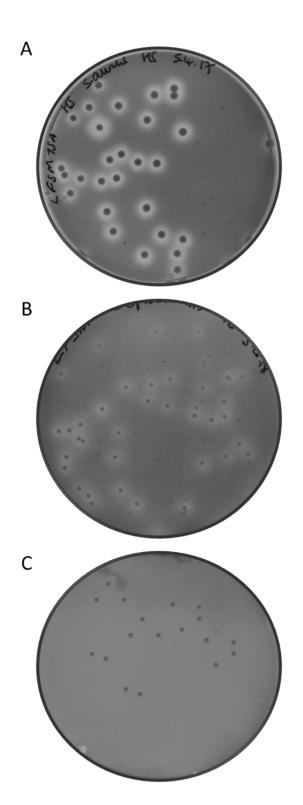


**Figure 8**. Layout of MIC plate and Preservative Concentrations as Found at Active Levels. Each row was a dilution of 1 in 2 dilution of the previous row, except for the last row which was minimal medium alone.

#### 3.19 Results

### 3.20 Using Lactose Free Skimmed-Milk Agar to Assess Whether the Bacteria Possess Extracellular Proteases

Both *Staphylococcus* spp. produced hydrolysed clearing zones and therefore tested positive for extracellular proteases. While colonies of *C. jeikeium* grew on the agar, no zones of clearing were observed and therefore do not possess extracellular proteases. See Figure 9 below.



### Figure 9. Extracellular Protease Production from The Three Skin Bacteria. A)

Staphylococcus aureus B) Staphylococcus epidermidis C) Corynebacterium jeikeium. Both Staphylococcus spp. display a clear zone of clearance around the colonies and therefore possess extracellular proteases. *C. jeikeium* colonies do not have a clear halo and therefore unlikely to possess these extracellular proteases.

### 3.21 Do the Preservatives found in the Proteins reach the Minimum Inhibitory Concentration or Limit Bacterial Growth?

To be classed as the minimum inhibitory concentration, 80% of total growth yield must be inhibited by addition of the preservative or preservative combination (Rushton et al. 2013). Both *Staphylococcus* spp. grew to their stationary phase within 24 hours as confirmed by the in-unison growth curves. The stationary phase was not achieved by *C. jeikeium* therefore the MIC could not be estimated. It was decided not to carry on the experiment for more than 24 hours as the proteins would be unlikely to be in contact for longer than that period on the skin. All results from this Section refer to the MIC values found in Figure 10, Figure 11 and Figure 12. All inhibition values and statistical data can be found in Table 16, A, B and C, in the Appendix, in Section 10.1.

# 3.21.1 Do the Preservatives found in Crosilk Lpc inhibit Visible Growth of Three Common Skin Bacteria?

At the active level in which the protein is originally sold (Section 3, Table 6), Crosilk Lpc was preserved with 0.5% sodium benzoate and 0.01% disodium EDTA. S. aureus (Figure 10) was, on average, inhibited 99.7% when grown with 4% active level of Crosilk Lpc and 90.3% inhibited when grown with 2%, however at 1% active level, inhibition was at 43.5%, therefore the MIC would be between 1.8-2% active. Below 1% active level, Crosilk Lpc preservatives inhibited between 15.2 and 2.07% dependent on active level. Similar results were observed with S. epidermidis (Figure 11), at 4% active level, the Crosilk Lpc inhibited the growth of S. epidermidis 100%, while at 2% the bacteria were inhibited 97.6%. At 1% active level, S. epidermidis was only inhibited by 46.3%, which puts the MIC likely between 1.7%-2% active level. C. jeikeium (Figure 12) was only inhibited by more than 80% when grown with 4% active level, Crosilk, at 2% or below it was inhibited between 41.4-2.28%. However, Crosilk significantly inhibited more C. jeikeium growth than S. epidermidis at, 0.5% (P=0.0214), 0.25% (P=0.0054) and 0.125% (P=0.0024) active level. When grown with 0.5% and 0.25% active level of Crosilk Lpc, C. jeikeium was significantly more inhibited than S. aureus (P<0.05). While S. epidermidis was significantly more inhibited by Crosilk at 2% than S. aureus was (P<0.001), at 0.5%, 0.125% and 0.0625% it was vice versa (P<0.05).

# 3.21.2 Do the Preservatives found in Hydroavena HPO inhibit Visible Growth of Three Common Skin Bacteria?

At the active level supplied, Hydroavena HPO was preserved with 0.5% sodium benzoate and 0.3% potassium sorbate. *S. aureus* (Figure 10) growth was inhibited by 93.2% when grown with 4% active level of Hydroavena HPO preservatives, but only 59.4% when grown with 2%. The MIC of Hydroavena preservatives on *S. aureus* would be upwards of 3.2% active level. At 1% active level and below, *S. aureus* was inhibited between 20.2-4.29%. Hydroavena preservatives inhibited

98.3% of *S. epidermidis* (Figure 11) when grown with 4% of the protein, while just 62.9% was inhibited at 2%. Therefore, the MIC was between 3-4% active level. At 1% and below, inhibition ranged from 16.9 to 1.03%. *C. jeikeium* (Figure 12) was inhibited by 87.4% when grown with 4% Hydroavena preservatives, and just 46.4% when grown with 2%. However, even at the lower active levels, most inhibited *C. jeikeium* growth more than either *Staphylococcus* spp.. From 0.0625-1% active levels, Hydroavena preservatives significantly inhibited *C. jeikeium* more than *S. epidermidis* (P<0.0007) and *S. aureus* (between P<0.0001 and P=0.01520). At 4% and 2% active levels, Hydroavena preservatives inhibited significantly more of *S. epidermidis*' growth than *S. aureus* (P<0.0471), but at 1% and below this was reversed (P<0.0103).

# 3.21.3 Do the Preservatives found in Hydrolactin Liquid PE inhibit Visible Growth of Three Common Skin Bacteria?

Hydrolactin Liquid PE is preserved with 1% phenoxyethanol and 0.2% disodium EDTA at the active level sold. The 80% inhibition for the MIC was not met against *S. aureus* (Figure 10). Hydrolactin preservatives inhibited *S. aureus* by 70.5% with the equivalent found at 4% active level. At 2% active level and below, the preservatives inhibit *S. aureus* between 0.0-19.3%. Hydrolactin preservatives inhibited *S. epidermidis* (Figure 11) by 97.7% with the 4% active level and 42.4% with the 2% active level. The MIC of the Hydrolactin preservatives would be around the 2.6% active level mark. At 4% and 2% active levels, the Hydrolactin preservatives only inhibited *C. jeikeium* (Figure 12) by 67.3% and 48.3% respectively. However, between 1% and 0.125%, the inhibition of *C. jeikeium* was significantly more than either *S. epidermidis* (P<0.0016) or *S. aureus* (P<0.001). Apart from a slight significant difference at 2% when *S. aureus* is more inhibited than *S. epidermidis* (P=0.0152), there is no significant difference between the two staphylococcal species at any other active level (P>0.05).

# 3.21.4 Do the Preservatives found in Hydrosativum P inhibit Visible Growth of Three Common Skin Bacteria?

Hydrosativum P is preserved with 1% phenoxyethanol and 0.3% potassium sorbate at the active level sold. The minimum inhibitory concentration was never reached for any of the species, both *Staphylococcus* spp. were only inhibited at 18.6% and 21.6% at what would be the highest dose (Figure 10, Figure 11). While there are some overlaps of inhibition percentages at different active levels, they all follow the expected trend. Similar high standard deviations were noted with *C. jeikeium* (Figure 12) but there was significantly greater inhibition between 4% and 0.5% than the other two species (P<0.0365).

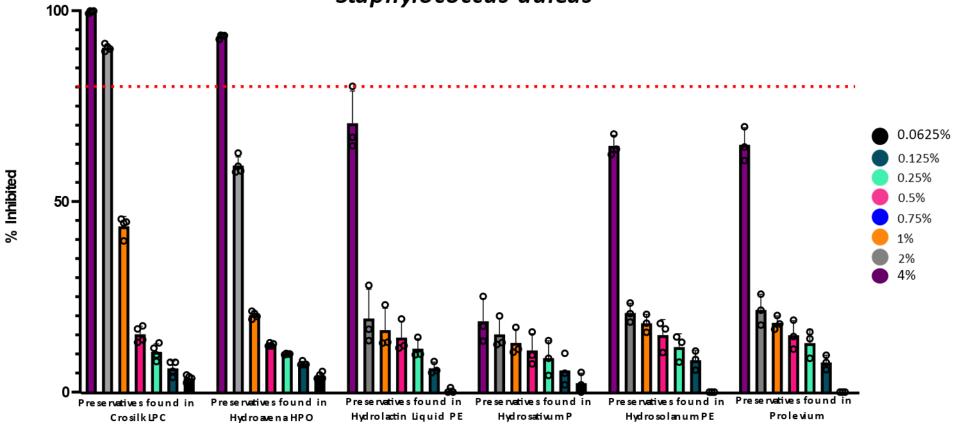
# 3.21.5 Do the Preservatives found in Hydrosolanum PE inhibit Visible Growth of Three Common Skin Bacteria?

Hydrosolanum PE is preserved with 1% phenoxyethanol, 0.3% potassium sorbate and 0.2% disodium EDTA at the active level sold. The minimum inhibitory concentration was not reach

when *S. aureus* (Figure 10) was exposed to the preservatives. Between 0.0625% and 4% active levels, *S. aureus* was inhibited by between 0-64.6%. With *S. epidermidis* (Figure 11), the Hydrosolanum preservatives inhibited 94.7% of growth at 4% active level and 44.7% at 2% active level. These results would suggest that the MIC of this preservative set would be upwards of 2.68% against *S. epidermidis*. At these higher preservative concentrations, *S. aureus* is significantly less inhibited than *S. epidermidis* when grown with the preservatives found in Hydrosolanum PE (P<0.0028). Again, while the MIC cannot be determined when grown with *C. jeikeium* (Figure 12), the lower preservative concentrations still inhibited significantly more growth than both *Staphylococcus* spp. (P<0.0221).

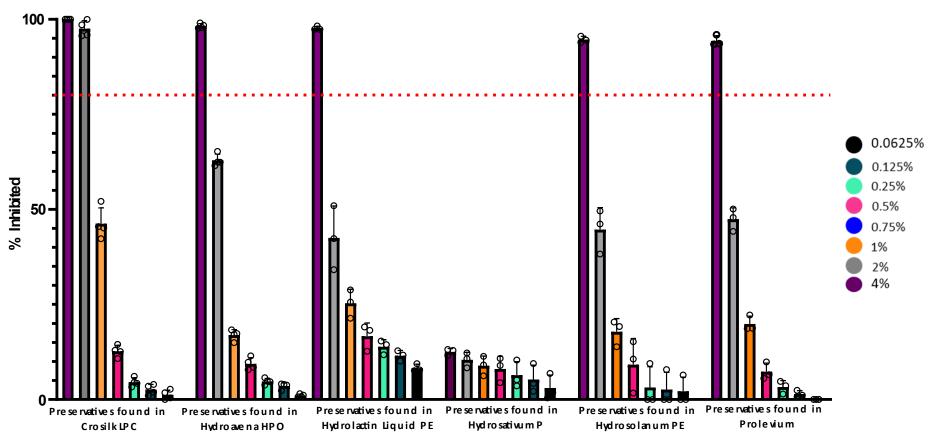
### 3.21.6 Do the Preservatives found in Prolevium inhibit Visible Growth of Three Common Skin Bacteria?

Prolevium was preserved with 1% phenoxyethanol, 0.3% potassium sorbate and 0.2% disodium EDTA at its sold active level. Again, the MIC was not reached for *S. aureus* (Figure 10), with the preservatives at 4% active level only inhibiting on average 64.9% of growth. Between 0.0625% and 2% active level, *S. aureus* was inhibited 0-21.6%. The growth of *S. epidermidis* however was inhibited 94.3% by the presence of the Prolevium preservatives at 4% active level. As the preservatives at 2% active level inhibited *S. epidermidis* by 47.4%, the MIC would be around 2.68% and above. At 0.5% and below, the susceptibility shifts, and more of *S. aureus* growth is significantly inhibited than *S. epidermidis* (Figure 11). For example, at 0.5% active level, *S. aureus* is inhibited, on average, twice as much and significantly more than *S. epidermidis* (P=0.0411). At the higher active levels, the preservatives do not inhibit *C. jeikeium* (Figure 12) to the extent of the other two species, but as with the other preservative measures, at the lower active levels, the preservatives inhibit *C. jeikeium* significantly more than both *Staphylococcus* spp. Inhibition was most significant at 0.125% active level where *C. jeikeium* was inhibited by 13.3% compared to *S. aureus* at 7.8% and *S. epidermidis* at 1.43% (P<0.02).



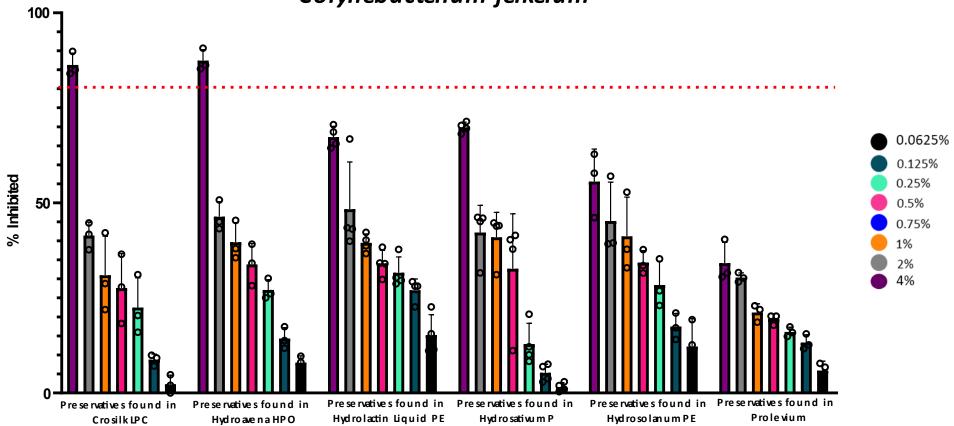
Staphylococcus aureus

**Figure 10. Inhibition of** *Staphylococcus aureus* by Preservatives found in Cosmetic Proteins. The experiment was repeated with three technical and biological replicates. The results seen in this Figure are discussed in Section 3.21. The red dotted line indicates the 80% inhibition threshold for the minimum inhibitory concentration. Only two preservative combinations met the inhibition percentage to be classed as the MIC.



Staphylococcus epidermidis

**Figure 11.** Inhibition of *Staphylococcus epidermidis* by Preservatives found in Cosmetic Proteins. The experiment was repeated with three technical and biological replicates. The results seen in this Figure are discussed in Section 3.21. The red dotted line indicates the 80% inhibition threshold for the minimum inhibitory concentration. Five preservative combinations met the percentage threshold to be classed as the MIC.



Corynebacterium jeikeium

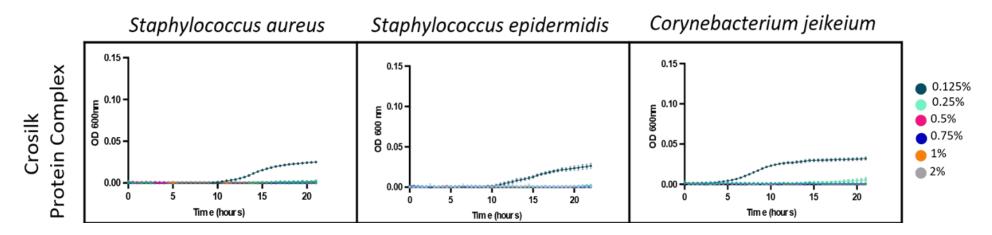
**Figure 12.** Inhibition of *Corynebacterium jeikeium* by Preservatives found in Cosmetic Proteins. The experiment was repeated with three technical and biological replicates. The results seen in this Figure are discussed in Section 3.21. The red dotted line indicates the 80% inhibition threshold for the minimum inhibitory concentration. Only two preservative combinations met the inhibition percentage to be classed as the MIC.

# 3.22 Using Growth Curves to Determine Whether Cosmetic Proteins Can Supplement Bacterial Growth

At 0% active level, which was minimal medium without a protein supplement, no growth was recorded for all three bacterial species.

### 3.22.1 Growth Curves of Three Skin Bacteria Supplemented with Crosilk Lpc

All results from this Section are referring to graphs in Figure 13. When grown with Crosilk, a classic growth curve was only observed at 0.125% active level for all three species. A slight growth with 0.25% active level was started by *C. jeikeium* at approximately 18 hours, but not enough to conduct statistical analysis. The exponential start time for both *Staphylococcus* spp. began at 10.5 hours, while the exponential phase for *C. jeikeium* started 6 hours earlier at 4.5 hours. At 0.125%, *S. aureus* had an exponential growth rate of 0.34 OD/hour, while *S. epidermidis* had a slightly slower rate of 0.31 OD/hour, with the slowest growth rate being *C. jeikeium* at 0.16 OD/hour. Total yield for both *S. aureus* and *S. epidermidis* was an of OD 0.026, but *C. jeikeium* had the highest yield with an OD reading of 0.032. There was no significant difference between the two *Staphylococcus* spp. growth curves at 0.125% active level (P=0.92), but both *S. aureus* and *S. epidermidis* had significantly different growth curve patterns than *C. jeikeium* (P<0.0001).



**Figure 13. Growth Curves of Three Skin Bacteria Supplemented with Crosilk Lpc.** The experiment was performed as three technical replicates and three biological replicates. Results were discussed in Section 3.22.1. A traditional growth curve was observed when all three species were supplemented with 0.125% active level of Crosilk LPC. Neither *Staphylococcus* spp. grew with any other active level supplemented and only a small growth was beginning to be observed when *C. jeikeium* grew with 0.25% Crosilk LPC. There was no significant difference between the growth curve pattern of the *Staphylococcus* spp. (P=0.96), but they were both significantly different to the *C. jeikeium* growth curve with 0.125% Crosilk (P<0.05).

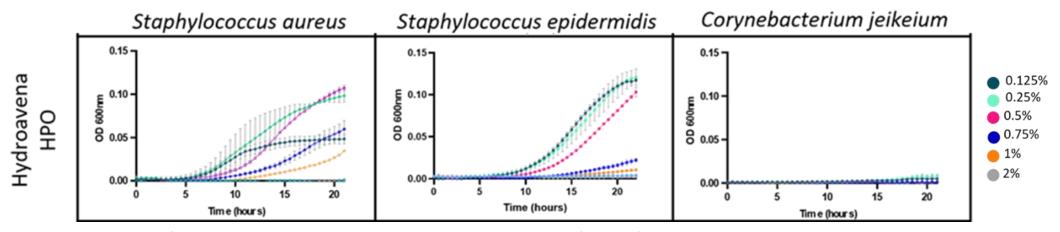
#### 3.22.2 Growth Curves of Three Skin Bacteria Supplemented with Hydroavena HPO

All results from this Section are referring to graphs in Figure 14. Growth Curves of Three Skin

Bacteria Supplemented with Hydroavena HPO. Figure 14. The addition of Hydroavena HPO to the minimal medium provided different growth curve patterns for all three species. Both Staphylococcus spp. grew with 1% active level Hydroavena HPO, while no growth at any active level was observed of C. jeikeium until around 19 hours when the start of some growth at 0.125% and 0.25% active level were observed. The log phase of the 0.125% and 0.25% growth curves started 5.5 hours, for 0.5% and 0.75% the lag phase started at 8 hours, while 1% active level the exponential phase started at 10.5 hours. No growth as observed at 2% active level. The growth rate of *S. aureus* when grown with 0.125% was 0.19 OD/hour, 0.25% was slightly faster at 0.24 OD/hour, at 0.5% the growth rate was 0.32 OD/hour, at 0.75% was 0.38 OD/hour and at 1% active level the growth rate was 0.45 OD/hour. The total OD yield reached for S. aureus when grown with 0.125% active level was 0.048, when grown with 0.25% active level was 0.099, 0.5% total yield was 0.110, 0.75% total yield was 0.063 and at 1% active level, the total OD for yield was 0.037. There were no significant differences between the growth of S. aureus with 0.125% and 0.5% Hydroavena HPO (P=0.42). There were also no significant differences between the growth curves produced by S. aureus at 0.25% active level and 0.5% active level (P>0.05). However, there were significant differences of the growth of S. aureus between all other active levels (P<0.04). The lag phase of *S. epidermidis* started at 7.5 hours with both 0.125% and 0.25% active levels, 8.5 hours with 0.5% active level, 14 hours with 0.75% and there was a slight growth starting at 17.5 hours with 1%. Again, no growth was observed with 2% active level Hydroavena HPO. The growth rate for S. epidermidis when grown with 0.125% active level Hydroavena HPO was 0.31 OD/hour, 0.32 OD/hour with 0.25%, 0.39 OD/hour with 0.5%, 0.38 OD/hour with 0.75% and 0.22 OD/hour with 1% active level Hydroavena HPO. The total OD yield reached by *S. epidermidis* varied when grown at each different active level, with 0.125% it reached 0.118, at 0.25% the bacteria reached 0.119, at 0.5% the total yield was 0.103, at 0.75% the yield was 0.022 and at 1% the total yield was 0.011. When grown with 2% Hydroavena HPO, S. epidermidis did not increase significantly past the starting OD (P>0.05). There was no significant difference between the growth curves of S. epidermidis when grown with 0.125%. 0.25% and 0.5% active levels Hydroavena HPO (P>0.10). There was also no significant difference in the growth of *S. epidermidis* when grown with 0.75% and 1% active levels (P=0.104). There was however a statistical difference between the lower active levels (0.125-0.5%) and the upper active levels (0.75%-2%) (P<0.0001). The small growth observed by C. jeikeium at any active level was not enough to statistically analyse. Until grown with 0.75% active level, there was no statistical difference between the growth of S. aureus and S. epidermidis (P>0.145). When grown with 0.75%, 1% and 2% active level Hydroavena, the two species' growth significantly differs (P<0.016). Both S. epidermidis and S. aureus significantly differ

in growth at all active levels compared to

*C. jeikeium* (P<0.001).

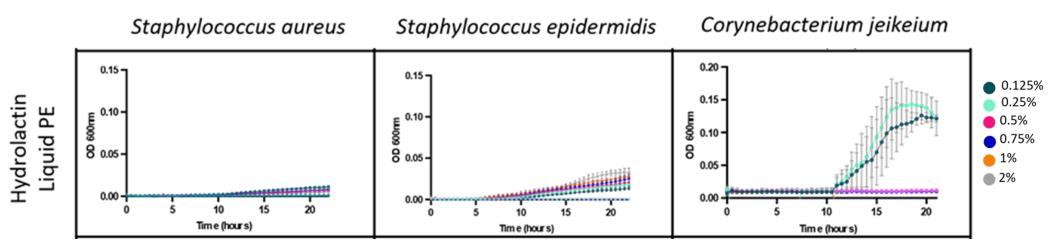


**Figure 14. Growth Curves of Three Skin Bacteria Supplemented with Hydroavena HPO.** Results from this figure were discussed in Section 3.22.2. The experiment was performed as three technical replicates and three biological replicates. Both *Staphylococcus* species grew with the greatest number of active levels of Hydroavena HPO, while there was barely any growth recorded of *C. jeikeium* with any of the active levels. There was no significant difference between growth curves of *S. aureus* when grown with 0.125% and 0.5%, as well as 0.25% and 0.5% Hydroavena HPO (P>0.05). There was no significant difference between the growth curves of *S. epidermidis* when grown with 0.125%. 0.25% and 0.5% active levels Hydroavena HPO (P>0.10).

3.22.3 Growth Curves of Three Skin Bacteria Supplemented with Hydrolactin Liquid PE All results from this Section are referring to graphs in Figure 15. *Staphylococcus aureus* did not achieve a high yield with the addition of Hydrolactin Liquid PE, while there was growth at all active levels the total yield was low. The log phase of growth of S. aureus started at the same time for all active levels, at 9.5 hours. If allowed to grow exponentially, the growth rate gradually declined as the active levels increased starting at 0.27 OD/hour when grown with 0.125% active level Hydrolactin, 0.26 OD/hour when grown with 0.25%, 0.24 OD/hour with 0.5%. 0.23 OD/hour with 0.75%, 0.21 OD/hour with 1% and 0.19 OD/hour when grown with 2% active level Hydrolactin Liquid PE. The total yield for S. aureus when grown with Hydrolactin also decreased as the active levels increased. The total OD yield when S. aureus was grown with 0.25% was 0.012, 0.011 with 0.25%, 0.008 with 0.5, 0.75% and 1% and 0.005 when grown with 2% Hydrolactin Liquid PE. Each growth curve is not statistically different from the previous growth curve, so growth at 2% active level is not statistically different from growth at 1%, which in turn is not significantly different from growth at 0.5% and so on (P>0.05). There is also no statistical difference between all the growth curves of S. aureus when grown with Hydrolactin Liquid PE between 0.125-1% active level. The only outlier is at 2% which is significantly different to 0.75% active level and below (P<0.0193). While total yield again was poor when S. epidermidis was grown with Hydrolactin Liquid PE, S. epidermidis grew at every active level. The start of the log phase for S. epidermidis when grown with 0.125% active level Hydrolactin started at 9 hours, with 0.25% exponential growth started at 8.5 hours, while when grown with both 0.5% and 0.75% the log phase started at 6.5 hours. S. epidermidis went into the log phase of growth at 5.5 hours when grown with 1% and 2% active level. Unlike previous proteins, the growth rate of S. epidermidis quickens as the active levels increase, starting at 0.256 OD/hour with 0.125% active level and ending up at 0.286 OD/hour with 2%. The total OD yield also increased as the active levels increased, at 0.125% the total OD yield was 0.013, which more than doubled when grown with 2% active level which was 0.033. Again, no growth curve was significantly different from the growth curve directly before it (P>0.05). There was a significant difference between growth at 2% and 0.5%, 0. 25% and 0.125% (P<0.05), as well as at 1% and 0.25% and 0.125% (P<0.0105), 0.75% and 0.125% (P=0.0036).

*C. jeikeium* achieved the highest total yield compared to the *Staphylococcus* spp. when grown with Hydrolactin Liquid PE. However, growth was only recorded with 0.125% and 0.25%. The log phase of growth for *C. jeikeium* when growth with both 0.125% and 0.25% Hydrolactin Liquid PE started at 10.5 hours. The growth rate of *C. jeikeium* when grown with 0.125% was 0.24 OD/hour, while growth at 0.25% was slightly slower at 0.20 OD/hour. The total yield for growth at 0.125% was an OD of 0.126 and slightly higher with 0.25% at an OD reading of 0.143. However, there was no statistical difference between the overall growth of *C. jeikeium* when grown with 0.125% or

0.25% active levels of Hydrolactin Liquid PE. Where growth was recorded all other growth curves between all three species were significantly different (P<0.05), except when both *Staphylococcus* species were grown with 0.125% active level there was no significant (P=0.52) differences between the growth patterns.



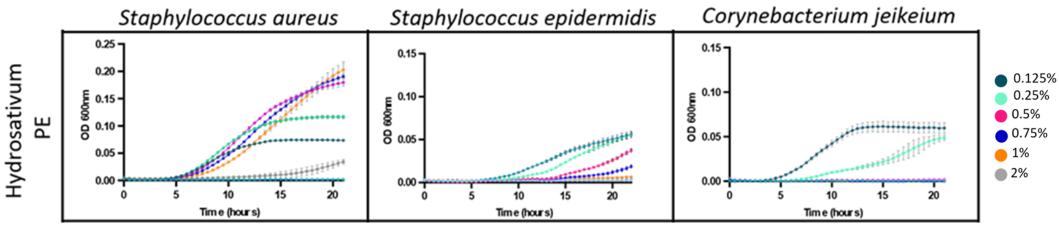
**Figure 15. Growth Curves of Three Skin Bacteria Supplemented with Hydrolactin Liquid PE.** The experiment was performed as three technical replicates and three biological replicates. The results from the figure above were discussed in Section 3.22.3. *S. aureus* did not grow well with Hydrolactin Liquid PE, and while *S. epidermidis* grew at every active level, the total yield was low. The highest yield with Hydrolactin was with *C. jeikeium*, however growth was only seen with 0.125% and 0.25% active. Each growth curve of *S. aureus* was not statistically different from the previous growth curve, so growth at 2% active level is not statistically different from growth at 1%, which in turn is not significantly different from growth at 0.5% and so on (P>0.05). Again, for *S. epidermidis*, no growth curve was significantly different from the growth curve directly before it (P>0.05). There was no statistical difference between the growth curves of *C. jeikeium* when grown with 0.125% or 0.25% active levels of Hydrolactin Liquid PE (P>0.05).

#### 3.22.4 Growth Curves of Three Skin Bacteria Supplemented with Hydrosativum P

All results from this Section are referring to graphs in Figure 16. S. aureus grew well with the addition of various levels of Hydrosativum P, growth was observed even with 2% active level. The log phase of growth started at 5 hours when S. aureus was grown with 0.125%, 0.25%, 0.5%, 0.75% and 1% active levels of Hydrosativum P. When grown with 2% active level, S. aureus started the log phase of growth at 13 hours. The exponential growth rate of S. aureus, when grown with Hydrosativum P, increased as the active levels increased, starting at 0.17 OD/hour with 0.125% active level, 0.19 OD/hour with 0.25%, 0.24 OD/hour with 0.5%, 0.27 OD/hour with 0.75%, 0.31 OD/hour with 1% and 0.33 OD/hour with 2% active level. The total yield also increased as the active levels increased, excepting with 2% where growth had only begun when the experiment ended. With 0.125% active level, *S. aureus* had a total OD yield of 0.074, 0.117 with 0.25% active level, 0.180 with 0.5%, 0.190 with 0.75% and 0.203 with 1% active level. At the end of the experiment, although growth had started, S. aureus had only reached an OD of 0.345 with 2% active level Hydrosativum P. There was no significant difference between the growth curves of S. aureus with 0.25%, 0.5%. 0.75% and 1% active level Hydrosativum P (P>0.231). Growth with both 0.125% and 2% created the outliers and S. aureus grew significantly different with both active levels (P<0.038) compared to each other and all other active levels.

S. epidermidis grew with the addition of Hydrosativum P, however, growth started very late with 0.75% and 1% active level and no growth was seen with 2% active level. The start log phase of S. epidermidis differed, dependent on what active level it was grown with. With 0.125% active level, the log phase of growth started at 7 hours, with 0.25% the log phase started at 9.5 hours, with 0.5% the log started at 14 hours, with 0.75% the log phase started at 16.5 hours, while S. epidermidis did not enter the log phase of growth with either 1% or 2% active levels of the product. The growth rate of S. epidermidis increased as the active level increased to 0.5% before slowing again. With 0.125% active level, S. epidermidis grew exponentially at a rate of 0.25 OD/hour, with 0.25% at 0.32 OD/hour, with 0.5% at 0.41 OD/hour, with 0.75% at 0.31 OD/hour. The total OD yield reached by S. epidermidis when grown with 0.125% active level of Hydrosativum P was 0.56, with 0.25% it was 0.056, with 0.5% was 0.37, with 0.75% was 0.019. Although no log phase was entered, S. epidermidis OD readings increased over time when grown at both 1% and 2% active levels and achieved a low total yield OD reading of 0.007 and 0.004, respectively. There was no significant difference between the growth of S. epidermidis with 0.125% and 0.25%, as well as between 0.75% and 1% active levels (P>0.05). The growth of S. epidermidis was significantly different between all other active levels (P<0.05). Again, growth of *C. jeikeium* was only observed with 0.25% and 0.125% active levels of Hydrosativum P. When grown with 0.125%, C. jeikeium entered a growth phase at 6.5 hours, which slowed before entering another log phase at 14 hours, before beginning to enter a

stationary phase at 21 hours. When grown with 0.125% active level of protein, *C. jeikeium* entered the one and only log phase at 4.5 hours. The growth rate of *C. jeikeium* with 0.125% active level was calculated at 0.17 OD/hour, while with 0.25% 0.33 OD/hour. However, due to the unconventional shape of the growth curve this may be inaccurate. There was a significant difference of growth between *C. jeikeium* with 0.125% and 0.25% active level of Hydrosativum P (P<0.001). All growth curves between all species were significantly different (P<0.05), except between *S. epidermidis* and *C. jeikeium* when both grown with 0.25% active level of Hydrosativum P (P=0.998).



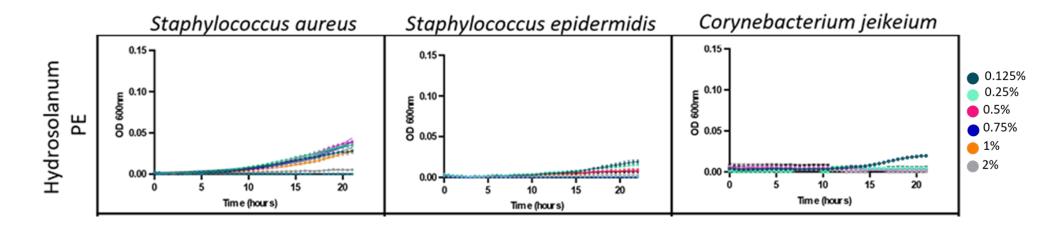
**Figure 16. Growth Curves of Three Skin Bacteria Supplemented with Hydrosativum P.** The experiment was performed as three technical replicates and three biological replicates. The results from the above figure were discussed in Section 3.22.4. *S. aureus* had growth at various active levels with Hydrosativum P, *S. epidermidis* grew but very little growth seen with the higher active levels, growth of *C. jeikeium* was only seen with 0.125% and 0.25% active. There was no significant difference between the growth curves of *S. aureus* with 0.25%, 0.5%. 0.75% and 1% active level Hydrosativum P (P>0.231). There was no significant difference between the growth of *S. epidermidis* with 0.125% and 0.25%, as well as between 0.75% and 1% active levels (P>0.05). There was a significant difference of growth between *C. jeikeium* with 0.125% and 0.25% active level of Hydrosativum P (P<0.001).

#### 3.22.5 Growth Curves of Three Skin Bacteria Supplemented with Hydrosolanum PE

All results from this Section are referring to graphs in **Error! Reference source not found.** When *S* . *aureus* was grown with Hydrosolanum P, there was growth at every active level, except at 2% active level where there was only a slight increase from the starting OD to the end OD. There was, however, a long lag phase of growth and log phase of growth had just started by the time of the last reading. Growth of the *S. aureus* started at 9 hours with 0.125-1% active levels. The growth with 2% active level was so slight it was not possible to calculate a start time. The growth rate of *S. aureus* was calculated at 0.274 OD/hour with 0.125%. 0.279 OD/hour with 0.25%, 0.3202 OD/hour with 0.5%, 0.329 OD/hour with 0.75% and 0.327 OD/hour with 1% active level. Total yield was not reached by *S. aureus* when grown with any active levels as the stationary phase was not attained, however, the final OD were similar across active levels 0.125-1% active level. *S. aureus* total OD of 0.0294 with 0.125%, 0.0382 with 0.25%, 0.0425 with 0.5%, 0.397 with 0.75%, 0.0306 with 1%. When grown with 2%, *S. aureus* reached a low OD of 0.006, which was still an 80% increase from the starting OD. There was no statistical difference between the growth of *S. aureus* with the active levels 0.125-1% (P=0.31). However, growth with 2% active level was significantly different from growth with all other active levels (P<0.001).

A similar pattern was seen when *S. epidermidis* was grown with Hydrosolanum PE. There was a long lag phase, the growth phase of *S. epidermidis* started at 11 hours with all the active levels where clear growth was recorded, 0.125%-1% active level. The growth rate of *S. epidermidis* when grown with 0.125% active level was 0.302 OD/hour, 0.211 OD/ hour with 0.25%, 0.167 OD/ hour with 0.5% and 0.136 OD/hour with 0.75%. *S. epidermidis* grew so gradually with 1% and 2% active level that any exponential growth rate could not be calculated. The final OD reached by *S. epidermidis* when grown with 0.125% active level of Hydrosolanum PE was 0.0192, 0.0151 with 0.25%, 0.009 with 0.5%, 0.007 with 0.75%, 0.008 with 1% and 0.003 with 2% level. There were no significant differences between the growth of *S. epidermidis* when grown with 0.125-0.5% active (P=0.12), or between growth with 0.5%-1% active (P=0.07). Growth with all active levels 0.125-1%, were significantly different from growth with 2% active level (P<0.005).

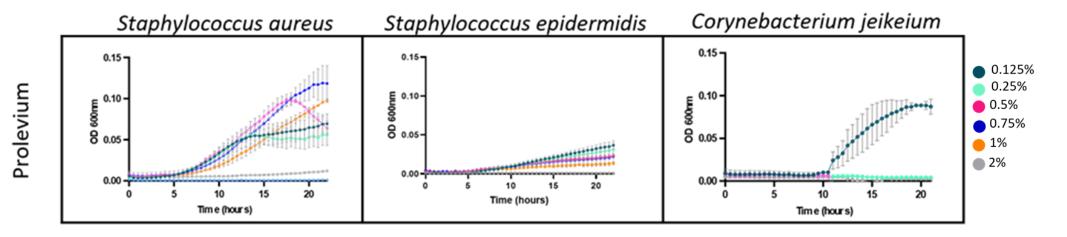
*C. jeikeium* only grew with one active level of Hydrosolanum PE, at 0.125%. Exponential growth of *C. jeikeium* started at 15 hours and appeared to just reach a stationary phase at 21 hours. The growth rate of *C. jeikeium* with 0.125% active level was 0.25 OD/hour and the total yield reach an OD reading of 0.021. There was no significant difference between the growth of *S. aureus* at 0.125% and the growth of *C. jeikeium* at 0.125% (P=0.097) or between *S. epidermidis* and *C. jeikeium* also with 0.125% active level of Hydrosolanum PE (P=0.1051). However, there was a significant difference in growth between *S. aureus* and *S. epidermidis* (P=0.004) with 0.25% active level, as well as a significant difference between the three bacteria at all active levels of Hydrosolanum PE (P>0.05).



**Figure 17. Growth Curves of Three Skin Bacteria Supplemented with Hydrosolanum PE.** The experiment was performed as three technical replicates and three biological replicates. The results from the figure above were discussed in 3.22.5. All three achieved very little yield when supplemented with Hydrosolanum PE, *S. aureus* had the higher total yield and *S. epidermidis* had some growth at the higher active levels, but *C. jeikeium* only grew with 0.125% and the yield was low. There was no statistical difference between the growth of *S. aureus* with the active levels 0.125-1% (P=0.31). There were no significant differences between the growth of *S. epidermidis* or between growth with 0.5%-1% active (P=0.07).

#### 3.22.6 Growth Curves of Three Skin Bacteria Supplemented with Prolevium

All results from this Section are referring to graphs in Figure 18. S. aureus grew with all active levels of Prolevium, although growth was very stagnant with 2% active level of the cosmetic protein. The log phase of growth started at 5.5 hours for S. aureus grown with 0.125-0.75% active level of Prolevium, with 1% active the log phase started at 6.5 hours. As the growth of *S. aureus* with 2% active level was so gradual an exponential growth was never achieved in the 21 hours. The growth rate of S. aureus with 0.125% active level of Prolevium was 0.176 OD/hour, 0.154 OD hour with 0.25%, 0.176 OD/hour with 0.5%, 0.247 OD/hour with 0.75% and 0.261 OD/hour with 1% active level. Due to the growth pattern of *S. aureus* with 2%, an exponential growth rate could not be calculated. With 0.125% active level, S. aureus had a total OD yield of 0.070, 0.0564 with 0.25% active level, 0.0984 with 0.5%, 0.119 with 0.75%, 0.0977 with 1% active level and 0.012 with 2% active level. There was no significant difference between the growth of *S. aureus* when grown with 0.125-1% (P=0.071) but growth with 2% active level was significantly different from growth with the other active levels (P>0.05). When grown with Prolevium, S. epidermidis grew with 0.125-1% active level of the protein. There was no recorded growth with 2% active level of Prolevium. The log phase of growth started at 5 hours with every active level where growth was recorded. The growth rate of S. epidermidis with 0.125% active level of Prolevium was 0.242 OD/hour, 0.221 OD hour with 0.25%, 0.179 OD/hour with 0.5%, 0.170 OD/hour with 0.75% and 0.138 OD/hour with 1% active level. With 0.125% active level, S. epidermidis had a total OD yield of 0.037, 0.031 with 0.25% active level, 0.023 with 0.5%, 0. 134 with 0.75% and 0.001 with 1% active level. There was no significant difference of S. epidermidis growth when grown with 0.125-0.75% Prolevium (P=0.307). There was significant difference in the growth of S. epidermidis with 1% active level compared to growth at all other active levels (P<0.003). When grown with Prolevium, C. jeikeium only grew with 0.125% active level of the protein. The exponential phase started at 10.5 hours and the growth rate was 0.265 OD/hour. The total OD yield of *C. jeikeium* with 0.125% Prolevium was 0.089. Between bacteria, the only non-significant difference in growth was between S. aureus and C. jeikeium with 0.125% active level of Prolevium (P=0.43).



**Figure 18. Growth Curves of Three Skin Bacteria Supplemented with Prolevium.** The experiment was performed as three technical replicates and three biological replicates. The results from the figure above were discussed in Section 3.22.6. The total yield of *S. aureus* when grown with Prolevium was higher than that of *S. epidermidis*, which grew at nearly all active levels, but yield was low. *C. jeikeium* only grew at 0.125% active, but the yield was better than *S. epidermidis* at any active level. There was no significant difference between the growth curves of *S. aureus* when grown with 0.125-1% (P=0.071) but growth with 2% active level was significantly different from growth with the other active levels (P>0.05). There was no significant difference of *S. epidermidis* growth when grown with 0.125-0.75% Prolevium (P=0.307).

# 3.23 If the Addition of Cosmetic Proteins Did Not Result in Visible Growth, Are the Cosmetic Proteins Bacteriostatic or Bactericidal Towards the Three Skin Species?

While no growth was recorded when each species was grown in minimal media alone, the colony count revealed that there was no significant (P>0.05) gain nor loss in of bacteria after 21 hours of incubation. Where no growth was recorded with a cosmetic protein, the colonies from plates were counted and the final cfu/ml calculated, if this did not significantly differ from the inoculated amount then the preserved cosmetic protein was bacteriostatic. If the final cfu/ml was significantly less than the inoculated amount, then the protein would be bactericidal. The efficacy of the preservatives may differ from previous results (Figure 10, Figure 11, Figure 12) as differences in medium composition can produce different results (Choi et al. 2014; Gomes et al. 2021).

### 3.23.1 Was the addition of any Active Level of Crosilk Lpc Bacteriostatic or Bactericidal?

When grown with Crosilk, no growth was recorded for both *Staphylococcus* spp. after 0.125% active level, and only a small amount of growth was recorded with *C. jeikeium* at 0.25%. There was a significantly lower (P<0.05) final cfu/ml than the inoculated amount when *S. aureus* was grown with 0.75% active level Crosilk and above. Both *S. epidermidis* and *C. jeikeium* had significantly less (P<0.01) final cfu/ml when grown with 0.5% active level of Crosilk and above.

# 3.23.2 Was the addition of any Active Level of Hydroavena HPO Bacteriostatic or Bactericidal?

When grown with Hydroavena HPO, no growth was recorded for *S. aureus* and *S. epidermidis* at 2% active level. Very little growth of *C. jeikeium* was recorded at any active level, but at 0.5% and above there was no growth. While there was, on average, a lower cfu/ml for *S. aureus* at 2% active level, it was not significantly less (P=0.064), so the protein was considered as bacteriostatic. *S. epidermidis* had a significantly(P<0.05) lower cfu/ml than inoculated when grown with 2% active level, so the protein was bactericidal at this active level. Hydroavena HPO was bactericidal for *C. jeikeium* at 0.75% and above.

# 3.23.3 Was the addition of any Active Level of Hydrolactin Liquid PE Bacteriostatic or Bactericidal?

While differing successes, there was growth with every active level of Hydrolactin Liquid PE for both *Staphylococcus* spp. The only active level in which Hydrolactin Liquid PE was bactericidal for *C. jeikeium* was with the 2% active level (P<0.01).

# 3.23.4 Was the addition of any Active Level of Hydrosativum P Bacteriostatic or Bactericidal?

*Staphylococcus aureus* grew with every active level of Hydrosativum P, and even though no growth was reported for *S. epidermidis* with 2% active level, the protein was not bactericidal.

Growth of *C. jeikeium* was only recorded with up to 0.25% active level, Hydrosativum P only significantly reduced the starting inoculum cfu/ml at 2% active level (P<0.05).

# 3.23.5 Was the addition of any Active Level of Hydrosolanum PE Bacteriostatic or Bactericidal?

Hydrosolanum PE was not bactericidal to *S. aureus* at any active level, and although reduced the final cfu/ml of *S. epidermidis* at 2% active level, it was not significant (P>0.05). However, the final cfu/ml of *C. jeikeium* was significantly lower than the inoculated amount at 0.5% active level and above (P<0.01).

#### 3.23.6 Was the addition of any Active Level of Prolevium Bacteriostatic or Bactericidal?

*Staphylococcus aureus* grew with every active level of Prolevium, even at 2% the final cfu/ml had significantly increased from the inoculated amount (P<0.01). However, Prolevium was bactericidal to *S. epidermidis* at 2% active level, and bactericidal to *C. jeikeium* with 0.75% active level and above.

# 3.24 Can Cosmetic Proteins Provide Enough Sustenance for the Bacteria to Form Biofilms

While all three species are known to produce biofilms, not all strains and isolates possess the genes capable of creating a biofilm (Zhang et al. 2003; Otto 2008; Martínez-García et al. 2019; Ozdemir et al. 2021). Quantification using the crystal violet method measured the extent of biofilm formation, unattached cells are washed away, and the crystal violet stained the remaining attached cells and extracellular matrix (O'Toole 2011; Welch et al. 2012). Preliminary experiments to determine whether the isolates of the three species could produce a biofilm all generated a positive result. All three species used in the research produced a quantifiable biofilm when grown with both TSB and MH at 37 °C, pH 7 for 24 hours. All other biofilm formation results are in reference to **Figure 19. Crystal Violet OD of Biofilm Formation of A) S. aureus, B) S. epidermidis and C) C. jeikeium when grown with the six cosmetic proteins.** These experiments were discussed in Section 3.24, including statistical analysis. The yellow column are the control biofilms, formed when the organisms were grown with the minimal medium plus 0.6% w/v casamino acid.Figure 19(A, B and C), which shows the quantity of crystal violet which had stained the adhered cells and biofilm matrix.

When the minimal medium was supplemented with 0.6% v/v casamino acids, the resulting biofilms were recorded. Significantly more cells of *S. epidermidis* adhered and produced a biofilm with these conditions than either *S. aureus* or *C. jeikeium* (P<0.001). However, both *S. aureus* and *C. jeikeium* produced biofilms in which the adhered quantity was significantly different to each other (P=0.72).

## 3.24.1 The Effect of Different Active Levels of Crosilk Lpc on Biofilm Formation in the 3 Common Skin Bacteria

When the minimal medium was supplemented with Crosilk Lpc, there were mixed results in biofilm formations. *S. aureus* (Figure 19, part A) produced a biofilm when grown with 0.125% and 0.25% active levels, there was no significant difference between the biofilms produced (P=0.57). *S. epidermidis* (Figure 19, part B) only produced a weak biofilm when grown with 0.125% active level. *C. jeikeium* (Figure 19, part C) produced a clearly quantifiable biofilm with 0.125%, 0.25% and 0.5% active level of Crosilk, in which there was no significant difference between these (P=0.97). There were also some adhered cells which were stained when *C. jeikeium* grew with 1% and even 2% active levels. There was no statistical difference between the biofilms of *S. aureus* and *C. jeikeium* when grown with both 0.125% and 0.25% active level of Crosilk (P>0.05), but both grew a significantly better biofilm with 0.125% active level than *S. epidermidis* did (P<0.02).

# 3.24.2 The Effect of Different Active Levels of Hydroavena HPO on Biofilm Formation in the 3 Common Skin Bacteria

When grown with Hydroavena HPO as the protein supplement, S. aureus produced a biofilm with 0.125%, 0.25% and 0.5% active levels. S. aureus' (Figure 19, part A) biofilm formation with both 0.25% and 0.5% active levels was more significant than with 0.125% (P<0.008). Biofilm formation was most extensive at 0.25% and significantly more than with 0.5% active level (P<0.001). Some adhered cells were stained when grown with 1%, 2% and 4% active levels. S. epidermidis (Figure 19, part B) was able to form a biofilm when grown with every active level of Hydroavena HPO (0.125%-4%). There was no significant difference of biofilm production at 0.125% and between 0.5-4% active levels (P<0.06). However, biofilm formation with 0.25% was only slightly significantly greater than with the other active levels (P=0.02). C. jeikeium (Figure 19, part C) formed a biofilm with all active levels of Hydroavena HPO, however at 1-4% active levels there were very few adhered cells stained and there was no statistical difference between the biofilm formations (P=0.99). There was no statistical difference between the biofilm formations of C. jeikeium with Hydroavena HPO at 0.125%-0.5%. However, there was a statistical difference between the two groups, C. jeikeium with 0.125-0.5% formed significantly more biofilm than with 1-4% active levels of Hydroavena HPO (P<0.04). There was no significant difference between the biofilms formed by S. aureus and S. epidermidis at 0.25%, 0.5% and 4% active level (P>0.05), however S. epidermidis had significantly more cell adherence when grown with 0.125%, 1% and 2% active levels Hydroavena HPO P<0.04). Except with 4% active level, S. epidermidis formed significantly more abundant biofilm than C. jeikeium with all other active levels (P>0.05). S. aureus formed had significantly more adhered cells than C. jeikeium at 0.25% and 0.5% (P<0.05), but not with the other active levels.

## 3.24.3 The Effect of Different Active Levels of Hydrolactin Liquid PE On Biofilm Formation in the 3 Common Skin Bacteria

S. aureus (Figure 19, part A) formed poor biofilms with Hydrolactin Liquid PE, there was no significant differences between the biofilms formed when grown with every active level tested (P>0.05). S. epidermidis (Figure 19, part B) formed biofilms with every active level of Hydrolactin Liquid PE tested. There was no significant difference between the biofilms with 0.125%, 0.25% and 0.5%, or between 1% and 2% active levels (P>0.05). However, the biofilm formed with 4% active level of Hydrolactin Liquid PE was significantly less than at all other active levels (P<0.04). C. *jeikeium* (Figure 19, part C) formed biofilms when grown with all active levels of Hydrolactin Liquid PE. There was no significant difference between the biofilms formed with 0.125%, 2% and 4% active levels of Hydrolactin Liquid PE (P=0.20). There was no significant difference in biofilm formation with 0.25% and 1% active levels (P=0.06) and the biofilm formed with 0.5% active level of Hydrolactin was significantly more than at any other active level (P<0.03). S. aureus formed significantly less biofilm with every active level of Hydrolactin compared to S. epidermidis (P<0.05). With 0.25% and 0.5% active level of Hydrolactin Liquid PE, S. aureus formed significantly less biofilm formation than C. jeikeium, However, at 0.125%, 2% and 4% there was no significant difference between the biofilms formed (P>0.06). Again, S. epidermidis formed significantly more abundant biofilms with every active level of Hydrolactin Liquid PE than *C. jeikeium* (P<0.01).

### 3.24.4 The Effect of Different Active Levels of Hydrosativum P On Biofilm Formation in the 3 Common Skin Bacteria

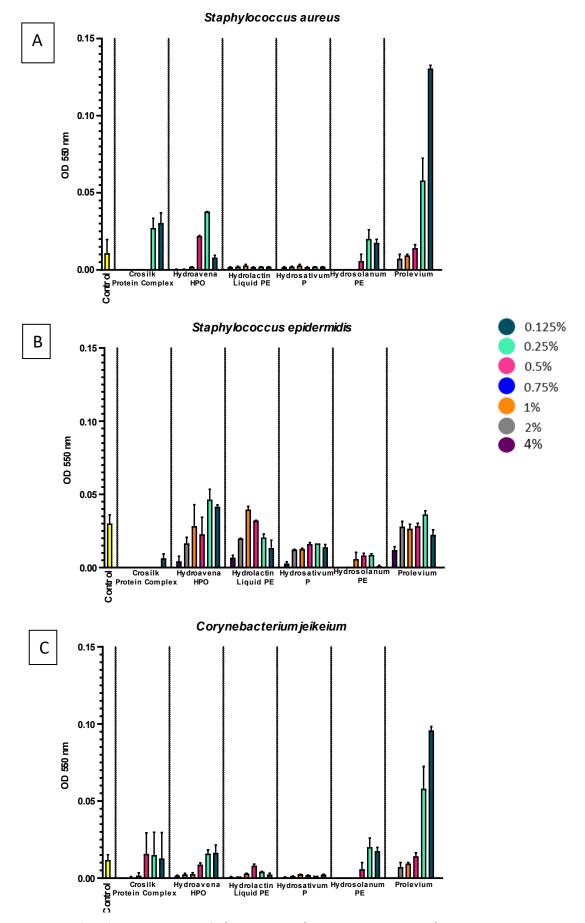
*S. aureus* (Figure 19, part A) was able to form a biofilm when grown with Hydrosativum P, although not abundantly. There was no significant difference between the quantity of adhered *S. aureus* when grown with any active level (P>0.05). *S. epidermidis* (Figure 19, part B) also was able to form biofilms when grown with every active level of Hydrosativum P, with many more cells adhering to the well than with *S. aureus* (P<0.05). When grown with Hydrosativum P, there was no significant differences between the biofilm formed with 0.125, 0.25. 0.5 and 1% active levels (P=0.08), 1 and 2% active levels (P=0.63). *S. epidermidis* formed the least abundant biofilm with 4% active level of Hydrosativum P (P<0.01). *C. jeikeium* (Figure 19, part C) was also able to form a biofilm formation with 0.125, 0.25 and 0.5% active levels (P>0.05), but there was a steady reduction in the numbers of adhered cells from 1-4% active levels, with no significant difference between biofilms with 2 and 4% (P>0.05). No significant differences between the abundance of biofilm formed by both *S. aureus* and *C. jeikeium* when grown with 0.125-1% active levels of Hydrosativum P. *S. epidermidis* produced more biofilm with every active level than the other two species (P<0.014).

# 3.24.5 The Effect of Different Active Levels of Hydrosolanum PE on Biofilm Formation in the 3 Common Skin Bacteria

S. aureus (Figure 19, part A) was only able to form a biofilm when grown with 0.125-0.5% active levels of Hydrosolanum PE, with 0.75-4% active level of Hydrosolanum PE there was no staining recorded and therefore no adhered cells. There was no significant difference between the biofilm formed with 0.125% and 0.25% active level of Hydrosolanum PE, but the amount of biofilm was significantly reduced with 0.5% active level (P<0.02). S. epidermidis (Figure 19, part B) formed a biofilm with 0.125-1% active level of Hydrosativum P, although the adherence was low at 0.125% and significantly less than with any other active level (P<0.001). There was no significant difference between the biofilms formed between 0.25-1% active level (P<0.05). C. jeikeium (Figure 19, part C) also only formed biofilms when grown up to 0.5% active level of Hydrosolanum PE, biofilms formed at 0.5% were significantly less abundant than at 0.125 or 0.25% (P<0.03). There were no significant differences between the biofilms formed by C. jeikeium at 0.125 and 0.25% (P=0.54). There were no significant differences between the biofilms formed by *S. aureus* and C. jeikeium when grown with 0.125 and 0.25% active levels of Hydrosolanum PE (P>0.05). But both species, with these active levels, formed significantly more abundant biofilms than S. epidermidis (P<0.05). With 0.5% active level, there was no statistical difference between the biofilms formed by the three species (P>0.05).

### 3.24.6 The Effect of Different Active Levels of Prolevium on Biofilm Formation in the 3 Common Skin Bacteria

When grown with Prolevium, *S. aureus* (Figure 19, part A) was able to form biofilms when grown with 0.125-2% active levels. The significantly most abundant biofilm was formed with 0.125% (P<0.001), followed by 0.25% (P<0.007), then 0.5% (P<0.023). There were no significant differences between the biofilms formed with 1 and 2% Prolevium (P=0.3). *S. epidermidis*, (Figure 19, part B) however was able to form biofilms with every active level of Prolevium. There were no significant differences between the abundance of biofilm formed at active levels 0.125-2%, but these were significantly more abundant than the biofilm grown with 4% active level (P=0.003). *C. jeikeium* followed a similar pattern to the biofilms formed by *S. aureus*, with the most abundant biofilm formation at 0.125% (P<0.02), then 0.25% *et cetera*, with no significant differences between the biofilms formed with 1 and 2% active level (P=0.3). Both *S. aureus* and *C. jeikeium* (Figure 19, part C) form non-statistically different biofilm abundance with 0.25, 0.5, 1 and 2% active levels of Prolevium. At 0.125 and 0.25% both species grew significantly more abundant biofilms than *S. epidermidis* with the same active level (P<0.05). However, this was reversed at 0.5% and above, when *S. epidermidis* grew more abundant biofilms than the other two species (P<0.04).



**Figure 19**. **Crystal Violet OD of Biofilm Formation of A)** *S. aureus*, **B)** *S. epidermidis* and **C)** *C. jeikeium* when grown with the six cosmetic proteins. These experiments were completed with three technical replicates and three biological replicates. The above results were discussed in Section 3.24, including statistical analysis. The yellow column are the control biofilms, formed when the organisms were grown with the minimal medium plus 0.6% w/v casamino acid.

#### 3.25 Discussion

We can reject the null hypothesis that cosmetic proteins do no provide support for any kind of bacterial growth.

#### 3.26 Identifying Bacteria with Extracellular Proteases

Many species of bacteria can release proteases into their surroundings. These extracellular proteases can be part of the organism's virulence portfolio or used to digest large, unusable proteins into smaller peptides and amino acids that are transported into the cell and utilised for cellular processes (Wandersman 1989). Most bacterial species have proteases which are stable and functional between a pH of 5-9 (Rao et al. 1998), while a common staphylococcal commensal has been found to possess resilient proteases which can operate at more extreme acidic and alkaline conditions (Uttatree and Charoenpanich 2018). Therefore, it could be assumed that any proteases secreted by the above bacteria would be likely functionable at most skin sites and in the presence of cosmetic products which have a pH to match skin.

Colonies of *Corynebacterium jeikeium* did not produce zones of clearing on the lactose-free skimmed milk agar. This result corroborates with previous research which found that most *Corynebacterium* spp. do not possess extracellular enzymes which other skin dwellers do, including proteases (Kwaszewska et al. 2014). It's likely that *Corynebacterium* spp. acquire their amino acids from the by-products of protease producing *Staphylococcus* spp. (Bojar and Holland 2002). This survival tactic would make *C. jeikeium* a social cheater, a species which acquires the products of other bacteria for their own metabolic gain (Chen et al. 2019).

Both *Staphylococcus* spp. gave a positive result for extracellular proteases using the LFSM agar method (Figure 9). Both *Staphylococcus* spp. having extracellular proteases corroborates with prior research, in which both *S. aureus* and *S. epidermidis* isolates have produced hydrolysed clear zones on similar media and thus exhibiting their extracellular protease activity (Sudagidan and Aydin 2009; Alkhafaji et al. 2013; Alizadeh-Sani et al. 2018).

While many studies confirm the presence of proteases, few describe the proteolytic activity against different protein sources. For instance, there is little to no research detailing protease activity of *Staphylococcus* spp. against silk proteins, the source of Crosilk Lpc. Silk proteins have been investigated for their antimicrobial potential (Kunz et al. 2016; Xue et al. 2016), and a few studies have examined their potential as a nutrient source (Weide 2003). There have even been studies on the ability of *S. aureus* to form biofilms on clinical silk stitches, which would suggest there is potential for utilisation of silk proteins in biofilms (Hess et al. 2011). To successfully degrade silk protein, either *Staphylococcus* spp. would need to possess the extracellular fibroinase like the Gram-negative soil dwelling species *Variovorax paradoxus* (Forlani et al. 2000). Casein however, which was the source for Hydrolactin Liquid PE, has been extensively researched

for its utilisation (Taylor 1951; Bryant and Robinson 1962; Reissbrodt et al. 1995). *Staphylococcus aureus* possesses the V8 extracellular protein, while *Staphylococcus epidermidis* possesses the SepA, both of which are caseinolytic (Arvidson 1973; Martínez-García et al. 2018). Therefore, if the proteolysis resulted in large fragments, it would be possible for both *Staphylococcus* spp. to utilise these products. Casein hydrolysates, both acid and enzymatic digests, are ingredients in, or supplemented into media (Moore 2015; Millipore 2018) capable of providing nutrients for a wide range of organisms, *Staphylococcus* spp. and *Corynebacterium* spp. included (Morita et al. 1979; Balci et al. 2002; Moore 2015). If the casein hydrolysis was successful in producing small fragments or free amino acids, then all three species would theoretically be able to grow with Hydrolactin Liquid PE.

Hydrosolanum PE is derived from potato protein and potatoes have long been used to cultivate microorganisms (Zumstein 1936). Potato peptones in bacterial cultivation are becoming more popular and if not equally as successful as meat derived peptones, due to the demand for animal-product free science (Heenan et al. 2002; Solabia 2019). As *Staphylococcus aureus* is a frequent potato contaminant, then it stands to reason that the bacteria can hydrolyse the proteins and utilise the peptones to enable proliferation (Huang 2015). Thus, potato peptones are suitable for a range of Gram-positive organisms and can supply at least some useable peptides. Similar results could be expected from the other vegetable protein source commonly used in cultivation media, Hydrosativum P, which is hydrolysed pea protein (Thermofisher 2018; Merck 2022).

Hydroavena HPO, sourced from oat protein prolamin avenin, has a similar structure to gluten (Balakireva and Zamyatnin 2016; Gilissen et al. 2016). Both *Staphylococcus aureus* and *Staphylococcus epidermidis* have been found to possess extracellular proteases which are effective against prolamins, although the latter was strain dependent (Herrán et al. 2017). Other research has found that even *Staphylococcus* spp. which reside above-ground on cereal species (Legard et al. 1994), do not possess these extracellular proteases (Herranen et al. 2010), highlighting that not all staphylococcal species or strains possess these prolamin degrading extracellular enzymes. However, if both *Staphylococcus* spp. in the experiment do possess these prolamin hydrolysing extracellular proteases then they would be able to easily breakdown and utilise any large peptide fragments.

Bacteria which can utilise cottonseed proteins, the protein source for Prolevium, express extracellular proteases, which also happen to be fibrinolytic, while they utilise the protein as a nitrogen source. The complex structure of cottonseed requires large quantities of protease production to break the proteins down and use the nitrogen source (Bajaj et al. 2013). Staphopains and cysteine proteases, released by *S. aureus* can degrade fibrinogen (Ohbayashi et

al. 2011), *S. epidermidis* also releases enzymes to degrade fibrin (Ma et al. 2017), and therefore could potentially also degrade the complex proteins found in cottonseed.

Due to *S. aureus* being a common contaminant in a range of food sources (Kadariya et al. 2014), it is highly likely that this will be the organism most tolerable at breaking down large fragments and utilising a range of peptide sizes, and as *S. epidermidis* possesses similar extracellular protease activity (Martínez-García et al. 2018), then the bacteria will also likely be able to degrade various protein sources. Though skin is a nutrient desert, free amino acids are easier to utilise, the smaller fragmented cosmetic proteins would provide better nutrients for the growth of both *Staphylococcus* spp. Both *Staphylococcus* spp. would have an advantage over the proteinase lacking *Corynebacterium jeikeium*, which would only be able to utilise the smallest of fragments and free amino acids.

# 3.27 Are Preservatives found in Cosmetic Proteins Effective Against the Three Skin Species?

The experiment above was not the standardised testing for the minimum inhibitory concentration as the investigation tested the preservative concentrations as found in the cosmetic protein active levels. Standard MIC tests are carried out on bacteria at  $5 \times 10^5$  cfu/ml, while here the test was carried out at  $1 \times 10^5$  cfu/ml to standardize with the other experiments in the thesis and to lessen the quantity to be more similar to the low biomass found on skin (Wilson 2004). The pH was also dropped to 5 to better represent the likely pH of the final formulations (Lukić et al. 2021; Schulte to Brinke et al. 2021) as well as the skin (Lambers et al. 2006). However, as with previous work, Mueller-Hinton broth was the testing medium (EUCAST 2003) and the minimum inhibitory concentration was met when the preservatives reduced bacterial growth by 80% or above (Rushton et al. 2013). The mechanisms for all preserving substances are found in the Section 1, Table 3.

Only three preservatives reached the 80% and above inhibition of *Staphylococcus aureus*, all at the highest active levels, which are not likely to be used in final formulations. However, even at the lower, widely used active levels, there was still inhibition of growth (Figure 10). Crosilk Lpc at the sold active level of 12.7% is preserved with 0.5% sodium benzoate and 0.01% disodium EDTA. As Crosilk Lpc was sold at the lowest active level of the all the proteins at 12%, therefore, to reach formulation levels, it was diluted the least and thus had the highest preservative concentrations. For example, at 4% active level, the preservative concentrations would have been 0.16% sodium benzoate and 0.00315% disodium EDTA. *Staphylococcus aureus* has shown to be highly sensitive to sodium benzoate at concentrations as low as 0.0032% (Karabay and Sahin 2005). Although ineffective alone (Sangcharoen et al. 2017), EDTA has also been found to enhance antimicrobial

agents against planktonic *S. aureus* through exposure of the inner cell membrane and allowing preservative partners to enter to the cell more easily (Walsh et al. 2003).

The preservatives in Hydroavena HPO at 22.4% active level, also contained 0.5% sodium benzoate, this time with the addition of 0.3% potassium sorbate. However, as Hydroavena HPO is sold at a high active level, it was diluted nearly twice as much as Crosilk Lpc to reach a working formulation active level. For example, at 4% active level, the concentration of sodium benzoate was 0.09%, while potassium sorbate was 0.05%. While the effectiveness of sodium benzoate against *S. aureus* has been noted, potassium sorbate has also shown to be effective at inhibiting *S. aureus*. At pH 5, a low concentration of 0.016% potassium sorbate alone has previously inhibited the growth of *S. aureus* in brain-heart infusion broth (Aminzare et al. 2014), but other work has found a much higher concentration of 0.4% was needed (Wang et al. 2018a). When used in conjunction together, sodium benzoate and potassium sorbate were classed as 'highly effective' against *S. aureus*, causing between 10-20% inhibition (Pinto et al. 2021). While the MIC of both sodium benzoate containing preserving measures were at active levels unlikely to be used in final formulations, *S. aureus* was still somewhat inhibited at the lowest active level concentrations.

The four remaining preservatives were the least effective at inhibiting *S. aureus*. All contained Phenoxyethanol and either disodium EDTA, potassium sorbate or both. Phenoxyethanol has been reported to be less effective against Gram-positive bacteria than Gram-negative bacteria (Wishart et al. 2015) At 18.3% active level, Hydrolactin Liquid PE was preserved with 1% phenoxyethanol and 0.2% disodium EDTA. Once diluted to 4% active level, the concentrations of preservatives were 0.3% phenoxyethanol and 0.06% disodium EDTA. The minimal inhibitory concentration was not reached, but *S. aureus* was inhibited by 70% at 4% active level. Previous work found that to reach the MIC to inhibit *S. aureus*, phenoxyethanol had to be twice as concentrated at 0.64% compared to other bacterial species (Deckner 2015). While the addition of 0.1-0.2% EDTA has shown to improve the efficacy of phenoxyethanol in inhibiting *S. aureus*, the levels found in the used active levels were far too low. If the addition of disodium EDTA had little effect at these low concentrations, then also using phenoxyethanol at pH 5 would also present less staphylococcal inhibition, as phenoxyethanol, alone, works best at pH 7 (Siegart 2013).

Hydrosativum P was sold at 20.3% active and at this concentration the protein was preserved with 1% phenoxyethanol and 0.3% potassium sorbate. At 4% active level this would equate to 0.2% phenoxyethanol and 0.06% potassium sorbate, 0.1% less than phenoxyethanol found in Hydrolactin Liquid PE at 4% active level and less than previous MIC concentrations (Deckner 2015). At the active level they were sold at, both Hydrosolanum PE and Prolevium were preserved with 1% phenoxyethanol, 0.3% potassium sorbate and 0.20% disodium EDTA. Therefore, Hydrosolanum PE when diluted to a 4% active level the protein contained 0.20%

phenoxyethanol, 0.060% potassium sorbate and 0.040% disodium EDTA. At 4% active level of Prolevium contains 0.19% phenoxyethanol, 0.056% potassium sorbate and 0.038% disodium EDTA. Both preservative mixtures faired similarly to each other, and with the preservatives found in Hydrolactin Liquid PE. If disodium EDTA was present in the preservative mixture, those preserving measure were more successful at inhibiting *S. aureus* than preservative mixtures without disodium EDTA, due to EDTA weakening of the cell wall (Miyahara and Arita 2020). The MIC of EDTA when used in conjunction with other antimicrobials has been put at approximately 0.049% (Lambert et al. 2004), which is close, but not quite the level reached at the 4% active level of any of the cosmetic proteins. To inhibit S. epidermidis, the MIC of phenoxyethanol alone has previously been calculated at 0.5% or higher (Wang et al. 2019). At 4% active level, the four phenoxyethanol containing cosmetic proteins only contained approximately 0.3% phenoxyethanol, however, three were still able to inhibit S. epidermidis by 80% or more. The addition of disodium EDTA to Hydrolactin Liquid PE, Hydrosolanum PE and Prolevium boosted the efficacy of phenoxyethanol, thus allowing greater inhibition at lower concentrations against Staphylococcus spp. (Miyahara and Arita 2020). However, the same inhibition 'boost' could not be said for the preserving measures of Hydrosativum P. While prior research found that most double preservative mixtures (both 0.1% concentrated) had completely inhibited the growth of S. epidermidis, any preservative paired with potassium sorbate did not repeat such results and growth was recorded (Lalitha and Prasada Rao 2015).

Preservative mixtures containing sodium benzoate were more effective against inhibiting *S. aureus* than other preserving measures. This corroborates with previous work which has highlighted that sodium benzoate is a more effective preservative against *S. aureus* below pH 6 than potassium sorbate. Although phenoxyethanol can be used from pH 3-9 (Williams et al. 2018), it is less effective at the lower the pH ranges (Siegart 2013). The addition of most of these preserving measures, except the preservative combination in Hydrosativum P, could still influence and potentially significantly inhibit *S. aureus* residing on the skin.

The preservatives found at 4% active level in five out of six of the proteins inhibited *S. epidermidis* by 80% or more. The preservatives found at 2% active level of Crosilk Lpc also inhibited *S. epidermidis* by more than 97%. The preservatives found at 2% active level of Hydroavena HPO still inhibited *S. epidermidis* by nearly 63% (Figure 11), corroborating with previous research which has found that like *S. aureus, S. epidermidis* is more sensitive to sodium benzoate than most other preservative types, with the MIC of sodium benzoate being as low as 0.0016% (Güven and Kaynak 2014). Figure 11 also shows that the proteins preserved with sodium benzoate were effective at inhibiting *S. epidermidis*, even at the lower concentrations. However, unlike *S. aureus, S. epidermidis* and the other preservative combinations, all of which

contain phenoxyethanol. While previous research found that phenoxyethanol alone had a MIC of between 0.5- 1% against *S. epidermidis* (Wang et al. 2019; Fournière et al. 2020), the addition of EDTA consistently lowers the MIC to 0.4% (Miyahara and Arita 2020). The preservatives found in Hydrosativum P were the least effective against *S. epidermidis*, the same as *S. aureus*. The lack of EDTA meant that the preserving efficacy of phenoxyethanol was not 'boosted' against *S. epidermidis*. Previous work has found that potassium sorbate is not as effective against *S. epidermidis* than other preserving measures, and the MIC was double that of sodium benzoate (Güven and Kaynak 2014).

As seen in Figure 6, when grown with Mueller-Hinton broth, *C. jeikeium* does not reach stationary phase within the 24-hour incubation. Extension of the incubation period could create inaccuracies as extending could make the MIC appear higher (EUCAST 2003), and the likelihood of products staying in contact with skin greater than this period of time would also be unlikely (Larson 2001; Purnamawati et al. 2017). If total growth is not reached, the MIC will likely appear to be higher and the organism less sensitive than it may be (Mouton et al. 2018).

Much of the previous research regarding *Corynebacterium* spp. and the effect of preservatives have focused on deodorant and antiperspirant preservatives (Halla et al. 2018) as the axilla is the *Corynebacterium* 'problem' area (Lam et al. 2018). These preservatives were chlorhexidine and Trichlorocarbanilide (Halla et al. 2018), which are highly effective at inhibiting skin bacteria (Fahimipour et al. 2018; Kates et al. 2019).

While little data is available about the effectiveness of sodium benzoate, potassium sorbate and disodium EDTA on inhibiting *C. jeikeium*, phenoxyethanol has been found to be highly effective when used in conjunction with other preserving measures. Phenoxyethanol constituted 53% of a preservative mixture which contained naturally found preservatives, the minimal inhibitory concentration of the preservation compound was found to have ranged between 0.025% and 1% dependent of the strain of *C. jeikeium* (Haustein et al. 1993). The strain of *C. jeikeium* used in the above experiments was sensitive to phenoxyethanol. In Prolevium at 0.0625% active level, phenoxyethanol would be found at a concentration of approximately 0.003%, a concentration which had no inhibition against *S. aureus* and *S. epidermidis*, while *C. jeikeium* was inhibited by nearly 6% (Figure 10, Figure 11, Figure 12). The lowest concentrations of phenoxyethanol containing mixtures inhibited *C. jeikeium* by up to 15.3%, while *S. epidermidis* was only inhibited up to 8.3% and *S. aureus* was only inhibited up to 2.6%. While no MIC was reached by the phenoxyethanol containing mixtures, giving the impression that *C. jeikeium* was less sensitive to these, the higher inhibition percentages at the lowest concentrations would suggest the opposite.

While an accurate picture of the sensitivity of *C. jeikeium* to the preservative mixtures is not necessarily possible as stationary phase was not reached, there was clear sensitivity to the

mixtures containing sodium benzoate. However, across the active levels, the sodium benzoate concentration found in Crosilk were nearly double the concentration found in Hydroavena HPO, but the inhibition percentages did not reflect this (Figure 19). The addition of disodium EDTA in Crosilk may have a reduced effect against *C. jeikeium* than other skin species. The cell wall of *Corynebacterium* spp. is considered more complex than other Gram-positive species. *Corynebacterium* spp. possess a layer of mycolic acid outside the peptidoglycan layer, which is comparable to the outer membrane of Gram-negative bacteria (Burkovski 2013,2018). This extra layer has been shown to reduce sensitivity to lytic substances which attack the cell membrane (Burkovski 2018; Theresia et al. 2018). The extra cell membrane layer may well be why the addition of the membrane targeting disodium EDTA (Virto et al. 2005) does not increase the effectiveness of sodium benzoate against *C. jeikeium* compared to the two *Staphylococcus* spp.

All three species showed sensitivity at some level to the preservative combinations found in cosmetic proteins. The addition of preservatives to cosmetic proteins may influence the natural balance of bacteria on the skin due to the varying sensitivities from species to species. This may even affect other microbes too, while the use of potassium sorbate may not widely inhibit most bacteria, fungi are quite sensitive to the preservative (Marshall et al. 2016; Alsudani 2017). *Staphylococcus aureus* has been shown to be the least sensitive to the preservative combinations, a worrying sign as it is the most pathogenic (Bush and Vazquez-Pertejo 2021) of the three species tested. However, this is not a certainty in how the preservatives will react with species when applied to the skin, there will always be strain-to-strain variation (Lambert and Pearson 2000) and previous work has found that the *in vitro* preservative experiment results have not always been repeated *in vivo* (Murphy et al. 2021).

#### 3.28 What do the Protease assay, MIC tests and Growth Experiments reveal?

As seen in Figure 9, both *Staphylococcus* spp. produced extracellular proteases, while *C. jeikeium* did not. These extracellular proteases are predominantly used for virulence, as bacteria favour utilisation of free amino acids as nutritional sources. However, in nutrient poor conditions such as the skin, proteases can be released to hydrolyse proteins into small peptides and amino acids (Kolar et al. 2013). Many of the cosmetic proteins which are used in formulations are derived from proteins, which both *Staphylococcus* spp. can hydrolyse, and contain hydrolysates used to promote bacterial growth under laboratory conditions (Arvidson 1973; Slifkin and Pouchet 1975; Swiatecka et al. 2010). Therefore, with thorough protein analysis of the fragment sizes or free amino acids available, then it would be highlight whether using a cosmetic protein could potentially favour bacteria with extracellular proteases. However, if the hydrolysis produces large fragments, using these proteins in formulations could favour certain species.

Another obstacle which may cause microbial perturbations is the addition of preservatives in the cosmetic proteins. Necessary in liquid products to avoid contamination, but many of these targeted contaminants also happen to be skin microbiota. Figure 10, Figure 11 and Figure 12 show that all three species have some degree of susceptibility to the preservatives found at the highest active levels of proteins tested. However, in nutrient depleted conditions, the efficacy of the preservatives can improve as there is less sustenance available to overcome the antimicrobial activity (Gomes et al. 2021). Therefore, choice of preservatives is important and species with less susceptibility to antimicrobials could be promoted over more sensitive species, in this experiment the most pathogenic species was the least susceptible. Many of these preservative combinations may not be as effective against bacteria, however, they could cause dysbiosis for the other microbiota that reside of skin (Leyva Salas et al. 2017). The cosmetic industry on whole is moving towards using less water in formulations and using dry ingredients (Embleton 2019; Turner 2021). Research into dry cosmetic proteins, in which preserving measures are not required, could be the next step (Halla et al. 2018). However, putting unprotected hydrolysates on skin could cause over-proliferation of species, throwing up new problems (Murphy et al. 2021).

A key question was, could these proteolysates provide amino acids/nitrogen source to sustain growth of the three skin species. Growth of all three species in the minimal medium was bacteriostatic, meaning there was no significant loss or rise in the number of cells inoculated. However, the addition of many of the cosmetic proteins, especially at the lower active levels when preservative concentration was low, provided the sustenance necessary for growth. Growth was not equal across the different bacteria and the differing amino acid content of the proteins provided various levels of nourishment for the three species. For example, *S. aureus* grew better when supplemented with cosmetic proteins which had higher levels of cysteine (Alreshidi et al. 2020). More proteomic analysis would also highlight if any of the hydrolysed proteins fragmented into peptides which could harm skin bacteria (Théolier et al. 2013). While providing sustenance, peptides can also have antibacterial qualities (Ouertani et al. 2018).

While the proteins could provide sustenance for planktonic growth, preservatives hindered growth with higher active levels of proteins. Biofilm formation shielded the skin species from these preserving measures and sessile cells were quantified even at the highest active levels (Dincer et al. 2020). The pH helped downregulate biofilm forming genes in *S. aureus* (Efthimiou et al. 2019), but many of the proteins still provided nutrition needed for adherence of the cells. *S. epidermidis* was able to form consistent biofilms, even with cosmetic proteins in which planktonic growth was poor. The slow growing *C. jeikeium*, also formed biofilms when supplemented with many of the cosmetic proteins, again including with active levels where no planktonic growth was recorded. The least formed biofilms were with the one cosmetic protein,

Crosilk Lpc, where D-amino acids could have been present. Research into using some of these Damino acids in formulations could curb any potential biofilm formations without harming the bacteria themselves (Kolodkin-Gal et al. 2010; Ampornaramveth et al. 2018).

Introduction of cosmetic proteins to the skin may favour the growth of organisms with extracellular proteins which could utilise large peptide fragments. Without mass spectrometry to analyse the peptide length and peptides produced, it is difficult to say whether they would be useful or even potentially antimicrobial. The use of preservatives could reduce growth of susceptible species and promote growth of less sensitive species. Overuse of low preservative concentrations could also increase resistance amongst skin bacteria (Capita et al. 2019). In amino acid depleted environments, the cosmetic proteins can provide sustenance to aid in growth of bacteria. If adherence of the bacteria begin, cosmetic proteins can also provide nutrients which aid in biofilm production, which can also reduce the efficacy of the preservatives. Promotion of one species over another, even when described as 'beneficial bacteria' could upset the overall balance, but actively promoting pathogens on skin is harmful. In a healthy individual, the most desirable outcome would be using an active level of a cosmetic protein which is bacteriostatic towards all species. 4 Planktonic Growth and Biofilm Formation of Co-Cultured *Staphylococcus* spp. with Cosmetic Proteins

### 4.1 Introduction

*Staphylococcus aureus* and *Staphylococcus epidermidis* are often described as the pathogenic and commensal cousin. While *S. epidermidis* is also a major cause of nosocomial infections, the associated virulence factors are not as severe as the ones used by *S. aureus* (Otto 2009,2012). Both species colonise similar areas of the skin and therefore interact with each other (Otto 2010; Gosbell and van Hal 2013). *S. epidermidis*, for example, can modulate *S. aureus* to limit the latter's ability to infect and form biofilms (Byrd et al. 2018). For these reasons, many publications investigate interactions between the two species (Iwase et al. 2010; Fredheim et al. 2015; Lee et al. 2019a; Hardy et al. 2020)

On healthy skin, both species can co-exist without causing any serious health issues (Grice and Segre 2011). However, the introduction of a substance which could manipulate the staphylococcal balance could promote inflammation leading to disease (Park et al. 2019).

### 4.2 Aims

- Investigate if cosmetic proteins can promote the growth of one staphylococcal species when grown together in a planktonic state
- Investigate whether cosmetic proteins promote the formation of biofilms by one staphylococcal species over another

### 4.3 Null Hypothesis

Addition of cometic proteins would not cause an imbalance of planktonic growth or biofilm production in a co-culture of *S. epidermidis* and *S. aureus*.

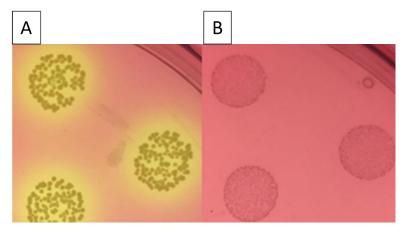
## 4.4 Methods

#### 4.5 Bacteria

Both the *Staphylococcus aureus* and *Staphylococcus epidermidis* isolates used were the same as in Section 2.6.

#### 4.6 Media

TSB and TSA were used to grow the species separately as found in Section 2.10. Minimal medium was used to co-culture the species (Section 2.8). Mannitol salt agar was used to differentiate and count the species. *S. aureus* can utilise mannitol and colonies are surrounded by yellow halo (**Error! Reference source not found.**), while *S. epidermidis* cannot utilise mannitol and therefore t he colonies are either colourless or red and the surrounding media stays red (Chapman 1945).



**Figure 20.** *Staphylococcus* species grown on Mannitol Salt Agar. *Staphylococcus aureus* (A) can utilise mannitol and therefore a yellow halo is formed around the colonies. *Staphylococcus epidermidis* (B) does not utilise mannitol, and therefore the colonies remain grey on a red background.

### 4.7 Preparation for Planktonic Growth

The minimal medium from Section 2.8, was used as a way of producing conditions which could reflect the skin environment better than traditional growth media. However, when testing the cosmetic proteins, the casamino acid growth supplement was removed from the recipe. Instead, the media was supplemented with the cosmetic protein at active levels in which they may be used in the final formulation 0, 0.125, 0.25, 0.5, 0.75, 1 and 2%.

Bacteria were grown as single colonies on TSA. A single colony was removed and place into 4 ml of TSB, which was grown for 18 hours at 37 °C on an orbital shaker at 150rpm. The optical density (OD) was measured at 600 nm and the cell suspensions were diluted 1x10<sup>5</sup> cfu/ml in minimal media containing the cosmetic protein. To produce the co-culture, 100 µl of each species were added and mixed in a well of a MicroWell<sup>™</sup> 96-Well Microplate well plate (Nunc, Denmark) and placed into a shaking incubator at 37 °C for 24 hours.

#### 4.8 Preparation for Sessile Growth

Bacteria were grown overnight, as stated above, and diluted to 1x10<sup>5</sup> cfu/ml in minimal media. The media was supplemented with the cosmetic protein at active levels in which they may be used in the final formulation 0, 0.125, 0.25, 0.5, 1, 2% and 4%. An 200 µl aliquot of a 1:1 ratio of *S. epidermidis* and *S. aureus* and supplemented minimal media were placed into a flat bottom MicroWell<sup>™</sup> 96-Well Microplate well plate (Nunc, Denmark). The layout of the plate was simultaneously duplicated so that they could be treated differently later. Flat bottom plates were chosen due to the non-motile nature of the organisms (O'Toole 2011). These plates were placed into a 37 °C incubator for 24 hours without shaking. After incubation, one of the plates was stained with crystal violet as per the protocol set by O'Toole (O'Toole 2011). The other plate was washed gently three times with 1 x PBS to removed unattached cells and the biofilm removed manually using a sterile pipette tip as suggested by Lemos and colleagues (Lemos et al. 2010). Once scraped, 100  $\mu$ l of 1x PBS was added to the well and the contents were serially diluted before being plated onto Mannitol salt agar for counting using the Miles and Misra method (Miles et al. 1938). The resulting cfu/ml were converted into percentages. A 100% domination by one species did not mean that the other species was not at all present, but at the dilution counted there were not any of the reduced species to count.

#### 4.9 Statistics

The final cfu/ml of both species for both planktonic growth and biofilm formations were analysed using GraphPad Software (Version 9.1.2). The mean of each were compared using t-tests and significant differences noted.

#### 4.10 Results

# 4.11 Does Incubation with Cosmetic Proteins Promote One *Staphylococcus* spp. Over Another in a Planktonic Growth Co-Culture?

There was never any significant difference (P>0.05) between the inoculated cfu/ml of the *Staphylococcus* spp. or after incubation with the minimal medium without supplements, see yellow and blue bars from Figure 21. All results below are in reference to the data shown on Figure 21.

# 4.11.1 Does Incubation with Crosilk Lpc Promote One *Staphylococcus* spp. Over Another in a Planktonic Growth Co-Culture?

The addition of Crosilk Lpc to the minimal medium resulted in the planktonic growth of *S. aureus* being favoured over the growth of *S. epidermidis*. When grown with Crosilk Lpc at active levels 0.125-0.75%, both the cfu/ml of *S. aureus* and *S. epidermidis* increased significantly from the starting inoculum. At 1% and 2% however, the total cfu/ml had significantly decreased from the starting inoculum (P<0.001).

# 4.11.2 Does Incubation with Hydroavena HPO Promote One *Staphylococcus* spp. Over Another in a Planktonic Growth Co-Culture?

The addition of Hydroavena HPO also showed no significant promotion of one species over another (P>0.05). There was significantly more growth with every active level of Hydroavena HPO than with Crosilk Lpc (P<0.0003). The final cfu/ml of both species were also significantly increased when grown with every active level of Hydroavena HPO (P<0.03), the final cfu/ml was never less than the inoculated amount.

# 4.11.3 Does Incubation with Hydrolactin Liquid PE Promote One *Staphylococcus* spp. Over Another in a Planktonic Growth Co-Culture?

When the co-culture was grown with supplemented Hydrolactin Liquid PE, there was no promotion of either *Staphylococcus* spp. with 0.125% active. However, with 0.25% Hydrolactin

Liquid PE and above, *S. epidermidis* was significantly promoted over *S. aureus* (P<0.0079). The final cfu/ml of *S. epidermidis* increased significantly compared to the initial inoculated amount with every active level (P<0.009) and continued to rise as the active levels increased. While the final cfu/ml of *S. aureus* was significantly higher than the inoculated amount with active levels 0.125-1% (P<0.008), the total cfu/ml of *S. aureus* peaked with 0.5% active and significantly reduced with active levels 0.75-2%.

### 4.11.4 Does Incubation with Hydrosativum P Promote One *Staphylococcus* spp. Over Another in a Planktonic Growth Co-Culture?

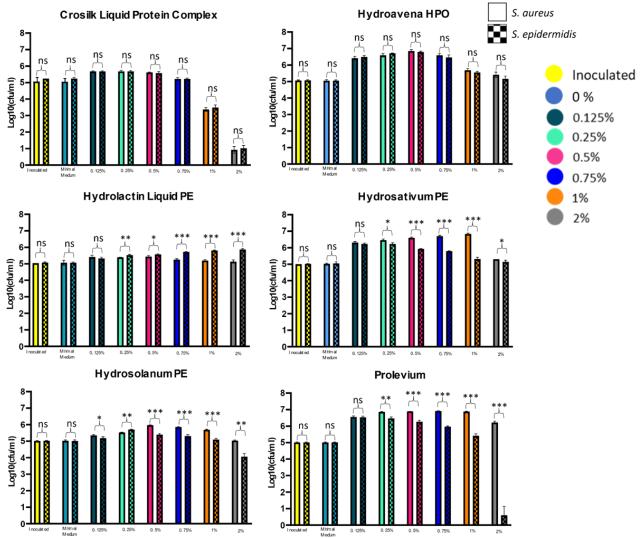
When grown with 0.125% Hydrosativum P, neither *S. aureus* nor *S. epidermidis* were significantly promoted over each other (P>0.05). However, with 0.25% upward, *S. aureus* was promoted significantly more than *S. epidermidis* (P<0.045). The total cfu/ml of *S. aureus* increased significantly until grown with 2% active, where the cfu/ml was significantly decreased compared to growth with 1% (P<0.001). However, even growth with 2% active resulted in a higher end cfu/ml than the initial inoculated amount (P<0.001). While *S. aureus* grew more successfully, the total cfu/ml of *S. epidermidis* never dropped significantly below the initial inoculated amount (P=0.09), but the final cfu/ml did significantly drop when grown with 0.5-2% compared to growth with both 0.125% and 0.25% (P<0.003).

### 4.11.5 Does Incubation with Hydrosolanum PE Promote One *Staphylococcus* spp. Over Another in a Planktonic Growth Co-Culture?

When grown with Hydrosolanum PE, *S. aureus* was significantly promoted over *S. epidermidis* when grown with 0.125% active, but only slightly (P=0.0475). When grown with 0.25% active Hydrosolanum PE, this is reversed and *S. epidermidis* is significantly promoted over S. aureus (P=0.0012). However, when grown with 0.5% active and above, *S. aureus* is significantly promoted over *S. epidermidis* (P<0.001). The final cfu/ml of *S. aureus* increased until 0.5%, when it decreased significantly from 0.75% active onwards. However, the final cfu/ml never significantly decreased below the initial inoculated amount, even with 2% active (P=0.44).

### 4.11.6 Does Incubation with Prolevium Promote One *Staphylococcus* spp. Over Another in a Planktonic Growth Co-Culture?

Growth with 0.125% Prolevium neither promoted the growth of *S. aureus* nor *S. epidermidis*. However, from 0.25% onward, *S. aureus* was significantly promoted over *S. epidermidis* (P<0.0012). The total cfu/ml of *S. aureus* significantly increased when grown with 0.25% compared with 0.125% active (P=0.0008). However, there was no significant difference between the final cfu/ml of *S. aureus* when grown with 0.25-1% active (P=0.149), with 2% active the final cfu/ml was significantly reduced (P=0.0002) but still significantly more than the starting inoculum (P<0.0001). The final cfu/ml of *S. epidermidis* decreased significantly when grown with 0.5-2% active Prolevium (P<0.05). However, the final cfu/ml only significantly decreased compared to the inoculated amount when grown with 2% active (P=0.0002).



**Figure 21. Final Cfu/ml of the Mixed** *Staphylococcus* **spp. Culture; Planktonic Growth**. These experiments were completed with three technical replicates and three biological replicates. *S. aureus* is represented by the non-patterned bars while *S. epidermidis* is referenced by the chequered bars. The yellow bars are the inoculated amount, the blue bars are the species when grown with minimal medium without supplement. There was never any significant difference between the inoculated numbers of each bacterium or the final cfu/ml after incubation with the minimal medium alone.

## 4.12 Does Incubation with Cosmetic Proteins Promote One *Staphylococcus* spp. Over Another in a Sessile Growth Co-Culture?

When grown in the minimal medium supplemented with 0.6% casamino acids, a biofilm was formed which comprised of 59% *S. epidermidis* and 41% *S. aureus*, as seen on the green bar from Figure 22. Results below are referencing data shown in Figure 22.

### 4.12.1 Does Incubation with Crosilk Lpc Promote One *Staphylococcus* spp. Over Another in a Sessile Growth Co-Culture?

When grown with Crosilk Lpc, a quantifiable biofilm was only formed with 0.125 and 0.25% active. There was no significant difference between the measurable biofilm formed at both active levels (P=0.23), however there were differences in the quantity of each species. While both biofilms were heavily *S. aureus* dominated, at 0.125%, 28% of the biofilm was formed by *S. epidermidis*. At 0.25% active level, only *S. aureus* was able to be measured using the Miles and Misra method.

### 4.12.2 Does Incubation with Hydroavena HPO Promote One *Staphylococcus* spp. Over Another in a Sessile Growth Co-Culture?

Biofilms were formed with every active level of Hydroavena HPO, with varying dominating species. With 0.125% active, the biofilm formation was split 24.1% *S. epidermidis* compared to 75.9% of *S. aureus*, there was significantly less quantifiable biofilm formed than at 0.5% and 1% active (P<0.03). There was no significant difference between the quantifiable biofilm formed with 0.25% and 0.5% active Hydroavena HPO (P>0.05), *S. aureus* was also the only detectable species in the biofilm with both active levels. With 1-4% active Hydroavena HPO, there was a significant drop in measurable biofilm compared to the lower active levels (P<0.0002). With active levels 1-4% there was also a shift in the dominating *Staphylococcus* spp., with 1% active the biofilm was dominated by 55% *S. epidermidis*, with 2% *S. epidermidis* made up 65% of the biofilm and 63.4% of the biofilm formed with 4%.

### 4.12.3 Does Incubation with Hydrolactin Liquid PE Promote One *Staphylococcus* spp. Over Another in a Sessile Growth Co-Culture?

Biofilms were formed with every active level of Hydrolactin Liquid PE, with the most significant biofilm structures were formed with 0.5 and 1% active (P<0.05). There was no significant difference between the biofilms formed with 1 and 2% (P>0.05), while the biofilm formed at 0.25% had significantly more established cells than with 0.125% active (P=0.007). *S. epidermidis* dominated the biofilm formations at every active level making up 69% with 0.125 and 0.25% active and 79.2% with 0.5% active. With 1%, 2% and 4% active the only quantifiable bacterium was *S. epidermidis*.

### 4.12.4 Does Incubation with Hydrosativum P Promote One *Staphylococcus* spp. Over Another in a Sessile Growth Co-Culture?

The bacteria were again able to form quantifiable biofilms with every active level of Hydrosativum P. There was no significant difference between the biofilms formed with 0.25 and 0.125% active

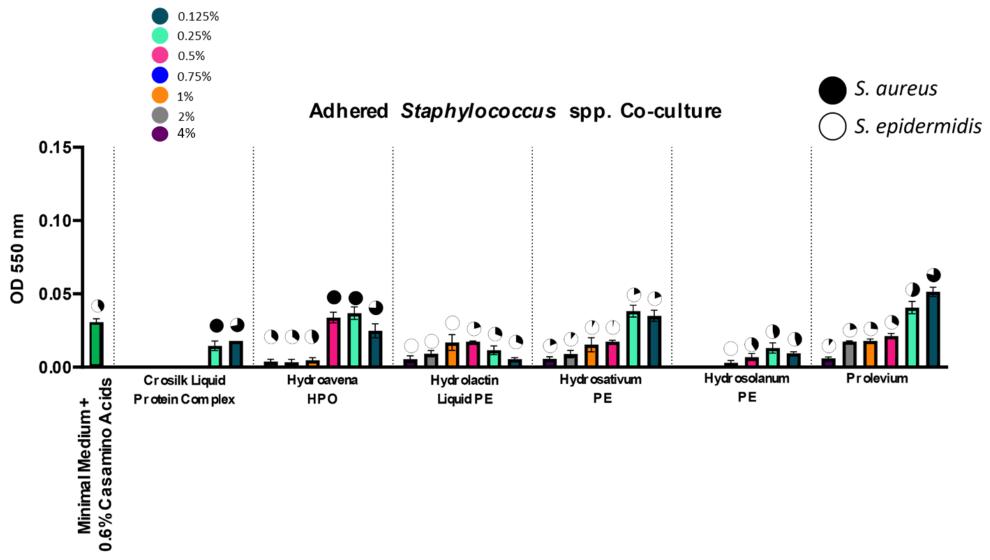
(P>0.05) which had significantly more established biofilm than with any other active level (P<0.0009). There was also no significance between biofilms formed with 0.5 and 1% active, 1% and 2% active and 2% and 4% active (P>0.05). Again, the dominant species of biofilms formed with every active level was *S. epidermidis*. With 0.125% active Hydrosativum P, *S. epidermidis* formed 66% of the biofilm, with 0.25% *S. epidermidis* made up 80.4%, followed by 97.5% with 0.5, 92.9% with 1%, 89.1% with 2% and formed 81.2% of the biofilm with 4% active Hydrosativum P.

### 4.12.5 Does Incubation with Hydrosolanum PE Promote One *Staphylococcus* spp. Over Another in a Sessile Growth Co-Culture?

Quantifiable biofilm was only detected with up to 1% Hydrosolanum PE, there was no significant difference between the biofilms formed with 0.125, 0.25 and 0.5% active (P>0.05). *S. epidermidis* narrowly dominated the biofilms formed with 0.125, 0.25 and 0.5% active, making up 54%, 53% and 58% respectively. *S. epidermidis* was the only species quantifiable from the biofilm formed with 1% active Hydrosolanum PE.

### 4.12.6 Does Incubation with Prolevium Promote One *Staphylococcus* spp. Over Another in a Sessile Growth Co-Culture?

A quantifiable biofilm was formed with every active level of Prolevium, with varying results as to which species dominated. The biofilm formed with the most significant number of adhered cells was with 0.125% (P<0.007), followed by 0.25%, 0.5%. 1% and 2% active. The biofilms formed with 0.125 and 0.25% active Prolevium were dominated with 79% and 55.4% *S. aureus,* respectively. From 0.5-4% active *S. epidermidis* was the dominant species in the biofilm, making up 65.2% of the biofilm with 0.5%, 74% of the biofilm with 1%, 79% of the biofilm with 2% and 90% of the biofilms formed with 4% active Prolevium.



**Figure 22. OD readings Of Crystal Violet which Stained Adhered Cells and the Ratio of** *Staphylococcus* **spp. in the Biofilm.** These experiments were completed with three technical replicates and three biological replicates. The first bar is the control of both species grown with minimal medium plus 0.6% w/v casamino acids. The ratios are represented by pie charts above the bars, black is *S. aureus* and white is *S. epidermidis*.

#### 4.13 Discussion

#### 4.14 Planktonic Mixed Species Growth Reflects Individual Species Growth

The planktonic growth of each species in co-culture were reflective of their individual planktonic growth from Section 3.22. If a species grew better than the other with a cosmetic protein, then that species was more likely to be the dominant species in the co-culture. For example, *S. epidermidis* achieved a higher yield and faster growth rates when grown with every active level of Hydrolactin Liquid PE compared to *S. aureus*. This result was reflected in the co-culture where the final cfu/ml of *S. epidermidis* was significantly higher than *S. aureus* when grown with 0.25% active level and up of Hydrolactin Liquid PE. This pattern is again presented when grown with Crosilk Lpc and Hydroavena HPO, both individual species grew equally poorly with Crosilk and well with Hydroavena HPO.

Previous work has shown that *S. aureus'* faster growth rate would make it dominate in a mixed culture with *S. epidermidis*, which was apparent when both were grown with proteins which *S. epidermidis* did not utilise well, Hydrosolanum PE and Prolevium (Figure 21). The slowed growth of *S. aureus* at pH 5 (Stewart et al. 2017), aided *S. epidermidis* to dominate growth with cosmetic proteins in which it grew well. The low pH of this experiment favoured growth of *S. epidermidis*, when a neutral pH may promote the growth of *S. aureus* and previous work at this pH has showed that *S. aureus* can grow with other bacterial species without interrupting the other species' health (Frapwell et al. 2018). This could explain why in cosmetic proteins, which both species either grew

#### 4.15 *Staphylococcus* species May Tolerate the Presence of Each Other

When co-cultured with both Crosilk and Hydroavena HPO, there were no significant differences between the species of their final cfu/ml. Most research has focused on *S. aureus* being an invasive pathogen, but little has been written about its commensal status (Cogen et al. 2008). This organism can be found on many peoples' skins as part of the natural microbiota in and around the nose, therefore interactions with *S. epidermidis* wouldn't always be antagonistic (Sakr et al. 2018; Boxberger et al. 2021). These *Staphylococcus* spp. have possibly previously benefitted from being in close contact, methicillin resistance gene cassettes are thought to have been passed on to *S. aureus* from *S. epidermidis*, through horizontal gene transfer (Otto 2009). As the results from Figure 21 show, the lack of domination by one species would suggest, perhaps not a cooperative relationship, but one of cohabitation.

#### 4.16 The Lower pH favours *S. epidermidis* in Biofilm Domination

*S. aureus* and *S. epidermidis*, have both been found in multispecies biofilms of skin ulcers (Johani et al. 2017). Proving that, while reported for reducing *S. aureus* colonisation, *S. epidermidis* can co-exist with its close relative in pathogenic circumstances. Both species can also dominate a

mixed staphylococcal biofilm, when equally inoculated and under alkali and neutral conditions, *S. aureus* dominates over *S. epidermidis*. However, at pH 5, this is reversed as in acidic conditions *the* genes which enable *S. aureus* cell adherence are downregulated (Efthimiou et al. 2019) and *S. epidermidis* has the ability to become the dominant species within the biofilm (Stewart et al. 2017; Efthimiou et al. 2019). The dominance of *S. epidermidis* is reflected in many of the results from Figure 22. The only instances in which *S. aureus* dominated the biofilms were with all levels of Crosilk Lpc and with the lower active levels of Hydroavena HPO and Prolevium. If the genes for *S. aureus* are downregulated, this would leave *S. aureus* at risk from the higher concentrations of preservatives, which *S. epidermidis* could tolerate. The dominance of *S. epidermidis* could also be down to the species' auto-inducing peptides which inhibits the quorum-sensing gene regulators (*agr*) of *S. aureus* (Boles and Horswill 2008), which are involved in biofilm formation (Yarwood et al. 2004).

#### 4.17 Planktonic Growth and Sessile Growths are Dominated by Different Bacteria

We can reject the null hypothesis for planktonic growth of the co-culture, when grown with most active levels of Hydrolactin Liquid PE, Hydrosativum P, Hydrosolanum PE and Prolevium. However, planktonic growth of the co-cultured species with either Crosilk Lpc or Hydroavena HPO did not promote one species over the other, therefore we can accept the null hypothesis for these cosmetic proteins. For biofilm production, we can reject the null hypothesis for all co-cultured growth with all the cosmetic proteins as one species was always promoted over another. Planktonic growth versus sessile growth, of all bacteria, differ in their nutritional requirements and susceptibility to antimicrobials (Donlan 2002). This is reflected in the difference in the species which dominated dependent on type of growth. S. aureus for example dominated in planktonic growth with most active levels of Hydrosativum P, Hydrosolanum PE and Prolevium. However, S. epidermidis made up more than 50% of the biofilm when grown with most active levels of these cosmetic proteins. Planktonic growth of S. aureus is not significantly affected by acidic pHs (Korting et al. 1992), that would explain why within the planktonic co-culture S. aureus could dominate. However, sensitivity of *S. aureus* to acidic stresses (lyer et al. 2021) can cause down regulation of biofilm related genes (Efthimiou et al. 2019). S. aureus' sensitivity can also cause a reduced colony size (Mirza et al. 1985), which affects the quantity of biomass within a biofilm (Yoshioka and Newell 2016). Therefore, the lack of sensitivity of *S. epidermidis* to lower pHs meant that this species was more capable of biofilm domination with nutrient appropriate cosmetic proteins. Throughout experiments from Sections 4, 3.22.1 and 3.24.1, S. epidermidis has never proliferated when grown in the minimal medium supplemented with Crosilk Lpc. The amino acid content of Crosilk had a high percentage of serine (Table 7), if racemization of serine had occurred, while both S. aureus and S. epidermidis have difficulty growing in the presence of Dserine, S. epidermidis is far more sensitive (Sakinç et al. 2009). However, the poor growth of S.

102

*epidermidis* could also have been due to the high concentration of disodium EDTA found in Crosilk Lpc. Disodium EDTA has been shown to have a bacteriostatic effect against planktonic cells and have the ability to inhibit growth and promote dispersal of *S. epidermidis* biofilms (Juda et al. 2008).

While promoting any type of biofilm formation is unadvisable, promotion of biofilm formations dominated by *S. aureus* over *S. epidermidis* could cause severe illness. Therefore, ensuring products do not alter the natural pH of the skin by keeping them at lower pHs would favour *S. epidermidis* health over *S. aureus*. To ensure that *S. epidermidis* can aid in downregulating *S. aureus* colonisation on the skin, formulations should avoid preservatives in which *S. epidermidis* is highly sensitive too, especially EDTA and EDTA derivatives.

5 *In Vitro* Stimulation of Immune Response Biomarkers of an Immortal Keratinocyte Cell-line by Addition of *Staphylococcus* spp. and Cosmetic Proteins

#### 5.1 Immune Response to Commensal Microbes

The importance of the human microbial community does not simply start and end with the microbes that reside there, but the interactions between them and the host cells. Commensal microbes are recognised by the immune system as little or no threat and induce homeostasis (Belkaid and Harrison 2017). The sheer presence, however, of skin microbes is enough to trigger and reinforce the immune response (Abdallah et al. 2017). This readies the immune system for any microbial dysbiosis, pathogenic invasions and quick wound repair (Linehan et al. 2018; Timm et al. 2020).

Exposing chemicals to the skin may cause its own immune response which manifest as contact dermatitis (Martin et al. 2011; Martin 2017; Nicolai et al. 2020). The addition of these substances may alter the natural composition of the bacterial environment, depleting or promoting species growth (Bouslimani et al. 2019). The change in the microbial arrangement could spark an immune response (Mezouar et al. 2018; Catinean et al. 2019; Faas et al. 2020; Swaney et al.).

#### 5.2 HaCaT Cells in Skin Studies

The cell-line HaCaT are immortal keratinocytes cells, more resilient and longer lasting than primary keratinocyte cell lines (Colombo et al. 2017; Griffoni et al. 2021). As the epidermis is >90% Keratinocytes, HaCaTs are used *in vitro* for numerous experiments regarding skin. This includes experiments which aim to measure the skin's innate immune response to pathogens and disease (Olaru and Jensen 2010; Henrot et al. 2020).

#### 5.3 Immune Response Biomarkers

The pathways of the immune markers can be found in Table 8.

#### IL-8

High levels of the chemokine Interleukin-8 (IL-8, CXCL8) are associated with numerous diseases (Shahzad et al. 2010). Many types of tissue release IL-8 as part of their immune response and therefore IL-8 is used as a biomarker for clinical diagnosis and *in vitro* experiments (Shahzad et al. 2010; Quist et al. 2016; Ke et al. 2019; Griffoni et al. 2021). Keratinocytes are one of the tissue types which release IL-8 in response to inflammatory stimuli and while this is mostly from pathogenic invasion, interleukins have been produced by HaCaT cells, when stimulated with known chemical skin irritants (Mohamadzadeh et al. 1994).

#### TNF-α

Tumour necrosis factor-  $\alpha$ , as the name suggests, is part of the innate immune system which targets and causes cancerous cells to undergo apoptosis (Wang and Lin 2008). However, production of TNF- $\alpha$  also increases in the presence of a bacterial infection (Ma et al. 2010). Different species or strains of bacteria could vary in the TNF- $\alpha$  levels expressed (Kragsbjerg et al. 1998). Keratinocytes express TNF- $\alpha$  through a multitude of stimulants including autoimmune diseases (Li et al. 2019c), bacterial infections (Johnston and Conly 2006) and UVB stimulation (Bashir et al. 2009).

#### IFN-¥

Interferon- $\gamma$  is a glycosylated proteins involved with the innate and adaptive immune system (Vilček et al. 1998). The specialised cytokine is synthesized mostly within immunity cells (Payne 2017), including Natural Killer cells and T regulatory cells (Griffin et al. 2008). IFN- $\Upsilon$  receptors are found throughout cells in the body. IFN- $\Upsilon$  has been used as a biomarker for an immune response against bacterial antigens delivered in vaccines (Weir et al. 2008). It is also used as a biomarker for skin conditions, increased IFN- $\Upsilon$  levels and IFN- $\Upsilon$  induced processes are found in individuals with atopic dermatitis (Rebane et al. 2012).

#### 5.4 Null Hypothesis

The addition of bacteria nor the exposure to cosmetic proteins would not cause any significant changes the concentration of immune markers found in the supernatant of HaCaT cells.

#### 5.5 Aims

- Investigate the effect of *Staphylococcus* spp. have on the concentration of immune marker concentration found in the supernatant of HaCaT keratinocytes
- Investigate how the exposure of keratinocytes and bacteria to cosmetic proteins effects the concentration of immune marker concentration found in the supernatant of HaCaT keratinocytes

Biomarker	Pathway
Interleukin-8 (IL-8)	When pathogen-associated molecular patterns are recognised, Toll-like receptors ligate which prompts the production of many pro-inflammatory proteins, including IL-8 (Christmas 2010). IL-8 then draws in neutrophils to the infection site to neutralise the
	microbial threat (Kobayashi et al. 2018) IL-8 also upregulates complement receptors on the surface of neutrophils, which boosts the adherence of the leukocytes (Zwahlen et al. 1993). Stimulates respiratory burst which releases reactive oxygen species when neutrophils are infected by a pathogen, which degrades the bacteria (Bréchard et al. 2005).
Tumour Necrosis Factor - α (TNF-α)	Mostly produced by macrophages (Parameswaran and Patial 2010), TNF- $\alpha$ are proteins which are involved in both the innate and acquired immune responses. It is predominantly involved in tissue degradation, repair and signalling. These signalling pathways are dependent on which of the transmemebrane TNF- receptors are activated. TNFR1 starts a pathway in which promotes inflammatory cytokine concentration and survival of the cells. TNFR2 signals a different pathway in which cell proliferation and migration. Both receptors are more focused on cell survival and can inhibit targeted cell apoptosis (Yang et al. 2018). However, TNF- $\alpha$ can also trigger hyper-inflammation which can lead to elongated wound healing times(Ashcroft et al. 2012).
Interferon- ¥ (IFN-¥)	When macrophages recognise a pathogenic invasion, IFN-X releasing interleukins are activated (Schroder et al. 2004). IFN-X itself binds to IFNG receptors, which are present on a range of cell types. This starts the activation of two Janus kinases JAK1 and JAK2 (Shtrichman and Samuel 2001). JAK1 and JAK2 release phosphate which signal transducer and activator of transcription (STATs) form a dimer with. The large dimer then moves into the cell and binds to DNA. This, in turn, triggers the activation of genes to further the immune response (Kisseleva et al. 2002).

#### 5.6 Materials

#### 5.7 Proteins

Hydrosolanum PE and Hydrosativum P were chosen for this experiment as both had previously shown either positive or very little negative effects on the growth of the commensal *S. epidermidis* or did not overly promote *S. aureus* over the growth of *S. epidermidis*. The proteins were also in-keeping with cosmetic trends of not having been derived from animal products. Hydroavena HPO fit both profiles, however this cosmetic protein differs from the others tested as a large percentage of the active level contains oligosaccharides rather than peptides. The proteins were diluted in sterile dH2O pH 5 to active levels of 0.125%, 0.25%, 0.5%, 0.75%, 1% and 2%. The controls were fresh media and 0% (sterile dH2O, pH 5).

#### 5.8 Bacteria

Both *Staphylococcus aureus* and *Staphylococcus epidermidis* used were as described previously in Section 2.6. *S .aureus* was stained with the fluorescent dye of CellTrace Red, and *S. epidermidis* was stained with flourescent CellTrace CFSE. Both *Staphylococcus* spp. were grown, as in Section 2.10, then spun at 6000 x g, washed twice with 1x PBS and incubated with the fluorescent dye. The bacteria were diluted down to  $0.5 \times 10^6$  cfu/ml ready to be seeded, this number was chosen because in the preliminary experiments it was the most consistent inoculation number to be able to produce quantifiable adhered cells. Fluorescence for CellTrace red was measured at 635 nm excitation, and at 488 nm excitation for CellTrace CFSE. Fluorescence staining was originally used so that the bacteria could be counted by flow cytometry, but was then used to ensure the bacteria were still present throughout the week long experiment.

#### 5.9 HaCaT Cells

HaCaT cells were kindly donated by the School of Dentistry at Cardiff University. Mycoplasma detection was carried out using polymerase chain reaction analysis involving mycoplasma specific primers (Hopert et al. 1993), the results were negative. The cells were cultivated as per suggestions from the dental school. HaCaTs were grown in high glucose DMEM plus pyruvate, 10% v/v fetal bovine serum, 1% v/v antibiotic-antimyotic (Streptomycin, Amphotericin B, Penicillin), 1% v/v L-Glutamine and in an incubator set at 5% CO<sub>2</sub>, 37 °C. For the experiments, where bacteria were involved, there was no antibiotic present in the media. Cells were split appropriately once approximately acheived 60-70% confluence. Although the ideal pH for this experiment would have been pH 5, due to the time required to adjust the cells to a new pH, the media was used at the pH supplied. Changing the medium to a lower pH has been shown to reduce viability and the migration rates of cultured keratinocytes (Lönnqvis et al. 2015).

#### 5.10 Methods

#### 5.11 Tissue Experiment

HaCaT cells were grown to approximately 60-70% confluent and diluted to  $0.5 \times 10^5$  cells/ml. These were seeded into 96 well plates for a final volume of 200 µl and incubated overnight. When a confluence of 40% across the plates was reached, this would be taken as time point 1 and the supernatent would be removed and stored for further work. The supernatent would be replaced with either fresh media, fresh media and *S. aureus*, fresh media and *S. epidermidis* or fresh media and a 1:1 *Staphylococcus* mix. Fluorescence was measured on a microplate reader to confirm presence of bacteria. After 48 hours to allow for sufficient bacterial adherence, the supernatent was removed and labelled as time point 2. The adhered cells were washed once with 1xPBS before being incubated with 100 µl of verying levels of proteins or controls for 15 minutes. The proteins were replaced with fresh media before fluorescence was measured to confirm bacterial presence and incubated. After 24 hours, supernatent for time point 3 was saved and the bacteria quantified.

#### 5.12 Microscope Images

After bacteria were seeded with the established HaCaT cells, they were left to incubate for 48 hours. The wells were examined using the GXM-XDS Inverted Biological Phase Contrast Microscope (GT-Vision Ltd, Sudbury) at 40x magnification and images captured using a GXM-camera extension (GT-Vision Ltd, Sudbury). The images taken were of the control of HaCaT cells alone, HaCaT cells that were incubated with *S. aureus*, HaCaT cells which were incubated with *S. epidermidis* and HaCaT cells which were incubated with a 1:1 ratio *Staphylococcus* spp. mix.

#### 5.13 Biomarker Assays

Sandwich ELISA assays for IL-8, IFN-Y and TNF- $\alpha$  were purchased from Peprotech. Assays were carried out per the manufacturer's protocols. Biomarker levels were measured in the supernatent that was removed at each time point, at neat, 1/25 and 1/50 dilutions.

#### 5.14 Measurement of Adhered Bacteria

The quantity of each *Staphylococcus* species which had adhered to the plate or HaCaT cells were due to be measured on a flow cytometer. However, due to pandemic restraints on the University equipment, the flow cytometer was unavailable for use. Instead, the adhered bacteria were twice washed with 1xPBS and scratched off with a pipette tip. To quanitify, the bacteria were diluted in 1xPBS, plated, incubated and counted using the Miles and Misra method. Indivudal species were plated onto TSA, while co-culutred species were plated onto MSA.

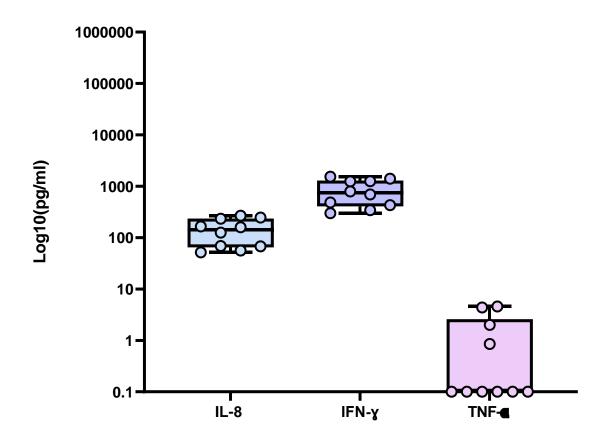
#### 5.15 Statistics

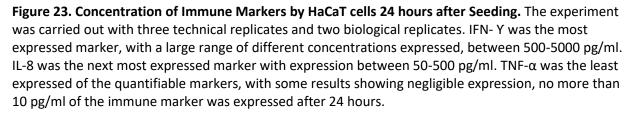
The mean concentrations of immune markers from the ELISA results and mean cfu/ml from the Miles and Misra method were analysed using t-tests using GraphPad Prism (Version 9.1.2). Graphs below were also made using this software.

#### 5.16 Results

#### 5.17 24 Hours After Seeding HaCaT Cells

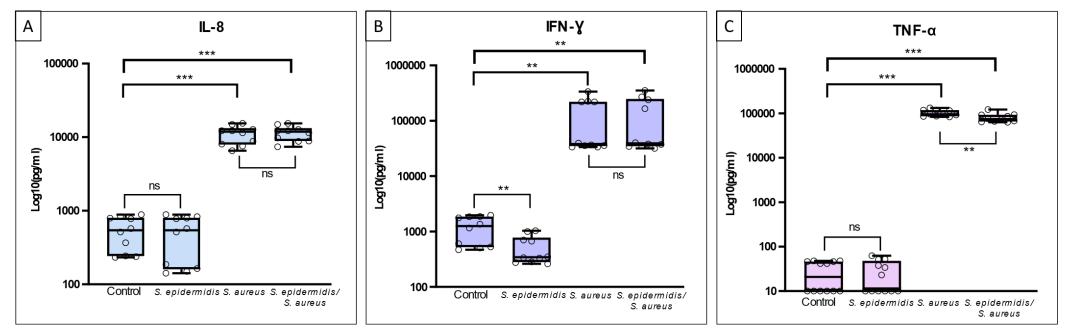
The following results are in reference to Figure 23. The other Immune markers were expressed 24 hours after seeding into the 96 well plate (Figure 23). IL-8 had a mean concentration of 144.0 pg/ml, with a range of 216.2 pg/ml and a standard deviation of 83.19 pg/ml. TNF- $\alpha$  concentration was on average 1.178 pg/ml with a range of 4.571 pg/ml and a standard deviation of 1.848 pg/ml. IFN- $\chi$  had the largest range of concentration with 1233 pg/ml and an average concentration of 846.7 pg/ml, due to this large discrepancy in concentration the standard deviation is 469.6 pg/ml.





#### 5.18 48 Hours After Incubation with Bacteria

The following results are in reference Figure 24 A, B and C. The addition of *S. epidermidis* to HaCaT cells did not increase the immune markers expressed by HaCaT cells. Both IL-8 (Figure 24A) and TNF- $\alpha$  (Figure 24C) concentration were not significantly changed by the addition of *S. epidermidis* (P>0.7), while IFN-Y (Figure 24B) concentration was significantly reduced (P=0.006). Incubation with *S. aureus* or the *Staphylococcus* spp. co-culture elevated the concentration of all immune markers. Increased concentration of IL-8 and TNF- $\alpha$  were the most prominent (P<0.0001), while IFN-Y still significantly increased (P=0.0044). Despite double the number of bacteria inoculated to the HaCaT cells, compared to *S. aureus* alone, the co-culture of bacteria did not significantly change the concentration of IL-8 and IFN-Y (P>0.07) and had significantly decreased the concentration of TNF- $\alpha$  (P=0.013).



**Figure 24. Concentration of Immune Markers measured in the HaCaT Supernatant after 48 hours Incubation with Bacteria.** The experiment was carried out with three technical replicates and two biological replicates. A) IL-8 B) IFN-Y and C) TNF-a. There was no significant difference between the concentration of IL-8 in HaCaT supernatant between the control and HaCaT cells incubated with *S. epidermidis* (P>0.05). However, incubation with *S. aureus* increased the concentration of IL-8 by at least 10-fold compared to both the control and HaCaT with *S. epidermidis* (P<0.001). A similar result is seen when HaCaT cells were incubated with both *Staphylococcus* spp., however the concentration of IL-8 was not significantly different from when HaCaT cells were incubated with *S. aureus* alone (P>0.05). A similar result to IL-8 was seen with IFN-Y, however incubation with *S. epidermidis* significantly decreased the concentration of IFN-Y in the supernatant (P<0.01). Again, incubation with S. aureus and the Staphylococcus spp. mix increased the concentration of TNF-a in the supernatant, however this was nearly 10,000-fold (P<0.001), as TNF-a was barely negligible when HaCaT cells were alone or incubated with *S. epidermidis*.

## 5.19 Microscope Images of HaCaT Cells After 48 hours, Incubation with and without Staphylococcus spp.

Images (Figure 25) from the microscope show the physiological health and attachment of the HaCaT cells 72 hours after initial seeding and 48 hours after introduction of *Staphylococcus* spp. The results in Section 5.18 are a qualitative and descriptive assessment of the images.

#### 5.19.1 How did the HaCaT Cells Look without Bacteria?

Without the addition of bacteria, the HaCaT cells had a continuous unbroken mosaic formation around the perimeter of the well and proliferation of the cells were moving towards the centre of the well. There was evidence of cell death, due to some shrivelled cells that had remained attached to the monolayer (Figure 25A).

#### 5.19.2 How did the HaCaT cells look when Grown with *Staphylococcus epidermidis*?

The HaCaT cells still were in a mosaic pattern, but there were more gaps between clumps of cells. Cells were still proliferating towards the centre of the well. There were more signs of dead cells and some cells had become swollen, and some cells had detached (Figure 25B).

#### 5.19.3 How did the HaCaT cells look when Grown with *Staphylococcus aureus*?

HaCaT cells were still mostly confined to the perimeter but were separated into clumps. The cells were extremely swollen, and many were shrivelled and dead. Any proliferation into the centre of the well had now stopped and there were many cells that had removed from attachment (Figure 25C).

#### 5.19.4 How did the HaCaT cells look when Grown with a Co-culture of *Staphylococcus*

#### spp.?

HaCaT cells were still surrounding the perimeter, but again, separated into lots of clumps of cells. The cells were again swollen, and many appeared shrivelled and detached, but not to the extent of *S. aureus* alone. There was no evidence that the cells were proliferating into the centre of the well. Again, many cells had detached from the bottom of the well (Figure 25D).

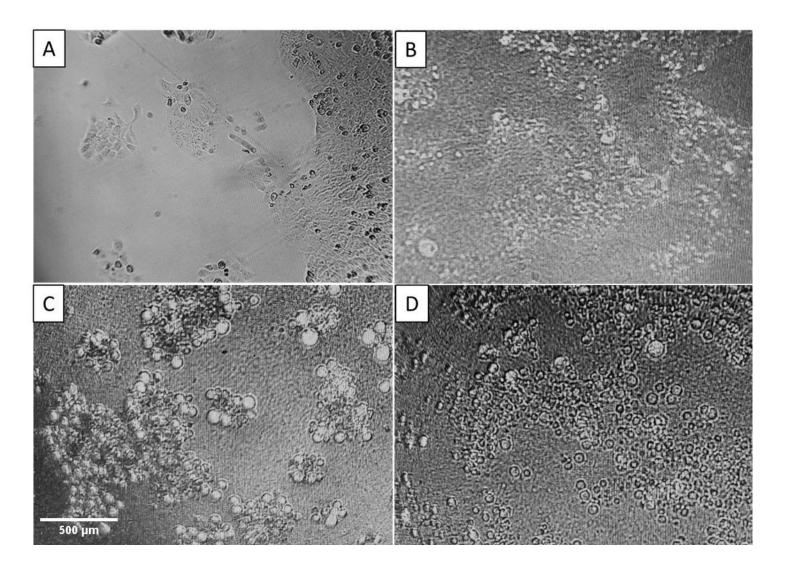


Figure 25. Microscope images of HaCaT cells Grown with and without *Staphylococcus* **spp.** A) HaCaT alone B) HaCaT with S. epidermidis C) HaCaT with S. aureus D) HaCaT with S. epidermidis and S. aureus Mix. After 48 hours of incubation, there are naturally dead cells present without the addition of bacteria. However, clear stress signs can be seen with HaCaT cells incubated with the bacteria, especially with S. aureus alone or with the co-culture. Reduced adhesion and cell swelling are clear indications of the keratanocytes are under immune stresses.

## 5.20 Does Exposure to Hydrosativum P Affect Interactions Between the *Staphylococcus* spp. and HaCaT Immune Marker Concentration?

### 5.20.1 How did exposure to Hydrosativum P alone Affect the Concentration of IL-8 from HaCaT cells?

All results below are in respect to Figure 26. Exposure of HaCaT cells to sterilised water (0%), 0.5% and 0.75% active levels of Hydrosativum P had no significant effect on the concentration of IL-8 (P>0.06). Exposure to 0.125, 0.25, 1 and 2% active levels of Hydrosativum P significantly reduced the amount of IL-8 expressed by the HaCaT cells (P<0.05). There were no significant differences between the amount of IL-8 expressed when exposed to 0.5 and 0.75% active levels compared to 2% active level of Hydrosativum P. Therefore, the concentration of IL-8 was on trend to be less when exposed to Hydrosativum P, compared to the control, reducing expressed IL-8 from an average of 509.6 pg/ml to as low as 362.6 pg/ml.

### 5.20.2 How did exposure to Hydrosativum P Affect the Concentration of IL-8 from HaCaT cells incubated with *S. epidermidis*?

The addition of S. epidermidis alone to HaCaT cells reduced the concentration of IL-8 significantly (P<0.001), from an average concentration of 551.7 pg/ml to 134.1 pg/ml. Exposure to water and the 0.125% active level of Hydrosativum P did not significantly change (P>0.10) the expressed IL-8 compared to S. epidermidis alone. Exposure to 0.25-0.75% active level significantly increased (P<0.001) the expressed IL-8 compared to S. epidermidis alone. With 0.25% active level concentration levels were still significantly less (P=0.005) than HaCaT cells without S. epidermidis, 509.6.7 pg/ml compared to 280.4 pg/ml. With 0.5 and 0.75% active level it was not significantly more than HaCaT cells without S. epidermidis (P>0.42), 509.6 pg/ml compared to 555.3 pg/ml and 522.2 pg/ml, respectively. Exposure of HaCaT cells with S. epidermidis to 1% active level of Hydrosativum P significantly increased the concentration of IL-8 compared to HaCaT cells alone (P<0.003). HaCaT cells alone expressed 509.6 pg/ml, while when grown with S. epidermidis and exposed with 1% active level this increased to 825.7 pg/ml. Exposure to 2% active levels of Hydrosativum P overall significantly reduced the concentration of IL-8 to 489.3 pg/ml, however the range of expressed IL-8 with this active level is large between 380-676.56 pg/ml. While S. epidermidis reduced the concentration of IL-8, exposing HaCaT grown with S. epidermidis to increased levels of Hydrosativum P increased the IL-8 expressed.

### 5.20.3 How did exposure to Hydrosativum P Affect the Concentration of IL-8 from HaCaT cells incubated with *S. aureus*?

Incubation of HaCaT cells with *S. aureus* significantly increases the average concentration of IL-8 compared to HaCaT cells alone or with *S. epidermidis* (P<0.001), concentration of IL-8 was raised up to 3039 pg/ml. Exposure to Hydrosativum P only slightly significantly raised the concentration level compared to HaCaT with *S. aureus* alone with active levels 0.125 and 0.25% (P<0.05). With 0, 0.5, 0.75, 1 and 2% active level of Hydrosativum P did not significantly change the concentration of IL-8

compared to HaCaT cells with *S. aureus* alone (P>0.05). As a trend, addition of Hydrosativum to HaCaT cells grown with *S. aureus* did not increase IL-8 concentration of the cells, and if there was an increase it was only just significant.

## 5.20.4 How did exposure to Hydrosativum P Affect the Concentration of IL-8 from HaCaT cells incubated with *Staphylococcus* spp. Co-culture?

Again, when HaCaT cells were incubated with the *Staphylococcus* spp. mix, the IL-8 levels were significantly higher than when HaCaT cells were grown alone (P<0.001) and with *S. epidermidis* (P<0.001). The concentration of IL-8 was also slightly significantly increased compared to HaCaT cells with *S. aureus* alone (P=0.04). Exposure to Hydrosativum P active levels 0.5 and 0.75% significantly increased the IL-8 levels expressed by the HaCaT cells grown with the *Staphylococcus* co-culture, however it was only a slight significant increase (P=0.02). When HaCaT cells grown with *Staphylococcus* co-culture was grown with 0, 0.125, 25, 1 and 2% active levels of Hydrosativum P there was no significant change in concentration levels (P>0.06). Again, the addition of Hydrosativum P, generally, did not significantly affect the concentration of IL-8 by HaCaT cells grown with the *Staphylococcus* spp. co-culture, and if it was increased it was only slightly significant.

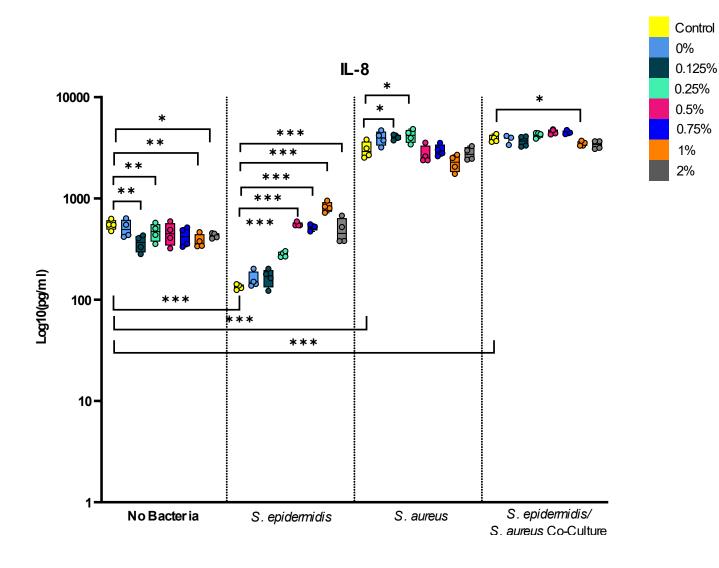


Figure 26. Concentration of IL-8 from HaCaT cells With or Without Bacteria after Being Exposed to Various Active Levels of Hydrosativum P. Yellow bars represent HaCaT cells (with or without bacteria) in which they have not been exposed to any outside source, only the media was changed out. The blue bar represents the HaCaT cells being exposed to 0% of the cosmetic protein, otherwise known as sterile water. The other colours are exposure to active levels 0.125-2% of the cosmetic proteins. Non-significant values were not added, nor values between species. \*<0.05, \*\*<0.01, \*\*\*<0.0001. For all statistics, please see above Section 5.19.1-5.19.4.

## 5.20.5 How did exposure to Hydrosativum P alone Affect the Concentration of IFN-Y from HaCaT cells?

The following results are in relation to Figure 27. HaCaT cells grown alone expressed a varied level of IFN-Y, but the average value was 443.8 pg/ml. When exposed to 0, 0.125, 0.25, 0.5, 0.5, 0.75 and 2% Hydrosativum P, there was no significant change in the IFN-Y expressed by the HaCaT cells. There was a slightly significant increase (P=0.045) in IFN-Y when HaCaT cells were incubated with 1% active level of Hydrosativum P, up to 818.4 pg/ml, but exposure to all active levels resulted in a large range of concentrations.

## 5.20.6 How did exposure to Hydrosativum P Affect the Concentration of IFN-¥ from HaCaT cells incubated with *S. epidermidis*?

While the addition of *S. epidermidis* did not significantly change the concentration of IFN-Y from HaCaT cells alone, the mean concentration at 206.6 pg/ml and only slightly significant result would suggest that it does have some reducing affect (P=0.054). The addition of 0.125-2% active levels of Hydrosativum also significantly increased (P<0.003) the concentration of IFN-Y compared to HaCaT cells grown with *S. epidermidis* alone, up to 1504 pg/ml. Even the exposure to 0%, (sterile water), increased the concentration of IFN-Y significantly to 994 pg/ml (P=0.0023). While the addition of *S. epidermidis* slightly decreased the concentration of IFN-Y, although not significantly, addition of water and Hydrosativum P increased the concentration significantly.

## 5.20.7 How did exposure to Hydrosativum P Affect the Concentration of IFN-Y from HaCaT cells incubated with *S. aureus*?

Addition of *S. aureus* to HaCaT cells significantly increased (P<0.001) to 35,616 pg/ml the production of IFN-X compared to HaCaT cells grown alone or with *S. epidermidis*. Exposure to 0-0.5% Hydrosativum P significantly increased the concentration (P<0.031) of IFN-X by HaCaT cells grown with *S. aureus* alone, up to 53,024 pg/ml with 0.5%. Exposure to 0.75-2% active level of Hydrosativum did not significantly change the concentration of IFN-X by HaCaT cells grown with *S. aureus* (P>0.15). Exposure of HaCaT cells grown with *S. aureus* to Hydrosativum P did increase the concentration of IFN-X, but not with 0.5% active level and above.

## 5.20.8 How did exposure to Hydrosativum P Affect the Concentration of IFN-Y from HaCaT cells incubated with *Staphylococcus* spp. Co-culture?

Incubation of HaCaT cells with the *Staphylococcus* spp. co-culture did increase the concentration of IFN-X compared to HaCaT cells grown alone, or with *S. epidermidis* (P<0.001). However, compared to HaCaT cells grown with *S. aureus* alone, there was no significant change in the IFN-X expressed (P=0.24). Exposure of HaCaT cells grown with *Staphylococcus* spp. mix to water, 0.125 or 2% active levels of Hydrosativum P did not significantly affect the concentration of IFN-X

(P>0.2). However, exposure to 0.25, 0.5, 0.75 and 1% active did significantly increase the concentration of IFN-Y (P<0.026).

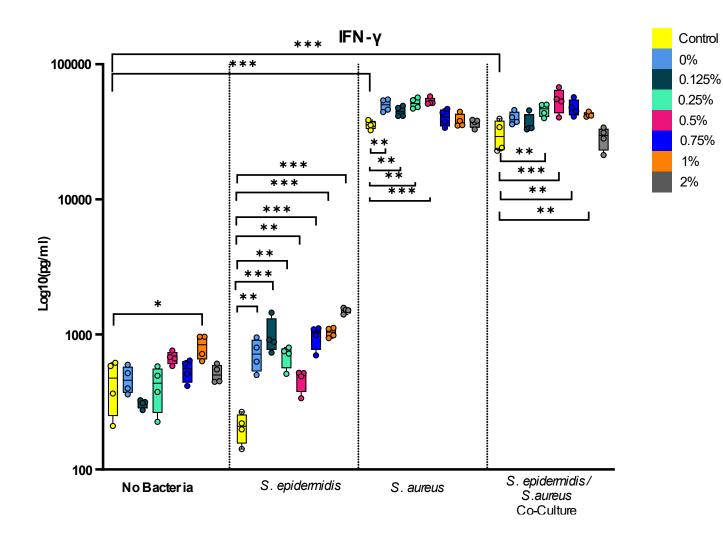


Figure 27. Concentration of IFN- X from HaCaT cells With or Without Bacteria after Being Exposed to Various Active Levels of Hydrosativum P. Yellow bars represent HaCaT cells (with or without bacteria) in which they have not been exposed to any outside source, only the media was changed out. The blue bar represents the HaCaT cells being exposed to 0% of the cosmetic protein, otherwise known as sterile water. The other colours are exposure to active levels 0.125-2% of the cosmetic proteins. Non-significant values were not added, nor values between species. \*<0.05, \*\*<0.01, \*\*\*<0.0001. For all statistics, please see Section 5.19.5-5.19.8.

# 5.20.9 How did exposure to Hydrosativum P alone Affect the Concentration of TNF- $\alpha$ from HaCaT cells?

All results below are in reference to Figure 28. HaCaT cells alone expressed 50.77 pg/ml of TNF- $\alpha$ . Exposure of Hydrosativum P to HaCaT cells alone increased concentration of TNF- $\alpha$  when exposed to 0, 0.125 and 0.25%, in which concentration increased up to 97.05 pg/ml (P<0.02). The biggest significant increase in TNF- $\alpha$  concentration was when HaCaT cells were exposed to Hydrosativum P at active level 2%, in which concentration shot up to 234.4 pg/ml (<0.001). However, exposure to 0.5, 0.75 and 1% active did not significantly increase concentration of TNF- $\alpha$  by HaCaT cells alone (P>0.05).

## 5.20.10 How did exposure to Hydrosativum P Affect the Concentration of TNF- $\alpha$ from HaCaT cells incubated with *S. epidermidis*?

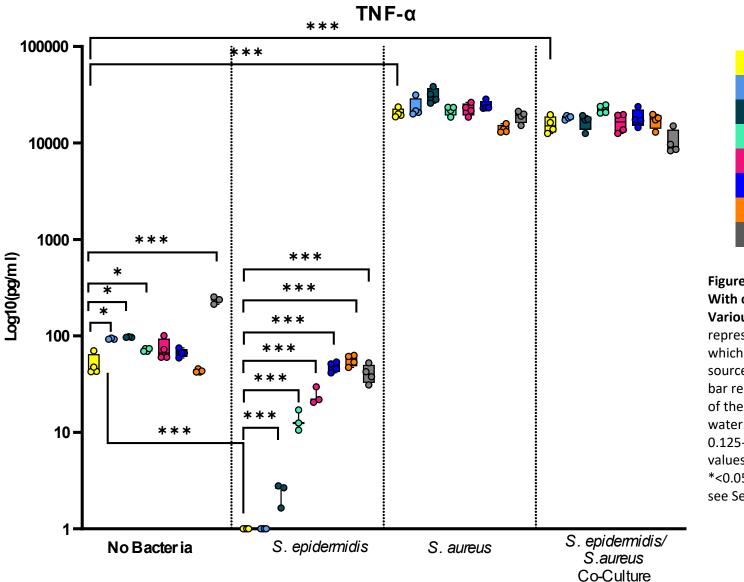
Growing HaCaT cells with *S. epidermidis* significantly reduced the concentration of TNF- $\alpha$  compared to HaCaT cells alone, no TNF- $\alpha$  was detected in the supernatant (P<0.001). Again, TNF- $\alpha$  was undetectable when HaCaT cells grown with *S. epidermidis* were exposed to sterile water (0%). However, exposure to 0.125% active level of Hydrosativum P and above increased the TNF- $\alpha$  expressed significantly compared to HaCaT cells with *S. epidermidis* alone (P<0.0006). However, exposure to 0.125, 0.25 and 0.5% Hydrosativum P still significantly reduced the concentration of TNF- $\alpha$  of HaCaT cells with *S. epidermidis* to Hydrosativum P at 0.75-2% active levels did not result in TNF- $\alpha$  concentration which was significantly more than HaCaT cells alone (P>0.2).

## 5.20.11 How did exposure to Hydrosativum P Affect the Concentration of TNF- $\alpha$ from HaCaT cells incubated with *S. aureus*?

*S. aureus* being incubated with HaCaT cells made their concentration increase to 20, 409 pg/ml, significantly more than HaCaT cells alone or with *S. epidermidis* (P<0.0001). Exposure of HaCaT cells incubated with *S. aureus*, to any level of Hydrosativum P did not significantly change the concentration levels of TNF- $\alpha$  (P>0.05).

## 5.20.12 How did exposure to Hydrosativum P Affect the Concentration of TNF- $\alpha$ from HaCaT cells incubated with *Staphylococcus* spp. Co-culture?

The *Staphylococcus* spp. co-culture being incubated with HaCaT cells made their concentration increase to 15, 597 pg/ml, significantly more than HaCaT cells alone or with *S. epidermidis* (P<0.001). However, this was significantly less concentration of TNF- $\alpha$  compared to HaCaT cells grown with *S. aureus* alone (P=0.045). Again, exposure of any active level of Hydrosativum P did not significantly change the concentration of TNF- $\alpha$  from HaCaT cells with *Staphylococcus* spp. mix (P>0.057).



Control 0% 0.125% 0.25% 0.5% 0.75% 1% 2%

Figure 28. Concentration of TNF-α from HaCaT cells With or Without Bacteria after Being Exposed to Various Active Levels of Hydrosativum P. Yellow bars represent HaCaT cells (with or without bacteria) in which they have not been exposed to any outside source, only the media was changed out. The blue bar represents the HaCaT cells being exposed to 0% of the cosmetic protein, otherwise known as sterile water. The other colours are exposure to active levels 0.125-2% of the cosmetic proteins. Non-significant values were not added, nor values between species. \*<0.05, \*\*<0.01, \*\*\*<0.0001. For all statistics, please see Section 5.19.9-5.19.12.

### 5.20.13 How did exposure to Hydrosativum P Affect the Final CFU/ml of *S.* epidermidis grown with HaCaT cells?

All results below are in reference to Figure 29. For the control, the final number of attached *S. epidermidis* grown with HaCaT cells was, on average, 2x10<sup>9</sup> cfu/ml. When exposed to the 0% control, i.e., sterile water, this final cfu/ml was not significantly reduced (p=0.55). However, when exposed to Hydrosativum P, the final cfu/ml of *S. epidermidis* was significantly reduced when exposed to active levels 0.125-2%, compared to both controls (for first control, P<0.0002, for 0% control P<0.004). The final cfu/ml of *S. epidermidis* was significantly reduced when grown with 0.25% compared to 0.125%, with 0.5% compared to 0.25% and with 2% compared to 1% (P<0.03). However, there was no statistical difference between the final cfu/ml of *S. epidermidis* when exposed to 0.5 and 0.75% active levels or 0.75% and 1% active levels of Hydrosativum P (P>0.05). The higher the active level of Hydrosativum P exposed to *S. epidermidis*; the fewer bacteria were able to remain attached. However, even at the highest active level tested, the final cfu/ml was still significantly higher than the original inoculated amount.

## 5.20.14 How did exposure to Hydrosativum P Affect the Final CFU/ml of *S. aureus* grown with HaCaT cells?

For the control, the final number of attached *S. aureus* grown with HaCaT cells was, on average, 2.2 x10<sup>9</sup> cfu/ml, not significantly different to the final number of adhered of *S. epidermidis* (P=0.44). Exposure to the 0% Hydrosativum P, sterile water, significantly reduced the final cfu/ml of adhered *S. aureus* (P=0.014), however after exposure to 0.125% active level of Hydrosativum P the final cfu/ml of adhered cells increased compared to 0% but was not significantly different to the original control (P=0.22). Exposure of 0.125-2% active levels of Hydrosativum P did not significantly change the number of adhered cells of *S. aureus* compared to the original control (P>0.2) and the final cfu/ml of *S. aureus* was not significantly different when all active levels were compared against each other (P=0.10). Although looking at the data from Figure 29 would suggest that increasing the active level of Hydrosativum P increased the final cfu/ml of adhered *S. aureus*, this was only a trend and was not significant.

## 5.20.15 How did exposure to Hydrosativum P Affect the Final CFU/ml of *Staphylococcus* spp. Co-culture grown with HaCaT cells?

For the control, the final number of attached *S. epidermidis* cells was on average 2.4x10<sup>8</sup> cfu/ml, while the number of attached *S. aureus* cells was on average 2.3x10<sup>8</sup> cfu/ml, no significant difference between the two (P=0.61). The final cfu/ml for both species did not significantly change when exposed to the 0% control (P>0.11). Exposure to 0.125-1% active levels of Hydrosativum P did not significantly alter the final cfu/ml of *S. epidermidis* compared to the control, with 2%

active level the final cfu/ml was significantly reduced to  $1.3 \times 10^8$  (P=0.0009). Exposure of *S. aureus* to 0.125 and 0.25% Hydrosativum P significantly increased the final cfu/ml to 2.8x10<sup>8</sup> with both active levels (P<0.02). However, exposure to 0.5-1% Hydrosativum P did not significantly alter the final cfu/ml of adhered cells compared to the control (P>0.05). Exposure of *S. aureus* to 2% active level of Hydrosativum P significantly reduced the final cfu/ml to  $1.5 \times 10^8$  (P=0.001). The only significant difference between adhered *Staphylococcus* spp. cells was when the two species were exposed to 0.25, 0.5 and 0.75% Hydrosativum P (P<0.04), *S. aureus* was the dominant species. When exposed to 0.125, 1 and 2% active level of Hydrosativum P there was no significant difference between the quantity of adhered cells (P>0.05).

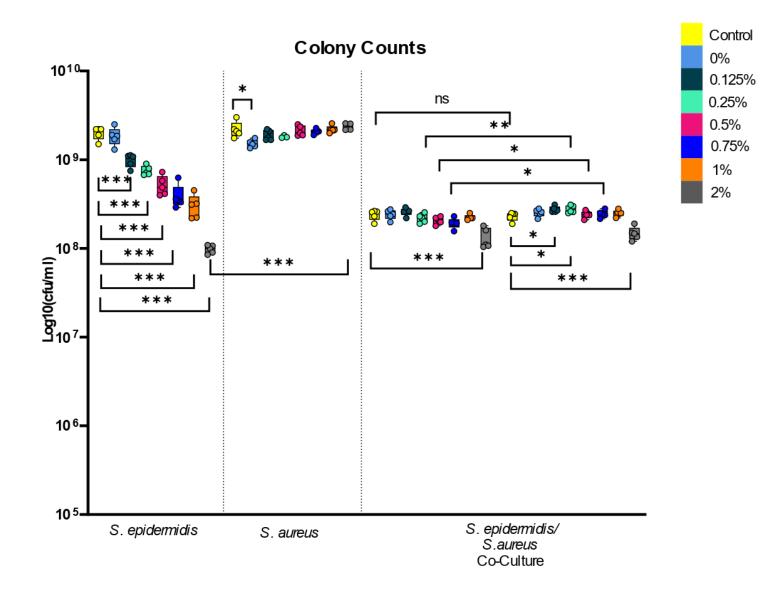


Figure 29. Final CFU/ml of *S. epidermidis*, alone, *S. aureus* alone and the *Staphylococcus* spp. Coculture after being exposed to Various Active levels of Hydrosativum P. Statistical values between individual species were not all added, when exposed to active levels 0.125-2%, individual *S. aureus* had a significantly higher cfu/ml than *S. epidermidis*. \*<0.05, \*\*<0.01, \*\*\*<0.0001. For all statistics, please see Section 5.19.13-5.19.15.

### 5.21 Does Exposure to Hydrosolanum PE Affect Interactions Between the *Staphylococcus* spp. and HaCaT Immune Marker Concentration?

## 5.21.1 How did exposure to Hydrosolanum PE alone Affect the Concentration of IL-8 from HaCaT cells?

All results below are in reference to Figure 30. HaCaT cells grown alone expressed 1092 pg/ml of IL-8, when exposed to 0-0.75% active levels of Hydrosolanum PE the concentration of IL-8 was significantly reduced (P<0.0007) to between 360.1-565.9 pg/ml. When exposed to 1 and 2% active levels of Hydrosolanum PE, the expressed IL-8 was increased compared to the lower active levels (P<0.05), but not significantly more than the control (P>0.06).

## 5.21.2 How did exposure to Hydrosolanum PE Affect the Concentration of IL-8 from HaCaT cells incubated with *S. epidermidis*?

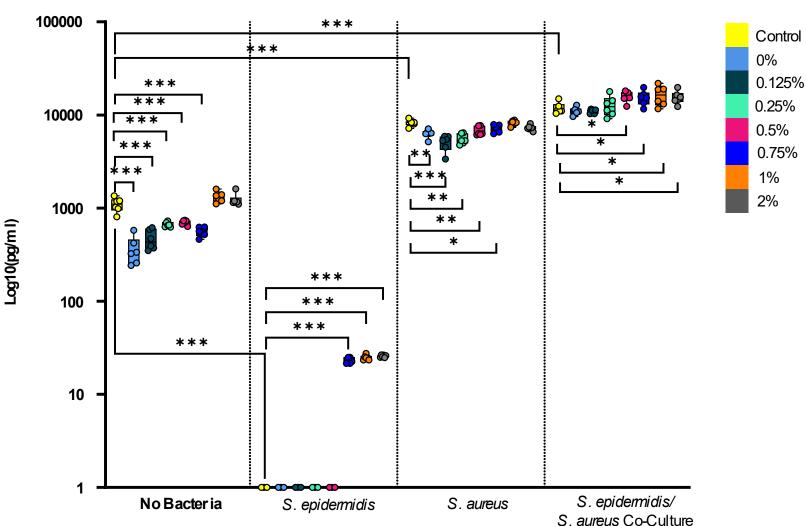
Addition of *S. epidermidis* to HaCaT cells significantly reduced the concentration of IL-8 compared to HaCaT cells alone, from 1092 pg/ml to negligible quantities (P<0.0001). No quantifiable IL-8 was measured by HaCaT cells with *S. epidermidis* when exposed to 0-0.5% Hydrosolanum PE. After being exposed to 0.75-2% active levels of Hydrosolanum PE, the concentration of IL-8 increased significantly (P<0.0001) to between 23-26 pg/ml but was still significantly less IL-8 than HaCaT cells expressed when grown alone (P<0.0001). There was no significant difference in the concentration of IL-8 from HaCaT cells grown with *S. epidermidis* exposed to 0.75 and 1%, or 1 and 2% Hydrosolanum PE (P<0.05).

### 5.21.3 How did exposure to Hydrosolanum PE Affect the Concentration of IL-8 from HaCaT cells incubated with *S. aureus*?

When incubated with *S. aureus*, HaCaT expressed 8229 pg/ml of IL-8, a significant increase compared to HaCaT cells alone or with *S. epidermidis* (P<0.0001). Exposure of HaCaT cells grown with *S. aureus* to between 0-0.75% Hydrosolanum PE significantly reduced the concentration of IL-8 to as low as 5065 pg/ml, compared to the *S. aureus* control (P<0.02). Exposure of HaCaT plus *S. aureus* to 1 and 2% active levels of Hydrosolanum significantly increased concentration of IL-8 compared to the lower active levels (P<0.009) but not significantly more than the *S. aureus* control (P>0.05). Addition of the lower active levels of Hydrosolanum PE reduced IL-8 concentration, but even at the higher active levels, the IL-8 concentration was not increased.

# 5.21.4 How did exposure to Hydrosolanum PE Affect the Concentration of IL-8 from HaCaT cells incubated with *Staphylococcus* spp. Co-culture?

Incubation of HaCaT cells with the *Staphylococcus* spp. co-culture significantly increased the concentration of IL-8 compared to HaCaT alone, with *S. epidermidis* and with *S. aureus* (P<0.0005). Exposure of the HaCaT cells with the *Staphylococcus* spp. mix to 0-0.25% active levels of Hydrosolanum PE did not significantly change the concentration of IL-8 (P>0.2). However, exposure to 0.5-2% Hydrosolanum PE significantly increased the concentration compared to the control (P<0.03). There was no significant difference between the concentration of HaCaT cells plus *Staphylococcus* spp. mix when exposed to 0.5-2% active levels of Hydrosolanum PE (P>0.6).



IL-8

Figure 30. Concentration of IL-8 from HaCaT cells With or Without Bacteria after Being Exposed to Various Active Levels of Hydrosolanum PE. Yellow bars represent HaCaT cells (with or without bacteria) in which they have not been exposed to any outside source, only the media was changed out. The blue bar represents the HaCaT cells being exposed to 0% of the cosmetic protein, otherwise known as sterile water. The other colours are exposure to active levels 0.125-2% of the cosmetic proteins. Non-significant values were not added, nor values between species. \*<0.05, \*\*<0.01, \*\*\*<0.0001. For all statistics, please see Section 5.20.1-5.20.4.

# 5.21.5 How did exposure to Hydrosolanum PE alone Affect the Concentration of IFN-X from HaCaT cells?

All results below are in reference to Figure 31. HaCaT cells grown alone expressed 2265 pg/ml of IFN-Y. Exposure of these cells to every active level of Hydrosolanum PE, including 0% control, increased the concentration of IFN-Y significantly to as high as 7825 pg/ml with an active level of 2% (P<0.0001). There was no significant difference with any active level in the concentration of IFN-Y from HaCaT cells when exposed to 0.125-2% Hydrosolanum PE (P>0.05), however concentration with active levels was significantly higher than concentration with the 0% control (P<0.02).

# 5.21.6 How did exposure to Hydrosolanum PE Affect the Concentration of IFN-X from HaCaT cells incubated with *S. epidermidis*?

HaCaT cells grown with *S. epidermidis* significantly reduced the concentration of IFN-X to 261.5 pg/ml, compared to HaCaT cells grown alone (P<0.0001). Exposure to 0, 0.125 and 0.75% Hydrosolanum PE did not significantly change the concentration of IFN-X from HaCaT cells with *S. epidermidis* (P>0.85). However, exposure to 0.25, 0.5, 1 and 2% Hydrosolanum PE significantly increased (P<0.05) the concentration of IFN-X to as high as 495 pg/ml, however this was still significantly less than HaCaT cells alone (P=0.0002).

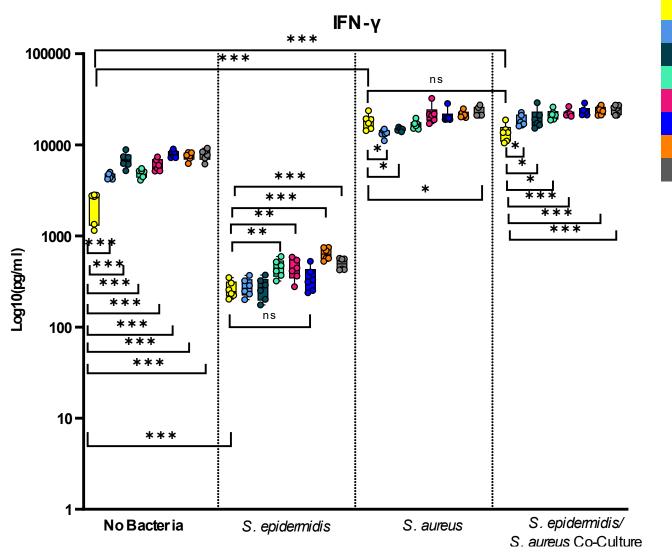
# 5.21.7 How did exposure to Hydrosolanum PE Affect the Concentration of IFN-X from HaCaT cells incubated with *S. aureus*?

Incubation of HaCaT cells with *S. aureus* increased the concentration of IFN- $\chi$  from 2265 pg/ml to 18105 pg/ml which is a significant increase (P<0.0001). Exposure to 0 and 0.125% Hydrosolanum PE significantly reduced the concentration of IFN- $\chi$  from HaCaT cells with *S. aureus* compared to the control (P<0.04). Exposure to 0.25-1% Hydrosolanum PE did not significantly alter the concentration of IFN- $\chi$  from HaCaT Cells with *S. aureus* (P>0.40), however exposure to 2% active level significantly increased the concentration of IFN- $\chi$  (P=0.024).

#### 5.21.8 How did exposure to Hydrosolanum PE Affect the Concentration of IFN-Y from

### HaCaT cells incubated with *Staphylococcus* spp. Co-culture?

Addition of the *Staphylococcus* spp. to the HaCaT cells significantly increased the concentration of IFN-X compared to HaCaT alone and with *S. epidermidis* (P<0.0001), up to 13,713 pg/ml. However, it did not significantly increase the concentration of IFN-Y compared to incubation with *S. aureus* alone (0.04). Exposure to 0-2% significantly increased the concentration of IFN-X compared to the control (P<0.001).



0% 0.125% 0.25% 0.5%  $_{0.75\%}$  Figure 31. Concentration of IFN-  $\tt X$  from HaCaT cells With or Without Bacteria after Being Exposed to 1% Various Active Levels of Hydrosolanum PE. Yellow 2% bars represent HaCaT cells (with or without bacteria) in which they have not been exposed to any outside source, only the media was changed out. The blue bar represents the HaCaT cells being exposed to 0% of the cosmetic protein, otherwise known as sterile water. The other colours are exposure to active levels 0.125-2% of the cosmetic proteins. Nonsignificant values were only added if important and not obvious from the figure, nor values between species. \*<0.05, \*\*<0.01, \*\*\*<0.0001. For all statistics, please see Section 5.20.5-5.20.8.

Control

# 5.21.9 How did exposure to Hydrosolanum PE alone Affect the Concentration of TNF- $\alpha$ from HaCaT cells?

All results below are in reference to Figure 32. HaCaT cells alone expressed an average 10.67 pg/ml of TNF- $\alpha$  and when exposed to the active levels 0 and 0.125% this did not significantly change (P>0.50). Exposure to active levels of 0.25-1% Hydrosolanum PE significantly increased (P<0.0002) the concentration of TNF- $\alpha$  from 10.67 pg/ml to between 41-35 pg/ml but these were not significantly different to each other (P=0.44). Exposure to 2% Hydrosolanum PE significantly increased the concentration of TNF- $\alpha$  compared to the other active levels (P<0.05), up to 66.99 pg/ml.

# 5.21.10 How did exposure to Hydrosolanum PE Affect the Concentration of TNF- $\alpha$ from HaCaT cells incubated with *S. epidermidis*?

Incubation of HaCaT cells with *S. epidermidis* significantly reduced the concentration of TNF- $\alpha$  (P<0.0001) to a negligible amount. Exposure to 0-2% active levels of Hydrosolanum PE did not significantly change this as there was no TNF- $\alpha$  detected (P>0.05).

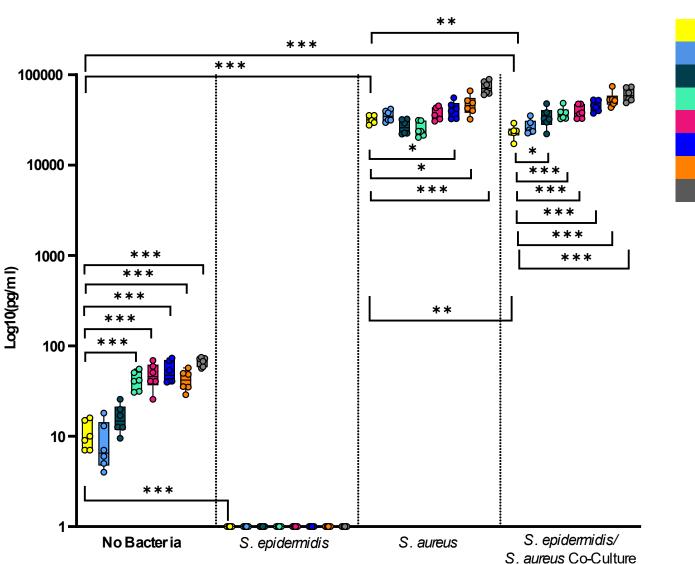
# 5.21.11 How did exposure to Hydrosolanum PE Affect the Concentration of TNF- $\alpha$ from HaCaT cells incubated with *S. aureus*?

Incubation with *S. aureus* significantly increased the concentration of TNF- $\alpha$  from HaCaT cells alone from 10.67 to 31,931 pg/ml (P<0.0001). Exposure to active levels 0, 0.125, 0.25 and 0.5% did not significantly change the concentration of TNF- $\alpha$  (P<0.2), although the exposure to 0.125% and 0.25% did reduce the concentration and was only just not significant (P>0.05). Exposure to 0.75 and 1% active levels of Hydrosolanum PE significantly increased (P<0.03) the concentration of TNF- $\alpha$  to 41,476 and 46,931 pg/ml respectively, but these Figures were not significant from each other (P=0.4). Exposure to 2% active level Hydrosolanum PE increased the concentration of TNF- $\alpha$  from the control (P<0.0001) and compared to the other active levels (P<0.0005).

# 5.21.12 How did exposure to Hydrosolanum PE Affect the Concentration of TNF-α from HaCaT cells incubated with *Staphylococcus* spp. Co-culture?

Incubation of HaCaT cells with the *Staphylococcus* spp. co-culture significantly increased the concentration of TNF- $\alpha$  to 23,351 pg/ml compared to HaCaT cells alone or with *S. epidermidis* (P<0.0001). However, the concentration of TNF- $\alpha$  was significantly less than when HaCaT cells were grown with *S. aureus* alone (P=0.002). Exposure to 0% control did not significantly alter (P=0.25) the concentration of TNF- $\alpha$  from the HaCaT cells, however exposure to 0.125-2% significantly increased the TNF- $\alpha$  concentration (P<0.02) to between 33,868-60,715 pg.ml. There was no significant difference in concentration of TNF- $\alpha$  when exposed to 0.125-0.75% active levels of Hydrosolanum PE (P>0.05). Exposure to 1 and 2% active levels significantly increased the

concentration compared to the lower active levels (P<0.002), but the concentration after incubation to 1 and 2% was not significantly different (P=0.30).



TNF-α

Figure 32. Concentration of TNF-α from HaCaT cells With or Without Bacteria after Being Exposed to Various Active Levels of Hydrosolanum PE. Yellow bars represent HaCaT cells (with or without bacteria) in which they have not been exposed to any outside source, only the media was changed out. The blue bar represents the HaCaT cells being exposed to 0% of the cosmetic protein, otherwise known as sterile water. The other colours are exposure to active levels 0.125-2% of the cosmetic proteins. Non-significant values were not added, nor values between species. \*<0.05, \*\*<0.01, \*\*\*<0.0001. For all statistics, please see Section 5.20.9-5.20.12.

Control

0.125%

0.25%

0.5%

1%

2%

0.75%

0%

# 5.21.13 How did exposure to Hydrosolanum PE Affect the Final CFU/ml of *S*.

## epidermidis grown with HaCaT cells?

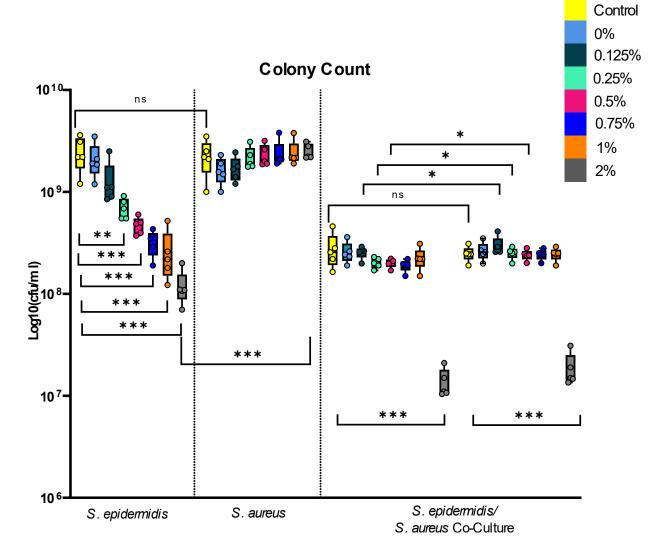
All results below are in reference to Figure 33. The final cfu/ml of adhered *S. epidermidis* cells when grown with HaCaT cells was 2.46 x  $10^9$ , when exposed to 0% control or 0.125% Hydrosolanum PE, this did not significantly change (P>0.053). Exposure to 0.25-2% active levels of Hydrosolanum PE did however significantly reduce the final cfu/ml to between 6.9 x  $10^8$  to 1.19 x  $10^8$  (P<0.003). Exposure to increasing active levels significantly decreased the number of attached *S. epidermidis* cells (P<0.05), except for 0.75 and 1% active (P=0.45).

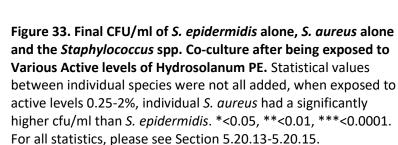
# 5.21.14 How did exposure to Hydrosolanum PE Affect the Final CFU/ml of *S. aureus* grown with HaCaT cells?

The final cfu/ml of adhered *S. aureus* cells when grown with HaCaT cells was 2.3 x 10<sup>9</sup> cfu/ml which was not significantly different to the adhered cells of *S. epidermidis* alone (P=0.74). Exposure to any active level of Hydrosolanum PE did not significantly alter the final cfu/ml of attached *S. aureus* cells (P=0.22).

# 5.21.15 How did exposure to Hydrosolanum PE Affect the Final CFU/ml of *Staphylococcus* spp. Co-culture grown with HaCaT cells?

The final cfu/ml of adhered *S. epidermidis* in the *Staphylococcus* spp. co-culture grown with HaCaT cells alone was 2.5 x  $10^8$  and the final cfu/ml of *S. aureus* was 2.8 x  $10^8$ , which were not significantly different from each other (P=0.61). Exposure to 0-1% Hydrosolanum PE, showed no significant reduction in adhered *S. epidermidis* cells (P>0.13), however the general trend is a reduction in adhered cells, from 2.5 x  $10^8$  cfu/ml down to  $1.9 \times 10^8$  cfu/ml. Exposure to 2% active level Hydrosolanum PE significantly reduced the number of adhered *S. epidermidis* cells down to  $1.36 \times 10^8$  cfu/ml, compared to the lower active levels (P<0.001) and the control (P=0.0008). Again, exposure to 0-1% active level of Hydrosolanum PE did not significantly alter (P>0.13) the final cfu/ml of attached *S. aureus* cells, however the trend again was a reduction down to  $1.9 \times 10^8$  cfu/ml. Exposure to 2% active level of Hydrosolanum PE did significantly reduce the final cfu/ml of *S. aureus*, down to  $1.36 \times 10^8$  cfu/ml (P<0.0008). Although both species final cfu/ml of adhered cells followed a similar pattern, *S. aureus* significantly dominated (P<0.04) the adhered cells when exposed to 0.25, 0.5 and 0.75% active levels of Hydrosolanum PE.





### 5.22 Discussion

# 5.23 Microscopic Observation of HaCaT cells shows addition of Bacteria Stresses the Cellular Monolayer

The images shown in Figure 25 were microscope images of the HaCaT cells after 48 hours of incubation with the bacteria. Without bacteria, there was clear adherence and continuous mosaic pattern around the periphery of the well, reaching in towards the centre of the well. Some of the cells had become condensed with uneven shrivelled edges which is a sign of normal developmental cell death (Ziegler and Groscurth 2004), the majority were forming a healthy merged structure. When grown with both *Staphylococcus* spp., separately and together, cell swelling was observed at varying degrees. Some swelling was noted when grown with *S. epidermidis*, but a larger proportion of swollen cells were found when incubated with *S. aureus* or the co-culture of both species.

Keratinocyte swelling is a morphological process which is attributed to several potential causes, commonly microbial infections which trigger oncosis (Rock and Kono 2008; Lauffer et al. 2018). Oncotic cell swelling is due to increased membrane permeability (Wei et al. 2020) causing an inflow of sodium and chloride ions and outflow of potassium ions. The resulting osmotic gradient swells the cell with water, eventually leading to death (Loh et al. 2019). The lack of membrane integrity during oncosis is linked to pore-forming toxins (Lin et al. 2010). Staphylococcus aureus releases a pore-forming cytotoxic agent called alpha toxin ( $\alpha$ -toxin) which is known to lyse human epithelial cells (Essmann et al. 2003). The  $\alpha$ -toxins are released and bind to monomers on the membrane of cells, converting them into a multicellular complex which forces a  $\beta$ -barrel through the lipid bilayer. This opens a new channel which leads to the cell swelling (Seilie and Bubeck Wardenburg 2017). In future, to explore whether the swelling was initiated through the release of Staphylococcal  $\alpha$ -toxin, there are highly sensitive enzyme-linked immunosorbent assays available. These assays can detect  $\alpha$ -toxins in highly diluted samples (Surujballi and Fackrell 2021). Staphylococcus epidermidis does not exhibit as many virulent factors as its more pathogenic cousin, however it does secrete  $\delta$ -toxin (Otto 2012). In other species,  $\delta$ -toxin shares similarities with  $\alpha$ -toxin, in that it forms pores in the cell membrane with  $\beta$ -strands (Manich et al. 2008). Some swelling could be attributed to this toxin and ELISAs have been used to confirm the presence of  $\delta$ -toxins (Scheifele et al. 1987). However, some of the bloated cells could be attributed by introduction of bacteria into the well, causing changes to the pH and utilisation of nutrients (Segeritz and Vallier 2017).

The HaCaT cells were also observed to have reduced adhesion when grown with all *Staphylococcus* spp. combinations, however the most pronounced was with *S. aureus* alone. HaCaT cells have been known to have reduced adherence when under different stress conditions

(Luangpraditkun et al. 2021), the presence of other bacteria species has also shown the ability to reduce the HaCaT adhesion (Siemens et al. 2011).

Due to the nature of this experiment, the focus was on the effect of cosmetic proteins on the final cfu/ml of the bacteria. Without performing an extra time-consuming control group, the exact viability of the HaCaT cells could not be quantified. This would be useful for future experiments to investigate the overall health of the keratinocytes.

### 5.24 Detection of Immune Biomarkers

#### 5.24.1 Immune Markers are Expressed without Stimulation

Even before the incubation for several days or incubation with bacteria, HaCaT cells expressed low levels of bioactive markers Figure 23. This was normal, as previous studies on immune marker concentration reported low levels of these markers from the control results, the added stimulant usually increases the concentration compared to the control level (Colombo et al. 2017; El Darzi et al. 2017; Lee et al. 2019b). As keratinocytes are the first line of defence, having low levels of immune responses allows for quick response when invading pathogens are detected (Nestle et al. 2009; Piipponen et al. 2020).

# 5.24.2 Addition of either Cosmetic Protein did not Increase Concentration of IL-8 but did increase Concentration of other Immune Markers

The exposure of either cosmetic protein to HaCaT cells alone did not significantly increase the concentration of IL-8 compared to HaCaT cells alone and some active levels even reduced the concentration compared to HaCaT cells alone. Cosmetic proteins are key ingredients in moisturising products which can be used in conjunction to help treat inflammatory diseases (Lynde 2008). While there was no significant change in IL-8 concentration with the pea protein derivative, Hydrosativum P, the trend was a reduction in concentration. Pea proteins have been shown to reduce excessive concentration of pro-inflammatory interleukins in atopic dermatitis damaged skin cells (Campolo et al. 2020). The lower active levels of the potato protein derived cosmetic protein, Hydrosolanum PE, significantly reduced HaCaT cell concentration of IL-8. When exposed to the higher active levels of Hydrosolanum PE, the concentration started to increase but still not more than HaCaT cells alone. While there's little research into anti-inflammatory effects of potato proteins, proteins from similar species have been found to promote wound healing in damaged skin (Suzuki et al. 1996). Unlike IL-8 concentration, both IFN-X and TNF- $\alpha$  were either significantly increased or the trend was increased concentration when exposed to both proteins. Both proteins were preserved with 1% phenoxyethanol (Section 3, Table 6), a substance which has been shown to able to cause slight erythema of skin, a rash which is associated with elevated levels of IFN-X and TNF- $\alpha$  (Caproni et al. 2006; Miller et al. 2009; Ma et al. 2021). It should be noted that any increase in immune marker concentration from HaCaT cells exposed to cosmetic proteins, does not compare to the increased concentration of bioactive markers from HaCaT cells

incubated with *S. aureus*. When HaCaT cells were incubated with S. aureus, the concentration of IL-8 in the supernatant increased by at least 10-fold, the concentration of IFN-  $\Upsilon$  increased by at least 100-fold and the concentration of TNF-  $\alpha$  increased by at least 1000-fold compared to HaCaT cells grown alone or with *S. epidermidis*. The extent of the immune marker increase by incubation of HaCaT cells with *S. aureus* was discussed in Section 5.25.

# 5.25 The Presence of *Staphylococcus epidermidis* Alone Reduces the Immune Response

When HaCaT cells were grown with *S. epidermidis*, concentration of immune markers compared to the control group was either significantly reduced, sometimes to negligible levels, or not significantly different (Figure 24ABC, 26-28, 30-32). However, as exposure to higher active levels of the cosmetic proteins decreased the final cfu/ml of *S. epidermidis*, the concentration levels of immune markers often increased, even when the bioactive marker concentration levels increased, they were often less compared to HaCaT cells grown alone (Figure 23, Figure 24). This resonates with previous literature in which *S. epidermidis* is recognised as a commensal by skin cells (Claudel et al. 2019) and has been shown to be able to reduce excessive immune responses (Skabytska and Biedermann 2016).

#### 5.25.1 S. epidermidis Possess Many TNF-α Reducing Techniques

Reduction in TNF- $\alpha$  concentration by HaCaT cells incubated with *S. epidermidis* was seen after 48 hours (Figure 24C) and when grown with both proteins (Figure 28, Figure 32). S. epidermidis modulates immune responses from skin cells to limit exaggerated reactions and promote wound healing through inhibition of toll-like receptor 3 facilitated inflammatory pathways (Li et al. 2019a). These pathways include the activation of TNF- $\alpha$  (Covacu et al. 2009), which is involved in the early stages of wound healing (Ritsu et al. 2017; Frank et al. 2021) but is also linked to persistent wounds due to hyper-inflammation (Ashcroft et al. 2012). Concentration of TNF- $\alpha$  can trigger an extreme build-up of glycation products at tissue sites, which initiate apoptosis of fibroblasts and integral vascular cells, thus stopping successful wound healing (Tanaka et al. 2000). S. epidermidis prevents TNF- $\alpha$  hyper-inflammation by targeting upstream processes. The bacterium produces a Lipopeptide (LP78), which activates  $\beta$ -catenin which is known to supress toll-like receptor 3 (Li et al. 2019a). One way to establish if TNF- $\alpha$  levels were suppressed due to the presence of S. epidermidis, previous work has used horseradish peroxidase (hrp) immunohistochemistry to identify elevated concentration of  $\beta$ -catenin in tissue samples. A primary antibody was used to detect the presence of  $\beta$ -catenin, with diaminobenzidine as the chromogen (Bhattacharya et al. 2019). Concentration was scored from multiplying the percentage of positive β-catenin expressed cells by their staining intensity (Mauri et al. 1998). Other research has found that *S. epidermidis* can reduce proinflammatory TNF- $\alpha$  over-expression caused by pathogens. It was deduced that staphylococcal lipoteichoic acid (LTA), a key component in the cell

membrane of *S. epidermidis*, induced certain miRNAs which inhibited pathogen induced cytokines (Skabytska and Biedermann 2016). Abrogation of TNF- $\alpha$  by systems triggered by LTA could be confirmed by sampling the supernatant and confirmation by use of an LTA sandwich ELISA kit (Tadler et al. 1989; LSBio 2022)

### 5.25.2 Modulation of IL-8 Can be Direct and Indirect

Incubation with *S. epidermidis* either did not significantly change the concentration of IL-8 by HaCaT cells (Figure 24A) or significantly reduced the concentration of IL-8 compared to HaCaT cells alone (Figure 26, Figure 30). However, exposure to the 1% active level Hydrosativum P did increase the concentration of IL-8 from HaCaT cells with *S. epidermidis* compared to HaCaT cells alone. Many of the TNF- $\alpha$  reducing strategies of *S. epidermidis* are also effective against suppression of IL-8. Lipoteichoic acid, effective against reduction in TNF- $\alpha$  over-expression, also limits IL-8 concentration in various tissues by other species (Blease et al. 1999; Im et al. 2015). Keratinocytes treated with a product isolated from *S. epidermidis* culture medium have found it successful in reducing multiple bioactive markers, including IL-8 (Lai et al. 2009). *S. epidermidis* released extracellular vesicles can directly increase IL-8 production, however they can also indirectly reduce the chemokine through modulation of LL37 which induces IL-8 production in psoriasis inflamed skin (Gómez-Chávez et al. 2021).

# 5.25.3 IFN-¥ Concentration May have Increased due to Irritation as well as Reduced *S. epidermidis*

IFN-Y concentration was reduced in HaCaT cells incubated with *S. epidermidis* (Figure 24B), however exposure to Hydrosativum P significantly increased concentration (Figure 27). Previous work has shown that *S. epidermidis*-produced biofilms interact with the immune system and can manipulate the immune response inhibiting inflammatory cytokines, including IFN-Y (Le et al. 2018). While the increased immune markers could be attributed to the decreased *S. epidermidis* levels, it is worth noting that the preservative phenoxyethanol is found in both of these cosmetic proteins (Section 3, Table 6), which has previously been found to cause slight erythema of the skin during patch tests (Ma et al. 2021). Higher levels of IFN-Y are associated with erythema and can exacerbate the symptoms (Miller et al. 2009). Therefore, phenoxyethanol could have reduced *S. epidermidis*, while potentially promoting skin irritation.

# 5.25.4 Adhered *S. epidermidis* Cells were Reduced as the Active Level of Proteins Increased

In Section 3.21.4, *S. epidermidis* was least sensitive to the preservative mix and concentrations found in Hydrosativum P (phenoxyethanol and potassium sorbate). However, in Figure 29, the final cfu/ml of *S. epidermidis* decreased as the active level concentration increased. While the pH of the proteins was pH 5  $\pm$  0.2, the rest of the experiment could only be undertaken at pH 7. Unlike other preservative types, phenoxyethanol is the most efficient at inhibiting microbes when

used at pH 7, including against *Staphylococcus* spp. (Siegart 2013). Phenoxyethanol has also been shown to be able to increase the permeability and reduce integrity of bacterial cell membranes which can increase the efficacy of the inhibition effect (Walsh et al. 2019). A reduction in final adhered cfu/ml was also noted when *S. epidermidis* was exposed to Hydrosolanum PE, the preservative mixture has the heightened preserving measure of disodium EDTA (Section 3, Table 6). Disodium EDTA increases cell membrane permeability which allows entry into the cell more easily and enhances the inhibition of preservatives (Walsh et al. 2003). *In vitro*, EDTA has been shown to be bacteriostatic against planktonic *S. epidermidis*, and also affective at stopping adhesion of the species and subsequent formation of biofilms (Juda et al. 2008). As discussed in 3.25, due to the lack of protein analysis of the hydrolysed cosmetic proteins, there is always a chance that some of the peptides produced could have antimicrobial effects against *Staphylococcus epidermidis*. However, simple size exclusion data, from Croda Europe Ltd., of both Hydrosativum P and Hydrosolanum PE did show that the hydrolysis produced a range of peptides at varying lengths. The size exclusion data is commercially confidential and cannot be added or be discussed in depth in this thesis.

# 5.25.5 Future Investigation into Whether *S. epidermidis* being a Commensal or a Pathogen?

As S. epidermidis can be both a useful commensal and an opportunistic pathogen, the bacteria's immune modulation could also be part of its immune evasion tactics (Otto 2009; Le et al. 2018). Pathogenic S. epidermidis has been shown to activate IL-8 (Sachse et al. 2008), while in this study the IL-8 levels were reduced and therefore unlikely to be acting as a pathogen. However, to investigate whether the reduced immune marker concentration across the board was caused by S. epidermidis acting as an immune calming commensal or an evasive pathogenic threat, previous research has identified several markers (Ortega-Peña et al. 2019). SesC is a surface protein in which elevated levels are associated with the latter stages of biofilm forming cells compared to their planktonic counterparts (Shahrooei et al. 2009). The SesC producing gene has been shown to be present in all S. epidermidis clinical isolates in multiple studies (Bowden et al. 2005; Khodaparast et al. 2016b), including the strain used in the above work (Bahonar et al. 2019). However, the protein has been absent in isolates from healthy skin (Shahrooei et al. 2009). Identification of this protein would involve separation of the adhered and planktonic cells of S. epidermidis from the wells. The next step would then be isolation of the proteins through electrophoresis and SesC antibody added before visualizing on a Western blot (Khodaparast et al. 2016a). Comparison of planktonic and adhered cells would show whether SesC levels were elevated and therefore the presence of a later-stage biofilm.

# 5.26 *Staphylococcus aureus* Increases Concentration of Immune Markers by HaCaT Cells

Incubation of the HaCaT cells with *S. aureus* saw the concentration of the three markers increase compared to the concentration for HaCaT cells alone or grown with *S. epidermidis. Staphylococcus aureus* is a pathogen which is targeted by the innate and acquired immune system (Karauzum and Datta 2017). The pH of this experiment would have suited *S. aureus* better than if the bacteria had found itself on the skin, *S. aureus* proliferates best at neutral pHs while growth is slowed in more acidic conditions (Mirza et al. 1985; Stewart et al. 2017). Multiple immune biomarkers are activated when keratinocytes have been incubated with the species *in vitro* (Hong et al. 2014). While there were some differing concentration levels after exposure to Hydrosativum P, the overall trend was that the cosmetic protein was unlikely to influence the concentration, when HaCaT cells were grown with *S. aureus*. When exposed to Hydrosolanum PE, the overall trend was, when exposed to the higher active levels of the protein the concentration of IFN-Y and TNF- $\alpha$ increased, while IL-8 was slightly reduced.

# 5.26.1 *S. aureus* increased IL-8 Concentration at least 10-Fold More Than HaCaT cells Alone

When HaCaT cells were grown with S. aureus, the concentration of IL-8 increased significantly compared to HaCaT cells grown alone or with S. epidermidis, whether exposed to cosmetic proteins or not (Figure 24A, Figure 26, Figure 30). Increased levels of IL-8 are an indication of a pathogenic infection (Arican et al. 2005), as a pro-inflammatory chemokine they can activate pathways which increase lesions and exacerbate skin disorders (Kemény et al. 1994; Oka et al. 2000; Amarbayasgalan et al. 2013), which is advantageous to bacteria (Bowler et al. 2001; Arican et al. 2005). S. aureus is one such species involved in skin diseases that is known for multiple virulence factors which trigger both direct and indirect IL-8 concentration (Sasaki et al. 2003; Bien et al. 2011). These virulence factors known for inducing IL-8 around all different parts of the body include protein A, enterotoxin B and haemolysin (Thakur et al. 1997; Räth et al. 2013; Ledo et al. 2021). While there was a slight increase in IL-8 when grown with Hydrosativum P, the trend was no change in concentration when exposed to the cosmetic protein. When HaCaT grown with S. aureus were exposed to Hydrosolanum P, the IL-8 concentration was reduced. Plant based peptides have been shown to be able to reduce inflammation markers, and potato hydrolysates can activate mechanisms in skin cells (Apone et al. 2019). Potato peptides have been found to have anti-inflammatory properties elsewhere in the body, including the gut (Basilicata et al. 2019).

#### 5.26.2 Could EDTA Induce a Stress Response in S. aureus?

Again, concentration of both IFN-X and TNF- $\alpha$  were significantly increased with HaCaT cells grown with S. aureus than compared to HaCaT cells grown alone or with S. epidermidis (Figure 24B&C, Figure 27, Figure 28, Figure 31, Figure 32). Many of the *S. aureus* virulence factors that modulate IL-8 concentration also promote concentration of both IFN- $\chi$  and TNF- $\alpha$ . Protein A had been shown to stimulate and cause over concentration of both TNF- $\alpha$ , IFN- $\Upsilon$  and an array of interleukins in soft nasal tissue (Patou et al. 2008) and keratinocytes (de Souza Feitosa Lima et al. 2019; Ledo et al. 2021). Skin cells recognise lipoproteins released from S. aureus as antigens and trigger inflammatory responses, including accumulation of CD4+ and CD8+ T-cells, which produce IFN- $\chi$  (Saito and Quadery 2018). While the concentration of both IFN- $\chi$  and TNF- $\alpha$  were, as a trend, not affected by being exposed to Hydrosativum P, both immune markers are increased when exposed to Hydrosolanum PE. One of the main differences between the two proteins is the addition of EDTA to the preservative mixture of Hydrosolanum PE. EDTA has been shown to spark stress responses in Gram-negative species, including release of extracellular vesicles (Steenhuis et al. 2020). It is thought that these stress responses might also be found in gram-positive species (Mozaheb and Mingeot-Leclercq 2020). It is already known that S. aureus can release extracellular vesicles which can release pore forming toxins (Wang et al. 2021). These toxins, as discussed above, can lead to cell swelling as seen in Figure 25 (Surewaard et al. 2018). So, the increase in some of the inflammatory bioactive markers could be due to exposure of EDTA, even if it did not affect the final cfu/ml. To investigate whether the addition of EDTA can cause these stress responses in S. aureus, techniques analysing supernatants could include RNA extraction and confirmatory western blots, size exclusion chromatography or microfluidics (Kang et al. 2017).

#### Adhered S. aureus Cells were not Reduced by Preservatives

Previous work in Section 3.21.5, found that the preservatives found in Hydrosolanum PE and even more so Hydrosativum P, were the least effective at inhibiting *S. aureus* (Figure 10). The minimal inhibitory concentration of phenoxyethanol against *S. aureus*, is higher than other preservatives at around 1%, (Lundov et al. 2011) more than both cosmetic proteins would be found in formulations. Exposure to EDTA can reduce biofilm formation in *S. aureus*, but over 24 hours and at higher concentrations than found in the cosmetic proteins (Liu et al. 2018). These reasons would explain why the increased active levels of each cosmetic protein did not significantly alter the final cfu/ml of adhered cells (Figure 29, Figure 33). Also, one of *S. aureus*' stress responses, sigma B has been shown to aid in overcoming antimicrobial stresses (Ranganathan et al. 2020).

### 5.27 The Co-culture of Staphylococcus spp. Increased the Immune Marker

#### Concentration

The original inoculation amount of the co-culture was twice as much as HaCaT cells with individual species. However, the final cfu/ml of both species was significantly less than individual species, as competition reduced total population due to limited resources (Celiker and Gore 2012; Osmond and de Mazancourt 2013), but concentration levels were not too dissimilar to *S. aureus* alone (Figure 24).

#### 5.27.1 Staphylococcus aureus Was More Likely to Dominate a Sample

Although there was not always a dominant species in the co-culture, when there was, the one species which was the most prevalent was *S. aureus*. The neutral pH would have favoured *S. aureus* as it has the faster growth rate at pHs close to neutral (Stewart et al. 2017). The increased levels of IFN-Y has also been shown to promote growth of *S. aureus*, but not commensal *Staphylococcus* spp. (Di Domenico et al. 2018). As both species had a reduction in the adhered population when exposed to the active level 2% of both cosmetic proteins, internalisation of *S. aureus* into the keratinocytes was unlikely to have occurred, as this would protect the species from high concentrations of preservatives (Al Kindi et al. 2019).

#### 5.27.2 Staphylococcus epidermidis alerts the Immune System to Staphylococcus aureus

As IL-8, IFN-Y and TNF- $\alpha$  levels were akin to the levels expressed by HaCaT cells with *S. aureus* alone, it could be hypothesized that *S. epidermidis* is now promoting the immune response. Instead of downregulating a hyper immune reaction, as *S. epidermidis* did when grown alone, the commensal may have aided in promoting the bioactives due to the presence of its pathogenic relative.

Previous work has found that *S. epidermidis* can stimulate the innate immune system into targeting invasive *S. aureus* (Laborel-Préneron et al. 2015; Pastar et al. 2020). *S. epidermidis* can activate a response to limit *S. aureus* virulence against the skin. This includes activating keratinocytes to produce the antimicrobial peptide LL-37 (Elias et al. 2021). As well as antimicrobial properties, the peptide can modulate the pro-inflammatory responses including early upregulation of IL-8 and suppression of TNF- $\alpha$  or IFN- $\Upsilon$  promoted interleukins (Chen et al. 2013b). The high concentration of IFN- $\Upsilon$  and TNF- $\alpha$  when HaCaT cells were incubated with *S. aureus* and the *Staphylococcus* spp. coculture could be why the HaCaT cells did not form a continuous mosaic pattern, and there were large gaps between adhered cells and less attachment. Previous work has shown that concentration of IL-8, along with TNF- $\alpha$ , IL-6 and IL-1B, has been postulated as a biomarker for staphylococcal sepsis (Sachse et al. 2008).

Other markers could be examined to further investigate interactions between the two *Staphylococcus* spp. The anti-inflammatory IL-10 is often induced by *S. epidermidis*, which can reduce tissue damage and help inhibit bacterial pathogenesis (Laborel-Préneron et al. 2015). However, *S. aureus* has been shown to be able to manipulate IL-10 into hyperexpression, thus supressing T-cell induction of the pathogen targeting proinflammatory bioactives and aiding *S. aureus* into evading the immune response (Leech et al. 2017; Islam et al. 2021). Using ELISAs to investigate IL-10 hyperexpression could explain why *S. aureus* could continue to successfully adhere even when grown with *S. epidermidis*. However, even with the pH advantage, the adhered cells of *S. aureus* did not excessively proliferate compared to *S. epidermidis* (Figure 29, Figure 33). Extracellular proteases released from *S. epidermidis*, discussed in 3.26, also aid in reduction of adherence and biofilm formation of *S. aureus*. The Esp protease targets the cell wall fractions and hydrolyses more than 50 proteins and nearly a dozen involved in biofilm forming, adherence and fibronectin binding proteins (lwase et al. 2010; Chen et al. 2013; Sugimoto et al. 2013).

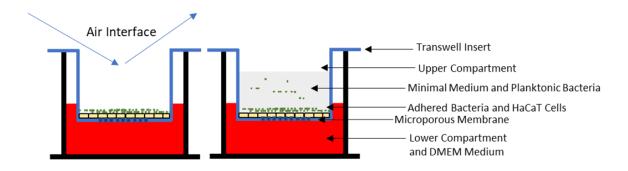
#### 5.27.3 Conclusion

Exposure of Hydrosolanum PE to HaCaT cells alone only increased the concentration of the three immune markers in the supernatant at the higher active levels. The exposure of Hydrosolanum PE increased the concentration of IL-8 at the higher active levels, but the exposure of Hydrosolanum PE increased both IFN-Y and TNF-a at most active levels. However, to highlight that while mostly the addition of the 0% control did not affect the concentration of the immune markers, sometimes the levels could be both increased and decreased. The uncertainty of the expression levels could be down to the inconsistent growth and stress responses of the HaCaT cells, rather than the introduction of the cosmetic proteins. However, the addition of *S. epidermidis* to HaCaT cells decreased the concentration of immune markers found in the supernatant. The higher active levels of both cosmetic proteins could reduce the final cfu/ml of *S. epidermidis* and therefore the concentration of immune markers, it was minimal compared to the 10-1000-fold increase of immune marker concentration when HaCaT cells were incubated with *S. aureus*, whether alone or in co-culture. When in co-culture, both *Staphylococcus* spp. can 'keep check' of each other and stop wild proliferation of either species.

#### 5.27.4 Future Work to Enhance the Experiment to be More Akin to the Habitat of Skin

As previously mentioned, this experiment was carried out at pH 7 which is not like the average acidic conditions of skin (Ali and Yosipov 2013). Keratinocytes grown in an acidic pH have shown to have reduced migration and viability (Lönnqvis et al. 2015), so conditioning HaCaT cells to grow in a lower pH may take extra time. Lowering the pH would reduce the advantages a neutral pH awards *S. aureus,* and *S. epidermidis* would likely dominate (Stewart and William Costerton 2001). To make the experiment more comprehensive, the total viability of the HaCaT cells would more

quantitively portray the overall keratinocyte health, rather than simply qualitatively as seen in Figure 25 and discussed in 5.18. An extra control experiment focussing on the viability of HaCaT cells rather than the final cfu/ml of the bacterial species would achieve this. Limiting access to highly nutritious media, as discussed in 3.26, would also allow growth of slower growing organisms if other species were to be added to the mixed culture (Davis et al. 2005). This could be achieved using Transwell inserts which can separate media, for instance DMEM in the lower compartment and minimal medium in the upper compartment (Sip et al. 2014). Transwells have also been successful in producing air-liquid interface, which would be more analogous to the skins ecosystem (Li et al. 2009) (Figure 34). The use of Transwells were investigated but was unsuccessful and abandoned due to time constraints.



**Figure 34**. **Using Transwells to Assimilate Conditions More Akin to Skin.** Using a liquid-air interface (left) and using minimal medium (right).

6 Investigating the Effect of Swab Head Type and Buffer Composition on Bacterial Collection using a Porcine Skin Model

#### 6.1 Introduction

# 6.2 Skin Microbe Research is Lagging

One of the largest organs of the human body and the first line of immunological defence is the skin (Byrd et al. 2018). However, the residing microbial community is often overlooked for areas of the body with greater microbial mass – mainly the gut microbiota (Proctor et al. 2019). The understanding of how the microbes within the gut are connected to nutrition, digestion and immunology is far from complete (Chang and Kao 2019) but the overall research topic is leaps and bounds ahead (Dréno et al. 2016). However with the emergence of modern skin diseases (Cordain et al. 2020) and the increased cases of skin cancers (Ishihara 2006), only recently has the microbial population of the skin been recognised as an equally important area of the human microbiota that requires investigation (Sohn 2018). To find a gold standard of collection of skin microbes could help ensure conformity across the research, bad collection technique could skew and cause inaccurate results (Ogai et al. 2018; Allaband et al. 2019).

# 6.3 Collecting Skin Microbiota

Understanding how these microbial skin communities could defend against or even influence these diseases and cancers are vital for cure and prevention (Grice and Segre 2011). This requires a robust and consistent method for collecting an accurate as possible representation of these skin communities. For example, a common method to produce a fingerprint of the microbial gut community is the analysis of faecal sample (Wang et al. 2018b).

There are numerous techniques used to collect skin microbiota including tape stripping, skin scraping, biopsies and swabbing (Ogai et al. 2018). Tape stripping is inexpensive but requires the area to be flat and without scarring (Kong et al. 2017) . Skin scraping and biopsies are useful for collecting low microbial mass but are invasive and not suitable for exploring multiple sites (Ogai et al. 2018). Swabbing is by far the easiest, least invasive and most versatile at collecting from all crevices of the skin (Grice et al. 2008). Nevertheless, previous papers have used varied methods in skin microbe collection using swabs, including numerous swab head types, and differing buffer compositions (Keyworth et al. 1990; Huttenhower et al. 2012; Ogai et al. 2018; Prast-Nielsen et al. 2019). Any previous research in to swab head types have either collected samples from surfaces dissimilar to the skin (Park et al. 2015) or have evaluated the release of microbial matter from swabs which have been dipped straight into a cell suspension (Van Horn et al. 2008; Mokomane et al. 2016).

#### 6.4 Skin Models

Animal skin models are commonly used as replacements for human skin in research (Abd et al. 2016). This includes cancer models (van der Weyden et al. 2016), permeation drug studies (Neupane et al. 2020), drug discovery (Avci et al. 2013), and as a practice for surgical techniques (Denadai et al. 2013). Animal skins are readily available in the large quantities needed to

undertake experiments (Schmook et al. 2001) and using them bypasses a lot of ethical and legal issues that would arise by using human skin (Petrini 2012). While a range of species are used, some animal skins are more akin to human skin than others. Murine (mouse and rat) skin have differing dermal thickness (Zomer and Trentin 2018) and higher permeability (van Ravenzwaay and Leibold 2004) than human skin. While porcine skin for example, is structurally similar to human skin, pigs have a similar number of dermal layers as well as comparable skin thickness and elasticity (Keiko et al. 2018). The number of follicles on the pigskin is also akin to our own and while there is often more hair on adult pig skin, this can be rectified by removal (Yu et al. 2015) or using neonatal subjects (Keiko et al. 2018).

#### 6.5 Aims

- Produce an ethically sound experiment in which human skin can be reproduced
- Compare different swab head types and buffer combinations at collecting bacteria from a skin model

# 6.6 Null Hypothesis

Swab head type or buffer composition have no significance on the quantity of bacteria collected from skin.

# 6.7 Materials

### 6.8 Bacteria

*Staphylococcus aureus* and *Staphylococcus epidermidis* used were the same isolates as previously described in Section 2.6.

### 6.9 Media

TSB and TSA were used to grow both species and quantify them for the experiment, preparation as seen in Section 2.10. Mannitol salt agar (MSA) from Thermo Scientific was prepared as to specifications on the packaging. MSA was used to quantify the species removed from the swab.

### 6.10 Porcine Skin

Porcine skin was purchased from a local supermarket butcher. Hair and subcutaneous fat were already removed, and this meant that no animal was killed specifically for the purpose of this investigation.

## 6.11 Swab and Buffer Types

The swab head types, and buffer compositions were all used in previous skin swabbing papers. For this study, the different buffer solutions were renamed buffer 1, buffer 2 and buffer 3. For swab types and buffer compositions please see

Paper	Swab Head Type	Buffer Composition	Buffer
			Name
(Keyworth et	Dacron™	0.075 mol litre-1 of phosphate	Buffer 1
al. 1990)	(Deltalab, Barcelona)	buffer [pH 7.9] containing 0.1%	
		v/v Triton X-100	
(Ogai et al.	Cotton	0.9% v/v Saline + 0.1% v/v Tween	Buffer 2
2018)	(Technical Service	20	
	Consultants, Heywood)		
(Huttenhower	Flocked	50 mM Tris buffer [pH 7.6], 1 mM	Buffer 3 <sup>9</sup>
et al. 2012)	(4N6FLOQSwabs™, Life	EDTA [pH 8.0] + 0.5% v/v Tween-	
	Technologies, Carlsbad)	20	

# Table 9. Swab head type and Buffer combinations used in Previous Swabbing Papers

# 6.12 Methods

# 6.13 Bacterial Suspension Preparation

Both species were cultured in TSB at 37 °C for 18 hours and then diluted to OD 1 as previously described in 2.9. These were then further diluted in 1xPBS to approximately  $1 \times 10^5$  cfu/ml. For mixed cultures, the species were diluted individually to approximately  $2 \times 10^5$  cfu/ml and added together at a 1:1 ratio to produce approximately  $1 \times 10^5$  cfu/ml of each. To verify the quantity of bacteria inoculated, the colonies were plated onto TSA and quantified using the Miles and Misra method (Miles et al. 1938).

# 6.14 Porcine Skin Preparation

The porcine skin was prepared by washing with 70% ethanol three times, to remove any contaminating microbes residing on the skin. The inoculation areas of 3 x 3 cm<sup>2</sup> were then drawn on using 70% ethanol washed templates and permanent marker. A control area was swabbed and plated onto a mannitol salt agar plate to confirm no residual *Staphylococcus* spp. on the porcine skin.

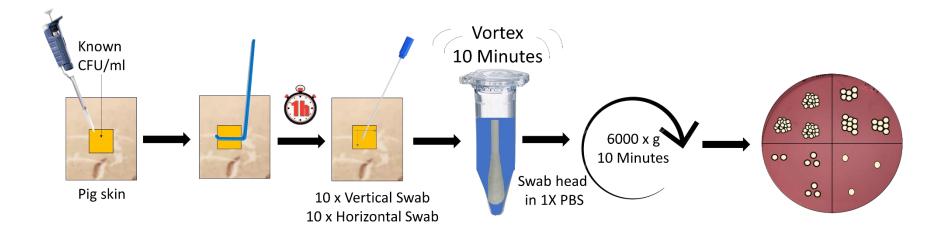
<sup>9</sup> For this study the buffers were renamed Buffer 1, Buffer 2, and Buffer 3

# 6.15 Inoculation of Porcine Skin

The porcine skin was inoculated with 50  $\mu$ l of either individual or mixed, bacterial suspension and, using an L-shaped cell spreader, spread evenly across the designated 3 x 3 cm<sup>2</sup> area. The bacterial suspension was allowed to dry into the skin for one hour. The segments were then swabbed similarly to the report by Ogai and co-workers (Ogai et al. 2018). The swabs were immersed into the buffer for 5 seconds to saturate the tip and swabbed the skin with 10 vertical and 10 horizontal rotational strokes. The swab tips were removed and immersed into sterile phosphate buffer saline (PBS). To shake out the collected biota, the swabs were vortexed for 10 minutes, followed by centrifugation at 6000 x g for 10 minutes and the swab removed. The pellet was resuspended and serially diluted in 1 ml of 1 x PBS, then 20  $\mu$ l plated onto mannitol salt agar plates. After overnight incubation at 37 °C, the colonies were quantified using the Miles and Misra method (Miles et al. 1938). Figure 35 illustrates the process.

# 6.16 Statistics

Graphs were made and data analysed using GraphPad Prism (Version 9.1.2). T-tests were used to compare the quantities of bacteria removed from the swabs.



**Figure 35**. **Inoculation, Swabbing and Quantification of** *Staphylococcus* **spp.**. 50  $\mu$ l of cell suspension was inoculated onto porcine skin and spread around the 3x3 cm<sup>2</sup> area. The bacteria were left to soak into the skin for 1 hour before being swabbed.

# 6.17 Results

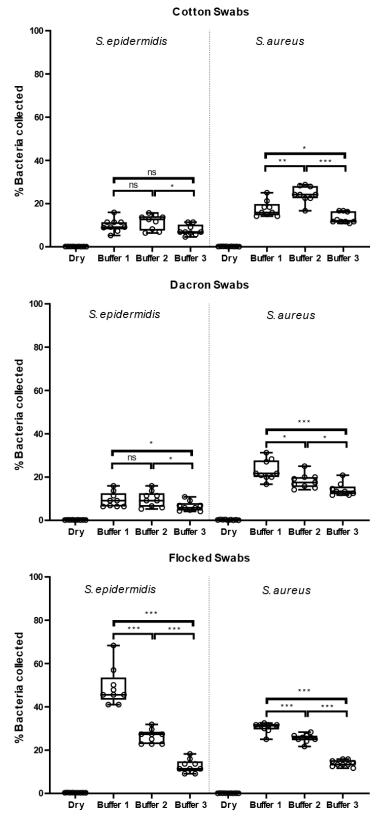
#### 6.18 Collecting Individual Species from Porcine Skin

The results below are in reference to Figure 36 and Figure 37. Both buffer composition and swab head type made a significant impact on the quantity of individual *Staphylococcus* spp. collected from the pig skin. Dry cotton swabs collected and released the lowest percentage of either species, consistently less than 1% of the inoculated amount. Cotton swabs used in conjunction with any buffer type collected and released between 7-12% of *S. epidermidis* and 10-29% of *S. aureus*. There was no significance between using buffer 1 or 2 to collect.

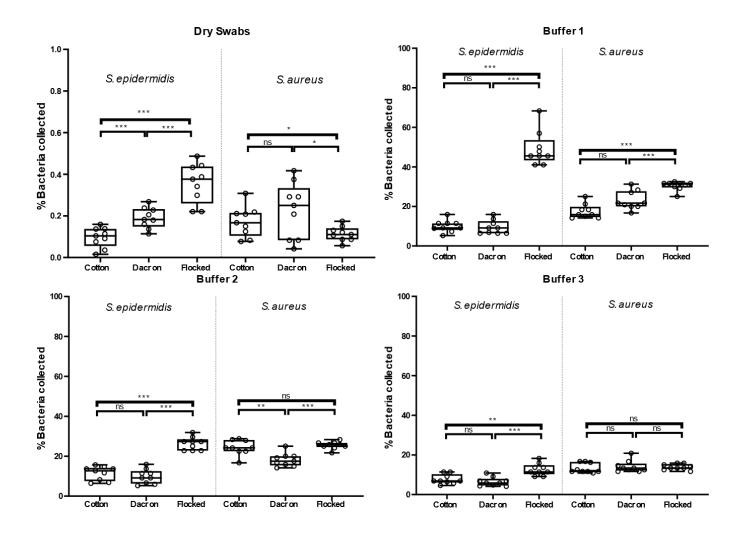
For *S. epidermidis* there was no difference between the buffers (P=0.339), however, buffer 2 was significantly better than buffer 1 when *S. aureus* was collected (P=0.001). Both buffer 1 and 2 were significantly more efficient at collecting and releasing both species than using buffer 3 (P<0.05). Again, dry Dacron swabs collected less than 1% of either species, which is significantly less than using any buffer type (P<0.001). While there was no significant difference between buffer 1 and 2 with Dacron swabs at collecting *S. epidermidis*, buffer 1 is slightly better than buffer 2 with a significance of P=0.022 when *S. aureus* was collected. Again, both buffer 1 and 2 still collected significantly more bacterial cells than buffer 3 when both species were collected (P<0.05). While there is inconsistency with which buffer is better when using cotton or Dacron swabs, the best buffer type is clear when using flocked swabs. Using a dry swab once again, resulted in the least number of bacterial cells being collected, less than 1%. Flocked swabs with any buffer collected and released between 12-50% of the inoculated *S. epidermidis* and 11-32% of *S. aureus*. When both species were collected, buffer 1 collected significantly more than both buffer 2 (P<0.001) and buffer 3 (P<0.001). Buffer 2 still collected significantly more of both species than buffer 3 (P<0.001).

When collecting both *S. epidermidis* and *S. aureus*, there was no clear dry swab which was better than any other. While flocked swabs were significantly better at collecting *S. epidermidis* (P<0.001), Dacron swabs were significantly the best at collecting *S. aureus* (P<0.05). No more than 0.6% of the original inoculum was collected by any swab. When utilising buffer 1, the results were very similar when collecting both species. There was no statistical difference between both cotton and Dacron swabs. When used with buffer 1, cotton swabs collected between 5-16%, Dacron collected between 6-16% and flocked between 41-69% of the inoculated *S. epidermidis*. There was no statistical difference between cotton or Dacron swabs, but flocked swabs collected significantly more (P<0.001). Similar results were seen with *S. aureus*, with buffer 1 cotton swabs collected between 14-25%, Dacron between 16-29% and flocked between 25-32%. Again, flocked swabs were significantly better than the other types, while there was no statistical difference between 6-15%, Dacron between 5-16% while flocked collected upwards of 41-

69% of *S. epidermidis*. Again, there was no significance between both cotton and Dacron swabs (P>0.05), but flocked swabs collect significantly more (P<0.001). There were much different results when *S. aureus* was collected, Cotton and flocked swabs collected percentages which were not significantly different, between 16-29% for cotton and 21-29% for flocked (P=0.44). However, Dacron collected 14-25% of the bacteria, which was significantly less than both cotton and flocked (P<0.002). When used with buffer 3, there was not a swab which consistently collected more than any other type. Flocked swabs collected between 9-13% of *S. epidermidis*, which was significantly more than the 4-11% collected by Dacron (P<0.001) and 5-15% collected by cotton (P=0.001). However, when *S. aureus* was collected there was no overall significant difference between the percentage of bacterial cells collected and released (P>0.05). Cotton collected between 10-17%, Dacron 11-21% and flocked between 11-16%.



**Figure 36**. Percentage of Bacteria Collected from Each Swab Type. Using a buffer was always significantly better than using a dry swab. Buffer 2 was either trending or significantly better than buffer 1 and 3 when used with cotton, or Dacron swabs. Buffer 3 consistently collected the least percentage of bacteria, most often significantly worse than the other buffers with any swab head type used. Buffer 1 was significantly more effective when used with flocked swabs. When used with buffer 1, flocked swabs collected mostly between 30-70% of the inoculated bacteria. While the range of collected is large, it is still significantly more than any other swab/buffer combination.

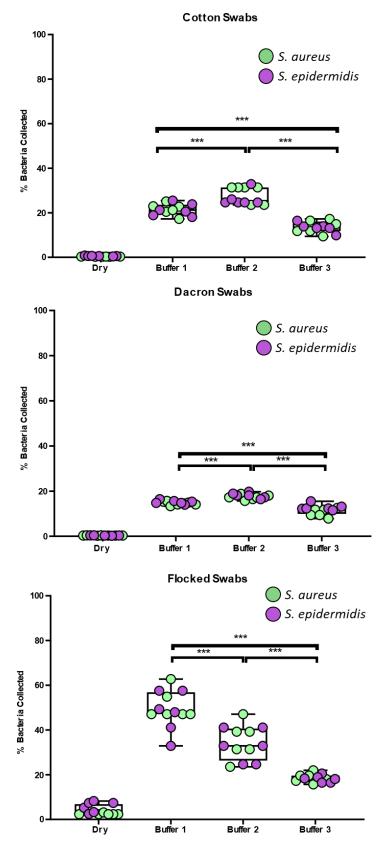


**Figure 37**. Comparison of Buffer Composition and Swab head Type on Bacterial Collection. Notice how with dry swabs the y-axis had to be changed from 0-100% to 0-1% as the collection percentage was so low. While there are statistical differences between swab head type, there is no pattern or one swab type which is significantly better, biomass collection was below 1%. Again, when used with buffer 1, flocked swabs collected a significantly higher percentage of bacteria than the other two swab head types. This is much more apparent when *S. epidermidis* was collected compared to *S. aureus*, but the pattern is the same. It is not completely clear when using buffer 2, but on trend flocked swabs collected more than cotton or Dacron, again more prevalent when S. epidermidis was collected. When using buffer 3 there was no clear 'winner' in swab head type, flocked swabs collected significantly more *S. epidermidis*, but not significantly more *S. aureus* than the other swab head types.

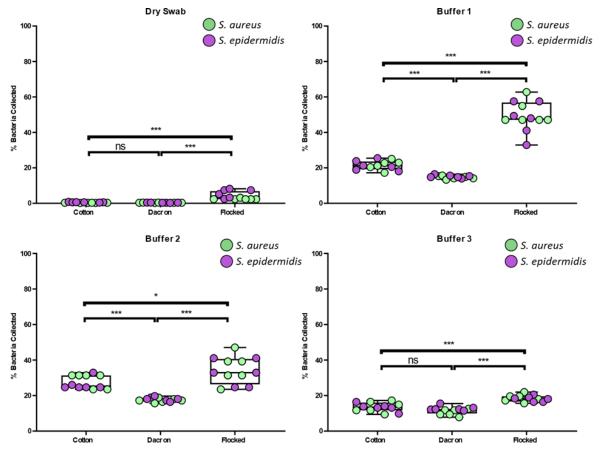
## 6.19 Collection of the Mixed Staphylococcus spp. from Porcine Skin

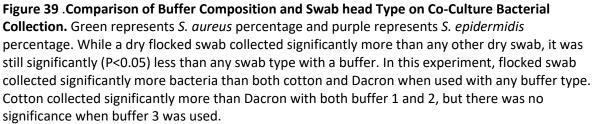
The following results are in reference to Figure 38 and Figure 39. Any dry swab head type, once again, reproduced the lowest recovery of bacteria. A dry cotton swab collected between 0.1-0.8% of both species, a dry Dacron between 0.2 and 0.5% and a dry flocked swab bucked the previous trend and collected between 2-8% of the inoculated bacteria, still significantly less than any buffer type with any swab head (P<0.001). Cotton swabs when using buffer 1 collected 17-26% of the inoculate, with buffer 2, 23-33% and with buffer 3 between 9-15%. As also seen when collecting S. aureus alone, cotton swabs with buffer 2 collected and released significantly more bacterial cells than buffer 1 or 3 (P<0.001). Cotton swabs with buffer 1 collected more than buffer 3 with a higher significance than the previous experiment in Section 6.18(P<0.001). When a Dacron swab was used to collect the mix of staphylococcal species, buffer 2 collected between 15-20% of the inoculate, which was significantly more than buffer 1 which was between 13-16% and buffer 3, 7-16% (P<0.001). Such significant differences between buffer efficiency were unlike the individual species collection, where there was either no significance between buffer 1 and 2 for S. epidermidis, or buffer 1 was only better by a small significance when S. aureus was collected. When a flocked swab was used, the results matched the results from Section 6.18, in which buffer 1 collected between 41-63% which was highly more significant than the 23-48% buffer 2 collected (P<0.001) and the 15-22% that buffer 3 did (P<0.001).

Dry flocked swabs were statistically better at collecting and releasing the staphylococcal mix than either of the other two swab head types (P<0.001). When flocked swabs collected the Staphylococcal mix, that was the only occurrence where a dry swab had achieved over 1% of the inoculant recovery. Flocked swabs again recovered more bacteria with both buffer 2 and 3 in this experiment than the other two swab head types. Therefore, in this experiment, flocked swabs consistently collected and released the highest percentage of the mixed *Staphylococcus* spp.. There was no significant difference between cotton and Dacron swabs when used with buffer 3 or a dry swab (P>0.05). Cotton swabs were significantly more efficient at recovery of biota than Dacron swabs when used with buffer 1 and buffer 2 (P<0.001).



**Figure 38.** Percentage of Co-Culture Bacteria Collected from Each Swab Type. Green represents *S. aureus* percentage and purple represents *S. epidermidis* percentage. Again, while buffer 2 collected the most bacteria when used with cotton or Dacron, buffer 1 significantly outperformed when used with the flocked head. Again, using any buffer collected significantly more than a dry swab.





#### 6.20 Discussion

To collect microbes from the gut in a non-invasive method, a faecal sample is the accepted protocol (Tang et al. 2020b). However, to collect a non-invasive microbial sample from the skin, there is no clear 'gold standard' and several previous studies have used a range of buffers and swab head types (Keyworth et al. 1990; Huttenhower et al. 2012; Ogai et al. 2018). The above experiments have shown that buffer type and swab head type have an impact on the quantity of bacteria collected from a skin model. Therefore, we can reject the null hypothesis, which stated, swab head type or buffer composition have no significance on the quantity of bacteria collected from skin.

# 6.21 Moistening the Tip of the Swab Improves Recovery of Bacterial Biomass from the Skin

Using a buffered solution to wet the swab before collecting a sample, significantly increased the quantity of bacteria removed from the skin model. Any combination of the three buffers with any swab head type always collected more than using a dry swab alone (Figure 36, Figure 38). Prior work that collected bacterial samples from various environmental surfaces have also found that using a wetting agent to premoisten swabs have increased collection sensitivity (Landers et al. 2010). Dry swabs are not highly utilised in skin microbe studies due to the repeated reduced biomass collected by them (Kong et al. 2017). However, a moistened swab head has been shown not to significantly alter the quantity of bacteria collected when sampling from a mucosal zone, such as inside the nasal cavity (Hagiya et al. 2013). Therefore, use of a wetting agent, to premoisten a swab, is likely only required when collecting from areas of skin which are not excessively moist like the inside the nose or the inner vulva.

# 6.22 Importance of Buffer Composition When Collecting Bacterial Biomass from the Skin

The composition of the solutions used in these previous papers include a non-ionic surfactant and an osmotic/pH buffering base. The addition of the non-ionic surfactant increases contact of the swab with the sample surface, the decreased surface tension also helps remove adhered cells and eventually release them from the swab (Moore and Griffith 2007). The solutions used in which the highest quantity of bacteria was collected across all the experiments were buffers 1 and 2 (Figure 36, Figure 38). Buffer 1 contained 0.1% v/v of the Triton-x-100, while buffer 2 contained 0.1% v/v Tween 20. Both non-ionic surfactants can cause damage to bacterial cell membranes and Triton-x-100 can be particularly potent against gram-negative bacteria (Helander and Mattila-Sandholm 2000; Johnson 2013). Tween 80, for example, has been shown to permeate membranes at a concentration as low as 0.1% (Nielsen et al. 2016).

As there was no overall significance of total bacteria collected between the two buffers, the nonionic surfactants were unlikely to have caused serious membrane damage at the concentration used. Buffer 3, however, significantly, and consistently collected the lowest number of bacteria from the porcine skin. While buffer 3 also contained Tween 20, the concentration was five times higher than found in buffer 2. The buffer may have initially removed the same quantity of the *Staphylococcus* spp., however, cell membrane damage could have reduced the number of viable cells. For future research into whether surfactant concentration has an effect on cell viability, the buffer compositions could have their surfactants switched, e.g., Buffer 1 made with 0.5% v/v Tween 20 rather than 0.1% v/v Tween 20.

### 6.23 The influence of Swab Head Types on Viable Bacterial Cells Collection

The number of viable bacterial cells collected from the skin was significantly affected by the swab head type used. Flocked swab heads collected, and deposited, significantly more bacteria when using buffer 1 or 2, across all experiments than either cotton or Dacron (Figure 37, **Error! R eference source not found.**). While not as consistently, flocked swabs still collected more than cotton or Dacron swabs using buffer 3, even without buffer. The results correspond with the published literature, which reports that flocked swabs are more efficient at uptake and release of biomass than traditional swab types (Daley et al. 2006; Dalmaso et al. 2008; Hernes et al. 2010; Finazzi et al. 2016). The design of flocked swabs differs to the traditional, as they have individual protruding nylon fibres which increase both surface area and surface tension. Individual strands and a lack of core also mean that the microbiota collected are less likely to be trapped amongst the fibres and therefore released with more ease (CopanDiagnostics 2010; Faoagali 2010; PuritanMedical 2019; Manoj et al. 2021).

While using flocked, the swab type consistently collected and released the most biomass, the same consistency could not be replicated with the cotton or Dacron swabs. Many of the experiments returned no significance between the two swab types, and neither regularly outperformed the other (Figure 37, **Error! Reference source not found**.). Previous work has found t hat while Dacron swabs were overall more efficient at absorption, extraction and recovery, many of these properties also overlapped with cotton swabs (Bruijns et al. 2018). Cotton swabs possess fatty acids which, if exposed long enough, can be toxic to certain bacteria (Zain and Bradbury 1995; Faoagali 2010). Irradiating the cotton swabs to sterilise them can also cause leaching of these fatty acids and exacerbate the issue (Dadd et al. 1970). The Centres for Disease Control and Prevention actively advise against the use of cotton swabs as their materials can inhibit PCRs (CDC 2017), while their high DNA content which could also cause issues in creating false results (Probst et al. 2010). Dacron swabs are still used for research and, when flocked swabs are unavailable, are an adequate substitute (Kline et al. 2021). However, due to their fibrous design, bacteria can become trapped and unable to be released. Nevertheless, Dacron swabs have been shown to

recover proteins better than other swab types and therefore would likely be more suited for experiments involving secreted bacterial toxins, for example (Zasada et al. 2020).

One of the reasons however that cotton and Dacron swabs were so inconsistent was the difficulty in repeating the swabbing technique. While the protocol remained the same, the pressure used in collection is extremely hard to replicate. Discrepancy between swabbing pressure has been noted in several studies that swabbing technique can impact the collection of viable bacteria and that other methods may be better suited (Ogai et al. 2018).

# 6.24 Conclusion

This study has highlighted the inconsistencies between previous research papers and how they may not have successfully created an accurate depiction of skin microbiota. While swabbing itself may not paint the most accurate microbial picture, there will always be a need for a non-invasive protocol involving swabs. Therefore, correct buffer and swab type selection could potentially increase the accuracy of microbial representation and it is imperative that the practise of skin swabbing becomes more standardised to help ensure consistent reproducibility across the research. The above results clearly show that using flocked swab head types in conjunction with buffer 1 recovered a significantly larger quantity of bacteria than any other combination. It also shows that regardless of swab type, a wet swab was always better than a dry swab.

7 Choosing a Suitable Swab Site for Skin Microbiome Experiments to Limit Background Contamination Interference

### 7.1 Introduction

Bacterial mass on skin is low compared to other areas of the body, collection of enough bacteria to produce an accurate picture of the microbial inhabitants can be difficult (Byrd et al. 2018). As discussed in the introduction, the skin has varying pHs, topography, temperature and dryness which results in the microbial fingerprint varying from region to region (Yousef et al. 2020; Zhou et al. 2020). If one were to design an experiment, it would be ideal to sample from areas in which the most bacterial DNA can be recovered. A logical continuation from the results of Section 6 would be to use the best swab and buffer combination to recover bacteria from the skin. Future general cosmetic studies could focus investigations on the areas that could give the biggest bacterial return and limit the relative abundance of background contamination which could skew results.

# 7.2 Microbial Inhabitants Differ from Person-to-Person

While different areas of the body will have different microbial communities, individuals themselves will differ in microbial biomass and inhabitants. Influences on skin's microbes include individual hygiene, sex, hormones, age, location, partners, and pets (Song et al. 2013; Ying et al. 2015; Gupta et al. 2017; Vandegrift et al. 2017). There's conflicting data as to whether men or women have more abundant or varied species on their skin (Marples 1982; Fierer et al. 2008), but cohabiting couples often have overlapping communities (ASM 2017; Ross et al. 2017). Pets also influence the microbiota that live on skin, with humans often harbouring microbiota more closely associated with their pets (Song et al. 2013; Wetzels et al. 2021). With such differences, you cannot say whether one community fingerprint is the 'best' as each microbial skin community is different. However, there are microbial signs in which someone's skin may be unhealthy (Liu et al. 2020a). Individuals with atopic dermatitis for instance often have a higher abundance of *S. aureus* (Ogonowska et al. 2021), or people with seborrheic dermatitis may have elevated levels of the fungal genus *Malassezia* residing on their scalp (Kim 2009).

### 7.3 Cosmetic Testing on Skin

Studies into how cosmetics affect skin often use the volar forearm as the testing location, called the forearm-controlled application technique (FCAT) (Ertel et al. 1995; Farage 2000; GSK 2017). The volar forearm has a large surface area, a second arm for control, a lack of interfering hair or secretions and can easily be covered up should any unsightly reactions to the product occur. It has also been shown to be a decent comparison for testing facial cosmetics as it has equivalent hydration and biochemical properties (Bazin and Fanchon 2006). However, if one were to investigate microbial composition of the skin and any changes which may occur, the volar forearm may not be the best location for such cosmetic investigations. Being classed as a 'dry' area of the skin (Grice et al. 2008), the bacteria which reside there would unlikely be comparable products

which are designed for oily or moist regions (Grice and Segre 2011). The microbial biomass available would be minimal (Breton 2018) and background contamination could dominate the samples, leaving the results with very little useful information (Salter et al. 2014; Glassing et al. 2016; Eisenhofer et al. 2019).

# 7.4 Background Contamination of Microbial Samples

DNA extraction from a microbial sample will always have background contamination, whether it be from the sampling equipment, extraction kit, the processing laboratory or simply from the environment which surrounds the collection site (CDC 2003). Steps can be taken to remove the background contamination through multiple negative controls including multiple negative controls of the sampling devices, surroundings and extraction methods and removing these from the samples using bioinformatics software (Grogan et al. 2019). However, many of the background contaminating bacteria are also normal inhabitants of the collection site and therefore are difficult to identify as a contaminant (Glassing et al. 2016). Contamination in low biomass samples have also been shown to have skewed data by dominating the sample and therefore inaccurately portrayed the microbial community (Hasrat et al. 2021). When choosing a site on skin to conduct a microbiome study, choosing a site with greater biomass will help reduce spikes in background contamination (Minich et al. 2019).

# 7.5 16S rRNA gene Sequencing to Identify Microbial Communities

The ribosome in prokaryotes have the same function as eukaryotes, they are the site of protein synthesis (Adams 2014). Prokaryotes 70S ribosome have a small 30S unit, which contains the subunit 16S rRNA, and a larger 50S unit, which contains the subunits 23S rRNA and 5S rRNA (Fox 2010). The 16S rRNA gene has more than 1500 base pairs and consists of nine hypervariable regions which are unique to each species (Bukin et al. 2019).16S rRNA gene sequencing has been used for many years to help identify microbial communities of different habitats, most research focuses on certain hypervariable regions which can usually identify down to genus level, but if the whole gene is sequenced then species can be identified (Janda and Abbott 2007). Amplification of different regions can influence the results of the communities (Soriano-Lerma et al. 2020), generally for identification of skin bacteria the V3-V4 region is used (Castelino et al. 2017). Previous work has shown that amplification of the V3-V4 region had high species richness and identified known skin species in abundance (Ross et al. 2018; Stehlikova et al. 2019).

## 7.6 Sequencing reads and Operational Taxononomic Units (OTUs)

16S rRNA gene sequencing recover total sequencing reads, taxon sequencing reads, unclassified sequencing reads, and unique sequencing reads from each sample. Total sequencing reads are the number of effective sequencing reads, taxon sequencing reads are the sequencing reads which can be attached to a taxon, unclassified sequencing reads are the that are not associated with

taxa and unique sequencing reads are sequencing reads which only one occur in one sample. Sequencing reads with an identical sequence of 97% or more are called operational taxonomic units (OTUs) which help determine the bacterial diversity present.

#### 7.7 Diversity Indices

#### 7.7.1 Alpha Diversity Indices

Alpha diversity ( $\alpha$ -diversity) indices evaluate the species diversity within a sample group based on either measurement of abundance of specific species or distribution within the sample, or as a combination (Willis 2019).

The Shannon diversity index uses the abundance and evenness of species within a sample to calculate how unpredictable a random species plucked from the sample would be. For example, if there are only 2 species within a sample at a 1:1 ratio then the diversity is low guessing a randomly picked species would be highly likely. However, if a sample has thousands of species at different proportions, then diversity would be high and the chances of guessing a random species would be highly unlikely. Therefore, the higher the resulting number, the higher the diversity within a sample (Thukral 2017). The Simpson diversity index is similar to the Shannon diversity index, but measures the probability that two randomly picked individuals from a sample were from the same grouping (Hunter and Gaston 1988). As 0 would be high diversity and 1 would be no diversity, the data is often represented as '1 – Probability Result' to maintain the 'high number equals high diversity' theme, this is called the Gini-Simpson index (Caso and Gil 1988). While the Shannon and Simpson's diversity indices measures abundance and evenness throughout the sample, both CHAO1 and Abundance Based Coverage Estimator (ACE), estimate the richness of a sample by abundance of different species present. CHAO1 weights the estimation on rarer species within a sample, only occurring once or twice, to approximate the number of missing species. ACE also calculates estimation of diversity and missing species through the using rare species, but these are classed as species occurring less than 10 times within a sample (Kim et al. 2017a). The Good's coverage calculates the coverage of a dominant species within a sample by measuring the number of rare OTUs with one appearance over the total OTUs within a sample (Good's Coverage = (1- frequency of rare OTUs/Total OTUs)), so the greater the result the less diversity within a sample or high domination by abundant species (Fouts et al. 2012). The phylogenetic diversity measures the total branch length of one group, the higher the total length the greater the diversity within a sample (Faith 1992).

#### 7.7.2 Beta Diversity

Beta diversity ( $\beta$ -diversity) measures similarity between samples as a distance between 0 to 1. Weighted unifrac distance and unweighted unifrac distance measure the dissimilarity coefficient between paired samples. The higher the unifrac distance the greater the diversity between samples, this is measured on 0-1 scale. Weighted unifrac calculates diversity by including the abundance of species/groups, while Unweighted unifrac only calculates using true or false, meaning simply do both samples contain this species/group (Lozupone et al. 2007). Both  $\alpha$ diversity and  $\beta$ -diversity indices are commonly used for skin studies (Silva et al. 2018).

### 7.8 Null Hypothesis

That the location site of skin swabbing, for the collection of bacteria, does not affect the relative background contamination.

### 7.9 Aims

- Investigate different swab sites and whether they are appropriate for cosmetic microbiome studies
- Choose a swab site with greater viable cells to limit background contamination
- Compare percentage of background contamination from swabs and extraction kit
- Compare the presence of bacterial taxa at each swabbing location and between participants

### 7.10 Materials

## 7.11 Swab type and Buffer

Section 6.2 highlighted how different swab head types and buffer compositions can retrieve significantly differing quantities of bacteria from skin. Using those results, this experiment used the flocked swabs (4N6FLOQSwabs<sup>™</sup>, Life Technologies, Carlsbad) and Buffer 1 (0.075 mol litre-1 of phosphate buffer [pH 7.9] containing 0.1% v/v Triton X-100) combination to recover bacteria from the skin.

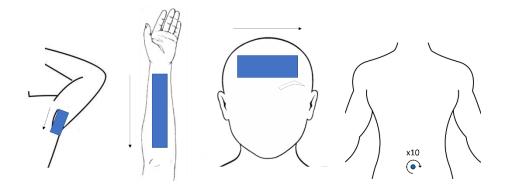
## 7.12 Swabbing Participants

One Caucasian male, age 34, and one Caucasian female, age 27, volunteered to be swabbed. Both individuals cohabited and owned two cats at time of participation. As the samples processed were microbial in nature and removed from skin cells they are not considered 'relevant material' under the Human Tissue Act and therefore no need for a license (HTA 2021). Swab heads which may have accidentally removed skin cells were discarded at the earliest convenience after use. Signed consent was obtained from both participants (See Appendix). Due to Covid restrictions and social distancing measures, the swabbing had to take place in the participants home environment, which was not ideal. Surfaces were cleaned with antimicrobial sprays and clean gloves were worn to take the sample. However, background contamination can come from anywhere, laboratories included (Weyrich et al. 2019). The number of participants would be classed as too low for robust study. If this experiment was to be repeated, possibly to investigate the background contamination of microbiological laboratories, then the number of participants would ideally be increased to between 10-20 partakers.

#### 7.13 Methods

#### 7.14 Swabbing Technique

The locations were chosen due to their differing dryness, the forehead is oily, the volar forearm is dry, the axilla is moist (Introduction, Figure 1). The volar forearm is also used in many cosmetic studies. The navel was chosen because its topography differs from the rest, as it can concave into or convex out of the skin (Fahmy 2018). Due to the differing topography and size of the location swabbed, a single technique was difficult to achieve. This work also wanted to be able to remove the highest quantity of DNA possible to achieve a more accurate representation of the microbial community. Swabbing took place first thing in the morning, before showering. A single swab was fully dipped into the buffer solution for 5 seconds and samples were taken from as much of the chosen area as possible. Figure 40 highlights the direction and area of the body that was swabbed. To swab the left axilla, the arm was raised and swabbed from the top furthest left to the bottom furthest right, swab direction was vertically downwards, the head was rotated after each line was completed. For the left volar forearm and axilla, the area was swabbed from the top left to the bottom right, one-way vertical strokes away from the wrist, with the head rotated a quarter turn after each line was completed. Care was taken not to swab the antecubital fossa. For the forehead, the same technique was repeated, but with horizontal strokes, left to right, care taken not to swab the hairline or eyebrows. Due to the shape of the navel, the swab was inserted until the bottom of the navel was achieved and the perimeter swabbed in a clockwise motion 10 times. Once the sample was collected, the swab head was removed from shaft and placed into an Eppendorf<sup>™</sup> (Eppendorf, Hamburg) polypropylene DNA Lo-bind polypropylene microcentrifuge tube ready for extraction.



**Figure 40. Body Parts Swabbed.** Blue indicates the areas swabbed. The axilla (left) the arm was raised and swabbed from the top furthest left to the bottom furthest right, swab direction was downwards. The left volar forearm (second from left) was swabbed away from the wrist in repetitive vertical strokes that covered the whole area. The forehead was swabbed horizontally left to right. The navel was swabbed once the swab hit the bottom, ten times in a clockwise rotation.

#### 7.15 Extraction of Bacterial DNA from Swabs

Bacterial DNA was extracted from the swabs using the PureLink<sup>™</sup> Microbiome DNA Purification Kit (Invitrogen, Massachusetts). The protocol was modified slightly to achieve greater yield. The swab heads were added to a bead tube containing the lysis buffer and lysis enhancer, the tubes were placed into the MP Biomedicals<sup>™</sup> FastPrep-24<sup>™</sup> 5G Instrument and lysed with a velocity of 6.5 m/s twice for 45 seconds with a 5-minute intermission. After a 10-minute incubation at 65 °C, the tubes were placed back into the FastPrep-24<sup>™</sup> at the same settings. From that point the protocol was followed until the DNA was eluted. RNase Free Water (Severn Biotech Ltd, Kidderminster) replaced the kit elution buffer. This was done as elution buffers have the potential to disrupt further applications. DNA was quantified using the Qubit 4 Fluorometer (Invitrogen, Massachusetts) using the protocol designed for the Qubit<sup>™</sup> dsDNA High Sensitivity assay. To confirm that downstream applications would not be affected by the chemicals used in the extraction, the V3-V4 hypervariable region of the bacterial 16S rRNA gene was amplified using primers 341F (5'->3') CCT AYG GGR BGC ASC AG and 806R (5'->3') GGA CTA CNN GGG TAT CTA AT. Products were run on a 1.5% agarose gel to confirm that bacterial DNA was present.

#### 7.16 16S rRNA Amplification and Sequencing

Genomic DNA extracted from the samples were sent to Novogene Co (China) for 16S rRNA amplicon metagenomics sequencing. Due to the low DNA concentration, 30,000 reads were undertaken per sample (~150k raw reads per sample). Again, the PCR was used to amplify the V3-V4 hypervariable regions using the same primers. The PCR products went through quantification and mixing, purification, library preparation and sequencing. Amplicon was sequenced on Illumina paired-end platform to generate 250 bp paired-end raw reads (Raw PE), and then merged and pre-treated to obtain Clean Sequencing reads. The chimeric sequences in Clean Sequencing reads were detected and removed to obtain the Effective Sequencing reads which can be used for subsequent analysis (Liu et al. 2019).

#### 7.17 Statistics

To study the microbial community composition in each sample, Operational Taxonomic Units (OTUs) were obtained by clustering with 97% identity on the Effective Sequencing reads of all samples, and then identified. The OTU analysis included species annotation, distribution,  $\alpha$ -diversity,  $\beta$ -diversity, and species variance statistics. To test for significance of differences between groups for both  $\alpha$ -diversity and  $\beta$ -diversity, this involved Wilcox and Tukey tests. Bacterial diversity analysis was performed using QIIME software (version 1.7.0). One-way ANOVA and t-tests were also carried out on the abundance of 'hits' sample groups and individual samples had on overall OTUs, using GraphPad Prism (version 9.3.1). The  $\beta$ -diversity weighted and unweighted unifrac calculations were visualised into non-metric multidimensional scaling using the Vegan and Mass packages in R (version 4.0.5) and illustrated using GraphPad Prism (version

9.3.1) The contamination percentage was achieved by removing the number of OTUs found in the male swab control, female swab control and kit control from the sample groups, this was performed in Excel (Version with Windows 11).

#### 7.18 Results

#### 7.19 Sequencing reads Recovered from Samples

The kit blank control returned 10,118 sequencing reads, in which 98.6% could be classified into 245 OTUs. This part of the results Section is in reference to Figure 41.

## 7.19.1 Male Participant's Results for Total, Usable, Percentage, Unique Sequencing reads and OTUs

For the male samples (Figure 41), the samples with the highest total sequencing reads were the axilla 83,488 of which 99.3% could be classified into 318 OTUs, 611 sequencing reads were unique to the sample. The forehead returned 81,474 sequencing reads, with 98.3% classified into 461 OTUs, 1204 sequencing reads were unique to the sample. The volar forearm returned 61,555 sequencing reads with 96.9% classified into 940 OTUs, 1879 sequencing reads were unique to the sample. The navel sample returned 32,735 sequencing reads with 97.7% being classified into 733 OTUs, 751 sequencing reads were unique to the sample. The male swab blank control also returned 14,802 sequencing reads in which 94.6% could be classified into 672 OTUs, 805 sequencing reads were also unique to that sample.

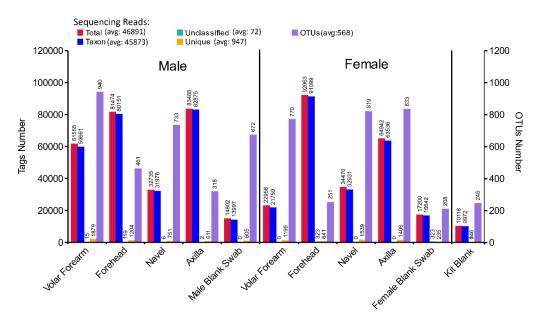
# 7.19.2 Female Participant's Results for Total, Usable, Percentage, Unique Sequencing reads and OTUs

For the female samples (Figure 41), the sample with the highest total sequencing reads was the forehead with 92,063 sequencing reads, of which 99.0% could be classified into 251 OTUs, 641 sequencing reads were unique to the sample. The axilla 64,942 of which 97.8% could be classified into 833 OTUs, 1406 sequencing reads were unique to the sample. The navel sample returned 34,470 sequencing reads with 95.5% being classified into 819 OTUs, 1539 sequencing reads were unique to the sample. The forearm returned 22,958 sequencing reads, with 94.7% classified into 770 OTUs, 1199 sequencing reads were unique to the sample. The female swab blank control also returned 17,200 sequencing reads in which 96.7% could be classified into 208 OTUs, 235 sequencing reads were also unique to that sample.

### 7.20 T-tests and One-way ANOVA of OTU abundance

One-way ANOVA analysis of the all-individual OTU abundance in all sample groups resulted in no statistical difference between the male-female-blank controls (P=0.3895). There was no statistical difference in the abundance of all individual OTUs when comparing male-female sample groups (P=0.5901), nor between male-blank controls (P=0.1298), nor female-blank controls (P=0.3002). Overall, while not statistically different, the male sample group had more dissimilar overall

individual OTU abundance than the blank controls than between the blank and female controls. However, using a t-test to analyse between two comparable individual groups did result in differences. Between male and female samples, the only statistical difference between overall individual OTU abundance was between the forearm samples (P=0.002). All the other comparable groups between male and female were not significantly different e.g., the male axilla did not have a significantly different individual OTU abundance than the female navel sample (P=0.9405). Only the male axilla sample was not significantly difference to both the male swab blank and kit blank controls (P>0.05), the rest were significantly different to their controls (P<0.03). Only the female forehead sample was not significantly different to the kit blank control (P>0.05), while the other female samples were significantly different to the kit blank control (P>0.05). Only the female axilla sample was significantly different to the kit blank control (P<0.02), the other samples were not significantly different to the swab control (P>0.05). None of the blank controls were significantly different to each other (P>0.30).



**Figure 41. Number of Sequencing reads and OTUs from Each Sample.** The most annotated sequencing reads from a male sample were from the axilla with 82,975, the lowest amount not including the blank was from the navel which was 31,978. The blank swab used when collecting male samples still resulted in 13,997 annotated sequencing reads. The most annotated sequencing reads from a female sample were from the forehead with 91,099, the lowest amount not including the blank was from the volar forearm which was 21,759. The blank swab used when collecting female samples still resulted in 16,642 annotated sequencing reads. The extraction kit itself produced 9972 annotated sequencing reads.

#### 7.21 Diversity Indices Results

#### 7.21.1 Alpha Diversity of Samples

These results refer to the top half of Table 10. The  $\alpha$ -diversity for the male's samples taken from body sites shows that the number of observed species mostly correlates with diversity. For example, the volar forearm had 634 observed species and the highest Shannon's (6.35), Gini-Simpson's (0.96), Chao1 (851) and ACE (927) results and the least amount of domination by one species of Good's Coverage (0.976). However, phylogenetic diversity measurement of the branch length was the second longest at 58.5 units compared to the forehead which was 81 units. The forehead sample was less diverse compared to the volar forearm with every other measurement. The blank swab, although it had the lowest number of useable taxonomic sequencing reads (Figure 41), had a high number of OTUs and individual species and therefore diversity results were high. Again, the most diverse of the female samples was the volar forearm with 607 observed species, it had the highest Shannon diversity (7.04), Gini-Simpson's diversity (0.981), Chao1 (730), ACE (742) and longest phylogenetic diversity unit (45.2). Only the navel sample had less coverage or dominance by the abundant species, at 0.979 compared to 0.984. Both the female blank swab control and kit blank control had less diversity compared to the male blank swab control; all other results can be seen in Table 10. Due to lack of replicates, comparison between samples is statistically difficult to achieve but comparison of overall diversity of the male and female total samples are possible. Although there were differences at sample levels of diversity, there was no statistical difference between male and female for all the  $\alpha$ -diversity indices (Table 11).

Participant	Sample Name	Number of Observed Species	Shannon Diversity Index	Gini- Simpson's Diversity Index	Chao1 Index	ACE Diversity Index	Good's Coverage	Phylogenetic Diversity
	Volar Forearm	634	6.354	0.960	851.107	926.519	0.976	58.495
	Forehead	296	4.202	0.849	501.857	514.764	0.987	81.091
Male	Navel	521	6.272	0.958	660.567	686.401	0.984	43.985
	Axilla	147	2.096	0.561	190.966	200.165	0.995	18.001
	Male Swab Blank	589	7.065	0.982	640.739	680.359	0.988	47.454
	Volar Forearm	607	7.040	0.981	730.367	741.897	0.984	45.227
	Forehead	94	1.240	0.393	183.438	215.605	0.995	16.477
Female	Navel	574	5.192	0.892	748.762	802.280	0.979	43.410
	Axilla	495	6.074	0.964	691.265	718.553	0.982	39.609
	Female Swab Blank	172	3.452	0.804	235.000	242.446	0.994	25.043
Kit Control	Kit Blank	245	4.426	0.917	328.133	344.657	0.991	23.787

Table 10. Alpha Diversity Index of All Samples

Table 11. Tukey and Wilcox Statistical results of the Overall Alpha Diversity Indices of the Male
and Female Participants

Alpha Index	Tukey	Wilcox
	P-Value <sup>10</sup>	
Observed Species	0.9613759	1
Shannon Diversity Index	0.9945016	0.9262
Gini-Simpson's Diversity Index	0.9852550	0.7080
Chao1 Diversity		
Index	0.9777527	0.7689
ACE	0.9796687	0.6226
Diversity Index		
Good's Coverage	0.9937061	0.8400
Phylogenetic Diversity	0.5742229	0.3365

Table 12. Tukey and Wilcox Statistical results of the Overall Alpha Diversity Indices of the Female and All Blank Controls

Alpha Index	Tukey	Wilcox
	P-Value <sup>11</sup>	
Observed Species	0.8144609	0.7525
Shannon Diversity Index	0.9982553	0.3333
Gini-Simpson's Diversity Index	0.8340474	0.8847
Chao1 Diversity	0.6326259	0.3463
Index		
ACE	0.6335160	0.3010
Diversity Index		
Good's Coverage	0.4913804	0.2802
Phylogenetic Diversity	0.9588387	0.9027

 $<sup>^{\</sup>rm 10}$  P<0.05 for a statistical difference

 $<sup>^{\</sup>rm 11}\,{\rm P}{<}0.05$  for a statistical difference

## Table 13. Tukey and Wilcox Statistical results of the Overall Alpha Diversity Indices of the Male and All Blank Controls

Alpha Index	Tukey	Wilcox
	P-Value <sup>12</sup>	I
Observed Species	0.9278945	0.7525
Shannon Diversity Index	0.9878695	0.5833
Gini-Simpson's Diversity Index	0.9049446	0.6244
Chao1 Diversity Index	0.7411215	0.4925
ACE	0.7372359	0.5451
Diversity Index		
	0.5450407	0.2027
Good's Coverage	0.5458487	0.3627
Phylogenetic Diversity	0.4646718	0.4358

## 7.22.1 Beta Diversity Between Samples

The weighted unifrac measured diversity based on shared species abundance, while the unweighted unifrac measured diversity based on whether both samples shared a species. The unifrac scores were converted into non-metric multidimensional scaling (nmds). The closer the samples were together on Figure 42, the less diversity between samples. The below results are all in reference to Figure 42.

The weighted unifrac samples were evenly spread across the graph, with both the female and male volar forearms and navels having the least diversity between samples. The four closest samples had more OTUs in common and abundancy with the male swab blank control sample than any other blank control group. The male axilla and female swab blank control were most like the kit blank control, but diverse from each other. The unweighted unifrac however had both much more distant diversity between samples, as well as samples which were so similar, they overlapped. The samples that were so similar they overlapped included the male swab blank control, female forearm, and female axilla. The male navel sample was very close to the overlapped trio of samples and around the perimeter of the cluster included female blank swab control, kit blank control and male volar forearm. The three outlier samples were the female forehead, male forehead, and male axilla samples. The female forehead had more OTU in common with the male axilla than the male forehead.

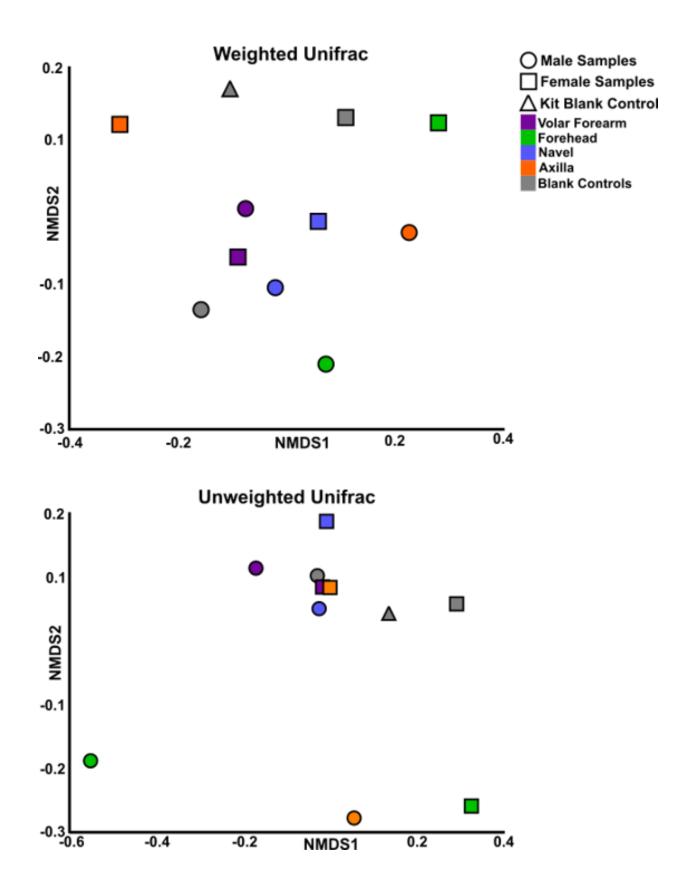
<sup>&</sup>lt;sup>12</sup> P<0.05 for a statistical difference

Due to a lack of replicates, a comparison between samples was statistically difficult to achieve, but comparison of overall diversity of the total male and female samples was possible. There were no statistical differences between the diversity between all the sample groups. However, though not significant there was more diversity between male and female groups than either male and the blank controls or female and the blank controls. (Table 14). All female samples and male samples had a diversity more alike the blank controls than each other.

Sample Comparison	Tukey P-Value <sup>13</sup>	Wilcox P-Value	
-	Weighted-Unifrac	Unweighted- Unifrac	
Male-Female	0.3277	0.2996	
Female-Blank Controls	0.9794	0.9943	
Male-Blank Controls	0.5753	0.4912	

Table 14. Tukey and Wilcox Statistical Differences between all Sample Groups

<sup>&</sup>lt;sup>13</sup> P<0.05 for a statistical difference



**Figure 42. NMDS of Weighted-Unifrac and Unweighted-Unifrac.** The closer the samples are together the less diversity between those samples. The weighted unifrac, which uses abundance and presence of OTUs, appears to a much more even spread of diversity from sample to sample than the unweighted unifrac. Both female and male navels and forearms were close in diversity, while the male and female foreheads and axilla were not so closely diverse. The unweighted unifrac only considers the binary of whether both samples contain an OTU. In the bottom of the unweighted, the male axilla and both sexes forehead samples are much farther away from the centre cluster. The centre cluster contains the samples with the low sequence reads and blanks controls.

#### 7.23 Top 10 Isolated Genera from the Samples

Figure 43 shows the top ten genera isolated from all the samples, these include the three common skin genera *Cutibacterium*, *Corynebacterium* and *Staphylococcus*. The kit blank control was made up of over 50% of the top ten genera, with the most abundant genera being *Cutibacterium*, *Staphylococcus*, *Enhydrobacter*, *Acidovorax* and *Bacillus*.

#### 7.23.1 Male Samples Genera Abundance

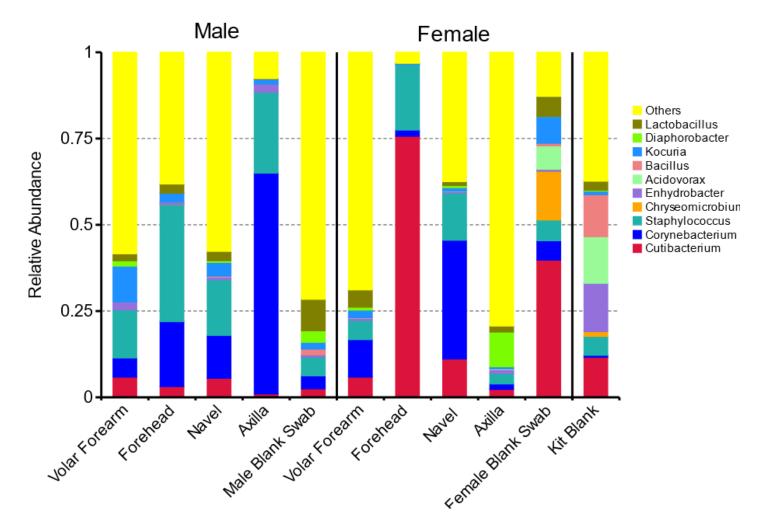
All the male samples were low in *Cutibacterium* abundance but were largely dominated by the genera *Corynebacterium* and *Staphylococcus*. Dominance from these two genera was most obvious from the axilla sample, where over 75% of the genera abundance was made up of *Staphylococcus* and *Corynebacterium*. The only other sample in which the three common skin genera made up over 50% of the relative abundance was from the forehead. The navel sample had over 25% abundance of the three common skin genera, with *Kocuria* being the next most prominent named genus. Both the volar forearm and the navel were dominated by the mixed, unnamed genera, others. The volar forearm only had 25% of its relative abundance as *Cutibacterium*, and *Corynebacterium* combined. The male blank swab had the top 10 genera even distributed to over 25% of the relative abundance, but most of the relative abundance consisted of mixed, unnamed genera.

#### 7.23.2 Female Samples Genera Abundance

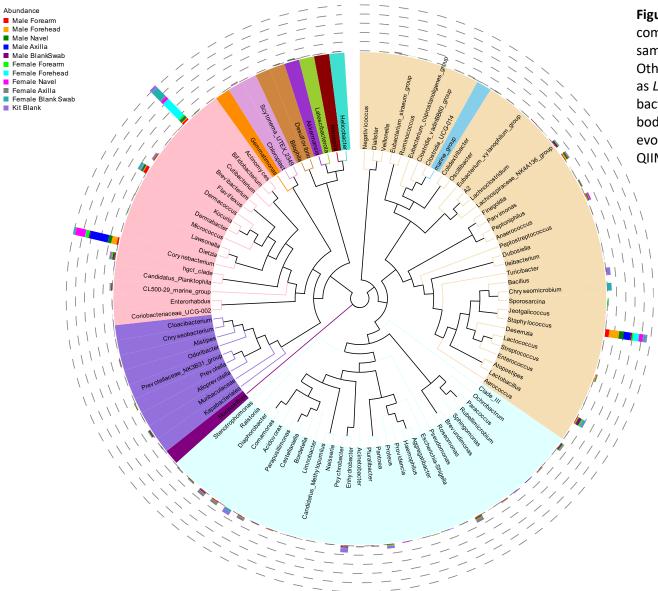
The female forehead was an abundance of 75% *Cutibacterium*, with the next most common genus being *Staphylococcus*, very little *Corynebacterium* was isolated from here. More than 50% of the abundance of genera isolated from the navel was dominated by the three common skin genera, while this dropped to under 25% for the volar forearm, and very little of the axilla was made up of the three. Both the volar forearm and axilla were dominated by the unnamed mixed genera, the volar forearm also had a good proportion on *Lactobacillus* isolated, while the axilla had a large abundance of *Diaphorobacter*. The female blank swab control was dominated by *Cutibacterium* and around 50% was made up of the three common skin bacteria, there was also a large abundance of *Chryseomicrobium*, *Acidovorax*, *Kocuria* and *Lactobacillus*.

#### 7.23.3 The Unnamed Genera Group

Figure 44 shows the evolutionary tree of all the genera isolated from all the samples, including the unnamed genera from Figure 43. This Figure highlights the unexpected genera in the background contaminations, such as *Helicobacter, Pantoea, Parapusillimonas* and *Muribaculaceae*.



**Figure 43. Top 10 Genera Found in Samples.** The classic skin genera *Cutibacterium, Staphylococcus* and *Corynebacterium* were found within the top 10 genera found in samples. Others found in the top 10 were questionable as to whether they were found on the skin or simply background within the blank controls. The genus *Chryseomicrobium* for example often have species isolated from soil or earthworms rather than human skin (Saha et al. 2018)



**Figure 44. Evolutionary Tree of Genera from All Samples**. Three common skin genera dominated the total abundance of all samples, *Cutibacterium, Staphylococcus* and *Corynebacterium*. Other genera also have a fair abundance of representation such as *Lactobacillus* and *Kocuria*. Many of the blank controls have bacteria which would be unexpected anywhere on the human body, let alone the skin. A stated in Section 7.17, analysis and evolutionary tree of bacterial diversity was produced using QIIME software (version 1.7.0).

#### 7.24 Percentage of Background Contamination and Likely Contaminants

In the appendix, is the list of OTUs and abundance of each OTU found in the sample. The percentage of contamination differed depending on which and how many control abundances were removed from the groups. If all controls were removed from the samples (male swab blank, female blank swab, and kit blank control), the most contaminated female sample was the Forearm sample at 62.1% and the most contaminated male sample was the navel at 46.3%. For all contamination percentages please see Table 15.

Figure 45 shows the phylogenetic tree of all samples, from kingdom all the way to identifiable species. Of the bacteria isolated nearly 57% were from the phylum Actinobacteriota, 33.3% were from the phylum Firmicutes and 9.77% were from the phylum Proteobacteria. While the phyla Actinobacteriota and Firmicutes were isolated from all samples, Proteobacteria were isolated from predominantly the kit blank control, the female swab blank control and the female axilla. This control group domination of isolated Proteobacteria filters through to the orders, families, genera and the one species identified, Moraxella osloensis. The only exception is the genus Diaphorobacter which was predominantly isolated from the female axilla. While the Firmicutes were evenly isolated from all samples, the order Bacillales was predominantly isolated from both the kit blank control and female blank swab control. The family and subsequent taxa of Bacillaceae was predominantly recovered from the kit blank control, while the family and subsequent taxa Planococcaceae were isolated from the female blank control. There were other taxa groups which were predominantly recovered from the control groups, Lactobacillus ingluviei, Lactobacillus johnsonii and Lactobacillus aviarius were predominantly isolated from the male blank swab control, while *Lactobacillus mucosae* was only isolated from the female blank swab control and kit blank swab control. Therefore, if a large percentage of recovered bacteria from a sample contain taxa which were predominantly isolated from a control group, then it could be deduced that these were likely from background contamination.

#### 7.24.1 The Sample from the Female Forehead was not Highly Contaminated

With the different control OTUs removed from the sample, the forehead was the least contaminated of the female samples, between 2.35-12.9% of the original sample was contaminated (Table 15). The abundance of phyla recovered from the female forehead included 80.3% Actinobacteriota, 19.7% Firmicutes and 0.02% Proteobacteria (Figure 46). The small percentage of Proteobacteria would have likely come from the kit blank control, as only the order Pseudomonadales was identifiable which was predominantly found in the kit. From the phyla Firmicutes, neither the likely contaminant species *Lactobacillus mucosae* nor any of the order Bacillales were detected in the sample. 7.24.2 The Sample from the Female Volar Forearm had Higher Contamination Levels The percentage of the volar forearm contamination was between 18.1-62.1% contaminated, the highest contamination percentage of any sample, male or female (Table 15). The sample from the female volar forearm had a higher percentage, 5.02%, of Proteobacteria identified from the sample Figure 47. This included the species *Moraxella osloensis* and genus *Acidovorax*, both predominantly isolated from the female blank swab control and kit blank control. From the phylum Firmicutes, the order Bacillales was also detected in the sample, likely to have come from the kit blank control as both *Bacillus thermoamylovorans* and *Bacillus lentus* were identifiable. Other samples with high Proteobacteria percentage included the female axilla (54.8%), the male forearm (9.1%) and the female forearm (5.02%), for all other phylogenetic trees *see appendix*.

	Sample Percentage Contaminated							
Controls	Male	Male	Male	Male	Female	Female	Female	Female
Removed	Forearm	Forehead	Navel	Axilla	Forearm	Forehead	Navel	Axilla
Male	17.3%	5.70%	27.7%	4.11%	42.4%	2.35%	23.2%	15.3%
Control								
Female	14.2%	6.93%	18.4%	4.29%	22.2%	9.15%	13.7%	8.45%
Control								
Kit Blank	10.2%	3.79%	11.5%	4.22%	18.1%	2.35%	9.47%	8.29%
Control								
Male + Kit	26.8%	8.77%	37.3%	7.73%	56.5%	4.28%	30.0%	22.7%
Female	22.0%	8.84%	24.3%	7.15%	30.7%	11.2%	18.3%	14.0%
+ Kit								
Male +	37.5%	13.5%	46.3%	10.2%	62.1%	12.9%	37.1%	26.2%
Female +								
Kit								

Table 15. Percentage of Sample Contaminated after Removal of Controls

## Figure 45 Phylogenetic Tree for all Samples.

Phylogenetic tree for all species highlights the groups which come from background contamination. Majority of the phylum Proteobacteria come from the contamination in the kit, while the order Bacillales is likely a joint contamination from the kit and the female blank swab. Some of the Lactobacillus spp. contaminants came from the male blank swab.

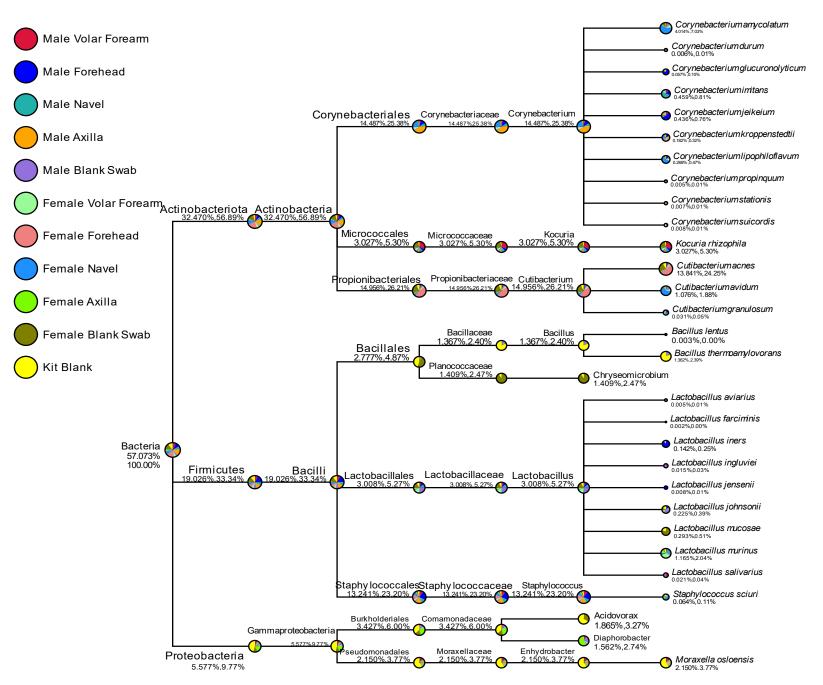


Figure 46. Phylogenetic Tree of the Identified Bacteria from the Female Forehead. The female forehead contained the least abundance of, the likely to be the main contaminant phylum Proteobacteria of any of the samples. Taxa in red were not detected in this sample.

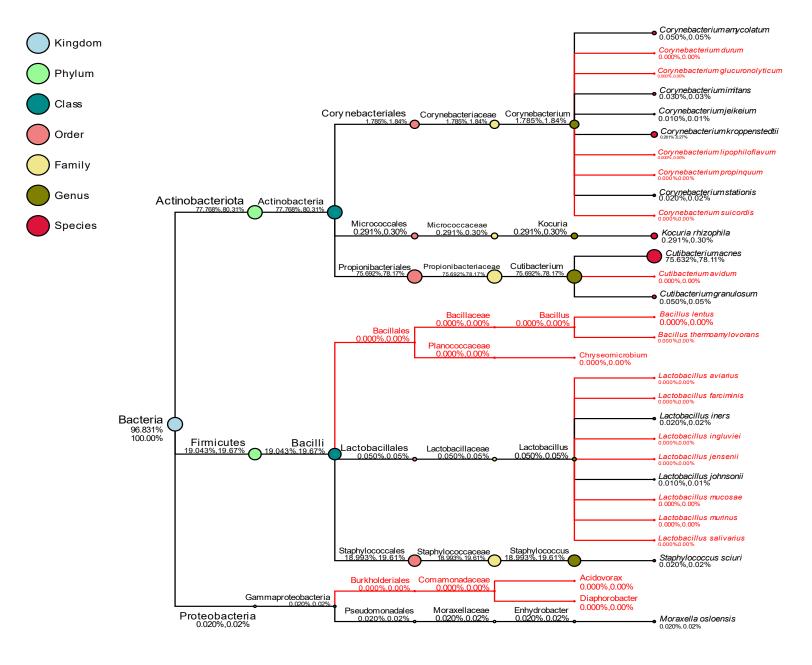
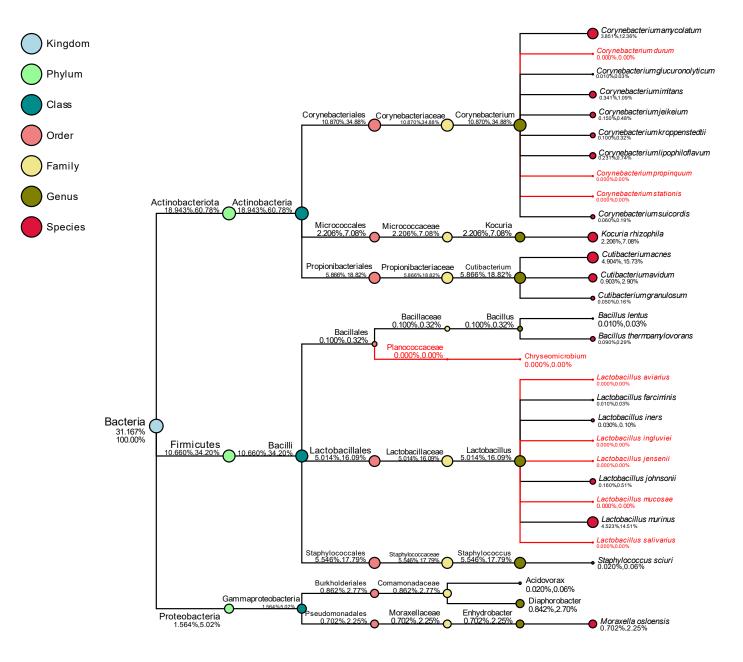


Figure 47. Phylogenetic Tree of the Identified Bacteria from the Female Forearm. The female forearm had 250 times more percentage of Proteobacteria isolated compared to the female forehead. The order Bacillales was also identified which was likely another background contaminant. Taxa in red were not detected in this sample.



## 7.25 Discussion

The site of swabbing does affect the relative background contamination and therefore the null hypothesis can be rejected.

#### 7.26 Ideal Number of Volunteers

Due to the pandemic regulations, the initial samples were taken in a non-laboratory setting and with only two volunteers. While undertaking the study would have been more appropriate in a laboratory setting, the ideal participant number was not so obvious. A range of issues have to considered when deciding the correct sample size for a skin studies including logistical, ethical, budgetary and time constraints (Martínez-Mesa et al. 2016). As this was a small study, with one person undertaking the sampling and initial protocol steps, then the volunteer numbers required would be lower, this would also allow for the time constraints and small budget. However, too small of a participant size could hinder statistical analysis and not provide a suitable conclusion to the study (Faber and Fonseca 2014). A prior study, comparing swabbing and tape-stripping to retrieve skin microbes, was able to conclude their results having used only three men and four women (Ogai et al. 2018), while another study, which had investigated skin microbes at different body sites, was able to successfully draw conclusions using 17 participants (Timm et al. 2020). Therefore, a participant size of around 10 would have been appropriate for this study.

#### 7.27 Likely Background Contaminants

There are always going to be background contaminants when working with microbial communities, even more so in low-biomass habitats like skin. Contamination of samples can come from the collection devices, the air around, the reagents in the kit and further along the process (CDC 2003). Acidovorax, Enhydrobacter, Lactobacillus and Bacillus were genera in which detection was predominantly found in the male blank swab control, female blank swab control or kit blank control (Figure 45), they have also been isolated from other negative control groups from previous microbiome studies (Eisenhofer et al. 2019). However, just because the contaminants mentioned are found predominantly on the control samples, it is possible that they can reside on skin, previous studies have found Proteobacteria such as Enhydrobacter and Acidovorax are naturally a component of the microbial community (Cosseau et al. 2016). If Proteobacteria were present on skin naturally, then the levels may have been too low compared to the controls and the dominant skin genera. While there are no records of background contamination by Chryseomicrobium spp., this genus is most likely to be isolated from aquatic ecosystems, deserts and from soil ejected from an earth worm's digestive tract (Shivaji et al. 2014; Saha et al. 2018), and therefore unlikely to part of the skin microbial community. The genera that also were isolated from the control samples included known skin bacteria, with over 50% of the genera isolated from the female blank control swab being Cutibacterium, Staphylococcus and Corynebacterium. Again, these common skin genera have been found in numerous experimental controls, all three have

been linked to being high abundance contaminants of DNA extraction and amplification kits (Salter et al. 2014; Glassing et al. 2016) and unsurprisingly contamination stemming from microbial laboratories (Weyrich et al. 2019).

#### 7.28 Were Transient Bacteria Present?

Some of the bacteria found on skin during this study may not be classed as normal skin bacteria. These taxa may also not have come from the background controls, and instead could be classed as temporary visitors to the skin, also known as transient bacteria (Kong et al. 2012). Transient species do not proliferate on skin but can multiply if the conditions are favourable, but due to sequencing limitations, these organisms could also be dead (Byrd et al. 2018). Transient species can be transferred to skin from other areas of the body, the surrounding environment or even from pets (WHO 2009). Staphylococcus sciuri, was found in the control samples (Figure 45) but there is little research on it as to its contamination status and was present in the sample which collected most bacterial mass (Figure 46). The largest abundance of S. sciuri were found at the female axilla and female navel. S. sciuri is predominantly part of several animal's microbiota and has been detected in the oral mucosa of cats, an animal which both participants are in direct contact with (Shida 2009; Otto 2010). Lactobacillus iners was also detected on the male forehead at a relative abundance of 2.22% (see appendix, Section 10.3), this species is more closely associated with the vaginal microbial community (Jakobsson and Forsum 2007; Petrova et al. 2017). Kocuria rhizophila was predominantly isolated form the male forearm as well as the female blank swab control. While the genus Kocuria has many species which are resident bacteria, Kocuria rhizophila is more associated with the soil, but has been isolated from mostly the skin of males (Takarada et al. 2008; Khayyira et al. 2020). K. rhizophila could possibly be classed as both transient and residential on human skin (Johnson et al. 2002), very similar to how S. aureus was previously classed (Cogen et al. 2008; Otto 2010; Bondurant et al. 2020).

#### 7.29 Contaminants influenced the Diversity Indices

Due to the low biomass collected from the skin, the overall samples from both male or female were not individually significantly less or more diverse than the blank control group (Table 11,

 Table 11. Tukey and Wilcox Statistical results of the Overall Alpha Diversity Indices of the Male

 and Female Participants

Alpha Index	Tukey	Wilcox
	P-Value	
Observed Species	0.8144609	0.7525
Shannon Diversity Index	0.9982553	0.3333
Gini-Simpson's Diversity Index	0.8340474	0.8847
Chao1 Diversity Index	0.6326259	0.3463
ACE Diversity Index	0.6335160	0.3010
Good's Coverage	0.4913804	0.2802
Phylogenetic Diversity	0.9588387	0.9027

 Table 12, Error! Reference source not found.). Also, although not significant from each other or

the blank controls, the diversity difference between the male and female groups were more

diverse than between both sexes' groups and the blank control groups (Table 11). Background contamination likely skewed the diversity results for the female axilla sample. The observed number of species for the male axilla was 147, while the female axilla observed 495. The male axilla was made up of more than 75% of the genera Corynebacterium and Staphylococcus (Figure 43), while more than 75% of the female axilla is made up of the least abundant genera grouped as others. The abundance of this 'other' group skewed the  $\alpha$ -diversity indices to result in higher diversity within the female axilla sample compared to the male sample. The skewed results are backed up by previous work, in which less than 20% of the phylum Proteobacteria, which many of the 'other' genera are classed, were found at the axilla site of both sexes (Li et al. 2019b). Less obviously, were the skewed evenness of taxa found at the site of both sexes' volar forearms. As a dry location, more diversity is to be expected at the volar forearm than perhaps elsewhere (Table 10). While the distribution of represented phyla was alike previous work, with less Proteobacteria if anything, the relative abundance of the top genera differed. Figure 43 shows the detected genera of Cutibacterium, Staphylococcus and Corynebacterium, together covered around 25% of the male volar forearm abundance and a little less for the female sample. The same three genera of previous work averaged an abundance coverage of 46.3% (Gao et al. 2007). Therefore, the reduced relative abundance of the expected top genera projected a more even distribution of taxa and therefore more diverse samples.

#### 7.30 Removal of Controls May Not Be So Easy

Using a multitude of negative controls and even positive controls can help eliminate the background contamination of samples (Kim et al. 2017b). Both males and female samples were taken together, but the decision was to use two blank swab controls dipped into the buffer for the study. Had this been an in-depth investigation, this would have very useful for the removal of contamination as there were differences in the numbers of OTUs and observed species for the male blank swab control was 672 and 589 respectively while the female blank swab control only had 208 OTUs and 172 observed species (Figure 41, Table 10). The diversity distance between the samples was also one of the longest with an Unifrac distance of 0.426 for weighted and 0.725 for unweighted. Removal of the different controls resulted in different contamination percentage, while the male axilla had a relatively small range of percentage contaminations, between 4.11-10.2%, the female axilla sample had a much larger percentage range between 8.29-26.2%. However, as there were such differences between the controls, this leaves questions as to whether the background contamination of the sample swabs so different. Many papers do not give in-depth descriptions of negative controls and previous work has presented results in which the data was not clearly distant from the contaminations. One of the main problems with microbial sampling is the lack of what is classed as true negative control e.g. a swab waved in the air is not really an accurate air control, or one swab's microbial composition might not reflect all swabs (Hornung et al. 2019). Kit contamination was also recorded from the above investigation (Figure 43). Salter (et al. 2014) found that not only do different kits have varied contamination, but that different batches of the same kit can have significant differences which can influence the microbial community resolution of low-biomass samples. Further potential issues come from choice of bioinformatics, problems reported included background contaminants missed, data skewed and contradictory outcomes (Glassing et al. 2016; Goig et al. 2020; Bharti and Grimm 2021) The way to reduce these problems would be to use multiple negative and positive controls, training for consistent technique, limit differing consumable batches and where possible, aim for sample sites with the greatest biomass available (Harris 2008; Eisenhofer et al. 2019).

#### 7.31 Microbial Communities and Biomass at Different Swab Sites

Both the female and male navel samples had high background contamination due to the low biomass collected from the site, up to 46.3% of the samples had contamination from the control groups. The microbial composition of the navel has previously been labelled as diverse yet 'predictable' (Hulcr et al. 2012). Domination by the classic skin genera of *Corynebacterium* and *Staphylococcus* were seen in the results (Figure 43), as well as the presence of not-so-commonly found on skin *Finegoldia* and *Anaerococcus* (see appendix). The species which were found in this study were all consistent with prior research into the bacterial composition of the navel (Hulcr et al. 2012). If considering a study of the navel microbial community, be sure to use plenty of background controls to cover the contaminating OTUs. Biomass retrieval from the axilla varied somewhat, with contamination of the male axilla being the lowest of all the sample at between 4.11-10.2%. The female axilla, while still relatively low, contamination for the sample was more contaminated than the male equivalent 8.29-26.2% (Table 15). The male axilla was dominated by the genus, Corynebacterium (Figure 43) while the female axilla was not and had much higher diversity. Men have been found to harbour more Corynebacterium than women, a genus associated with axillary odour (Troccaz et al. 2015). Women are more likely to shave their axilla (Basow 1991) and hair removal of the axilla have been shown to reduce malodour, which could explain the reduced Corynebacterium (Lanzalaco et al. 2016). Female axilla also had Lactobacillus present, which has also been previously identified in female axilla (Anukam et al. 2020). Many past cosmetic studies have used the FCAT technique, as it was assessed that the volar forearm was interchangeable with the face (Ertel et al. 1995; Farage 2000). This may have been true for hydration retention and biochemical processes but as the above in 7.23, and prior research have shown, the lack of biomass and bacteria recovered were not akin to the microbial community of the face. As the volar forearm is a dry area of skin, this would make it much more diverse compared to the oily face (Grice and Segre 2011). Prior work found that the forehead genera was dominated by either *Cutibacterium*, as seen with the female forehead sample (Figure 43), or has a large percentage of Corynebacterium, as seen with the male forehead sample (Figure 43). While the sampling of individuals' forearms resulted in much more variable ratios of different taxa, including larger proportions of Lactobacillales and Proteobacteria, as seen in this study with both male (see appendix) and female samples (Figure 45) (Staudinger et al. 2011). The biomass collected from the sampled areas also differed. Both the male forehead sample, and female forehead sample resulted in many more useable sequencing reads than the corresponding volar forearm samples (Figure 41). The volar forearm samples also contained a higher relative abundance than the forehead samples of background contamination (Table 15), the female volar forearm sample had the highest contamination of any sample, between 18.1-62.1%. The male forearm sample also had a high abundance of background contamination, between 10.2-37.5%. If future cosmetic studies wish to investigate a facial product, while the volar forearm could be used for traditional formulation testing, any microbial community investigations should be done on the area in question or more research done into areas with similar biomass and composition.

#### 7.32 What about Shotgun Metagenomic Sequencing?

*Staphylococcus* spp. are widely regarded as top inhabitants of the skin (Otto 2010; Grice and Segre 2011), yet only *S. sciuri* was identified to species level using the 16S rRNA gene sequencing. This amplification technique has its limits with such closely related species and cannot always distinguish between *Staphylococcus* spp. which reside on the skin (Ghebremedhin et al. 2008). Again, in the above study *Corynebacterium* spp. constituted 25% of the bacteria present, when

only 9.5% were identified to species level (Figure 45). There can also be different representation of microbial communities dependent on hypervariable region covered or primer choices (Johnson et al. 2019) 16S rRNA sequencing is still a useful tool in small microbial community studies, to have an idea of what a mixed sample contains, or studies that are not human-associated microbiome based (Poretsky et al. 2014; Ames et al. 2017).

Shotgun Metagenomic Sequencing fragments all the given genomic DNA, sequences it and compares to a reference genome database. This technique covers all genetic information across the three domains so studies can include fungi and archaea instead of focusing on bacteria as with 16S rRNA sequencing (Durazzi et al. 2021). The taxonomic resolution can determine species or strain level, metabolic functions can also be investigated or identification of antimicrobial resistance genes (Hamady and Knight 2009). There are a few disadvantages to this technique, as a reference database is required to compare sequences to, if the genome is not available there would be a high chance of false positive species. Also, due to the cross-domain identification, there is a risk of host DNA interfering with the results (Cattonaro et al. 2018). There is also cost to consider, the cost of shotgun metagenomic sequencing can be two to three times more costly than 16S rRNA sequencing, which can get expensive if there is a large sample size.

#### 7.33 Conclusion

The skin has low microbial biomass, but different areas are better for bacterial recovery than others. For instance, oily areas may be the least diverse, but the bacterial mass is much higher than dry or moist areas. Using areas with higher bacterial biomass for skin research can help reduce the relative background contamination from the surroundings, equipment, and consumables. To help identify background contaminants for skin experiments, multiple controls would be required, this includes equipment, kit, and consumable controls as well as a positive control, something scarcely used previously.

Previous skin research techniques may not translate well for studies which would include microbes. The forearm-controlled application technique (FCAT), for example, uses the forearm as a suitable control for the face and rest of the body, while in terms of microbial mass and species found on the forearm can be significantly different to the face.

Future microbial studies would also need to decide how in-depth the study should be, species level recovery can be limited with 16S rRNA sequencing, especially between closely related species like found in the *Staphylococcus* genus. There are more in-depth and accurate culture-independent techniques but the cost increases with accuracy.

8 Conclusions of Sections 2-7

#### 8.1 Introduction

The microbial community of skin is a recent area of research compared to other areas of the human body. With the increased prevalence of skin disorders, cosmetic companies have also started to investigate and formulate products which claim to either sustain the microbial balance or promote good bacteria. However, many of these products contain ingredients which could both provide nutrients and prevent growth of the skin residents. Therefore, many cosmetic products could be counterintuitive and imbalance a healthy microbial community. The promotion of 'good' bacteria could also be problematic, S. epidermidis can help reduce the adherence and infection of its more pathogenic cousin S. aureus, but itself is an opportunistic pathogen and can cause serious nosocomial infections. Before labelling these products with any microbe-related claims, thorough investigations into their potential interactions with skin microbiota is vital. This thesis focused on cosmetic proteins, peptide rich moisturising agents, and their interactions with common skin bacteria, however many of these in-vitro experiments could use different formulation ingredients. The work started with creating laboratory-based studies which used minimal nutritional medium and investigated how the cosmetic proteins affect the fundamentals of the species, including both planktonic and sessile growth. Then moved onto experimental design using tissue culture, a popular alternative to the out-dated animal trials. Before finally investigating suitable devices for retrieving bacteria from skin and locations for commencing human panel studies.

#### 8.2 Laboratory-based Studies

Lab-based work was never going to accurately create conditions which reflect the skin but were useful to study how cosmetics affect the fundamentals of skin species. Lactose-free skimmed medium helped identify species isolates that could be promoted if the cosmetic proteins contained large peptides. The use of a minimal medium with a pH lowered to 5 created an environment more akin to skin compared to the commonly used high nutritional media. The minimal medium also balanced the conditions between the faster *Staphylococcus* spp. and slower growing *C. jeikeium*, as well as downregulating the pathogen *S. aureus*, which favours neutral pH. Section 3 highlighted how using a minimal medium to investigate skin bacteria 'levels the playing field' and allows for slower growing organisms to compete with the faster organisms. Unfortunately, a minimal medium agar (1-2% w/v) was either not able to support consistent growth or only small unusable colonies were formed on the surface (Section 2.8). Therefore, a minimal medium agar could be something in which future investigations could attempt. The reduced water content and air interface would increase the homology to the skin environment.

Preliminary work for Section 4 investigated if the preservative as found at formulation concentrations could have bactericidal or bacteriostatic effects on skin bacteria, as many of these species are also targeted as products contaminations. The cosmetic proteins were preserved with

different combinations of common preservatives, many of the are used to target skin species which are also formulation contaminants. While the minimum inhibitory concentration was unlikely to be used in products, the low concentration of preservatives still had detrimental effect on the skin species. Sodium benzoate and EDTA were the most effective at inhibiting the growth of all species but worryingly so, the pathogenic *Staphylococcus* spp. was less effected than the commensal *S. epidermidis*. Future research into cosmetic proteins could investigate whether dry, and therefore unpreserved, proteins affect this skin microbes. The lack of preservation of the dry cosmetic proteins could increase the total nutrition available, reduce the environmental stresses and cause imbalances by promoting the faster growing species.

Removal of the casamino acid supplement from the minimal medium and replacement with the varied active level of cosmetic proteins showed whether the bacteria could utilise the cosmetic proteins as a source of nutrition and nitrogen for both planktonic and sessile growth. Without indepth proteomic analysis, peptide size could not be determined, but the two extracellular protease possessing *Staphylococcus* spp., grew with more of the cosmetic protein at a range of active levels. The variation between cosmetic proteins was highlighted in this thesis, as each individual cosmetic protein had a varying effect on the growth of individual species. However, it was clear that Crosilk LPC, the protein with the highest concentration of preservatives, had a negative effect on all three species tested. Similar results were seen when the two *Staphylococcus* spp. were grown together, the species which grew best with a certain cosmetic protein. Future work could delve into producing more varied culture mixes, expand into different common genera on skin. Further investigations could also consider the expression of the extracellular proteases in planktonic growth when supplemented with cosmetic proteins.

The degree of biofilm formation did not necessary reflect the planktonic growth. At pH 5, *S. aureus* could grow well planktonically, but biofilm formation was poor. The poor biofilm formation of *S. aureus* was highlighted when co-cultured with *S. epidermidis*, in which the commensal dominated the biofilm percentage when grown with the minimal medium and when supplemented with cosmetic proteins. Again, further investigations could include producing biofilms with more skin microbiota involved and studying gene expression when in biofilm formation. The biofilm quantification experiments could also be moved from microwell plates onto a material more akin to skin.

#### 8.3 Tissue Culture

The skin community does not just start and end with its microbial residents, but interactions with the skin cells and the immune response. Section 5 covered the experiments which involved with tissue culture. The skin naturally expresses a low level of immune responses to help recognition of commensal species and be on alert for invading pathogens. HaCaT cells expressed these low levels of immune markers without being extra stimulated by the exposure to cosmetic proteins or bacteria or both. The addition of S. epidermidis however lowered the concentration of immune markers expressed by the HaCaT cells in the surrounding supernatant, sometimes to a negligible result. Exposure of S. epidermidis to the higher active level concentrations reduced the number of adhered cells, and the concentration of immune markers increased. However, the concentration of immune markers in the supernatant whether the HaCaT cells were alone or grown with S. epidermidis, were insignificant compared to when HaCaT cells were grown with S. aureus, in which the immune marker concentration significantly increased. The increased immune marker concentration was also noted with a co-culture of Staphylococcus spp. However, the number of adhered cells was so much lower, suggesting that S. epidermidis had now switched from reducing, to promoting these immune markers to help the cells with the S. aureus infection. This work also highlighted the importance of a low pH on the skin, if one species dominated the biofilm formation of the mixed co-culture, it was S. aureus. In previous Section 4.12, S. epidermidis was likely to dominate a mixed biofilm, but the pH was lower. Future work could investigate either lowering the pH of the experiment or taking it a step further and create a liquid air interface which would be much more akin to the skin. Again, increasing the genera in the mixed species experiments, including slower growing organisms such as C. jeikeium or species who thrive on lower oxygen levels like *Cutibacterium acnes*.

#### 8.4 Designing a Human Panel Study

While not the most efficient way of recovering bacteria and bacterial DNA from skin, there will always be a need for swabbing skin as a non-intrusive method. Over the years different studies have used different swab types and buffers to remove bacteria and bacterial DNA from skin. In Section 6, a porcine skin model was inoculated with known quantities of *Staphylococcus* spp. before being recovered by three different swab and three different buffer combinations. Using any wet swab was better at recovering bacteria than any dry swab. Using a flocked swab recovered the most bacteria compared to a dacron or cotton swab.

Many cosmetic studies use the volar forearm as a comparable skin site to the face to test facial products. However, while comparable for hydration and moisturising studies, this may not be so for microbial studies. Using the best buffer and swab composition, microbes were removed from several different skin sites and sequenced using 16S rRNA. The volar forearm, a dry area of the skin, had some of the highest background contamination from both the swab controls and kit controls. The forehead samples, an oily area of the skin, had some of the least amount of background contamination. Both areas also had different dominating genera of bacteria. Section 7

highlighted that cosmetic studies will likely need to change their testing processes, as the volar forearm is not a good equivalence to the face for microbial composition and mass.

## 8.5 What Have all the Sections from this Thesis achieved?

With cosmetic companies moving into more studies involving microbes on the skin, new protocols are required to take these experiments from the fundamental lab work all through to skin panel studies. The basic, but essential investigations into both planktonic and sessile growth can help identify possible problematic ingredients that may promote pathogenic species or negatively affect commensal species. The tissue culture experiments are an alternative to the now very unpopular animal models, after all the cosmetics are going on the skin and the microbiome involves the cells which react to both bacteria which reside on the skin and cosmetics which are added. Finally, skin panel studies are used throughout industry to test the skin's properties after exposure to cosmetic ingredients, however, many of these practices do not translate well into microbial investigations. Areas of the skin which may have similar hydration properties may have completely different microbial inhabitants and biomass available. The final Sections emphasized which swabs and buffers, used in prior studies, were able to collect the most bacteria from skin, as well as where to target skin studies and how to overcome background contamination.

## 9 References

Abd, E. Et Al. 2016. Skin Models For The Testing Of Transdermal Drugs. *Clinical Pharmacology: Advances And Applications* 8, Pp. 163-176. Doi: 10.2147/Cpaa.S64788

Abdallah, F., Mijouin, L. And Pichon, C. 2017. Skin Immune Landscape: Inside And Outside The Organism. *Mediators Of Inflammation* 2017, Pp. 5095293-5095293. Doi: 10.1155/2017/5095293

Adams, J. 2014. How Do Cells Decode Genetic Information Into Functional Proteins? In: O' Connor, C. Ed. *Essentials Of Cell Biology*.

Adedeji, W. 2016. The Treasure Called Antibiotics. Ann Ib Postgrad Med. Vol. 14. Pp. 56-57.

Aguirre-Cruz, G., León-López, A., Cruz-Gómez, V., Jiménez-Alvarado, R. And Aguirre-Álvarez, G. 2020. Collagen Hydrolysates For Skin Protection: Oral Administration And Topical Formulation. *Antioxidants (Basel, Switzerland)* 9(2), P. 181. Doi: 10.3390/Antiox9020181

Al Kindi, A., Alkahtani, A. M., Nalubega, M., El-Chami, C., O'neill, C., Arkwright, P. D. And Pennock, J. L. 2019. Staphylococcus Aureus Internalized By Skin Keratinocytes Evade Antibiotic Killing. *Front Microbiol* 10, P. 2242. Doi: 10.3389/Fmicb.2019.02242

Albanesi, C., Scarponi, C., Giustizieri, M. L. And Girolomoni, G. 2005. Keratinocytes In Inflammatory Skin Diseases. Doi: Info:Doi/10.2174/1568010054022033

Alberts, B., Johnson, A., Lewis, J. And Al., E. 2002. Carrier Proteins And Active Membrane Transport. *Molecular Biology Of The Cell*. Vol. 4. New York: Garland Science.

Albrecht, V. S. Et Al. 2015. Staphylococcus Aureus Colonization And Strain Type At Various Body Sites Among Patients With A Closed Abscess And Uninfected Controls At U.S. Emergency Departments. *Journal Of Clinical Microbiology* 53(11), Pp. 3478-3484. Doi: 10.1128/Jcm.01371-15

Ali, S. And Yosipov, G. 2013. Skin Ph: From Basic Science To Basic Skin Care. Acta Dermato Venereologica 93, Pp. 261–267.

Alizadeh-Sani, M. Et Al. 2018. Bioemulsifiers Derived From Microorganisms: Applications In The Drug And Food Industry. *Adv Pharm Bull* 8(2), Pp. 191-199. Doi: 10.15171/Apb.2018.023

Alkhafaji, M., Flayyih, M. And Arsheed, M. 2013. Isolation, Identification And Detection Of Some Virulence Factors Of Staphylococci In Milk And Cheese In Baghdad, *Iraqi Journal Of Science* 54. . Pp. 1057-1067

Allaband, C. Et Al. 2019. Microbiome 101: Studying, Analyzing, And Interpreting Gut Microbiome Data For Clinicians. (1542-7714 (Electronic)),

Allen, L. J., 22 (4), 288–293. 2018. Quality Control: Water Activity Considerations For Beyond-Use Dates. *International Journal Of Pharmaceutical Compounding* 22(4), Pp. 288-293.

Allen, R. J. And Waclaw, B. 2019. Bacterial Growth: A Statistical Physicist's Guide. *Reports On Progress In Physics. Physical Society (Great Britain)* 82(1), Pp. 016601-016601. Doi: 10.1088/1361-6633/Aae546

Alreshidi, M. M., Dunstan, R. H., Macdonald, M. M., Gottfries, J. And Roberts, T. K. 2020. The Uptake And Release Of Amino Acids By Staphylococcus Aureus At Mid-Exponential And Stationary Phases And Their Corresponding Responses To Changes In Temperature, Ph And Osmolality. *Frontiers In Microbiology* 10, P. 3059.

Alreshidi, M. M., Dunstan, R. H., Macdonald, M. M., Smith, N. D., Gottfries, J. And Roberts, T. K. 2019. Amino Acids And Proteomic Acclimation Of Staphylococcus Aureus When Incubated In A Defined Minimal Medium Supplemented With 5% Sodium Chloride. *Microbiologyopen* 8(6), P. E00772. Doi: <u>Https://Doi.Org/10.1002/Mbo3.772</u>

Alsudani, A. 2017. In Vitro Antifungal Effect Of Potassium Sorbate And Sodium Benzoate On The Growth Of Fungi Causing Sinusitis. *African Journal Of Microbiology Research* 11, Pp. 232-236. Doi: 10.5897/Ajmr2016.8414

Altuntas, F., Yildiz, O., Eser, B., Gündogan, K., Sumerkan, B. And Çetin, M. 2004. Catheter-Related Bacteremia Due To Kocuria Rosea In A Patient Undergoing Peripheral Blood Stem Cell Transplantation. *Bmc Infectious Diseases* 4(1), Pp. 1-3. Doi: Doi:10.1186/1471-2334-4-62

Aly, R. 1996. Microbial Infections Of Skin And Nails. In: Baron, S. Ed. *Medical Microbiology*. 4 Ed. Galveston University Of Texas.

Amarbayasgalan, T., Takahashi, H., Dekio, I. And Morita, E. 2013. Interleukin-8 Content In The Stratum Corneum As An Indicator Of The Severity Of Inflammation In The Lesions Of Atopic Dermatitis. *International Archives Of Allergy And Immunology* 160(1), Pp. 63-74. Doi: 10.1159/000339666

Ames, N. J., Ranucci, A., Moriyama, B. And Wallen, G. R. 2017. The Human Microbiome And Understanding The 16s Rrna Gene In Translational Nursing Science. *Nursing Research* 66(2), Pp. 184-197. Doi: 10.1097/Nnr.000000000000212

Aminzare, M., Rohani, S., Raeisi, M., Hosseini, S. And Hashemi, M. 2014. Antibacterial Effects Of Monolaurin, Sorbic Acid And Potassium Sorbate On Staphylococcus Aureus And Escherichia Coli. *Journal Of Food Quality And Hazards Control* 1, Pp. 52-55.

Ammons, M. C. B., Tripet, B., Carlson, R. P., Kirker, K. R., Gross, M., Stanisich, J. J. And Copié, V. 2014. Quantitative Nmr Metabolite Profiling Of Methicillin-Resistant And Methicillin-Susceptible Staphylococcus Aureus Discriminates Between Biofilm And Planktonic Phenotypes. *J Proteome Res* 13(6), Pp. 2973-2985. Doi: 10.1021/Pr500120c

Amorim Franco, T. M. And Blanchard, J. S. 2017. Bacterial Branched-Chain Amino Acid Biosynthesis: Structures, Mechanisms, And Drugability. *Biochemistry* 56(44), Pp. 5849-5865. Doi: 10.1021/Acs.Biochem.7b00849 Ampornaramveth, R. S., Akeatichod, N., Lertnukkhid, J. And Songsang, N. 2018. Application Of D-Amino Acids As Biofilm Dispersing Agent In Dental Unit Waterlines. *Int J Dent* 2018, Doi: 10.1155/2018/9413925

Anukam, K. C., Nmewurum, V. And Agbakoba, N. R. 2020. Axillary Microbiota Compositions From Men And Women In A Tertiary Institution-South East Nigeria: Effects Of Deodorants/Antiperspirants On Bacterial Communities. *Biorxiv*, P. 2020.2003.2011.986364. Doi: 10.1101/2020.03.11.986364

Apone, F., Barbulova, A. And Colucci, M. G. 2019. Plant And Microalgae Derived Peptides Are Advantageously Employed As Bioactive Compounds In Cosmetics. *Frontiers In Plant Science* 10,

Arens, E. A. And Zhang, H. 2006. The Skin's Role In Human Thermoregulation And Comfort.*Thermal And Moisture Transport In Fibrous Materials*. Uc Berkeley: Center For The Built Environment.

Arican, O., Aral, M., Sasmaz, S. And Ciragil, P. 2005. Serum Levels Of Tnf-Alpha, Ifn-Gamma, II-6, II-8, II-12, II-17, And II-18 In Patients With Active Psoriasis And Correlation With Disease Severity. *Mediators Of Inflammation* 2005(5), Pp. 273-279. Doi: 10.1155/Mi.2005.273

Arimoto, T., Yambe, R., Morisaki, H., Umezawa, H., Kataoka, H., Matsui, S. And Kuwata, H. 2017. Influence Of Excess Branched-Chain Amino Acid Uptake By Streptococcus Mutans In Human Host Cells. *Fems Microbiology Letters* 365(3), Doi: 10.1093/Femsle/Fnx273

Arvidson, S. 1973. Hydrolysis Of Casein By Three Extracellular Proteolytic Enzymes From Staphylococcus Aureus, Strain V8. *Acta Pathologica Microbiologica Scandinavica Section B Microbiology And Immunology* 81b(5), Pp. 538-544. Doi: <u>Https://Doi.Org/10.1111/J.1699-0463.1973.Tb02239.X</u>

Ashcroft, G. S. Et Al. 2012. Tumor Necrosis Factor-Alpha (Tnf-A) Is A Therapeutic Target For Impaired Cutaneous Wound Healing. *Wound Repair And Regeneration : Official Publication Of The Wound Healing Society [And] The European Tissue Repair Society* 20(1), Pp. 38-49. Doi: 10.1111/J.1524-475x.2011.00748.X

Asm. 2017. Not Under The Skin, But On It: Living Together Brings Couples' Microbiomes Together. *American Society For Microbiology*,

Atlas, R. M. 2010. *Handbook Of Microbiological Media*. 4th Ed. Ed. Boca Raton, Fl: Boca Raton, Fl : Crc Press.

Attar Nasseri, A., Aboofazeli, R., Zia, H. And Needham, T. 2010. Lecithin - Stabilized Microemulsion - Based Organogels For Topical Application Of Ketorolac Tromethamine. Ii. Invitro Release Study. *Iranian Journal Of Pharmaceutical Research* Volume 2(Number 2), Pp. 117-124. Doi: 10.22037/Ijpr.2010.23 Avci, P. Et Al. 2013. Animal Models Of Skin Disease For Drug Discovery. *Expert Opin Drug Discov* 8(3), Pp. 331-355. Doi: 10.1517/17460441.2013.761202

Baas-Becking, L. And Parks, G. 1927. Energy Relations In The Metabolism Of Autotrophic

Bacteria. Physiological Reviews,

Bagatin, E., De Freitas, T. H. P., Machado, M. C. R., Ribeiro, B. M., Nunes, S. And Da Rocha, M. A. D. 2019. Adult Female Acne: A Guide To Clinical Practice. *An Bras Dermatol* 94(1), Pp. 62-75. Doi: 10.1590/Abd1806-4841.20198203

Bahonar, S., Ghazvinian, M., Haghshenas, M., Goli, H. And Mirzaei, B. 2019. Purification Of Pia And Rsesc As Putative Vaccine Candidates Against Staphylococcus Aureus. *Reports Of Biochemistry & Molecular Biology* 8(2),

Bajaj, B. K., Sharma, N. And Singh, S. 2013. Enhanced Production Of Fibrinolytic Protease From Bacillus Cereus Ns-2 Using Cotton Seed Cake As Nitrogen Source. *Biocatalysis And Agricultural Biotechnology* 2(3), Pp. 204-209. Doi: <u>Https://Doi.Org/10.1016/J.Bcab.2013.04.003</u>

Balakireva, A. V. And Zamyatnin, A. A. 2016. Properties Of Gluten Intolerance: Gluten Structure, Evolution, Pathogenicity And Detoxification Capabilities. *Nutrients* 8(10), P. 644. Doi: 10.3390/Nu8100644

Balamurugan, K. 2019. Corynebacterium Spp. In: Balamurugan, K. And Udayakumar, P. Eds. *Pocket Guide To Bacterial Infections*. 1 Ed. Taylor & Francis, P. 306.

Balci, I., Ekşi, F. And Bayram, A. 2002. Coryneform Bacteria Isolated From Blood Cultures And Their Antibiotic Susceptibilities. *The Journal Of International Medical Research* 30(4), Doi: 10.1177/147323000203000409

Bashir, M., Sharma, M. And Werth, V. 2009. Tnf-Alpha Production In The Skin. Archives Of Dermatological Research 301(1), Doi: 10.1007/S00403-008-0893-7

Basilicata, M. G. Et Al. 2019. Anti-Inflammatory And Antioxidant Properties Of Dehydrated Potato-Derived Bioactive Compounds In Intestinal Cells. *Int J Mol Sci* 20(23), Doi: 10.3390/Ijms20236087

Basow, S. A. 1991. The Hairless Ideal: Women And Their Body Hair. *Psychology Of Women Quarterly* 15(1), Pp. 83-96. Doi: 10.1111/J.1471-6402.1991.Tb00479.X

Bazin, R. And Fanchon, C. 2006. Equivalence Of Face And Volar Forearm For The Testing Of Moisturizing And Firming Effect Of Cosmetics In Hydration And Biomechanical Studies. *International Journal Of Cosmetic Science* 28(6), Pp. 453-461. Doi: <u>Https://Doi.Org/10.1111/J.1467-2494.2006.00352.X</u>

Becker, K., Skov, R. And Von Eiff, C. 2015. Staphylococcus, Micrococcus, And Other Catalase-Positive Cocci. In: Jorgensen, J.H., Pfaller, M.A., Carroll, K.C., Funke, G., Landry, M., Richter, S. And Warnock, D. Eds. *Manual Of Clinical Microbiology*. Vol. 11. Pub2web. Behbehani, M. J., Jordan, H. V. And Santoro, D. L. 1982. Simple And Convenient Method For Culturing Anaerobic Bacteria. *Applied And Environmental Microbiology* 43(1), Pp. 255-256. Doi: 10.1128/Aem.43.1.255-256.1982

Belkaid, Y. And Harrison, O. J. 2017. Homeostatic Immunity And The Microbiota. *Immunity* 46(4), Pp. 562-576. Doi: 10.1016/J.Immuni.2017.04.008

Bendia, A. G. Et Al. 2018. Surviving In Hot And Cold: Psychrophiles And Thermophiles From Deception Island Volcano, Antarctica. *Extremophiles* 22(6), Pp. 917-929. Doi: 10.1007/S00792-018-1048-1

Bernard, K. 2012. The Genus <Span Class="Named-Content Genus-Species" Id="Named-Content-1">Corynebacterium</Span> And Other Medically Relevant Coryneform-Like Bacteria. *Journal Of Clinical Microbiology* 50(10), P. 3152. Doi: 10.1128/Jcm.00796-12

Berry, B. J., Jenkins, D. G. And Schuerger, A. C. 2010. Effects Of Simulated Mars Conditions On The Survival And Growth Of <Em>Escherichia Coli</Em> And <Em>Serratia Liquefaciens</Em>. *Applied And Environmental Microbiology* 76(8), P. 2377. Doi: 10.1128/Aem.02147-09

Betts, G. Et Al. 2016. Layers Of The Skin. Anatomy And Physiology. Openstax.

Beuchat, L. R. 1981. Microbial Stability As Affected By Water Activity. *Cereal Foods World* 26, Pp. 345-349.

Bhakdi, S. And Tranum-Jensen, J. 1991. Alpha-Toxin Of Staphylococcus Aureus. *Microbiological Reviews* 55(4), Pp. 733-751.

Bharti, R. And Grimm, D. G. 2021. Current Challenges And Best-Practice Protocols For Microbiome Analysis. *Briefings In Bioinformatics* 22(1), Pp. 178-193. Doi: 10.1093/Bib/Bbz155

Bhate, K. And Williams, H. C. 2013. Epidemiology Of Acne Vulgaris. *British Journal Of Dermatology* 168(3), Pp. 474-485. Doi: 10.1111/Bjd.12149

Bhatia, A., Maisonneuve, J. And Persing, D. 2004. Propionibacterium Acnes And Chronic Diseases. In: Knobler, S., O'connor, S. And Lemon, S. Eds. *The Infectious Etiology Of Chronic Diseases: Defining The Relationship, Enhancing The Research, And Mitigating The Effects*. Washington: National Academies Press (Us).

Bhattacharya, I., Barman, N., Maiti, M. And Sarkar, R. 2019. Assessment Of Beta-Catenin Expression By Immunohistochemistry In Colorectal Neoplasms And Its Role As An Additional Prognostic Marker In Colorectal Adenocarcinoma. *Medicine And Pharmacy Reports* 92(3), Pp. 246-252. Doi: 10.15386/Mpr-1218

Bien, J., Sokolova, O. And Bozko, P. 2011. Characterization Of Virulence Factors Of <I>Staphylococcus Aureus</I>: Novel Function Of Known Virulence Factors That Are Implicated In

Activation Of Airway Epithelial Proinflammatory Response. *Journal Of Pathogens* 2011, P. 601905. Doi: 10.4061/2011/601905

Blank, I. 1938. Measurement Of Ph Of The Skin Surface II. Ph Of The Exposed Surfaces Of Adults With No Apparent Skin Lesions. *Investigative Dermatology*,

Blaser, M. Et Al. 2013. Distinct Cutaneous Bacterial Assemblages In A Sampling Of South American Amerindians And Us Residents. *The Isme Journal* 7(1), Doi: 10.1038/Ismej.2012.81

Blease, K., Chen, Y., Hellewell, P. And Burke-Gaffney, A. 1999. Lipoteichoic Acid Inhibits Lipopolysaccharide-Induced Adhesion Molecule Expression And II-8 Release In Human Lung Microvascular Endothelial Cells. *Journal Of Immunology (Baltimore, Md. : 1950)* 163(11),

Blum, R. And Rodvold, K. 1987. Recognition And Importance Of Staphylococcus Epidermidis Infections. *Clinical Pharmacy* 6(6),

Boer, M., Duchnik, E., Maleszka, R. And Marchlewicz, M. 2016. Structural And Biophysical Characteristics Of Human Skin In Maintaining Proper Epidermal Barrier Function. *Postepy Dermatol Alergol*. Vol. 33. Pp. 1-5.

Bojar, R. A. And Holland, K. T. 2002. Review: The Human Cutaneous Microflora And Factors Controlling Colonisation. *World Journal Of Microbiology And Biotechnology* 18(9), Pp. 889-903. Doi: 10.1023/A:1021271028979

Bojar, R. A. And Holland, K. T. 2004. Acne And Propionibacterium Acnes. *Clinics In Dermatology* 22(5), Pp. 375-379. Doi: <u>Https://Doi.Org/10.1016/J.Clindermatol.2004.03.005</u>

Boles, B. R. And Horswill, A. R. 2008. Agr-Mediated Dispersal Of Staphylococcus Aureus Biofilms. *Plos Pathogens* 4(4), Pp. E1000052-E1000052. Doi: 10.1371/Journal.Ppat.1000052

Bondurant, S., Mckinney, T., Bondurant, L. And Fitzpatrick, L. 2020. Evaluation Of A Benzalkonium Chloride Hand Sanitizer In Reducing Transient Staphylococcus Aureus Bacterial Skin Contamination In Health Care Workers. *Am J Infect Control* 48(5), Pp. 522-526. Doi: 10.1016/J.Ajic.2019.08.030

Bonnet, M., Lagier, J. C., Raoult, D. And Khelaifia, S. 2019. Bacterial Culture Through Selective And Non-Selective Conditions: The Evolution Of Culture Media In Clinical Microbiology. *New Microbes And New Infections* 34, Pp. 100622-100622. Doi: 10.1016/J.Nmni.2019.100622

Borody, T. J., Paramsothy, S. And Agrawal, G. 2013. Fecal Microbiota Transplantation: Indications, Methods, Evidence, And Future Directions. *Current Gastroenterology Reports* 15(8), Pp. 337-337. Doi: 10.1007/S11894-013-0337-1

Boundless. 2017. Culture Media. Microbiology. Libretexts.

Boundless. 2021. Chemical Analysis Of Microbial Cytoplasm.

Bouslimani, A. Et Al. 2019. The Impact Of Skin Care Products On Skin Chemistry And Microbiome Dynamics. *Bmc Biology* 17(1), P. 47. Doi: 10.1186/S12915-019-0660-6

Bowden, M. Et Al. 2005. Identification And Preliminary Characterization Of Cell-Wall-Anchored Proteins Of Staphylococcus Epidermidis. *Microbiology (Reading, England)* 151(Pt 5), Doi: 10.1099/Mic.0.27534-0

Bowler, P. G., Duerden, B. I. And Armstrong, D. G. 2001. Wound Microbiology And Associated Approaches To Wound Management. *Clinical Microbiology Reviews* 14(2), Pp. 244-269. Doi: 10.1128/Cmr.14.2.244-269.2001

Boxberger, M., Cenizo, V., Cassir, N. And La Scola, B. 2021. Challenges In Exploring And Manipulating The Human Skin Microbiome. *Microbiome* 9(1), P. 125. Doi: 10.1186/S40168-021-01062-5

Brabb, T., Newsome, D., Burich, A., Hanes, M., Suckow, M. A., Stevens, K. A. And Wilson, R. P. 2012. Chapter 23 - Infectious Diseases. *The Laboratory Rabbit, Guinea Pig, Hamster, And Other Rodents*. Boston: Academic Press, Pp. 637-683.

Bragg, R., Van Der Westhuizen, W., Lee, J., Coetsee, E. And Boucher, C. 2014. Bacteriophages As Potential Treatment Option For Antibiotic Resistant Bacteria. *Advances In Experimental Medicine And Biology* 807, Doi: 10.1007/978-81-322-1777-0\_7

Brandwein, M., Katz, I., Katz, A. And Kohen, R. 2019. Beyond The Gut: Skin Microbiome Compositional Changes Are Associated With Bmi. *Human Microbiome Journal* 13, P. 100063. Doi: <u>Https://Doi.Org/10.1016/J.Humic.2019.100063</u>

Brandwein, M., Steinberg, D. And Meshner, S. 2016. Microbial Biofilms And The Human Skin Microbiome. *Npj Biofilms And Microbiomes* 2(1), Pp. 1-6. Doi: Doi:10.1038/S41522-016-0004-Z

Bren, A., Park, J. O., Towbin, B. D., Dekel, E., Rabinowitz, J. D. And Alon, U. 2016. Glucose Becomes One Of The Worst Carbon Sources For E.Coli On Poor Nitrogen Sources Due To Suboptimal Levels Of Camp. *Scientific Reports* 6(1), P. 24834. Doi: 10.1038/Srep24834

Breton, H. 2018. 4 Critical Considerations For Collecting Skin Microbiome Samples. Dna Genotek,

Brianti, P., De Flammineis, E. And Mercuri, S. 2017. Review Of Hpv-Related Diseases And Cancers. *The New Microbiologica* 40(2),

Bruslind, L. 2017. Microbial Growth. *Microbiology*. Oregon: Pressbooks.

Bryant, M. P. And Robinson, I. M. 1962. Some Nutritional Characteristics Of Predominant Culturable Ruminal Bacteria. *Journal Of Bacteriology* 84(4), Pp. 605-614. Doi: 10.1128/Jb.84.4.605-614.1962 Brzuszkiewicz, E. Et Al. 2011. Comparative Genomics And Transcriptomics Of Propionibacterium Acnes. *Plos One* 6(6), Pp. E21581-E21581. Doi: 10.1371/Journal.Pone.0021581

Bréchard, S., Bueb, J. And Tschirhart, E. 2005. Interleukin-8 Primes Oxidative Burst In Neutrophil-Like HI-60 Through Changes In Cytosolic Calcium. *Cell Calcium* 37(6), Doi: 10.1016/J.Ceca.2005.01.019

Budd, J. And Spencer, C. 1968. The Utilisation Of Alkylated Amines By Marine Bacteria. *Marine Biology* 2(1), Pp. 92-101. Doi: Doi:10.1007/Bf00351645

Bukin, Y. S., Galachyants, Y. P., Morozov, I. V., Bukin, S. V., Zakharenko, A. S. And Zemskaya, T. I. 2019. The Effect Of 16s Rrna Region Choice On Bacterial Community Metabarcoding Results. *Scientific Data* 6(1), P. 190007. Doi: 10.1038/Sdata.2019.7

Burkovski, A. 2013. Cell Envelope Of Corynebacteria: Structure And Influence On Pathogenicity. *Isrn Microbiology* 2013, Pp. 935736-935736. Doi: 10.1155/2013/935736

Burkovski, A. 2018. The Role Of Corynomycolic Acids In Corynebacterium-Host Interaction. *Antonie Van Leeuwenhoek* 111(5), Pp. 717-725. Doi: 10.1007/S10482-018-1036-6

Burnett, C. Et Al. 2014. Safety Assessment Of Animal- And Plant-Derived Amino Acids As Used In Cosmetics. *International Journal Of Toxicology* 33(4 Suppl), Doi: 10.1177/1091581814554774

Bush, L. And Vazquez-Pertejo, M. 2021. Staphylococcal Infections. In: Msd Ed. *Msd Manual Professional - Infectious Diseases*. Merck And Co.

Byrd, A. L., Belkaid, Y. And Segre, J. A. 2018. The Human Skin Microbiome. *Nature Reviews Microbiology* 16(3), Pp. 143-155. Doi: 10.1038/Nrmicro.2017.157

Böni, R. And Nehrhoff, B. 2003. Treatment Of Gram-Negative Folliculitis In Patients With Acne. *American Journal Of Clinical Dermatology* 4(4), Doi: 10.2165/00128071-200304040-00005

Callewaert, C., Knödlseder, N., Karoglan, A., Güell, M. And Paetzold, B. 2021. Skin Microbiome Transplantation And Manipulation: Current State Of The Art. *Computational And Structural Biotechnology Journal* 19, Pp. 624-631. Doi: <u>Https://Doi.Org/10.1016/J.Csbj.2021.01.001</u>

Campana, R., Scesa, C., Patrone, V., Vittoria, E. And Baffone , W. 2006. Microbiological Study Of Cosmetic Products During Their Use By Consumers: Health Risk And Efficacy Of Preservative Systems. *Letters In Applied Microbiology* 43(3), Doi: 10.1111/J.1472-765x.2006.01952.X

Campolo, M. Et Al. 2020. Effect Of A Product Containing Xyloglucan And Pea Protein On A Murine Model Of Atopic Dermatitis. *International Journal Of Molecular Sciences* 21(10), P. 3596. Doi: 10.3390/Ijms21103596

Capita, R., Vicente-Velasco, M., Rodríguez-Melcón, C., García-Fernández, C., Carballo, J. And Alonso-Calleja, C. 2019. Effect Of Low Doses Of Biocides On The Antimicrobial Resistance And The Biofilms Of Cronobacter Sakazakii And Yersinia Enterocolitica. *Scientific Reports* 9(1), P. 15905. Doi: 10.1038/S41598-019-51907-1

Caproni, M. Et Al. 2006. Expression Of Cytokines And Chemokine Receptors In The Cutaneous Lesions Of Erythema Multiforme And Stevens–Johnson Syndrome/Toxic Epidermal Necrolysis. *British Journal Of Dermatology* 155(4), Pp. 722-728. Doi: <u>Https://Doi.Org/10.1111/J.1365-2133.2006.07398.X</u>

Cartwright, C. P., Stock, F., Kruczak-Filipov, P. M. And Gill, V. J. 1993. Rapid Method For Presumptive Identification Of Corynebacterium Jeikeium. *J Clin Microbiol* 31(12), Pp. 3320-3322.

Caso, C. And Gil, M. A. 1988. The Gini-Simpson Index Of Diversity: Estimation In The Stratified Sampling. *Communications In Statistics-Theory And Methods - Commun Statist-Theor Method* 17, Pp. 2981-2995. Doi: 10.1080/03610928808829784

Caso, G., Mcnurlan, M. A., Mileva, I., Zemlyak, A., Mynarcik, D. C. And Gelato, M. C. 2013. Peripheral Fat Loss And Decline In Adipogenesis In Older Humans. *Metabolism* 62(3), Pp. 337-340. Doi: 10.1016/J.Metabol.2012.08.007

Castelino, M. Et Al. 2017. Optimisation Of Methods For Bacterial Skin Microbiome Investigation: Primer Selection And Comparison Of The 454 Versus Miseq Platform. *Bmc Microbiol* 17(1), P. 23. Doi: 10.1186/S12866-017-0927-4

Catinean, A., Neag, M. A., Mitre, A. O., Bocsan, C. I. And Buzoianu, A. D. 2019. Microbiota And Immune-Mediated Skin Diseases—An Overview. *Microorganisms* 7(9), Doi: 10.3390/Microorganisms7090279

Cattonaro, F., Spadotto, A., Radovic, S. And Marroni, F. 2018. Do You Cov Me? Effect Of Coverage Reduction On Metagenome Shotgun Sequencing Studies. *F1000research* 7, Pp. 1767-1767. Doi: 10.12688/F1000research.16804.4

Cdc. 2003. Guidelines For Environmental Infection Control In Health-Care Facilities. Centers For Disease Control And Prevention.

Celiker, H. And Gore, J. 2012. Competition Between Species Can Stabilize Public-Goods Cooperation Within A Species. *Molecular Systems Biology* 8, Pp. 621-621. Doi: 10.1038/Msb.2012.54

Chabi, R. And Momtaz, H. 2019. Virulence Factors And Antibiotic Resistance Properties Of The Staphylococcus Epidermidis Strains Isolated From Hospital Infections In Ahvaz, Iran. *Tropical Medicine And Health* 47(1), Pp. 1-9. Doi: Doi:10.1186/S41182-019-0180-7

Chan, K. And Leung, O. C. 1979. Nutrition And Growth Of The Moderately Halophilic Bacteria Micrococcus Morrhuae K-17 And Micrococcus Luteus K-15. *Microbios* 25(100), Pp. 71-84.

Chang, C.-S. And Kao, C.-Y. 2019. Current Understanding Of The Gut Microbiota Shaping Mechanisms. *Journal Of Biomedical Science* 26(1), Pp. 1-11. Doi: Doi:10.1186/S12929-019-0554-5

Chapman, G. H. 1945. The Significance Of Sodium Chloride In Studies Of Staphylococci. *J Bacteriol* 50(2), Pp. 201-203.

Chaudhary, D. K., Khulan, A. And Kim, J. 2019. Development Of A Novel Cultivation Technique For Uncultured Soil Bacteria. *Scientific Reports* 9(1), P. 6666. Doi: 10.1038/S41598-019-43182-X

Chen, C., Krishnan, V., K, M., Manne, K., Narayana, S. And Schneewind, O. 2013a. Secreted Proteases Control Autolysin-Mediated Biofilm Growth Of Staphylococcus Aureus. *The Journal Of Biological Chemistry* 288(41), Doi: 10.1074/Jbc.M113.502039

Chen, R., Déziel, E., Groleau, M.-C., Schaefer, A. L. And Greenberg, E. P. 2019. Social Cheating In A <Em>Pseudomonas Aeruginosa</Em> Quorum-Sensing Variant. *Proceedings Of The National Academy Of Sciences* 116(14), P. 7021. Doi: 10.1073/Pnas.1819801116

Chen, X., Takai, T., Xie, Y., Niyonsaba, F., Okumura, K. And Ogawa, H. 2013b. Human Antimicrobial Peptide LI-37 Modulates Proinflammatory Responses Induced By Cytokine Milieus And Double-Stranded Rna In Human Keratinocytes. *Biochem Biophys Res Commun* 433(4), Pp. 532-537. Doi: 10.1016/J.Bbrc.2013.03.024

Chevalier, J., Pommier, M. And Crémieux, A. 1987. [Role Of Tween-80 Used In The Culture Of Cutaneous Corynebacteria (Jk Group) On The Composition Of Cellular Fatty Acids]. *Annales De L'institut Pasteur. Microbiology* 138(4), Doi: 10.1016/0769-2609(87)90060-3

Chi, C.-Y., Lin, C.-C., Liao, I.-C., Yao, Y.-C., Shen, F.-C., Liu, C.-C. And Lin, C.-F. 2013. Panton-Valentine Leukocidin Facilitates The Escape Of Staphylococcus Aureus From Human Keratinocyte Endosomes And Induces Apoptosis. *The Journal Of Infectious Diseases* 209(2), Pp. 224-235. Doi: 10.1093/Infdis/Jit445

Chiller, K., Selkin, B. And Murakawa, G. 2001. Skin Microflora And Bacterial Infections Of The Skin. *The Journal Of Investigative Dermatology. Symposium Proceedings* 6(3), Doi: 10.1046/J.0022-202x.2001.00043.X

Cho, S.-H., Strickland, I., Boguniewicz, M. And Leung, D. Y. M. 2001. Fibronectin And Fibrinogen Contribute To The Enhanced Binding Of Staphylococcus Aureus To Atopic Skin. *Journal Of Allergy And Clinical Immunology* 108(2), Pp. 269-274. Doi: <u>Https://Doi.Org/10.1067/Mai.2001.117455</u>

Choi, H., Chakraborty, S., Liu, R., Gellman, S. H. And Weisshaar, J. C. 2014. Medium Effects On Minimum Inhibitory Concentrations Of Nylon-3 Polymers Against E. Coli. *Plos One* 9(8), Pp. E104500-E104500. Doi: 10.1371/Journal.Pone.0104500

Chomnawang, M. T., Surassmo, S., Nukoolkarn, V. S. And Gritsanapan, W. 2005. Antimicrobial Effects Of Thai Medicinal Plants Against Acne-Inducing Bacteria. *Journal Of Ethnopharmacology* 101(1), Pp. 330-333. Doi: <u>Https://Doi.Org/10.1016/J.Jep.2005.04.038</u>

Christmas, P. 2010. Toll-Like Receptors: Sensors That Detect Infection. *Nature Education* 3(9), P. 85.

Chu, D. And Barnes, D. J. 2016. The Lag-Phase During Diauxic Growth Is A Trade-Off Between Fast Adaptation And High Growth Rate. *Scientific Reports* 6(1), P. 25191. Doi: 10.1038/Srep25191

Chu, S., Mehrmal, S., Uppal, P., Giesey, R. L., Delost, M. E. And Delost, G. R. 2017. Burden Of Skin Disease And Associated Socioeconomic Status In Europe: An Ecologic Study From The Global Burden Of Disease Study. (2666-3287 (Electronic)),

Chu, W. M. 2013. Tumor Necrosis Factor. *Cancer Letters* 328(2), Pp. 222-225. Doi: 10.1016/J.Canlet.2012.10.014

Claudel, J. P., Auffret, N., Leccia, M. T., Poli, F., Corvec, S. And Dréno, B. 2019. <B><I>Staphylococcus Epidermidis</I></B>: A Potential New Player In The Physiopathology Of Acne? *Dermatology* 235(4), Pp. 287-294. Doi: 10.1159/000499858

Clauditz, A., Resch, A., Wieland, K.-P., Peschel, A. And Götz, F. 2006. Staphyloxanthin Plays A Role In The Fitness Of Staphylococcus Aureus And Its Ability To Cope With Oxidative Stress. *Infection And Immunity* 74(8), Pp. 4950-4953. Doi: 10.1128/lai.00204-06

Clokie, M. R., Millard, A. D., Letarov, A. V. And Heaphy, S. 2011. Phages In Nature. *Bacteriophage* 1(1), Pp. 31-45. Doi: 10.4161/Bact.1.1.14942

Coates, M., Blanchard, S. And Macleod, A. S. 2018. Innate Antimicrobial Immunity In The Skin: A Protective Barrier Against Bacteria, Viruses, And Fungi. *Plos Pathogens* 14(12), Doi: 10.1371/Journal.Ppat.1007353

Coates, M., Lee, M. J., Norton, D. And Macleod, A. S. 2019. The Skin And Intestinal Microbiota And Their Specific Innate Immune Systems. *Frontiers In Immunology* 10, P. 2950.

Coffin, R. B. 1989. Bacterial Uptake Of Dissolved Free And Combined Amino Acids In Estuarine Waters. *Limnology And Oceanography* 34(3), Pp. 531-542. Doi: <u>Https://Doi.Org/10.4319/Lo.1989.34.3.0531</u>

Cogen, A. L., Nizet, V. And Gallo, R. L. 2008. Skin Microbiota: A Source Of Disease Or Defence? *The British Journal Of Dermatology* 158(3), Pp. 442-455. Doi: 10.1111/J.1365-2133.2008.08437.X

Collins, L. A. And Thune, R. L. 1996. Development Of A Defined Minimal Medium For The Growth Of Edwardsiella Ictaluri. *Applied And Environmental Microbiology* 62(3), Pp. 848-852. Doi: 10.1128/Aem.62.3.848-852.1996

Colombo, I. Et Al. 2017. Hacat Cells As A Reliable In Vitro Differentiation Model To Dissect The Inflammatory/Repair Response Of Human Keratinocytes. *Mediators Of Inflammation* 2017, P. 7435621. Doi: 10.1155/2017/7435621

Conlan, S., Kong Hh Fau - Segre, J. A. And Segre, J. A. 2012. Species-Level Analysis Of Dna Sequence Data From The Nih Human Microbiome Project. (1932-6203 (Electronic)),

Cooper, G. 2000a. The Biosynthesis Of Cell Constituents. *The Cell: A Molecular Approach*. 2 Ed. Sunderland: Sinauer Associates.

Cooper, G. 2000b. Transport Of Small Molecules. *The Cell: A Molecular Approach*. 2nd Edition Ed. Sunderland: Sinauer Associates.

Cordain, L., Lindeberg, S., Hurtado, M., Hill, K., Eaton, S. B. And Brand-Miller, J. 2020. Acne Vulgaris: A Disease Of Western Civilization. *Archives Of Dermatology* 138(12), Pp. 1584-1590. Doi: 10.1001/Archderm.138.12.1584

Corey, G. R. 2009. Staphylococcus Aureus Bloodstream Infections: Definitions And Treatment. *Clinical Infectious Diseases* 48(Supplement\_4), Pp. S254-S259. Doi: 10.1086/598186

Corvec, S. 2018. Clinical And Biological Features Of Cutibacterium (Formerly Propionibacterium) Avidum, An Underrecognized Microorganism. *Clinical Microbiology Reviews* 31(3), Doi: 10.1128/Cmr.00064-17

Cosseau, C. Et Al. 2016. Proteobacteria From The Human Skin Microbiota: Species-Level Diversity And Hypotheses. *One Health* 2, Pp. 33-41. Doi: <u>Https://Doi.Org/10.1016/J.Onehlt.2016.02.002</u>

Costello, E. K., Lauber, C. L., Hamady, M., Fierer, N., Gordon, J. I. And Knight, R. 2009. Bacterial Community Variation In Human Body Habitats Across Space And Time. *Science (New York, N.Y.)* 326(5960), Pp. 1694-1697. Doi: 10.1126/Science.1177486

Covacu, R. Et Al. 2009. Tlr Activation Induces Tnf-Alpha Production From Adult Neural Stem/Progenitor Cells. *Journal Of Immunology (Baltimore, Md. : 1950)* 182(11), Doi: 10.4049/Jimmunol.0802907

Cox, M. E. And Mangels, J. I. 1976. Improved Chamber For The Isolation Of Anaerobic Microorganisms. *Journal Of Clinical Microbiology* 4(1), Pp. 40-45.

Crawford, F. 2009. Athlete's Foot. Bmj Clin Evid 2009(1712),

Croda. 2022. Crodapersonalcare.Com. Available At: <u>Https://Www.Crodapersonalcare.Com/En-Gb/Product-Finder/</u>[Accessed.

D'amico, S., Collins, T., Marx, J.-C., Feller, G. And Gerday, C. 2006. Psychrophilic Microorganisms: Challenges For Life. *Embo Reports* 7(4), Pp. 385-389. Doi: 10.1038/Sj.Embor.7400662

Dalbey, R. E., Wang, P. And Van Dijl, J. M. 2012. Membrane Proteases In The Bacterial Protein Secretion And Quality Control Pathway. *Microbiology And Molecular Biology Reviews : Mmbr* 76(2), Pp. 311-330. Doi: 10.1128/Mmbr.05019-11

Davis, C. 1996. Normal Flora. In: Baron, S. Ed. *Medical Microbiology*. 4 Ed. Galveston: University Of Texas Medical Branch.

Davis, K. E. R., Joseph, S. J. And Janssen, P. H. 2005. Effects Of Growth Medium, Inoculum Size, And Incubation Time On Culturability And Isolation Of Soil Bacteria. *Applied And Environmental Microbiology* 71(2), Pp. 826-834. Doi: 10.1128/Aem.71.2.826-834.2005

De Souza Feitosa Lima, I. M. Et Al. 2019. Schinus Terebinthifolia Leaf Lectin (Stell) Has Anti-Infective Action And Modulates The Response Of Staphylococcus Aureus-Infected Macrophages. *Scientific Reports* 9(1), P. 18159. Doi: 10.1038/S41598-019-54616-X

Deckner, G. 2015. Phenoxyethanol: A Globally Approved Preservative. Available At: <u>Https://Knowledge.Ulprospector.Com/2532/Pcc-Phenoxyethanol-Globally-Approved-</u> Preservative/ [Accessed: 2015-05-29].

Denadai, R., Saad-Hossne, R. And Martinhão Souto, L. R. 2013. Simulation-Based Cutaneous Surgical-Skill Training On A Chicken-Skin Bench Model In A Medical Undergraduate Program. *Indian Journal Of Dermatology* 58(3), Pp. 200-207. Doi: 10.4103/0019-5154.110829

Di Domenico, E. G. Et Al. 2018. Inflammatory Cytokines And Biofilm Production Sustain Staphylococcus Aureus Outgrowth And Persistence: A Pivotal Interplay In The Pathogenesis Of Atopic Dermatitis. *Scientific Reports* 8(1), P. 9573. Doi: 10.1038/S41598-018-27421-1

Diepgen, T. L. And Mahler, V. 2002. The Epidemiology Of Skin Cancer. *British Journal Of Dermatology* 146(61), Pp. 1-6.

Dimitriu, P. A. Et Al. 2019. New Insights Into The Intrinsic And Extrinsic Factors That Shape The Human Skin Microbiome. *Mbio* 10(4), Doi: 10.1128/Mbio.00839-19

Dincer, S., Uslu, F. M. And Delik, A. 2020. Antibiotic Resistance In Biofilm. In: Dincer, S., Özdenefe, M. And Arkut, A. Eds. *Bacterial Biofilms*. London: Intechopen.

Divakaruni, A. S., Paradyse, A., Ferrick, D. A., Murphy, A. N., Jastroch, M. And Chan, D. C. 2014. Chapter Sixteen - Analysis And Interpretation Of Microplate-Based Oxygen Consumption And Ph Data.*Methods In Enzymology*. Vol. 547. Academic Press, Pp. 309-354.

Dobler, D., Schmidts, T., Wildenhain, S., Seewald, I., Merzhäuser, M. And Runkel, F. 2019. Impact Of Selected Cosmetic Ingredients On Common Microorganisms Of Healthy Human Skin. *Cosmetics* 6(3), Doi: 10.3390/Cosmetics6030045

Donlan, R. M. 2002. Biofilms: Microbial Life On Surfaces. *Emerging Infectious Diseases* 8(9), Pp. 881-890. Doi: 10.3201/Eid0809.020063

Dotis, J., Printza, N., Stabouli, S. And Papachristou, F. 2015. Kocuria Species Peritonitis: Although Rare, We Have To Care. *Perit Dial Int* 35(1), Pp. 26-30. Doi: 10.3747/Pdi.2013.00138

Draelos, Z. D. 2014. Facial Skin Care Products And Cosmetics. (1879-1131 (Electronic)),

Dreger, M. And Wielgus, K. 2013. Application Of Essential Oils As Natural Cosmetic Preservatives. *Herba Polonica* 59(4), Doi: 10.2478/Hepo-2013-0030

Dréno, B. Et Al. 2016. Microbiome In Healthy Skin, Update For Dermatologists. *J Eur Acad Dermatol Venereol*. Vol. 30. Pp. 2038-2047.

Dréno, B., Pécastaings, S., Corvec, S., Veraldi, S., Khammari, A. And Roques, C. 2018. Cutibacterium Acnes (Propionibacterium Acnes) And Acne Vulgaris: A Brief Look At The Latest Updates. *Journal Of The European Academy Of Dermatology And Venereology* 32(S2), Pp. 5-14. Doi: 10.1111/Jdv.15043

Dunn, A. B., Jordan, S., Baker, B. J. And Carlson, N. S. 2017. The Maternal Infant Microbiome: Considerations For Labor And Birth. *Mcn Am J Matern Child Nurs* 42(6), Pp. 318-325. Doi: 10.1097/Nmc.000000000000373

Dunn, R., Bares, S. And David, M. 2011. Central Venous Catheter-Related Bacteremia Caused By Kocuria Kristinae : Case Report And Review Of The Literature. *Annals Of Clinical Microbiology And Antimicrobials* 10(1), Pp. 1-5. Doi: Doi:10.1186/1476-0711-10-31

Durazzi, F., Sala, C., Castellani, G., Manfreda, G., Remondini, D. And De Cesare, A. 2021. Comparison Between 16s Rrna And Shotgun Sequencing Data For The Taxonomic Characterization Of The Gut Microbiota. *Scientific Reports* 11(1), P. 3030. Doi: 10.1038/S41598-021-82726-Y

Ebashi, S., Nonomura, Y. And Bourne, G. H. 1973. 7 - Proteins Of The Myofibril. *Physiology And Biochemistry (Second Edition)*. Academic Press, Pp. 285-362.

Efthimiou, G., Tsiamis, G., Typas, M. And Pappas, K. 2019. Transcriptomic Adjustments Of Staphylococcus Aureus Col (Mrsa) Forming Biofilms Under Acidic And Alkaline Conditions. *Frontiers In Microbiology* 10(2393), Doi: Doi:10.3389/Fmicb.2019.02393

Egelrud, T. 1995. New Knowledge Of The Skin's Horny Layer May Improve Understanding Of Skin Diseases. *Nordisk Medicin* 110(3),

Eisenhofer, R., Minich, J. J., Marotz, C., Cooper, A., Knight, R. And Weyrich, L. S. 2019. Contamination In Low Microbial Biomass Microbiome Studies: Issues And Recommendations. *Trends In Microbiology* 27(2), Pp. 105-117. Doi: <u>Https://Doi.Org/10.1016/J.Tim.2018.11.003</u>

Ekkelenkamp, M. B., Rooijakkers, S. H. M., Bonten, M. J. M., Cohen, J., Opal, S. M. And Powderly, W. G. 2010. Chapter 165 - Staphylococci And Micrococci.*Infectious Diseases (Third Edition)*. London: Content Repository Only!, Pp. 1632-1644.

El Darzi, E., Bazzi, S., Daoud, S., Echtay, K. S. And Bahr, G. M. 2017. Differential Regulation Of Surface Receptor Expression, Proliferation, And Apoptosis In Hacat Cells Stimulated With Interferon-Γ, Interleukin-4, Tumor Necrosis Factor-A, Or Muramyl Dipeptide. *International Journal Of Immunopathology And Pharmacology* 30(2), Pp. 130-145. Doi: 10.1177/0394632017707611 Elias, A., Mcbain, A. And O'neill, C. 2021. The Role Of The Skin Microbiota In The Modulation Of Cutaneous Inflammation-Lessons From The Gut. *Experimental Dermatology* 30(10), Doi: 10.1111/Exd.14420

Ellis, S., Nguyen, M., Vaughn, A., Notay, M., Burney, W., Sandhu, S. And Sivamani, R. 2019. The Skin And Gut Microbiome And Its Role In Common Dermatologic Conditions. *Microorganisms* 7(11), Doi: 10.3390/Microorganisms7110550

Elvers, B., Hawkins, S. And Russey, W. 2003. *Ullmann's Encyclopedia Of Industrial Chemistry*. Weinheim: Wiley-Vch.

Embleton, F. 2019. Waterless Beauty: Save Water And Face With These Eco-Friendly Products | Marie Claire. *Marie Claire* 2019-10-29. Available At: <u>Https://Www.Marieclaire.Co.Uk/Beauty/Waterless-Beauty-672042</u>

Epstein, W. 2003. The Roles And Regulation Of Potassium In Bacteria. *Prog Nucleic Acid Res Mol Biol* 75, Pp. 293-320.

Ertel, K. D., Keswick, B. H. And Bryant, P. B. 1995. A Forearm Controlled Application Technique For Estimating The Relative Mildness Of Personal Cleansing Products. *Journal Of The Society Of Cosmetic Chemists* 46, Pp. 67-76.

Essmann, F., Bantel, H., Totzke, G., Engels, I., Sinha, B., Schulze-Osthoff, K. And Jänicke, R. 2003. Staphylococcus Aureus Alpha-Toxin-Induced Cell Death: Predominant Necrosis Despite Apoptotic Caspase Activation. *Cell Death And Differentiation* 10(11), Doi: 10.1038/Sj.Cdd.4401301

Eu. 2015. Potassium Sorbate.

Eucast. 2003. Determination Of Minimum Inhibitory Concentrations (Mics) Of Antibacterial Agents By Broth Dilution. *Clinical Microbiology And Infection* 9(8), Pp. Ix-Xv. Doi: <u>Https://Doi.Org/10.1046/J.1469-0691.2003.00790.X</u>

Evans, C., Smith, W., Johnston, E. And Giblett, E. 1950. Bacterial Flora Of The Normal Human Skin. *The Journal Of Investigative Dermatology* 15(4), Doi: 10.1038/Jid.1950.105

Faas, M. M., Liu, Y., Borghuis, T., Van Loo-Bouwman, C. A., Harmsen, H. And De Vos, P. 2020. Microbiota Induced Changes In The Immune Response In Pregnant Mice. *Frontiers In Immunology* 10, P. 2976.

Fabbrocini, G. Et Al. 2010. Acne Scars: Pathogenesis, Classification And Treatment. *Dermatol Res Pract* 20(10), Doi: 10.1155/2010/893080

Faber, J. And Fonseca, L. 2014. How Sample Size Influences Research Outcomes. (2177-6709 (Electronic)),

Fagerbakke, K., Heldal, M. And Norland, S. 1996. Content Of Carbon, Nitrogen, Oxygen, Sulfur And Phosphorus In Native Aquatic And Cultured Bacteria. *Aquatic Microbial Ecology* 10, Pp. 15-27.

Fahimipour, A. K. Et Al. 2018. Antimicrobial Chemicals Associate With Microbial Function And Antibiotic Resistance Indoors. *Msystems* 3(6), Pp. E00200-00218. Doi: 10.1128/Msystems.00200-18

Fahmy, M. 2018. Umbilicus Types And Shapes. In: Fahmy, M. Ed. *Umbilicus And Umbilical Cord*. Cham: Springer International Publishing, Pp. 105-108.

Faith, D. P. 1992. Conservation Evaluation And Phylogenetic Diversity. *Biological Conservation* 61(1), Pp. 1-10. Doi: <u>Https://Doi.Org/10.1016/0006-3207(92)91201-3</u>

Fallah, M., Bahram, S. And Javadian, S. R. 2015. Fish Peptone Development Using Enzymatic Hydrolysis Of Silver Carp By-Products As A Nitrogen Source In Staphylococcus Aureus Media. *Food Science & Nutrition* 3(2), Pp. 153-157. Doi: <u>Https://Doi.Org/10.1002/Fsn3.198</u>

Farage, M. 2000. Development Of A Modified Forearm Controlled Application Test Method For Evaluating The Skin Mildness Of Disposable Wipe Products. *J Cosmet Sci* 51,

Fda. 1984-2014. *Water Activity (Aw) In Foods*. Available At: <u>Https://Www.Fda.Gov/Inspections-Compliance-Enforcement-And-Criminal-Investigations/Inspection-Technical-Guides/Water-Activity-Aw-Foods</u>

Ferla, M. And Wayne, P. 2014. Bacterial Methionine Biosynthesis. *Miocrobiology* 160, Pp. 1571-1584.

Fierer, N., Hamady, M., Lauber, C. And Knight, R. 2008. The Influence Of Sex, Handedness, And Washing On The Diversity Of Hand Surface Bacteria. *Pnas* 105(46), Doi: 10.1073/Pnas.0807920105

Findley, K. Et Al. 2013. Human Skin Fungal Diversity. *Nature* 498(7454), Pp. 367-370. Doi: 10.1038/Nature12171

Finnegan, S. And Percival, S. L. 2015. Edta: An Antimicrobial And Antibiofilm Agent For Use In Wound Care. *Adv Wound Care (New Rochelle)*. Vol. 4. Pp. 415-421.

Fiume, Z. 2001. Final Report On The Safety Assessment Of Lecithin And Hydrogenated Lecithin. *International Journal Of Toxicology* 20 Suppl 1, Doi: 10.1080/109158101750300937

Flores, M., Morillo, M. And Crespo, M. L. 1997. Deterioration Of Raw Materials And Cosmetic Products By Preservative Resistant Microorganisms. *International Biodeterioration & Biodegradation* 40(2), Pp. 157-160. Doi: <u>Https://Doi.Org/10.1016/S0964-8305(97)00037-1</u>

Forlani, G., Maria Seves, A. And Ciferri, O. 2000. A Bacterial Extracellular Proteinase Degrading Silk Fibroin. *International Biodeterioration & Biodegradation* 46(4), Pp. 271-275. Doi: <u>Https://Doi.Org/10.1016/S0964-8305(00)00099-8</u>

Forouzan, P. And Cohen, P. R. 2020. Erythrasma Revisited: Diagnosis, Differential Diagnoses, And Comprehensive Review Of Treatment. *Cureus* 12(9), Pp. E10733-E10733. Doi: 10.7759/Cureus.10733

Foster, T. 1996. Staphylococcus. In: Baron, S. Ed. *Medical Microbiology*. 4th Ed. Texas: University Of Texas Medical Branch

Foster, T. J., Geoghegan, J. A., Ganesh, V. K. And Höök, M. 2014. Adhesion, Invasion And Evasion: The Many Functions Of The Surface Proteins Of Staphylococcus Aureus. *Nature Reviews. Microbiology* 12(1), Pp. 49-62. Doi: 10.1038/Nrmicro3161

Fournière, M., Latire, T., Souak, D., Feuilloley, M. G. J. And Bedoux, G. 2020. Staphylococcus Epidermidis And Cutibacterium Acnes: Two Major Sentinels Of Skin Microbiota And The Influence Of Cosmetics. *Microorganisms* 8(11), Doi: 10.3390/Microorganisms8111752

Fouts, D. E. Et Al. 2012. Next Generation Sequencing To Define Prokaryotic And Fungal Diversity In The Bovine Rumen. *Plos One* 7(11), Pp. E48289-E48289. Doi: 10.1371/Journal.Pone.0048289

Fox, G. E. 2010. Origin And Evolution Of The Ribosome. *Cold Spring Harbor Perspectives In Biology* 2(9), Pp. A003483-A003483. Doi: 10.1101/Cshperspect.A003483

Frank, J., Born, K., Barker, J. H. And Marzi, I. 2021. In Vivo Effect Of Tumor Necrosis Factor Alpha On Wound Angiogenesis And Epithelialization. *European Journal Of Trauma* 29(4), Pp. 208-219. Doi: Doi:10.1007/S00068-003-1284-6

Frapwell, C. J. Et Al. 2018. Increased Rates Of Genomic Mutation In A Biofilm Co-Culture Model Of <Em>Pseudomonas Aeruginosa</Em> And <Em>Staphylococcus Aureus</Em>. *Biorxiv*, P. 387233. Doi: 10.1101/387233

Fredheim, E., Flægstad, T., Askarian, F. And Klingenberg, C. 2015. Colonisation And Interaction Between S. Epidermidis And S. Aureus In The Nose And Throat Of Healthy Adolescents. *European Journal Of Clinical Microbiology & Infectious Diseases : Official Publication Of The European Society Of Clinical Microbiology* 34(1), Doi: 10.1007/S10096-014-2197-5

Fromstein, S. R., Harthan, J. S., Patel, J. And Opitz, D. L. 2018. Demodex Blepharitis: Clinical Perspectives. *Clin Optom (Auckl)* 10, Pp. 57-63. Doi: 10.2147/Opto.S142708

Fujimura, S. And Nakamura, T. 1978. Purification And Properties Of A Bacteriocin-Like Substance (Acnecin) Of Oral Propionibacterium Acnes. *Antimicrobial Agents And Chemotherapy* 14(6), Pp. 893-898.

Funke, G., Von Graevenitz, A., Clarridge, J. E. And Bernard, K. A. 1997. Clinical Microbiology Of Coryneform Bacteria. *Clin Microbiol Rev* 10(1), Pp. 125-159.

Gagliano, V. And Hinsdill, R. 1970. Characterization Of A Staphylococcus Aureus Bacteriocin. *Journal Of Bacteriology* 104(1),

Gale, E. F. 1947. The Assimilation Of Amino-Acids By Bacteria: 1. The Passage Of Certain Amino-Acids Across The Cell Wall And Their Concentration In The Internal Environment Of Streptococcus Faecalis. *Journal Of Microbiology* 1(1), Pp. 53-76.

Gallo, R. L. 2015. S. Epidermidis Influence On Host Immunity: More Than Skin Deep. *Cell Host & Microbe* 17(2), Pp. 143-144. Doi: 10.1016/J.Chom.2015.01.012

Gao, Z., Tseng, C.-H., Pei, Z. And Blaser Martin, J. 2007. Molecular Analysis Of Human Forearm Superficial Skin Bacterial Biota. *Proceedings Of The National Academy Of Sciences* 104(8), Pp. 2927-2932. Doi: 10.1073/Pnas.0607077104

Garai, P., Chandra, K. And Chakravortty, D. 2017. Bacterial Peptide Transporters: Messengers Of Nutrition To Virulence. *Virulence* 8(3), Pp. 297-309. Doi: 10.1080/21505594.2016.1221025

Geary, C. And Stevens, M. 1986. Rapid Lysostaphin Test To Differentiate Staphylococcus And Micrococcus Species. *J Clin Microbiol* 23(6), Pp. 1044-1045.

Gharamti, A. And Kanafani, Z. 2017. Cutibacterium (Formerly Propionibacterium) Acnes Infections Associated With Implantable Devices. *Expert Review Of Anti-Infective Therapy* 15(12), Doi: 10.1080/14787210.2017.1404452

Ghazvini P, Treadwell P, Woodberry K, Nerette E Jr And Ii, P. H. 2017. Impetigo In The Pediatric Population. J Dermatolog Clin Re S 5(1), P. 1092.

Ghebremedhin, B., Layer, F., König, W. And König, B. 2008. Genetic Classification And Distinguishing Of Staphylococcus Species Based On Different Partial Gap, 16s Rrna, Hsp60, Rpob, Soda, And Tuf Gene Sequences. *Journal Of Clinical Microbiology* 46(3), Pp. 1019-1025. Doi: 10.1128/Jcm.02058-07

Giacomoni, P., Mammone, T. And Teri, M. 2009. Gender-Linked Differences In Human Skin. *Journal Of Dermatological Science* 55(3), Doi: 10.1016/J.Jdermsci.2009.06.001

Gilissen, L. J. W. J., Van Der Meer, I. M. And Smulders, M. J. M. 2016. Why Oats Are Safe And Healthy For Celiac Disease Patients. *Medical Sciences (Basel, Switzerland)* 4(4), P. 21. Doi: 10.3390/Medsci4040021

Glassing, A., Dowd, S. E., Galandiuk, S., Davis, B. And Chiodini, R. J. 2016. Inherent Bacterial Dna Contamination Of Extraction And Sequencing Reagents May Affect Interpretation Of Microbiota In Low Bacterial Biomass Samples. *Gut Pathogens* 8(1), P. 24. Doi: 10.1186/S13099-016-0103-7

Goig, G. A., Blanco, S., Garcia-Basteiro, A. L. And Comas, I. 2020. Contaminant Dna In Bacterial Sequencing Experiments Is A Major Source Of False Genetic Variability. *Bmc Biology* 18(1), Pp. 24-24. Doi: 10.1186/S12915-020-0748-Z

Gomes, F., Teixeira, P., Azeredo, J. And Oliveira, R. 2009. Effect Of Farnesol On Planktonic And Biofilm Cells Of Staphylococcus Epidermidis. *Current Microbiology* 59(2), Pp. 118-122. Doi: Doi:10.1007/S00284-009-9408-9

Gomes, J., Barbosa, J. And Teixeira, P. 2021. The Inhibitory Concentration Of Natural Food Preservatives May Be Biased By The Determination Methods. *Foods (Basel, Switzerland)* 10(5), P. 1009. Doi: 10.3390/Foods10051009

Gonzalez, A. O., Costa, T. F., Andrade Zde, A. And Medrado, A. 2016. Wound Healing - A Literature Review\*. *An Bras Dermatol* 91(5), Pp. 614-620. Doi: 10.1590/Abd1806-4841.20164741

Gosbell, I. And Van Hal, S. 2013. Staphylococcus Aureus Colonisation: Some Questions Answered. *The Lancet Infectious Diseases* 13(5), Pp. 380-381. Doi: 10.1016/S1473-3099(13)70048-3

Gravitz, L. 2018. Skin. Nature 563(7732), Pp. S83-S83. Doi: 10.1038/D41586-018-07428-4

Grice, E. A. Et Al. 2008. A Diversity Profile Of The Human Skin Microbiota. *Genome Res* 18(7), Pp. 1043-1050. Doi: 10.1101/Gr.075549.107

Grice, E. A. And Segre, J. A. 2011. The Skin Microbiome. *Nature Reviews. Microbiology* 9(4), Pp. 244-253. Doi: 10.1038/Nrmicro2537

Griffin, D. E., Mahy, B. W. J. And Van Regenmortel, M. H. V. 2008. Cytokines And Chemokines. *Encyclopedia Of Virology (Third Edition)*. Oxford: Academic Press, Pp. 620-624.

Griffoni, C. Et Al. 2021. In Vitro Skin Culture Media Influence The Viability And Inflammatory Response Of Primary Macrophages. *Scientific Reports* 11(1), P. 7070. Doi: 10.1038/S41598-021-86486-7

Grogan, M. D., Bartow-Mckenney, C., Flowers, L., Knight, S. A. B., Uberoi, A. And Grice, E. A. 2019. Research Techniques Made Simple: Profiling The Skin Microbiota. *The Journal Of Investigative Dermatology* 139(4), Pp. 747-752.E741. Doi: 10.1016/J.Jid.2019.01.024

Groven, F. M. V., Zwakhalen, S. M. G., Odekerken-Schröder, G., Joosten, E. J. T. And Hamers, J. P. H. 2017. How Does Washing Without Water Perform Compared To The Traditional Bed Bath: A Systematic Review. *Bmc Geriatr* 17(31), Doi: 10.1186/S12877-017-0425-4

Gsk. 2017. A Clinical Study To Assess The Mildness Of A Cosmetic Cleanser In Healthy Subjects Using The Forearm-Controlled Application Technique (Fcat). Available At: <u>Https://lchgcp.Net/Clinical-Trials-Registry/Nct03119688</u>

Guerra, A., Orille, E. And Waseem, M. 2022. Hand Foot And Mouth Disease. Treasure Island: Statspearls.

Guerriero, G. Et Al. 2018. Production Of Plant Secondary Metabolites: Examples, Tips And Suggestions For Biotechnologists. *Genes (Basel)*. Vol. 9.

Gunn, A. And Pitt, S. J. 2012. Parasitology: An Integrated Approach. Chichester: Wiley-Blackwell.

Guo, S. And Dipietro, L. 2010. Factors Affecting Wound Healing. J Dent Res. Vol. 89. Pp. 219-229.

Gupta, A. K. Et Al. 2018. Topical Treatments For Athlete's Foot. *Cochrane Database Syst Rev* 2018(1), Doi: 10.1002/14651858.Cd010863.Pub2

Gupta, V. K., Paul, S. And Dutta, C. 2017. Geography, Ethnicity Or Subsistence-Specific Variations In Human Microbiome Composition And Diversity. *Frontiers In Microbiology* 8,

Gálvez, A., Abriouel, H., López, R. And Ben, O. N. 2007. Bacteriocin-Based Strategies For Food Biopreservation. *International Journal Of Food Microbiology* 120(1-2), Doi: 10.1016/J.Ijfoodmicro.2007.06.001

Gómez-Chávez, F. Et Al. 2021. The Extracellular Vesicles From The Commensal Staphylococcus Epidermidis Atcc12228 Strain Regulate Skin Inflammation In The Imiquimod-Induced Psoriasis Murine Model. *International Journal Of Molecular Sciences* 22(23), Doi: 10.3390/Ijms222313029

Güven, N. And Kaynak, O., F. 2014. [Investigation Of Antimicrobial And Antibiofilm Effects Of Some Preservatives Used In Drugs, Cosmetics And Food Products]. *Mikrobiyoloji Bulteni* 48(1),

Hahn-Hägerdal, B. 1986. Water Activity: A Possible External Regulator In Biotechnical Processes. *Enzyme And Microbial Technology* 8(6), Pp. 322-327.

Hall, K. K. And Lyman, J. A. 2006. Updated Review Of Blood Culture Contamination. *Clin Microbiol Rev* 19(4), Pp. 788-802. Doi: 10.1128/Cmr.00062-05

Halla, N. Et Al. 2018. Cosmetics Preservation: A Review On Present Strategies. *Molecules* 23(7), P. 41. Doi: 10.3390/Molecules23071571

Hamady, M. And Knight, R. 2009. Microbial Community Profiling For Human Microbiome Projects: Tools, Techniques, And Challenges. *Genome Research* 19(7), Pp. 1141-1152. Doi: 10.1101/Gr.085464.108

Hardy, A. And Rollinson, G. 2012. Cosmetics For Eternity In Ancient Egypt. (0079-1393 (Print)),

Hardy, B. L. Et Al. 2020. Antimicrobial Activity Of Clinically Isolated Bacterial Species Against Staphylococcus Aureus. *Frontiers In Microbiology* 10,

Harris, K. 2008. Best Practices For Using Microbiological Sampling. In: Council, B.I.F.S. Ed. < Div Style=""> International Haccp Alliance.

Harrison, C. 2019. *Disappearance Of The Human Microbiota: How We May Be Losing Our Oldest Allies | Asm.Org.* American Society For Microbiology.

Hasrat, R. Et Al. 2021. Benchmarking Laboratory Processes To Characterise Low-Biomass Respiratory Microbiota. *Scientific Reports* 11(1), P. 17148. Doi: 10.1038/S41598-021-96556-5

Haustein, U.-F., Herrmann, J., Hoppe, U. And Engel, W. 1993. Growth Inhibition Of Coryneform Bacteria By A Mixture Of Three Natural Products Farnesol, Glyceryl Monolaurate, And Phenoxyethanol' Hgq. *J Soc Cosmet Chem* 44,

Hazan, S. 2020. Rapid Improvement In Alzheimer's Disease Symptoms Following Fecal Microbiota Transplantation: A Case Report:. *International Medical Research* 48(6), Doi: 10.1177\_0300060520925930

Hecker, M. T., Obrenovich, M. E., Cadnum, J. L., Jencson, A. L., Jain, A. K., Ho, E. And Donskey, C. J. 2016. Fecal Microbiota Transplantation By Freeze-Dried Oral Capsules For Recurrent Clostridium Difficile Infection. *Open Forum Infectious Diseases* 3(2), Pp. Ofw091-Ofw091. Doi: 10.1093/Ofid/Ofw091

Heenan, C. N., Adams, M. C., Hosken, R. W. And Fleet, G. H. 2002. Growth Medium For Culturing Probiotic Bacteria For Applications In Vegetarian Food Products. *Lwt - Food Science And Technology* 35(2), Pp. 171-176. Doi: <u>Https://Doi.Org/10.1006/Fstl.2001.0833</u>

Hendricks, A. J., Mills, B. W. And Shi, V. Y. 2019. Skin Bacterial Transplant In Atopic Dermatitis: Knowns, Unknowns And Emerging Trends. *Journal Of Dermatological Science* 95(2), Pp. 56-61. Doi: <u>Https://Doi.Org/10.1016/J.Jdermsci.2019.07.001</u>

Henrot, P., Laurent, P., Levionnois, E., Leleu, D., Pain, C., Truchetet, M.-E. And Cario, M. 2020. A Method For Isolating And Culturing Skin Cells: Application To Endothelial Cells, Fibroblasts, Keratinocytes, And Melanocytes From Punch Biopsies In Systemic Sclerosis Skin. *Frontiers In Immunology* 11, P. 2408.

Hentges, D. 1996. Anaerobes: General Characteristics. In: Baron, S. Ed. *Medical Microbiology*. 4 Ed. Galveston: University Of Texas Medical Branch At Galveston.

Herranen, M. Et Al. 2010. Isolation And Characterization Of Folate-Producing Bacteria From Oat Bran And Rye Flakes. *International Journal Of Food Microbiology* 142(3), Pp. 277-285. Doi: <u>Https://Doi.Org/10.1016/J.Ijfoodmicro.2010.07.002</u>

Herrán, A. R., Pérez-Andrés, J., Caminero, A., Nistal, E., Vivas, S., Ruiz De Morales, J. M. And Casqueiro, J. 2017. Gluten-Degrading Bacteria Are Present In The Human Small Intestine Of Healthy Volunteers And Celiac Patients. *Research In Microbiology* 168(7), Pp. 673-684. Doi: <u>Https://Doi.Org/10.1016/J.Resmic.2017.04.008</u>

Hess, D. J., Henry-Stanley, M. J. And Wells, C. L. 2011. Gentamicin Promotes Staphylococcus Aureus Biofilms On Silk Suture. *The Journal Of Surgical Research* 170(2), Pp. 302-308. Doi: 10.1016/J.Jss.2011.06.011

Hetem, D. J., Rooijakkers, S. H. M., Ekkelenkamp, M. B., Cohen, J., Powderly, W. G. And Opal, S. M. 2017. 176 - Staphylococci And Micrococci.*Infectious Diseases (Fourth Edition)*. Elsevier, Pp. 1509-1522.E1502.

Heyne, R. I., De Vrij, W., Crielaard, W. And Konings, W. N. 1991. Sodium Ion-Dependent Amino Acid Transport In Membrane Vesicles Of Bacillus Stearothermophilus. *Journal Of Bacteriology* 173(2), Pp. 791-800. Doi: 10.1128/Jb.173.2.791-800.1991

Ho, J. Et Al. 2015. Human Polyomavirus 7–Associated Pruritic Rash And Viremia In Transplant Recipients. *J Infect Dis*. Vol. 211. Pp. 1560-1565.

Hobot, J. A., Tang, Y.-W., Sussman, M., Liu, D., Poxton, I. And Schwartzman, J. 2015. Chapter 2 -Bacterial Ultrastructure.*Molecular Medical Microbiology (Second Edition)*. Boston: Academic Press, Pp. 7-32.

Hochbaum, A. I., Kolodkin-Gal, I., Foulston, L., Kolter, R., Aizenberg, J. And Losick, R. 2011. Inhibitory Effects Of D-Amino Acids On Staphylococcus Aureus Biofilm Development v +.*J Bacteriol*. Vol. 193. Pp. 5616-5622.

Holland, K. T. And Bojar, R. A. 2002. Cosmetics: What Is Their Influence On The Skin Microflora? *American Journal Of Clinical Dermatology* 3(7), Pp. 445-449. Doi: 10.2165/00128071-200203070-00001

Hong, S.-W. Et Al. 2014. An Important Role Of A-Hemolysin In Extracellular Vesicles On The Development Of Atopic Dermatitis Induced By Staphylococcus Aureus. *Plos One* 9(7), Pp. E100499-E100499. Doi: 10.1371/Journal.Pone.0100499

Hopert, A., Uphoff, C. C., Wirth, M., Hauser, H. And Drexler, H. G. 1993. Mycoplasma Detection By Pcr Analysis. *In Vitro Cellular & Developmental Biology - Animal* 29(10), Pp. 819-821. Doi: 10.1007/Bf02634350

Horikoshi, K. 1999. Alkaliphiles: Some Applications Of Their Products For Biotechnology. *Microbiology And Molecular Biology Reviews : Mmbr* 63(4), Pp. 735-750.

Hornung, B. V. H., Zwittink, R. D. And Kuijper, E. J. 2019. Issues And Current Standards Of Controls In Microbiome Research. *Fems Microbiology Ecology* 95(5), P. Fiz045. Doi: 10.1093/Femsec/Fiz045

Hou, Y., Wu, Z., Dai, Z., Wang, G. And Wu, G. 2017. Protein Hydrolysates In Animal Nutrition: Industrial Production, Bioactive Peptides, And Functional Significance. *Journal Of Animal Science And Biotechnology* 8(1), P. 24. Doi: 10.1186/S40104-017-0153-9

Hovelius, B. And Mardh, P. A. 1984. Staphylococcus Saprophyticus As A Common Cause Of Urinary Tract Infections. *Rev Infect Dis* 6(3), Pp. 328-337. Doi: 10.1093/Clinids/6.3.328

Hta. 2021. *List Of Materials Considered To Be 'Relevant Material' Under The Human Tissue Act 2004*. Human Tissue Authority. Available At: <u>Https://Www.Hta.Gov.Uk/Guidance-</u>

<u>Professionals/Hta-Legislation/Relevant-Material-Under-Human-Tissue-Act-2004/List-Materials</u> [Accessed.

Huang, L. 2015. Growth Of Staphylococcus Aureus In Cooked Potato And Potato Salad--A One-Step Kinetic Analysis. *J Food Sci* 80(12), Pp. M2837-2844. Doi: 10.1111/1750-3841.13110

Hulcr, J. Et Al. 2012. A Jungle In There: Bacteria In Belly Buttons Are Highly Diverse, But Predictable. *Plos One* 7(11), Pp. E47712-E47712. Doi: 10.1371/Journal.Pone.0047712

Hunter, P. R. And Gaston, M. A. 1988. Numerical Index Of The Discriminatory Ability Of Typing Systems: An Application Of Simpson's Index Of Diversity. *Journal Of Clinical Microbiology* 26(11), Pp. 2465-2466. Doi: 10.1128/Jcm.26.11.2465-2466.1988

Huovinen, P. 2001. Bacteriotherapy: The Time Has Come. (0959-8138 (Print)),

Huttenhower, C. Et Al. 2012. Structure, Function And Diversity Of The Healthy Human Microbiome. *Nature* 486(7402), Pp. 207-214. Doi: 10.1038/Nature11234

Huus, K. Et Al. 2020. Changes In Iga-Targeted Microbiota Following Fecal Transplantation For Recurrent Clostridioides Difficile Infection. <u>*Https://Doi.Org/10.1080/19490976.2020.1862027</u> 13(1), Doi: 202406448</u>* 

Ifantidou, A., Diamantidis, M., Tseliki, G., Angelou, A., Christidou, P., Papa, A. And Pentilas, D. 2010. Corynebacterium Jeikeium Bacteremia In A Hemodialyzed Patient. *International Journal Of Infectious Diseases : Ijid : Official Publication Of The International Society For Infectious Diseases* 14 Suppl 3, Doi: 10.1016/J.Ijid.2009.11.008

Ijabadeniyi, O. A. And Pillay, Y. 2017. Microbial Safety Of Low Water Activity Foods: Study Of Simulated And Durban Household Samples. *Journal Of Food Quality* 2017, Doi: <u>Https://Doi.Org/10.1155/2017/4931521</u>

Im, J. Et Al. 2015. Enterococcus Faecalis Lipoteichoic Acid Suppresses Aggregatibacter Actinomycetemcomitans Lipopolysaccharide-Induced II-8 Expression In Human Periodontal Ligament Cells. *International Immunology* 27(8), Pp. 381-391. Doi: 10.1093/Intimm/Dxv016

Inamadar, A. And Palit, A. 2003. The Genus Malassezia And Human Disease. *Indian Journal Of Dermatology, Venereology & Leprology* 69(4), Pp. 265-270.

Inman, M. 2011. How Bacteria Turn Fiber Into Food. *Plos Biology* 9(12), Pp. E1001227-E1001227. Doi: 10.1371/Journal.Pbio.1001227

Ishihara, K. 2006. [Reasons For The Increased Incidence Of Skin Cancer]. *Gan To Kagaku Ryoho* 33(10), Pp. 1380-1385.

Islam, H., Chamberlain, T. C., Mui, A. L. And Little, J. P. 2021. Elevated Interleukin-10 Levels In Covid-19: Potentiation Of Pro-Inflammatory Responses Or Impaired Anti-Inflammatory Action? *Frontiers In Immunology* 12,

Iwase, T. Et Al. 2010. Staphylococcus Epidermidis Esp Inhibits Staphylococcus Aureus Biofilm Formation And Nasal Colonization. *Nature* 465(7296), Pp. 346-349. Doi: 10.1038/Nature09074

Iyer, V., Raut, J. And Dasgupta, A. 2021. Impact Of Ph On Growth Of Staphylococcus Epidermidis And Staphylococcus Aureus In Vitro. *J Med Microbiol* 70(9), Doi: 10.1099/Jmm.0.001421

Izumi, A. K., Marples, R. R. And Kligman, A. M. 1970. Bacteriology Of Acne Comedones. *Archives Of Dermatology* 102(4), Pp. 397-399. Doi: 10.1001/Archderm.1970.04000100045010

Izzat, I. And Bennett, E. 1979. Effect Of Varying Concentrations Of Edta On The Antimicrobial Properties Of Cutting Fluid Preservatives. *Microbios* 26(103),

Jacquez, J. A. 1972. Na-Linked Transport Of Organic Solute. In: Heinz, E. Ed. *Ion Gradient Hypotheses And The Energy Requirement For Active Transport Of Amino Acids*. Germany: Springer.

Jakobsson, T. And Forsum, U. 2007. Lactobacillus Iners: A Marker Of Changes In The Vaginal Flora? *Journal Of Clinical Microbiology* 45(9), Pp. 3145-3145. Doi: 10.1128/Jcm.00558-07

Janda, J. M. And Abbott, S., L. 2007. 16s Rrna Gene Sequencing For Bacterial Identification In The Diagnostic Laboratory: Pluses, Perils, And Pitfalls. *Journal Of Clinical Microbiology* 45(9), Pp. 2761-2764. Doi: 10.1128/Jcm.01228-07

Janssen, P., Yates, P., Grinton, B., Taylor, P. And Sait, M. 2002. Improved Culturability Of Soil Bacteria And Isolation In Pure Culture Of Novel Members Of The Divisions Acidobacteria, Actinobacteria, Proteobacteria, And Verrucomicrobia. *Applied And Environmental Microbiology* 68(5), Doi: 10.1128/Aem.68.5.2391-2396.2002

Jarmuda, S., O'reilly, N., Żaba, R., Jakubowicz, O., Szkaradkiewicz, A. And Kavanagh, K. Potential Role Of Demodex Mites And Bacteria In The Induction Of Rosacea. (1473-5644 (Electronic)),

Jaśkiewicz, M., Neubauer, D. And Kamysz, W. 2017. Comparative Study On Antistaphylococcal Activity Of Lipopeptides In Various Culture Media. *Antibiotics (Basel, Switzerland)* 6(3), P. 15. Doi: 10.3390/Antibiotics6030015

Ji-Young, L., Yong-Suk, K. And Dong-Hwa, S. 2002. Antimicrobial Synergistic Effect Of Linolenic Acid And Monoglyceride Against Bacillus Cereus And Staphylococcus Aureus. 50(7), Pp. 2193-2199. Doi: 10.1021/Jf011175a

Jiang, Y., Geng, M. And Bai, L. 2020. Targeting Biofilms Therapy: Current Research Strategies And Development Hurdles. *Microorganisms* 8(8), P. 1222. Doi: 10.3390/Microorganisms8081222

Jin, Q. And Kirk, M. F. 2018. Ph As A Primary Control In Environmental Microbiology: 1. Thermodynamic Perspective. *Frontiers In Environmental Science* 6, P. 21.

Johani, K., Malone, M., Jensen, S., Gosbell, I., Dickson, H., Hu, H. And Vickery, K. 2017. Microscopy Visualisation Confirms Multi-Species Biofilms Are Ubiquitous In Diabetic Foot Ulcers. *International Wound Journal* 14(6), Pp. 1160-1169. Doi: <u>Https://Doi.Org/10.1111/lwj.12777</u>

Johnson, J. S. Et Al. 2019. Evaluation Of 16s Rrna Gene Sequencing For Species And Strain-Level Microbiome Analysis. *Nature Communications* 10(1), P. 5029. Doi: 10.1038/S41467-019-13036-1

Johnson, S. A., Goddard, P. A., Iliffe, C., Timmins, B., Rickard, A. H., Robson, G. And Handley, P. S. 2002. Comparative Susceptibility Of Resident And Transient Hand Bacteria To Para-Chloro-Meta-Xylenol And Triclosan. *J Appl Microbiol* 93(2), Pp. 336-344. Doi: 10.1046/J.1365-2672.2002.01691.X

Johnston, B. And Conly, J. 2006. Tumour Necrosis Factor Inhibitors And Infection: What Is There To Know For Infectious Diseases Physicians? *The Canadian Journal Of Infectious Diseases & Medical Microbiology = Journal Canadien Des Maladies Infectieuses Et De La Microbiologie Medicale* 17(4), Pp. 209-212. Doi: 10.1155/2006/385789

Juda, M., Paprota, K., Jałoza, D., Malm, A., Rybojad, P. And Goździuk, K. 2008. Edta As A Potential Agent Preventing Formation Of Staphylococcus Epidermidis Biofilm On Polichloride Vinyl Biomaterials. *Ann Agric Environ Med* 15(2), Pp. 237-241.

Juhász, M. And Marmur, E. 2014. A Review Of Selected Chemical Additives In Cosmetic Products. *Dermatologic Therapy* 27(6), Doi: 10.1111/Dth.12146

Jung, Y. O. Et Al. 2019. Lysates Of A Probiotic, Lactobacillus Rhamnosus, Can Improve Skin Barrier Function In A Reconstructed Human Epidermis Model. *Int J Mol Sci* 20(17), Doi: 10.3390/Ijms20174289

Jurtshuk, P. 1996. Bacterial Metabolism. *Medical Microbiology*. 4 Ed. University Of Texas Medical Branch At Galveston.

Kabene, S. And Baadel, S. 2019. Bioethics: A Look At Animal Testing In Medicine And Cosmetics In The Uk. *J Med Ethics Hist Med* 12, Doi: 10.18502/Jmehm.V12i15.1875

Kabongo, M. M., Sowar, M. And Nutini, L. 1982. A Simplified Medium For Detecting The Effect Of Lecithin On The Growth Of Propionibacterium Acnes. *Microbiologica* 5(1),

Kadariya, J., Smith, T. C. And Thapaliya, D. 2014. <I>Staphylococcus Aureus</I> And Staphylococcal Food-Borne Disease: An Ongoing Challenge In Public Health. *Biomed Research International* 2014, P. 827965. Doi: 10.1155/2014/827965

Kammon, A., Almaeyoufi, A. And Asheg, A. 2019. In Vitro Antimicrobial Activity Of Clove Oil Against Gram Negative Bacteria Isolated From Chickens. *Approaches In Poultry, Dairy & Veterinary Sciences* 6(2), Pp. 1-6.

Kang, H., Kim, J. And Park, J. 2017. Methods To Isolate Extracellular Vesicles For Diagnosis. *Micro And Nano Systems Letters* 5(1), P. 15. Doi: 10.1186/S40486-017-0049-7

Kantor, G. R., Taylor, J. S., Ratz, J. L. And Evey, P. L. 1985. Acute Allergic Contact Dermatitis From Diazolidinyl Urea (Germall Ii) In A Hair Gel. *Journal Of The American Academy Of Dermatology* 13(1), Pp. 116-119. Doi: <u>Https://Doi.Org/10.1016/S0190-9622(85)70153-3</u>

Karabay, O. And Sahin, I. 2005. In Vitro Activity Of Sodium-Benzoate Against Isolates Of Methicillin-Resistant Staphylococcus Aureus. *The West Indian Medical Journal* 54(2), P. 107. Doi: 10.1590/S0043-31442005000200004

Karastergiou, K., Smith, S. R., Greenberg, A. S. And Fried, S. K. 2012. Sex Differences In Human Adipose Tissues – The Biology Of Pear Shape. *Biol Sex Differ*. Vol. 3. P. 13.

Karauzum, H. And Datta, S. K. 2017. Adaptive Immunity Against Staphylococcus Aureus. *Current Topics In Microbiology And Immunology* 409, Pp. 419-439. Doi: 10.1007/82\_2016\_1

Karray, M. And Mckinney, W. P. 2020. Tinea (Pityriasis) Versicolor. *Statpearls*, Doi: <u>Https://Www.Ncbi.Nlm.Nih.Gov/Books/Nbk482500/</u>

Kasman, L. And Porter, L. 2020. Bacteriophages. Doi: <u>Https://Www.Ncbi.Nlm.Nih.Gov/Books/Nbk493185/</u>

Kates, A. E., Zimbric, M. L., Mitchell, K., Skarlupka, J. And Safdar, N. 2019. The Impact Of Chlorhexidine Gluconate On The Skin Microbiota Of Children And Adults: A Pilot Study. *American Journal Of Infection Control* 47(8), Pp. 1014-1016. Doi: 10.1016/J.Ajic.2019.01.024

Kaur, T., Jindal, N., Bansal, R. And Mahajan, B. B. 2012. Facial Demodicidosis: A Diagnostic Challenge. *Indian J Dermatol* 57(1), Pp. 72-73. Doi: 10.4103/0019-5154.92688

Ke, D., Kitamura, Y., Lejtenyi, D., Mazer, B., Brouillette, R. T. And Brown, K. 2019. Enhanced Interleukin-8 Production In Mononuclear Cells In Severe Pediatric Obstructive Sleep Apnea. *Allergy, Asthma, And Clinical Immunology : Official Journal Of The Canadian Society Of Allergy And Clinical Immunology* 15, Pp. 23-23. Doi: 10.1186/S13223-019-0338-1

Kechagia, M., Basoulis, D., Konstantopoulou, S., Dimitriadi, D., Gyftopoulou, K., Skarmoutsou, N. And Fakiri, E. M. 2013. Health Benefits Of Probiotics: A Review. *Isrn Nutrition* 2013, Doi: 10.5402/2013/481651

Keenleyside, W. 2019. The Effects Of Ph On Microbial Growth. *Microbiology*. Pressbooks.

Keiko, A. Et Al. 2018. Human Skin Cancers - Pathways, Mechanisms, Targets And Treatments. Doi: 10.5772/Intechopen.75788

Kelesidis, T. And Tsiodras, S. 2010. Staphylococcus Intermedius Is Not Only A Zoonotic Pathogen, But May Also Cause Skin Abscesses In Humans After Exposure To Saliva. *International Journal Of Infectious Diseases* 14(10), Doi: 10.1016/J.Ijid.2010.02.2249

Kellett, S. C. And Gawkrodger, D. J. 1999. The Psychological And Emotional Impact Of Acne And The Effect Of Treatment With Isotretinoin. *The British Journal Of Dermatology* 140(2), Pp. 273-282. Doi: 10.1046/J.1365-2133.1999.02662.X

Kemény, L., Ruzicka, T., Dobozy, A. And Michel, G. 1994. Role Of Interleukin-8 Receptor In Skin. *Int Arch Allergy Immunol* 104(4), Pp. 317-322. Doi: 10.1159/000236686

Kennedy, W. R. And Wendelschafer-Crabb, G. 1993. The Innervation Of Human Epidermis. . *Neurological Sciences* 115(2), Pp. 184–190.

Keyworth, N., Millar, M. R. And Holland, K. T. 1990. Swab-Wash Method For Quantitation Of Cutaneous Microflora. *Journal Of Clinical Microbiology* 28(5), P. 941.

Khayyira, A. S., Rosdina, A. E., Irianti, M. I. And Malik, A. 2020. Simultaneous Profiling And Cultivation Of The Skin Microbiome Of Healthy Young Adult Skin For The Development Of Therapeutic Agents. *Heliyon* 6(4), Pp. E03700-E03700. Doi: 10.1016/J.Heliyon.2020.E03700

Khodaparast, L. Et Al. 2016a. The Possible Role Of Staphylococcus Epidermidis Lpxtg Surface Protein Sesc In Biofilm Formation. *Plos One* 11(1), P. E0146704.

Khodaparast, L., Khodaparast, L., Van Mellaert, L., Shahrooei, M., Van Ranst, M. And Van Eldere, J. 2016b. Sesc As A Genetic Marker For Easy Identification Of Staphylococcus Epidermidis From Other Isolates. *Infection, Genetics And Evolution : Journal Of Molecular Epidemiology And Evolutionary Genetics In Infectious Diseases* 43, Doi: 10.1016/J.Meegid.2016.05.037

Ki, V. And Rotstein, C. 2008. Bacterial Skin And Soft Tissue Infections In Adults: A Review Of Their Epidemiology, Pathogenesis, Diagnosis, Treatment And Site Of Care.*Can J Infect Dis Med Microbiol*. Vol. 19. Pp. 173-184.

Kim, B. R. Et Al. 2017a. Deciphering Diversity Indices For A Better Understanding Of Microbial Communities. *J Microbiol Biotechnol* 27(12), Pp. 2089-2093. Doi: 10.4014/Jmb.1709.09027

Kim, D. Et Al. 2017b. Optimizing Methods And Dodging Pitfalls In Microbiome Research. *Microbiome* 5(1), Pp. 52-52. Doi: 10.1186/S40168-017-0267-5

Kim, G. K. 2009. Seborrheic Dermatitis And Malassezia Species: How Are They Related? *The Journal Of Clinical And Aesthetic Dermatology* 2(11), Pp. 14-17.

Kim, H. Et Al. 2015a. Effects Of Oral Intake Of Kimchi-Derived Lactobacillus Plantarum K8 Lysates On Skin Moisturizing. *Journal Of Microbiology And Biotechnology* 25(1), Doi: 10.4014/Jmb.1407.07078 Kim, R., Reboli, A. C., Bennett, J. E., Dolin, R. And Blaser, M. J. 2015b. 207 - Other Coryneform Bacteria And Rhodococci.*Mandell, Douglas, And Bennett's Principles And Practice Of Infectious Diseases (Eighth Edition)*. Philadelphia: Content Repository Only!, Pp. 2373-2382.E2374.

Kirchman, D. 1994. The Uptake Of Inorganic Nutrients By Heterotrophic Bacteria. *Microbial Ecology* 28, Pp. 255-271.

Kisseleva, T., Bhattacharya, S., Braunstein, J. And Schindler, C. 2002. Signaling Through The Jak/Stat Pathway, Recent Advances And Future Challenges. *Gene* 285(1-2), Doi: 10.1016/S0378-1119(02)00398-0

Kloos, W. E. And Musselwhite, M. S. 1975. Distribution And Persistence Of Staphylococcus And Micrococcus Species And Other Aerobic Bacteria On Human Skin. *Appl Microbiol* 30(3), Pp. 381-385.

Kneifel, W. 2009. In Vitro Growth Behaviour Of Probiotic Bacteria In Culture Media With Carbohydrates Of Prebiotic Importance. *Microbial Ecology In Health And Disease* 12(1), Doi: 10.1080/089106000435563

Kobayashi, S. D. And Deleo, F. R. 2013. Staphylococcus Aureus Protein A Promotes Immune Suppression. *Mbio* 4(5), P. E00764. Doi: 10.1128/Mbio.00764-13

Kobayashi, S. D., Malachowa, N. And Deleo, F. R. 2015. Pathogenesis Of Staphylococcus Aureus Abscesses. *The American Journal Of Pathology* 185(6), Pp. 1518-1527. Doi: 10.1016/J.Ajpath.2014.11.030

Kobayashi, S. D., Malachowa, N. And Deleo, F. R. 2018. Neutrophils And Bacterial Immune Evasion. *Journal Of Innate Immunity* 10(5-6), Pp. 432-441. Doi: 10.1159/000487756

Kober, M. M. And Bowe, W. P. 2015. The Effect Of Probiotics On Immune Regulation, Acne, And Photoaging.*Int J Womens Dermatol*. Vol. 1. Pp. 85-89.

Kolar, S. Et Al. 2013. Extracellular Proteases Are Key Mediators Of Staphylococcus Aureus Virulence Via The Global Modulation Of Virulence-Determinant Stability. *Microbiologyopen* 2(1), Doi: 10.1002/Mbo3.55

Kolodkin-Gal, I., Romero, D., Cao, S., Clardy, J., Kolter, R. And Losick, R. 2010. D-Amino Acids Trigger Biofilm Disassembly. *Science (New York, N.Y.)* 328(5978), Doi: 10.1126/Science.1188628

Kong, H. And Segre, J. 2012. Skin Microbiome: Looking Back To Move Forward. *The Journal Of Investigative Dermatology* 132(3.2), Doi: 10.1038/Jid.2011.417

Kong, H. H. Et Al. 2017. Performing Skin Microbiome Research: A Method To The Madness. *Journal Of Investigative Dermatology* 137(3), Pp. 561-568. Doi: 10.1016/J.Jid.2016.10.033

Kong, H. H. Et Al. 2012. Temporal Shifts In The Skin Microbiome Associated With Disease Flares And Treatment In Children With Atopic Dermatitis. *Genome Res* 22(5), Pp. 850-859. Doi: 10.1101/Gr.131029.111

Korting, H. C., Lukacs, A., Vogt, N., Urban, J., Ehret, W. And Ruckdeschel, G. 1992. Influence Of The Ph-Value On The Growth Of Staphylococcus Epidermidis, Staphylococcus Aureus And Propionibacterium Acnes In Continuous Culture. *Zentralbl Hyg Umweltmed* 193(1), Pp. 78-90.

Kostakioti, M., Hadjifrangiskou, M. And Hultgren, S. J. 2013. Bacterial Biofilms: Development, Dispersal, And Therapeutic Strategies In The Dawn Of The Postantibiotic Era. *Cold Spring Harbor Perspectives In Medicine* 3(4), Pp. A010306-A010306. Doi: 10.1101/Cshperspect.A010306

Kousha, M., Yeganeh, S. And Keramat Amirkolaie, A. 2017. Effect Of Sodium Selenite On The Bacteria Growth, Selenium Accumulation, And Selenium Biotransformation In Pediococcus Acidilactici. *Food Science And Biotechnology* 26(4), Pp. 1013-1018. Doi: 10.1007/S10068-017-0142-Y

Kragsbjerg, P., Söderquist, B., Holmberg, H., Vikerfors, T. And Danielsson, D. 1998. Production Of Tumor Necrosis Factor-A And Interleukin-6 In Whole Blood Stimulated By Live Gram-Negative And Gram-Positive Bacteria. *Clinical Microbiology And Infection* 4(3), Pp. 129-134. Doi: <u>Https://Doi.Org/10.1111/J.1469-0691.1998.Tb00375.X</u>

Kram, K. E. And Finkel, S. E. 2015. Rich Medium Composition Affects Escherichia Coli Survival, Glycation, And Mutation Frequency During Long-Term Batch Culture. *Applied And Environmental Microbiology* 81(13), Pp. 4442-4450. Doi: 10.1128/Aem.00722-15

Krismer, B., Weidenmaier, C., Zipperer, A. And Peschel, A. 2017. The Commensal Lifestyle Of Staphylococcus Aureus And Its Interactions With The Nasal Microbiota. *Nature Reviews Microbiology* 15, P. 675.

Kumar, S., Tsai, C. And Nussinov, R. 2000. Factors Enhancing Protein Thermostability. *Protein Engineering, Design And Selection* 13(3), Pp. 179-191. Doi: 10.1093/Protein/13.3.179

Kunz, R. I., Brancalhão, R. M. C., Ribeiro, L. D. F. C. And Natali, M. R. M. 2016. Silkworm Sericin: Properties And Biomedical Applications. *Biomed Research International* 2016, Pp. 8175701-8175701. Doi: 10.1155/2016/8175701

Kushkevych, I., Cejnar, J., Treml, J., Dordević, D., Kollar, P. And Vítězová, M. 2020. Recent Advances In Metabolic Pathways Of Sulfate Reduction In Intestinal Bacteria. *Cells* 9(3), P. 698. Doi: 10.3390/Cells9030698

Kwaszewska, A., Sobiś-Glinkowska, M. And Szewczyk, E. M. 2014. Cohabitation--Relationships Of Corynebacteria And Staphylococci On Human Skin. *Folia Microbiologica* 59(6), Pp. 495-502. Doi: 10.1007/S12223-014-0326-2

Laborel-Préneron, E. Et Al. 2015. Effects Of The Staphylococcus Aureus And Staphylococcus Epidermidis Secretomes Isolated From The Skin Microbiota Of Atopic Children On Cd4+ T Cell Activation. *Plos One* 10(10), Pp. E0141067-E0141067. Doi: 10.1371/Journal.Pone.0141067

Lacoma, A., Edwards, A. M., Young, B. C., Domínguez, J., Prat, C. And Laabei, M. 2019. Cigarette Smoke Exposure Redirects Staphylococcus Aureus To A Virulence Profile Associated With Persistent Infection. *Scientific Reports* 9(1), Pp. 1-15. Doi: Doi:10.1038/S41598-019-47258-6

Lai, Y. Et Al. 2009. Commensal Bacteria Regulate Toll-Like Receptor 3-Dependent Inflammation After Skin Injury. *Nature Medicine* 15(12), Pp. 1377-1382. Doi: 10.1038/Nm.2062

Lalitha, C. And Prasada Rao, P. 2015. Abstract Of Antimicrobial Efficacy Of Preservatives Used In Sk. *International Journal Of Science And Research* 4(6),

Lam, T. Et Al. 2018. Understanding The Microbial Basis Of Body Odor In Pre-Pubescent Children And Teenagers. *Microbiome* 6(1), Pp. 1-14. Doi: 10.1186/S40168-018-0588-Z

Lambers, H., Piessens, S., Bloem, A., Pronk, H. And Finkel, P. 2006. Natural Skin Surface Ph Is On Average Below 5, Which Is Beneficial For Its Resident Flora. *International Journal Of Cosmetic Science* 28(5), Pp. 359-370. Doi: 10.1111/J.1467-2494.2006.00344.X

Lambert, R. J. W., Hanlon, G. W. And Denyer, S. P. 2004. The Synergistic Effect Of Edta/Antimicrobial Combinations On Pseudomonas Aeruginosa. *Journal Of Applied Microbiology* 96(2), Pp. 244-253. Doi: <u>Https://Doi.Org/10.1046/J.1365-2672.2004.02135.X</u>

Lambert, R. J. W. And Pearson, J. 2000. Susceptibility Testing: Accurate And Reproducible Minimum Inhibitory Concentration (Mic) And Non-Inhibitory Concentration (Nic) Values. *Journal Of Applied Microbiology* 88(5), Pp. 784-790. Doi: <u>Https://Doi.Org/10.1046/J.1365-</u> 2672.2000.01017.X

Langdon, A., Crook, N. And Dantas, G. 2016. The Effects Of Antibiotics On The Microbiome Throughout Development And Alternative Approaches For Therapeutic Modulation.*Genome Med*. Vol. 8.

Lanzalaco, A., Vanoosthuyze, K., Stark, C., Swaile, D., Rocchetta, H. And Spruell, R. 2016. A Comparative Clinical Study Of Different Hair Removal Procedures And Their Impact On Axillary Odor Reduction In Men. *Journal Of Cosmetic Dermatology* 15(1), Pp. 58-65. Doi: 10.1111/Jocd.12197

Larson, E. 2001. Hygiene Of The Skin: When Is Clean Too Clean? *Emerging Infectious Diseases* 7(2), Pp. 225-230. Doi: 10.3201/Eid0702.010215

Lauffer, F. Et Al. 2018. Type I Immune Response Induces Keratinocyte Necroptosis And Is Associated With Interface Dermatitis. *Journal Of Investigative Dermatology* 138(8), Pp. 1785-1794. Doi: <u>Https://Doi.Org/10.1016/J.Jid.2018.02.034</u> Lbèr, C., Buraczewska-Norin, I., Kocherbitov, V., Saleem, S., Lodén, M. And Engblom, J. 2014. Effects Of Water Activity And Low Molecular Weight Humectants On Skin Permeability And Hydration Dynamics – A Double-Blind, Randomized And Controlled Study. *International Journal Of Cosmetic Science* 36(5), Pp. 412-418.

Le, K. Y., Park, M. D. And Otto, M. 2018. Immune Evasion Mechanisms Of Staphylococcus Epidermidis Biofilm Infection. *Frontiers In Microbiology* 9, Pp. 359-359. Doi: 10.3389/Fmicb.2018.00359

Ledo, C. Et Al. 2021. Protein A Modulates Neutrophil And Keratinocyte Signaling And Survival In Response To Staphylococcus Aureus. *Frontiers In Immunology* 11,

Lee, D. C. Et Al. 2019a. Bacterial Colonization Of The Hospitalized Newborn: Competition Between Staphylococcus Aureus And Staphylococcus Epidermidis. *The Pediatric Infectious Disease Journal* 38(7), Pp. 682-686. Doi: 10.1097/Inf.00000000002285

Lee, H. S. Et Al. 2019b. Anti-Inflammatory Effects Of Ethanol Extract From The Leaves And Shoots Of Cedrela Odorata L. In Cytokine-Stimulated Keratinocytes. *Exp Ther Med* 18(1), Pp. 833-840. Doi: 10.3892/Etm.2019.7639

Lee, K., Lee, H., Cho, H. And Kim, Y. 2005. Role Of The Conjugated Linoleic Acid In The Prevention Of Cancer. *Critical Reviews In Food Science And Nutrition* 45(2), Doi: 10.1080/10408690490911800

Leech, J. M., Lacey, K. A., Mulcahy, M. E., Medina, E. And Mcloughlin, R. M. 2017. II-10 Plays Opposing Roles During Staphylococcus Aureus Systemic And Localized Infections. *Journal Of Immunology (Baltimore, Md. : 1950)* 198(6), Pp. 2352-2365. Doi: 10.4049/Jimmunol.1601018

Legard, D. E. Et Al. 1994. Studies Of Seasonal Changes In The Microbial Populations On The Phyllosphere Of Spring Wheat As A Prelude To The Release Of A Genetically Modified Microorganism. *Agriculture, Ecosystems & Environment* 50(2), Pp. 87-101. Doi: <u>Https://Doi.Org/10.1016/0167-8809(94)90128-7</u>

Lemos, J. A., Abranches, J., Koo, H., Marquis, R. E. And Burne, R. A. 2010. Protocols To Study The Physiology Of Oral Biofilms. *Methods In Molecular Biology (Clifton, N.J.)* 666, Pp. 87-102. Doi: 10.1007/978-1-60761-820-1\_7

Lenczewski, M., Mcgavin, S. And Van Dyke, K. 1996. Comparison Of Automated And Traditional Minimum Inhibitory Concentration Procedures For Microbiological Cosmetic Preservatives. *Journal Of Aoac International* 79(6),

Leung, M. H. Y., Wilkins, D. And Lee, P. K. H. 2015. Insights Into The Pan-Microbiome: Skin Microbial Communities Of Chinese Individuals Differ From Other Racial Groups. *Sci Rep*. Vol. 5.

Leyden, J., Mcginley, K., Hölzle, E., Labows, J. And Kligman, A. 1981. The Microbiology Of The Human Axilla And Its Relationship To Axillary Odor. *The Journal Of Investigative Dermatology* 77(5), Doi: 10.1111/1523-1747.Ep12494624

Leyden, J. J. And Del Rosso, J. Q. 2011. Oral Antibiotic Therapy For Acne Vulgaris: Pharmacokinetic And Pharmacodynamic Perspectives. *J Clin Aesthet Dermatol* 4(2), Pp. 40-47.

Leyden, J. J., Marples, R. R. And Kligman, A. M. 1974. Staphylococcus Aureus In The Lesions Of Atopic Dermatitis. *British Journal Of Dermatology* 90(5), Pp. 525-525. Doi: 10.1111/J.1365-2133.1974.Tb06447.X

Leyva Salas, M., Mounier, J., Valence, F., Coton, M., Thierry, A. And Coton, E. 2017. Antifungal Microbial Agents For Food Biopreservation-A Review. *Microorganisms* 5(3), P. 37. Doi: 10.3390/Microorganisms5030037

Li, D., Wang, W., Wu, Y., Ma, X., Zhou, W. And Lai, Y. 2019a. Lipopeptide 78 From <Em>Staphylococcus Epidermidis</Em> Activates B-Catenin To Inhibit Skin Inflammation. *The Journal Of Immunology* 202(4), P. 1219. Doi: 10.4049/Jimmunol.1800813

Li, M., Budding, A. E., Van Der Lugt-Degen, M., Du-Thumm, L., Vandeven, M. And Fan, A. 2019b. The Influence Of Age, Gender And Race/Ethnicity On The Composition Of The Human Axillary Microbiome. *International Journal Of Cosmetic Science* 41(4), Pp. 371-377. Doi: <u>Https://Doi.Org/10.1111/lcs.12549</u>

Li, S. J., Perez-Chada, L. M. And Merola, J. F. 2019c. Tnf Inhibitor-Induced Psoriasis: Proposed Algorithm For Treatment And Management. *Journal Of Psoriasis And Psoriatic Arthritis* 4(2), Pp. 70-80. Doi: 10.1177/2475530318810851

Li, Y. J., Jiao, J. L., Zhang, D. C., Xuan, X. M., Wang, B. S. And Xiu, H. M. 2009. Organotypic Culture (Air-Liquid Interface) Of Keratinocytes Skin-Like Structure Using Transwell Plates Paved With Rat Tail Collagen. *Journal Of Clinical Rehabilitative Tissue Engineering Research* 13, Pp. 8211-8215. Doi: 10.3969/J.Issn.1673-8225.2009.42.001

Liang, X., Zhang, L., Natarajan, S. K. And Becker, D. F. 2013. Proline Mechanisms Of Stress Survival. *Antioxid Redox Signal*. Vol. 19. Pp. 998-1011.

Liavonchanka, A., Hornung, E., Feussner, I. And Rudolph, M. 2006. Structure And Mechanism Of The Propionibacterium Acnes Polyunsaturated Fatty Acid Isomerase. *Proceedings Of The National Academy Of Sciences Of The United States Of America* 103(8), Doi: 10.1073/Pnas.0510144103

Lieberl, M. 1990. Final Report On The Safety Assessment Of Diazolidinyl Urea. *Journal Of The American College Of Toxicology* 9(2),

Lilley, B. And Brewer, J. 1953. The Selective Antibacterial Action Of Phenylethyl Alcohol. *Journal Of The American Pharmaceutical Association* 42(1), Pp. 6-8.

Limon, J. J., Skalski, J. H. And Underhill, D. M. 2017. Commensal Fungi In Health And Disease. *Cell Host Microbe* 22(2), Pp. 156-165. Doi: 10.1016/J.Chom.2017.07.002

Lin, C.-F., Chen, C.-L., Huang, W.-C., Cheng, Y.-L., Hsieh, C.-Y., Wang, C.-Y. And Hong, M.-Y. 2010. Different Types Of Cell Death Induced By Enterotoxins. *Toxins* 2(8), Pp. 2158-2176. Doi: 10.3390/Toxins2082158

Linehan, J. Et Al. 2018. Non-Classical Immunity Controls Microbiota Impact On Skin Immunity And Tissue Repair. *Cell* 172(4), Doi: 10.1016/J.Cell.2017.12.033

Liu, F. Et Al. 2018. Tetrasodium Edta Is Effective At Eradicating Biofilms Formed By Clinically Relevant Microorganisms From Patients' Central Venous Catheters. *Msphere* 3(6), Pp. E00525-00518. Doi: 10.1128/Msphere.00525-18

Liu, Y. Et Al. 2020a. Distinct Skin Microbiota Imbalance And Responses To Clinical Treatment In Children With Atopic Dermatitis. *Frontiers In Cellular And Infection Microbiology* 10,

Liu, Y.-K., Kuo, H.-C., Lai, C.-H. And Chou, C.-C. 2020b. Single Amino Acid Utilization For Bacterial Categorization. *Scientific Reports* 10(1), P. 12686. Doi: 10.1038/S41598-020-69686-5

Liu, Z. Et Al. 2019. Bacterial Community And Composition In Jiang-Shui And Suan-Cai Revealed By High-Throughput Sequencing Of 16s Rrna. *International Journal Of Food Microbiology* 306, P. 108271. Doi: <u>Https://Doi.Org/10.1016/J.ljfoodmicro.2019.108271</u>.

Llor, C. And Bjerrum, L. 2014. Antimicrobial Resistance: Risk Associated With Antibiotic Overuse And Initiatives To Reduce The Problem. *Ther Adv Drug Saf*. Vol. 5. Pp. 229-241.

Lodish, H., Berk, A. And Zipursky, S. 2000. Structure Of Nucleic Acids.*Molecular Cell Biology*. 4 Ed. New York: Wh Freeman.

Loh, K., Wang, Z. And Liao, P. 2019. Oncotic Cell Death In Stroke. *Reviews Of Physiology, Biochemistry And Pharmacology* 176, Pp. 37-64. Doi: 10.1007/112\_2018\_13

Lowy, F. D. 1998. Staphylococcus Aureus Infections. *New England Journal Of Medicine* 339(8), Pp. 520-532. Doi: 10.1056/Nejm199808203390806

Lozupone, C. A., Hamady, M., Kelley, S. T. And Knight, R. 2007. Quantitative And Qualitative Beta Diversity Measures Lead To Different Insights Into Factors That Structure Microbial Communities. *Applied And Environmental Microbiology* 73(5), Pp. 1576-1585. Doi: 10.1128/Aem.01996-06

Lsbio. 2022. Monoclonal Mouse Anti-Staphylococcus Epidermidis Lta / Lipoteichoic Acid Antibody Ls-C760114. *Antibodies*.

Luangpraditkun, K., Tissot, M., Joompang, A., Charoensit, P., Grandmottet, F., Viyoch, J. And Viennet, C. 2021. Prevention By The Natural Artocarpin Of Morphological And Biochemical Alterations On Uvb-Induced Hacat Cells. *Oxidative Medicine And Cellular Longevity* 2021, Doi: <u>Https://Doi.Org/10.1155/2021/5067957</u>

Lukić, M., Pantelić, I. And Savić, S. D. 2021. Towards Optimal Ph Of The Skin And Topical Formulations: From The Current State Of The Art To Tailored Products. *Cosmetics* 8(3), Doi: 10.3390/Cosmetics8030069

Lumen. 2020. *Hypodermis | Biology For Majors Ii*. Lumen. Available At: <u>Https://Courses.Lumenlearning.Com/Wm-Biology2/Chapter/Hypodermis/</u> [Accessed: 30/04/2020].

Lundov, M. D., Johansen, J. D., Zachariae, C. And Moesby, L. 2011. Low-Level Efficacy Of Cosmetic Preservatives. *International Journal Of Cosmetic Science* 33(2), Pp. 190-196. Doi: <u>Https://Doi.Org/10.1111/J.1468-2494.2010.00619.X</u>

Lynde, C. 2008. Moisturizers For The Treatment Of Inflammatory Skin Conditions. *Journal Of Drugs In Dermatology* 7(11), Pp. 1038-1043.

Lönnqvis, S., Emanuelsson, P. And Kratz, G. 2015. Influence Of Acidic Ph On Keratinocyte Function And Re-Epithelialisation Of Human In Vitro Wounds. <u>Https://Doi.Org/10.3109/2000656x.2015.1053397</u>, Doi: 1053397

Ma, J., Zhang, Y.-G., Xia, Y. And Sun, J. 2010. The Inflammatory Cytokine Tumor Necrosis Factor Modulates The Expression Of Salmonella Typhimurium Effector Proteins. *Journal Of Inflammation* 7(1), P. 42. Doi: 10.1186/1476-9255-7-42

Ma, T. M., Vanepps, J. S. And Solomon, M. J. 2017. Structure, Mechanics, And Instability Of Fibrin Clot Infected With Staphylococcus Epidermidis. *Biophysical Journal* 113(9), Pp. 2100-2109. Doi: 10.1016/J.Bpj.2017.09.001

Ma, X., Wang, H., Song, Y. And Pan, Y. 2021. Skin Irritation Potential Of Cosmetic Preservatives: An Exposure-Relevant Study. *Journal Of Cosmetic Dermatology* 20(1), Pp. 195-203. Doi: <u>Https://Doi.Org/10.1111/Jocd.13502</u>

Ma, Z. And Li, W. 2019. How And Why Men And Women Differ In Their Microbiomes: Medical Ecology And Network Analyses Of The Microgenderome. *Advanced Science* 6(23), P. 1902054. Doi: <u>Https://Doi.Org/10.1002/Advs.201902054</u>

Madigan, M. T., Martinko, J. M., Bender, K. S., Buckley, D. H. And Stahl, D. A. 2014. *Brock Biology Of Microorganisms*.

Mahizan, N. A. Et Al. 2019. Terpene Derivatives As A Potential Agent Against Antimicrobial Resistance (Amr) Pathogens. *Molecules*. Vol. 24.

Majdabadi, N. Et Al. 2018. Effect Of 2-Phenylethanol As Antifungal Agent And Common Antifungals (Amphotericin B, Fluconazole, And Itraconazole) On Candida Species Isolated From Chronic And Recurrent Cases Of Candidal Vulvovaginitis. *Assay And Drug Development Technologies* 16(3), Doi: 10.1089/Adt.2017.837 Manich, M. Et Al. 2008. Clostridium Perfringens Delta Toxin Is Sequence Related To Beta Toxin, Netb, And Staphylococcus Pore-Forming Toxins, But Shows Functional Differences. *Plos One* 3(11), P. E3764.

Marples, R. 1982. Sex, Constancy, And Skin Bacteria. Archives Of Dermatological Research 272(3-4), Pp. 317-320.

Marshall, D. L., Dickson, J. S., Nguyen, N. H., Dossey, A. T., Morales-Ramos, J. A. And Rojas, M. G. 2016. Chapter 8 - Ensuring Food Safety In Insect Based Foods: Mitigating Microbiological And Other Foodborne Hazards. *Insects As Sustainable Food Ingredients*. San Diego: Academic Press, Pp. 223-253.

Martin, S., Esser, P., Weber, F., Jakob, T., Freudenberg, M., Schmidt, M. And Goebeler, M. 2011. Mechanisms Of Chemical-Induced Innate Immunity In Allergic Contact Dermatitis. *Allergy* 66(9), Doi: 10.1111/J.1398-9995.2011.02652.X

Martin, S. F. 2017. The Role Of The Innate Immune System In Allergic Contact Dermatitis. *Allergologie Select* 1(1), Pp. 39-43. Doi: 10.5414/Alx01274e

Martínez-García, S. Et Al. 2019. Non-Biofilm-Forming Commensal Staphylococcus Epidermidis Isolates Produce Biofilm In The Presence Of Trypsin. *Microbiologyopen* 8(10), P. E906. Doi: 10.1002/Mbo3.906

Martínez-García, S., Rodríguez-Martínez, S., Cancino-Diaz, M. E. And Cancino-Diaz, J. C. 2018. Extracellular Proteases Of Staphylococcus Epidermidis: Roles As Virulence Factors And Their Participation In Biofilm. *Apmis* 126(3), Pp. 177-185. Doi: <u>Https://Doi.Org/10.1111/Apm.12805</u>

Martínez-Mesa, J., González-Chica, D. A., Duquia, R. P., Bonamigo, R. R. And Bastos, J. L. 2016. Sampling: How To Select Participants In My Research Study? (1806-4841 (Electronic)),

Matejuk, A. 2018. Skin Immunity. Arch Immunol Ther Exp (Warsz). Vol. 66. Pp. 45-54.

Matevosyan, L., Bazukyan, I. And Trchounian, A. 2019. Comparative Analysis Of The Effect Of Ca And Mg Ions On Antibacterial Activity Of Lactic Acid Bacteria Isolates And Their Associations Depending On Cultivation Conditions. *Amb Express* 9(1), Pp. 32-32. Doi: 10.1186/S13568-019-0758-9

Mauldin, E. A., Peters-Kennedy, J. And Maxie, M. G. 2016. Chapter 6 - Integumentary System. *Jubb, Kennedy & Palmer's Pathology Of Domestic Animals: Volume 1 (Sixth Edition)*. W.B. Saunders, Pp. 509-736. E501.

Mauri, F. A. Et Al. 1998. Tissue Carcinoembryonic Antigen And Oestrogen Receptor Status In Breast Carcinoma: An Immunohistochemical Study Of Clinical Outcome In A Series Of 252 Patients With Long-Term Follow-Up. *British Journal Of Cancer* 77(10), Pp. 1661-1668. Doi: 10.1038/Bjc.1998.273 Mayser, P., Schäfer, U., Krämer, H., Irlinger, B. And Steglich, W. 2002. Pityriacitrin -- An Ultraviolet-Absorbing Indole Alkaloid From The Yeast Malassezia Furfur. *Archives Of Dermatological Research* 294(3), Doi: 10.1007/S00403-002-0294-2

Mcauliffe, O., Hill, C. And Ross, R. P. 2001. Lantibiotics: Structure, Biosynthesis And Mode Of Action. *Fems Microbiology Reviews* 25(3), Pp. 285-308. Doi: 10.1111/J.1574-6976.2001.Tb00579.X

Mclaughlin, J., Watterson, S., Layton, A. M., Bjourson, A. J., Barnard, E. And Mcdowell, A. 2019. Propionibacterium Acnes And Acne Vulgaris: New Insights From The Integration Of Population Genetic, Multi-Omic, Biochemical And Host-Microbe Studies. *Microorganisms* 7(5), Doi: 10.3390/Microorganisms7050128

Medina, D., Walke, J. B., Gajewski, Z., Becker, M. H., Swartwout, M. C. And Belden, L. K. 2017. Culture Media And Individual Hosts Affect The Recovery Of Culturable Bacterial Diversity From Amphibian Skin. *Frontiers In Microbiology* 8, Pp. 1574-1574. Doi: 10.3389/Fmicb.2017.01574

Meletiadis, J., Meis, J. F. G. M., Mouton, J. W. And Verweij, P. E. 2001. Analysis Of Growth Characteristics Of Filamentous Fungi In Different Nutrient Media. *Journal Of Clinical Microbiology* 39(2), P. 478. Doi: 10.1128/Jcm.39.2.478-484.2001

Melkonian, E. And Schury, M. 2020. Biochemistry, Anaerobic Glycolysis. *Statpearls*. Florida: Statpearls Publishing.

Merck. 2022. *Microbiology In Plant Peptones*. Available At: <u>Https://Www.Sigmaaldrich.Com/Gb/En/Technical-Documents/Technical-Article/Food-And-Beverage-Testing-And-Manufacturing/Microbiological-Analysis-For-Food-And-Beverage/Plant-Peptones</u>

Mezouar, S. Et Al. 2018. Microbiome And The Immune System: From A Healthy Steady-State To Allergy Associated Disruption. *Human Microbiome Journal* 10, Pp. 11-20. Doi: <u>Https://Doi.Org/10.1016/J.Humic.2018.10.001</u>

Miles, A. A., Misra, S. S. And Irwin, J. O. 1938. The Estimation Of The Bactericidal Power Of The Blood. *The Journal Of Hygiene* 38(6), Pp. 732-749.

Miller, C. H. T., Maher, S. G. And Young, H. A. 2009. Clinical Use Of Interferon-Gamma. *Annals Of The New York Academy Of Sciences* 1182, Pp. 69-79. Doi: 10.1111/J.1749-6632.2009.05069.X

Miller, J. E. Et Al. 2020. Mode Of Birth And Risk Of Infection-Related Hospitalisation In Childhood: A Population Cohort Study Of 7.17 Million Births From 4 High-Income Countries. *Plos Medicine* 17(11), P. E1003429.

Millipore. 2018. C8845 Casein Hydrolysate Broth.

Minich, J. J., Sanders, J. G., Amir, A., Humphrey, G., Gilbert, J. A. And Knight, R. 2019. Quantifying And Understanding Well-To-Well Contamination In Microbiome Research. *Msystems* 4(4), Doi: 10.1128/Msystems.00186-19

Mirza, J., Kim, Y. And Lorian, V. 1985. Effect Of Ph On The Morphology Of Staphylococcus Aureus. *Drugs Exp Clin Res* 11(3), Pp. 149-153.

Mittal, D., Gubin, M. M., Schreiber, R. D. And Smyth, M. J. 2014. New Insights Into Cancer Immunoediting And Its Three Component Phases — Elimination, Equilibrium And Escape. *Curr Opin Immunol* 27, Pp. 16-25. Doi: 10.1016/J.Coi.2014.01.004

Miyahara, Y. And Arita, K. 2020. Antimicrobial Boost: Edta For Robust Yet Low-Preservative Natural Formulas. *Cosmetics & Toiletries*,

Miyazawa, T., Shimode, S. And Nakagawa, S. 2016. Rd-114 Virus Story: From Rna Rumor Virus To A Useful Viral Tool For Elucidating The World Cats' Journey. *Uirusu* 66(1), Doi: 10.2222/Jsv.66.21

Mo, X., Preston, S. And Zaidi, M. 2019. Macroenvironment-Gene-Microenvironment Interactions In Ultraviolet Radiation-Induced Melanomagenesis.*Advances In Cancer Research Volume*. Vol. 144. Pp. 1-54.

Mohamadzadeh, M., Müller, M., Hultsch, T., Enk, A., Saloga, J. And Knop, J. 1994. Enhanced Expression Of II-8 In Normal Human Keratinocytes And Human Keratinocyte Cell Line Hacat In Vitro After Stimulation With Contact Sensitizers, Tolerogens And Irritants. *Experimental Dermatology* 3(6), Doi: 10.1111/J.1600-0625.1994.Tb00292.X

Mokomane, M. Et Al. 2016. A Comparison Of Flocked Swabs And Traditional Swabs, Using Multiplex Real Timepcr For Detection Of Common Gastroenteritis Pathogens In Botswana. *Diagn Microbiol Infect Dis* 86(2), Pp. 141-143. Doi: 10.1016/J.Diagmicrobio.2016.07.007

Monahan, L. G., Hajduk, I. V., Blaber, S. P., Charles, I. G. And Harry, E. J. 2014. Coordinating Bacterial Cell Division With Nutrient Availability: A Role For Glycolysis. *Mbio* 5(3), Pp. E00935-00914. Doi: 10.1128/Mbio.00935-14

Moore, T. 2015. Media Ingredients, Peptones & Hydrolysates. General Lab & Cleanroom Supply.

Morita, T., Patterson, J. And Woodburn, M. 1979. Magnesium And Iron Addition To Casein Hydrolysate Medium For Production Of Staphylococcal Enterotoxins A, B, And C. *Applied And Environmental Microbiology* 38(1), Doi: 10.1128/Aem.38.1.39-42.1979

Morris, L. S., Evans, J. And Marchesi, J. R. 2012. A Robust Plate Assay For Detection Of Extracellular Microbial Protease Activity In Metagenomic Screens And Pure Cultures. *Journal Of Microbiological Methods* 91(1), Pp. 144-146. Doi: <u>Https://Doi.Org/10.1016/J.Mimet.2012.08.006</u>

Morris, R. L. And Schmidt, T. M. 2013. Shallow Breathing: Bacterial Life At Low O(2). *Nature Reviews. Microbiology* 11(3), Pp. 205-212. Doi: 10.1038/Nrmicro2970

Moskovicz, V., Gross, A. And Mizrahi, B. 2020. Extrinsic Factors Shaping The Skin Microbiome. *Microorganisms* 8(7), P. 1023. Doi: 10.3390/Microorganisms8071023

Moss, C. W. And Speck, M. L. 1966. Identification Of Nutritional Components In Trypticase Responsible For Recovery Of Escherichia Coli Injured By Freezing. *Journal Of Bacteriology* 91(3), Pp. 1098-1104. Doi: 10.1128/Jb.91.3.1098-1104.1966

Mouton, J. W., Muller, A. E., Canton, R., Giske, C. G., Kahlmeter, G. And Turnidge, J. 2018. Mic-Based Dose Adjustment: Facts And Fables. *Journal Of Antimicrobial Chemotherapy* 73(3), Pp. 564-568. Doi: 10.1093/Jac/Dkx427

Moy, R. L. And Levenson, C. 2017. Sandalwood Album Oil As A Botanical Therapeutic In Dermatology. *J Clin Aesthet Dermatol* 10(10), Pp. 34-39.

Mozaheb, N. And Mingeot-Leclercq, M.-P. 2020. Membrane Vesicle Production As A Bacterial Defense Against Stress. *Frontiers In Microbiology* 11,

Mueller, J. H. And Hinton, J. 1941. A Protein-Free Medium For Primary Isolation Of The Gonococcus And Meningococcus. *Proceedings Of The Society For Experimental Biology And Medicine* 48(1), Pp. 330-333. Doi: 10.3181/00379727-48-13311

Mullish, B. Et Al. 2019. Microbial Bile Salt Hydrolases Mediate The Efficacy Of Faecal Microbiota Transplant In The Treatment Of Recurrent Clostridioides Difficile Infection. *British Medical Journal* 68(10), Doi: 10.1136/Gutjnl-2018-317842

Mullish, B. H. Et Al. 2018. The Use Of Faecal Microbiota Transplant As Treatment For Recurrent Or Refractory <Em>Clostridium Difficile</Em> Infection And Other Potential Indications: Joint British Society Of Gastroenterology (Bsg) And Healthcare Infection Society (His) Guidelines. *Gut* 67(11), P. 1920. Doi: 10.1136/Gutjnl-2018-316818

Murphy, B., Hoptroff, M., Arnold, D., Eccles, R. And Campbell-Lee, S. 2021. In-Vivo Impact Of Common Cosmetic Preservative Systems In Full Formulation On The Skin Microbiome. *Plos One* 16(7), P. E0254172.

Murphy, J. 1996. Corynebacterium Diphtheriae. In: Baron, S. Ed. *Medical Microbiology*. 4th Ed. Texas: University Of Texas Medical Branch At Galveston.

Myles, I., Reckhow, J., Williams, K., Sastalla, I., Frank, K. And Datta, S. 2016. A Method For Culturing Gram-Negative Skin Microbiota. *Bmc Microbiology* 16(1), Pp. 1-6. Doi: Doi:10.1186/S12866-016-0684-9

Nafisi, S. And Maibach, H. 2018. Skin Penetration Of Nanoparticles. *Emerging Nanotechnologies In Immunology*. Boston: Elsevier, Pp. 47-88.

Nakatsuji, T. Et Al. 2018. A Commensal Strain Of Staphylococcus Epidermidis Protects Against Skin Neoplasia. *Science Advances* 4(2), Doi: 10.1126/Sciadv.Aao4502

Neely, W. B. 1963. Action Of Formaldehyde On Microorganisms Iii. : Bactericidal Action Of Sublethal Concentrations Of Formaldehyde On Aerobacter Aerogenes. *J Bacteriol* 86(3), Pp. 445-448.

Nehete, J. Y., Bhambar, R. S., Narkhede, M. R. And Gawali, S. R. 2013. Natural Proteins: Sources, Isolation, Characterization And Applications. *Pharmacogn Rev.* Vol. 7. Pp. 107-116.

Nestle, F. O., Di Meglio, P., Qin, J.-Z. And Nickoloff, B. J. 2009. Skin Immune Sentinels In Health And Disease. *Nature Reviews. Immunology* 9(10), Pp. 679-691. Doi: 10.1038/Nri2622

Neu, J. And Rushing, J. 2011. Cesarean Versus Vaginal Delivery: Long-Term Infant Outcomes And The Hygiene Hypothesis. *Clinics In Perinatology* 38(2), Pp. 321-331. Doi: 10.1016/J.Clp.2011.03.008

Neupane, R., Boddu, S., Renukuntla, J., Babu, R. And Tiwari, A. 2020. Alternatives To Biological Skin In Permeation Studies: Current Trends And Possibilities. *Pharmaceutics* 12(2), Doi: 10.3390/Pharmaceutics12020152

Newstead, L. L., Varjonen, K., Nuttall, T. And Paterson, G. K. 2020. Staphylococcal-Produced Bacteriocins And Antimicrobial Peptides: Their Potential As Alternative Treatments For Staphylococcus Aureus Infections. *Antibiotics (Basel)*. Vol. 9.

Nickel, J. C. And Costerton, J. W. 1992. Bacterial Biofilms And Catheters: A Key To Understanding Bacterial Strategies In Catheter-Associated Urinary Tract Infection. *The Canadian Journal Of Infectious Diseases = Journal Canadian Des Maladies Infectieuses* 3(5), Pp. 261-267.

Nicolai, S. Et Al. 2020. Human T Cell Response To Cd1a And Contact Dermatitis Allergens In Botanical Extracts And Commercial Skin Care Products. 5(43), Doi: 10.1126/Sciimmunol.Aax5430

Nielsen, C. K., Kjems, J., Mygind, T., Snabe, T. And Meyer, R. L. 2016. Effects Of Tween 80 On Growth And Biofilm Formation In Laboratory Media. *Front Microbiol* 7, Doi: 10.3389/Fmicb.2016.01878

Nishijima, S., Kurokawa, I., Katoh, N. And Watanabe, K. 2000. The Bacteriology Of Acne Vulgaris And Antimicrobial Susceptibility Of Propionibacterium Acnes And Staphylococcus Epidermidis Isolated From Acne Lesions. *The Journal Of Dermatology* 27(5), Pp. 318-323. Doi: 10.1111/J.1346-8138.2000.Tb02174.X

Novak, N., Yu, C., Bieber, T. And Allam, J. 2008. Toll-Like Receptor 7 Agonists And Skin. *Drug News* & *Perspectives* 21(3),

Nóbrega, C. S., Pauleta, S. R. And Poole, R. K. 2019. Chapter Seven - Reduction Of Hydrogen Peroxide In Gram-Negative Bacteria – Bacterial Peroxidases.*Advances In Microbial Physiology*. Vol. 74. Academic Press, Pp. 415-464.

O'toole, G. A. 2011. Microtiter Dish Biofilm Formation Assay. *Journal Of Visualized Experiments : Jove* (47), P. 2437. Doi: 10.3791/2437

Ogai, K. Et Al. 2018. A Comparison Of Techniques For Collecting Skin Microbiome Samples: Swabbing Versus Tape-Stripping. (1664-302x (Print)),

Ogonowska, P., Gilaberte, Y., Barańska-Rybak, W. And Nakonieczna, J. 2021. Colonization With Staphylococcus Aureus In Atopic Dermatitis Patients: Attempts To Reveal The Unknown. *Frontiers In Microbiology* 11,

Oh, J., Conlan, S., Polley, E. C., Segre, J. A. And Kong, H. H. 2012. Shifts In Human Skin And Nares Microbiota Of Healthy Children And Adults. *Genome Medicine* 4(10), Pp. 77-77. Doi: 10.1186/Gm378

Ohbayashi, T. Et Al. 2011. Degradation Of Fibrinogen And Collagen By Staphopains, Cysteine Proteases Released From Staphylococcus Aureus. *Microbiology (Reading)* 157(Pt 3), Pp. 786-792. Doi: 10.1099/Mic.0.044503-0

Oka, M. Et Al. 2000. Interleukin-8 Overexpression Is Present In Pyoderma Gangrenosum Ulcers And Leads To Ulcer Formation In Human Skin Xenografts. *Laboratory Investigation* 80(4), Pp. 595-604. Doi: 10.1038/Labinvest.3780064

Okada, H., Kuhn, C., Feillet, H. And Bach, J. F. 2010. The 'Hygiene Hypothesis' For Autoimmune And Allergic Diseases: An Update. *Clin Exp Immunol* 160(1), Pp. 1-9. Doi: 10.1111/J.1365-2249.2010.04139.X

Olaru, F. And Jensen, L. 2010. Chemokine Expression By Human Keratinocyte Cell Lines After Activation Of Toll-Like Receptors. *Experimental Dermatology* 19(8), Doi: 10.1111/J.1600-0625.2009.01026.X

Olsen, A. M. And Scott, W. J. 1946. Influence Of Starch In Media Used For The Detection Of Heated Bacterial Spores. *Nature* 157(3985), Pp. 337-337. Doi: Doi:10.1038/157337a0

Ortega-Peña, S. Et Al. 2019. Sesa, Sesb, Sesc, Sesd, Sese, Sesg, Sesh, And Embp Genes Are Genetic Markers That Differentiate Commensal Isolates Of Staphylococcus Epidermidis From Isolates That Cause Prosthetic Joint Infection. *Infectious Diseases (London, England)* 51(6), Doi: 10.1080/23744235.2019.1597276

Osmond, M. M. And De Mazancourt, C. 2013. How Competition Affects Evolutionary Rescue. *Philosophical Transactions Of The Royal Society Of London. Series B, Biological Sciences* 368(1610), Pp. 20120085-20120085. Doi: 10.1098/Rstb.2012.0085

Otto, M. 2008. Staphylococcal Biofilms. *Current Topics In Microbiology And Immunology* 322, Pp. 207-228. Doi: 10.1007/978-3-540-75418-3\_10

Otto, M. 2009. Staphylococcus Epidermidis--The 'Accidental' Pathogen. *Nature Reviews. Microbiology* 7(8), Pp. 555-567. Doi: 10.1038/Nrmicro2182

Otto, M. 2010. Staphylococcus Colonization Of The Skin And Antimicrobial Peptides. *Expert Review Of Dermatology* 5(2), Pp. 183-195. Doi: 10.1586/Edm.10.6

Otto, M. 2012. Molecular Basis Of Staphylococcus Epidermidis Infections. *Seminars In Immunopathology* 34(2), Pp. 201-214. Doi: 10.1007/S00281-011-0296-2

Ouertani, A. Et Al. 2018. Two New Secreted Proteases Generate A Casein-Derived Antimicrobial Peptide In Bacillus Cereus Food Born Isolate Leading To Bacterial Competition In Milk. *Frontiers In Microbiology* 9, P. 1148.

Ouwehand, A. C., Tiihonen, K. And Lahtinen, S. 2010. The Potential Of Probiotics And Prebiotics For Skin Health. *Textbook Of Aging Skin* Pp. 799–809.

Ozdemir, S., Aydogan, O. And Koksal Cakirlar, F. 2021. Biofilm Formation And Antimicrobial Susceptibility Of Non-Diphtheria Corynebacterium Strains Isolated From Blood Cultures: First Report From Turkey. *Medeniyet Medical Journal* 36(2), Pp. 123-129. Doi: 10.5222/Mmj.2021.60252

Pandey, A. K., Kumar, P., Singh, P., Tripathi, N. N. And Bajpai, V. K. 2016. Essential Oils: Sources Of Antimicrobials And Food Preservatives. *Front Microbiol* 7, Doi: 10.3389/Fmicb.2016.02161

Pandya, P. H., Murray, M. E., Pollok, K. E. And Renbarger, J. L. 2016. The Immune System In Cancer Pathogenesis: Potential Therapeutic Approaches. *J Immunol Res* 2016, Doi: 10.1155/2016/4273943

Panico, A. Et Al. 2019. Skin Safety And Health Prevention: An Overview Of Chemicals In Cosmetic Products. *J Prev Med Hyg* 60(1), Pp. E50-57. Doi: 10.15167/2421-4248/Jpmh2019.60.1.1080

Parajuli, A. Et Al. 2018. Urbanization Reduces Transfer Of Diverse Environmental Microbiota Indoors. *Front Microbiol* 9, Doi: 10.3389/Fmicb.2018.00084

Parameswaran, N. And Patial, S. 2010. Tumor Necrosis Factor-A Signaling In Macrophages. *Critical Reviews In Eukaryotic Gene Expression* 20(2), Pp. 87-103. Doi: 10.1615/Critreveukargeneexpr.V20.I2.10

Park, G. W., Lee, D., Treffiletti, A., Hrsak, M., Shugart, J. And Vinjé, J. 2015. Evaluation Of A New Environmental Sampling Protocol For Detection Of Human Norovirus On Inanimate Surfaces. *Appl Environ Microbiol*. Vol. 81. Pp. 5987-5992.

Park, H. K., Ha, M. H., Park, S. G., Kim, M. N., Kim, B. J. And Kim, W. 2012. Characterization Of The Fungal Microbiota (Mycobiome) In Healthy And Dandruff-Afflicted Human Scalps. *Plos One*. Vol. 7.

Park, Y. J., Kim, C. W. And Lee, H. K. 2019. Interactions Between Host Immunity And Skin-Colonizing Staphylococci: No Two Siblings Are Alike. *International Journal Of Molecular Sciences* 20(3), Doi: 10.3390/Ijms20030718 Parke, D. And Lewis, D. 1992. Safety Aspects Of Food Preservatives. *Food Additives And Contaminants* 9(5), Doi: 10.1080/02652039209374110

Partridge, D., Lloyd, K. A., Rhodes, J. M., Walker, A. W., Johnstone, A. M. And Campbell, B. J. 2019. Food Additives: Assessing The Impact Of Exposure To Permitted Emulsifiers On Bowel And Metabolic Health – Introducing The Fadiets Study.*Nutr Bull*. Vol. 44. Pp. 329-349.

Partridge, J. D., Sanguinetti, G., Dibden, D. P., Roberts, R. E., Poole, R. K. And Green, J. 2007. Transition Of <Em>Escherichia Coli</Em> From Aerobic To Micro-Aerobic Conditions Involves Fast And Slow Reacting Regulatory Components \*<Sup> &#X9;&#X9;</Sup>. *Journal Of Biological Chemistry* 282(15), Pp. 11230-11237. Doi: 10.1074/Jbc.M700728200

Pastar, I. Et Al. 2020. Staphylococcus Epidermidis Boosts Innate Immune Response By Activation Of Gamma Delta T Cells And Induction Of Perforin-2 In Human Skin. *Frontiers In Immunology* 11,

Patel, B., Treister, A., Mccausland, C. And Lio, P. 2019. Anatomy, Skin, Sudoriferous Gland. Treasure Island (FI): Statpearls Publishing.

Patou, J., Gevaert, P., Van Zele, T., Holtappels, G., Van Cauwenberge, P. And Bachert, C. 2008. Staphylococcus Aureus Enterotoxin B, Protein A, And Lipoteichoic Acid Stimulations In Nasal Polyps. *Journal Of Allergy And Clinical Immunology* 121(1), Pp. 110-115. Doi: <u>Https://Doi.Org/10.1016/J.Jaci.2007.08.059</u>

Payne, S. 2017. Chapter 6 - Immunity And Resistance To Viruses. *Viruses*. Academic Press, Pp. 61-71.

Percival, S. L., Mccarty, S. M. And Lipsky, B. 2014. Biofilms And Wounds: An Overview Of The Evidence. (2162-1918 (Print)),

Perin, B., Addetia, A. And Qin, X. 2019. Transfer Of Skin Microbiota Between Two Dissimilar Autologous Microenvironments: A Pilot Study. *Plos One* 14(12), Pp. E0226857-E0226857. Doi: 10.1371/Journal.Pone.0226857

Petrini, C. 2012. Ethical And Legal Considerations Regarding The Ownership And Commercial Use Of Human Biological Materials And Their Derivatives. *J Blood Med* 3, Pp. 87-96. Doi: 10.2147/Jbm.S36134

Petrova, M. I., Reid, G., Vaneechoutte, M. And Lebeer, S. 2017. Lactobacillus Iners: Friend Or Foe? *Trends Microbiol* 25(3), Pp. 182-191. Doi: 10.1016/J.Tim.2016.11.007

Picardo, M., Ottaviani, M., Camera, E. And Mastrofrancesco, A. 2009. Sebaceous Gland Lipids. *Dermatoendocrinol*. Vol. 1. Pp. 68-71.

Piipponen, M., Li, D. And Landén, N. X. 2020. The Immune Functions Of Keratinocytes In Skin Wound Healing. *International Journal Of Molecular Sciences* 21(22), P. 8790. Doi: 10.3390/Ijms21228790

Pinto, D., Ciardiello, T., Franzoni, M., Pasini, F., Giuliani, G. And Rinaldi, F. 2021. Effect Of Commonly Used Cosmetic Preservatives On Skin Resident Microflora Dynamics. *Scientific Reports* 11(1), Pp. 1-7. Doi: Doi:10.1038/S41598-021-88072-3

Poretsky, R., Rodriguez-R, L. M., Luo, C., Tsementzi, D. And Konstantinidis, K. T. 2014. Strengths And Limitations Of 16s Rrna Gene Amplicon Sequencing In Revealing Temporal Microbial Community Dynamics. *Plos One* 9(4), P. E93827. Doi: 10.1371/Journal.Pone.0093827

Pradeep, J. And Sarika, S. 2008. Neutrophiles: Acid Challenge And Comparison With Acidophiles. *The Internet Journal Of Microbiology* 7(1),

Prado Barragán, L. A., Figueroa, J. J. B., Rodríguez Durán, L. V., Aguilar González, C. N., Hennigs, C., Poltronieri, P. And D'urso, O. F. 2016. Chapter 7 - Fermentative Production Methods.*Biotransformation Of Agricultural Waste And By-Products*. Elsevier, Pp. 189-217.

Prast-Nielsen, S. Et Al. 2019. Investigation Of The Skin Microbiome: Swabs Vs. Biopsies. *British Journal Of Dermatology* 181(3), Pp. 572-579. Doi: 10.1111/Bjd.17691

Price, M. N., Zane, G. M., Kuehl, J. V., Melnyk, R. A., Wall, J. D., Deutschbauer, A. M. And Arkin, A. P. 2018. Filling Gaps In Bacterial Amino Acid Biosynthesis Pathways With High-Throughput Genetics. *Plos Genetics* 14(1), Pp. E1007147-E1007147. Doi: 10.1371/Journal.Pgen.1007147

Principi, N., Silvestri, E. And Esposito, S. 2019. Advantages And Limitations Of Bacteriophages For The Treatment Of Bacterial Infections. *Frontiers In Pharmacology* 10, P. 513.

Proctor, L., Lotempio, J. And Marquitz, A. 2019. A Review Of 10 Years Of Human Microbiome Research Activities At The Us National Institutes Of Health, Fiscal Years 2007-2016. *Microbiome* 7(1), Pp. 1-19. Doi: Doi:10.1186/S40168-019-0620-Y

Prokopowicz, M. And Różycki, K. M. 2017. Innovation In Cosmetics. *World Scientific News* 72, Pp. 448-456.

Proksch, E., Brandner, J.M. And Jensen, J.-M. 2008. The Skin: An Indispensable Barrier. *Experimental Dermatology* 17(12), Pp. 1063-1072.

Purnamawati, S., Indrastuti, N., Danarti, R. And Saefudin, T. 2017. The Role Of Moisturizers In Addressing Various Kinds Of Dermatitis: A Review. *Clinical Medicine & Research* 15(3-4), Pp. 75-87. Doi: 10.3121/Cmr.2017.1363

Purty, S. Et Al. 2013. The Expanding Spectrum Of Human Infections Caused By Kocuria Species: A Case Report And Literature Review. <u>*Https://Doi.Org/10.1038/Emi.2013.71*</u> 2(1), Doi: 10.1038/Emi.2013.71

Quigley, E. M. M. 2013. Gut Bacteria In Health And Disease. *Gastroenterology & Hepatology* 9(9), Pp. 560-569.

Quist, S., Wiswedel, I., J, Q. And Gollnick, H. 2016. Kinetic Profile Of Inflammation Markers In Human Skin In Vivo Following Exposure To Ultraviolet B Indicates Synchronic Release Of Cytokines And Prostanoids. *Acta Dermato-Venereologica* 96(7), Doi: 10.2340/00015555-2406

Rahman, M. 2009. Food Stability Beyond Water Activity And Glass Transtion: Macro-Micro Region Concept In The State Diagram. *International Journal Of Food Properties* 12(4), Doi: International Journal Of Food Properties, Vol. 12, No. 4, October-December 2009: Pp. 726–740

Ramos, R. Et Al. 2011. Wound Healing Activity Of The Human Antimicrobial Peptide Ll37. *Peptides* 32(7), Doi: 10.1016/J.Peptides.2011.06.005

Rampelotto, P. H. 2013. Extremophiles And Extreme Environments. *Life (Basel, Switzerland)* 3(3), Pp. 482-485. Doi: 10.3390/Life3030482

Ranganathan, N., Johnson, R. And Edwards, A. M. 2020. The General Stress Response Of Staphylococcus Aureus Promotes Tolerance Of Antibiotics And Survival In Whole Human Blood. *Microbiology (Reading, England)* 166(11), Pp. 1088-1094. Doi: 10.1099/Mic.0.000983

Rao, M. B., Tanksale, A. M., Ghatge, M. S. And Deshpande, V. V. 1998. Molecular And Biotechnological Aspects Of Microbial Proteases. *Microbiology And Molecular Biology Reviews : Mmbr* 62(3), Pp. 597-635. Doi: 10.1128/Mmbr.62.3.597-635.1998

Rather, P. A. And Hassan, I. 2014. Human Demodex Mite: The Versatile Mite Of Dermatological Importance. *Indian J Dermatol* 59(1), Pp. 60-66. Doi: 10.4103/0019-5154.123498

Raut, S., Bhadoriya, S. S., Uplanchiwar, V., Mishra, V., Gahane, A. And Jain, S. K. 2012. Lecithin Organogel: A Unique Micellar System For The Delivery Of Bioactive Agents In The Treatment Of Skin Aging. *Acta Pharmaceutica Sinica B* 2(1), Pp. 8-15. Doi: Https://Doi.Org/10.1016/J.Apsb.2011.12.005

Ray, L. And Kellum, R. 1970. Corynebacterium Acnes From Human Skin: Identification By Morphologic, Cultural, Biochemical, Serological, And Chromatographic Methods. *Archives Of Dermatology* 101(1), Pp. 36-40. Doi: 10.1001/Archderm.1970.04000010038005

Rebane, A., Zimmerman, M., Aab, A. And Novak, N. 2012. Mechanisms Of Ifn- $\Gamma$ –Induced Apoptosis Of Human Skin Keratinocytes In Patients With Atopic Dermatitis. *Journal Of Allergy And Clinical Immunology* 129(5), Pp. 1297-1306. Doi: 10.1016/J.Jaci.2012.02.020

Reid, G. 2005. The Importance Of Guidelines In The Development And Application Of Probiotics. *Current Pharmaceutical Design* 11(1), Pp. 11-16.

Reissbrodt, R., Beer, W., Claus, H. And Müller, R. 1995. Characterization Of Casein Peptones By Hplc Profiles And Microbiological Growth Parameters. *Acta Biotechnologica* 15(2), Pp. 223-231. Doi: <u>Https://Doi.Org/10.1002/Abio.370150212</u>

Richmond, J. M. And Harris, J. E. 2014. Immunology And Skin In Health And Disease. *Cold Spring Harb Perspect Med*. Vol. 4.

Riegel, P. 1998. Bacteriological And Clinical Aspects Of Corynebacterium. *Annales De Biologie Clinique* 56(3),

Rippa, A. L., Kalabusheva, E. P. And Vorotelyak, E. A. 2019. Regeneration Of Dermis: Scarring And Cells Involved. *Cells*. Vol. 8.

Ritsu, M. Et Al. 2017. Critical Role Of Tumor Necrosis Factor-A In The Early Process Of Wound Healing In Skin. *Journal Of Dermatology & Dermatologic Surgery* 21(1), Pp. 14-19. Doi: <u>Https://Doi.Org/10.1016/J.Jdds.2016.09.001</u>

Rivière, A., Selak, M., Lantin, D., Leroy, F. And De Vuyst, L. 2016. Bifidobacteria And Butyrate-Producing Colon Bacteria: Importance And Strategies For Their Stimulation In The Human Gut. *Frontiers In Microbiology* 7, Pp. 979-979. Doi: 10.3389/Fmicb.2016.00979

Robinson, H. C. And Rettger, L. F. 1918. The Growth Of Bacteria In Protein-Free Enzyme- And Acid-Digestion Products. *Journal Of Bacteriology* 3(3), P. 209.

Rock, K. L. And Kono, H. 2008. The Inflammatory Response To Cell Death. *Annual Review Of Pathology* 3, Pp. 99-126. Doi: 10.1146/Annurev.Pathmechdis.3.121806.151456

Rodrigues Hoffmann, A. 2017. The Cutaneous Ecosystem: The Roles Of The Skin Microbiome In Health And Its Association With Inflammatory Skin Conditions In Humans And Animals. *Veterinary Dermatology* 28(1), Doi: 10.1111/Vde.12408

Rogers, K. And Kadner, R. 2020. Physical Requirements. *Bacteria*, Available At: <u>Https://Www.Britannica.Com/Science/Bacteria</u>.

Roghmann, M., Lydecker, A., Hittle, L., Deboy, R., Nowak, R., Johnson, J. And Mongodin, E. 2017. Comparison Of The Microbiota Of Older Adults Living In Nursing Homes And The Community. *American Society For Microbiology Journals* 2(5), Doi: 10.1128/Msphere.00210-17

Rolfe, M. Et Al. 2012. Lag Phase Is A Distinct Growth Phase That Prepares Bacteria For Exponential Growth And Involves Transient Metal Accumulation. *Journal Of Bacteriology* 194(3), Pp. 686-701. Doi: 10.1128/Jb.06112-11

Ross, A. A., Doxey, A., C., Neufeld, J. D. And Sharpton, T. 2017. The Skin Microbiome Of Cohabiting Couples. *Msystems* 2(4), Pp. E00043-00017. Doi: 10.1128/Msystems.00043-17

Ross, A. A., Müller, K. M., Weese, J. S. And Neufeld, J. D. 2018. Comprehensive Skin Microbiome Analysis Reveals The Uniqueness Of Human Skin And Evidence For Phylosymbiosis Within The Class Mammalia. *Proceedings Of The National Academy Of Sciences* 115(25), Pp. E5786-E5795. Doi: 10.1073/Pnas.1801302115 Rossi, F., Amadoro, C. And Colavita, G. 2019. Members Of The Lactobacillus Genus Complex (Lgc) As Opportunistic Pathogens: A Review.*Microorganisms*. Vol. 7.

Roth, R. R. And James, W. D. 1988. Microbial Ecology Of The Skin. *Annual Review Of Microbiology* 42(1), Pp. 441-464. Doi: 10.1146/Annurev.Mi.42.100188.002301

Rushton, L., Sass, A., Baldwin, A., Dowson, C., Donoghue, D. And Mahenthiralingam, E. 2013. Key Role For Efflux In The Preservative Susceptibility And Adaptive Resistance Of Burkholderia Cepacia Complex Bacteria. *Antimicrobial Agents And Chemotherapy* 57(7), Doi: 10.1128/Aac.00140-13

Räth, S. Et Al. 2013. S. Aureus Haemolysin A-Induced II-8 And II-6 Release From Human Airway Epithelial Cells Is Mediated By Activation Of P38- And Erk-Map Kinases And Additional, Cell Type-Specific Signalling Mechanisms. *Cellular Microbiology* 15(7), Doi: 10.1111/Cmi.12113

Sabbuba, N., Hughes, G. And Stickler, D. 2008. The Migration Of Proteus Mirabilis And Other Urinary Tract Pathogens Over Foley Catheters. *Bju Internationa* 89(1), Doi: 10.1046/J.1464-410x.2002.02560.X

Sachse, F., Von Eiff, C., Becker, K., Steinhoff, M. And Rudack, C. 2008. Proinflammatory Impact Of Staphylococcus Epidermidis On The Nasal Epithelium Quantified By II-8 And Gro-Alpha Responses In Primary Human Nasal Epithelial Cells. *International Archives Of Allergy And Immunology* 145(1), Doi: 10.1159/000107463

Saha, T., Chakraborty, B., Das, S., Thakur, N. And Chakraborty, R. 2018. Chryseomicrobium Excrementi Sp. Nov., A Gram-Stain-Positive Rod-Shaped Bacterium Isolated From An Earthworm (Eisenia Fetida) Cast. *Int J Syst Evol Microbiol* 68(7), Pp. 2165-2171. Doi: 10.1099/ljsem.0.002791

Saito, S. And Quadery, A. F. 2018. Staphylococcus Aureus Lipoprotein Induces Skin Inflammation, Accompanied With Ifn-Γ-Producing T Cell Accumulation Through Dermal Dendritic Cells. *Pathogens* 7(3), Doi: 10.3390/Pathogens7030064

Sakinç, T., Michalski, N., Kleine, B. And Gatermann, S. G. 2009. The Uropathogenic Species Staphylococcus Saprophyticus Tolerates A High Concentration Of D-Serine. *Fems Microbiology Letters* 299(1), Pp. 60-64. Doi: 10.1111/J.1574-6968.2009.01731.X

Sakr, A., Brégeon, F., Mège, J.-L., Rolain, J.-M. And Blin, O. 2018. Staphylococcus Aureus Nasal Colonization: An Update On Mechanisms, Epidemiology, Risk Factors, And Subsequent Infections. *Frontiers In Microbiology* 9, Pp. 2419-2419. Doi: 10.3389/Fmicb.2018.02419

Salter, S. J. Et Al. 2014. Reagent And Laboratory Contamination Can Critically Impact Sequence-Based Microbiome Analyses. *Bmc Biology* 12, Pp. 87-87. Doi: 10.1186/S12915-014-0087-Z

Sanchez, S., Rodríguez-Sanoja, R., Ramos, A. And *Al., E.* 2018. Our Microbes Not Only Produce Antibiotics, They Also Overproduce Amino Acids. *Journal Of Antibiotics* 71, Pp. 26-36.

Sanders, E. R. 2012. Aseptic Laboratory Techniques: Plating Methods. *Jove (Journal Of Visualized Experiments)* (63), Doi: 10.3791/3064

Sanford, J. A. And Gallo, R. L. 2013. Functions Of The Skin Microbiota In Health And Disease. Seminars In Immunology 25(5), Pp. 370-377. Doi: <u>Https://Doi.Org/10.1016/J.Smim.2013.09.005</u>

Sangcharoen, N., Klaypradit, W. And Wilaipun, P. 2017. Antimicrobial Activity Optimization Of Nisin, Ascorbic Acid And Ethylenediamine Tetraacetic Acid Disodium Salt (Edta) Against Salmonella Enteritidis Atcc 13076 Using Response Surface Methodology. *Agriculture And Natural Resources* 51(5), Pp. 355-364. Doi: <u>Https://Doi.Org/10.1016/J.Anres.2017.12.005</u>

Sanz, J. L. 2011. Anaerobe. *Encyclopedia Of Astrobiology*. Berlin, Heidelberg: Springer Berlin Heidelberg, Pp. 44-44.

Sasaki, T., Kano, R., Sato, H., Nakamura, Y., Watanabe, S. And Hasegawa, A. 2003. Effects Of Staphylococci On Cytokine Production From Human Keratinocytes. *Br J Dermatol* 148(1), Pp. 46-50. Doi: 10.1046/J.1365-2133.2003.05017.X

Saunte, D. M. L., Gaitanis, G. And Hay, R. J. 2020. Malassezia-Associated Skin Diseases, The Use Of Diagnostics And Treatment. *Frontiers In Cellular And Infection Microbiology* 10, Pp. 112-112. Doi: 10.3389/Fcimb.2020.00112

Scheifele, D., Bjornson, G., Dyer, R. And Dimmick, J. 1987. Delta-Like Toxin Produced By Coagulase-Negative Staphylococci Is Associated With Neonatal Necrotizing Enterocolitis. *Infection And Immunity* 55(9), Doi: 10.1128/Iai.55.9.2268-2273.1987

Schiraldi, C. And De Rosa, M. 2016. Mesophilic Organisms. *Encyclopedia Of Membranes*. Berlin, Heidelberg: Springer Berlin Heidelberg, Pp. 1-2.

Schittek, B., Paulmann, M., Senyürek, I. And Steffen, H. 2008. The Role Of Antimicrobial Peptides In Human Skin And In Skin Infectious Diseases. *Infectious Disorders Drug Targets* 8(3), Doi: 10.2174/1871526510808030135

Schmook, F. P., Meingassner, J. G. And Billich, A. 2001. Comparison Of Human Skin Or Epidermis Models With Human And Animal Skin In In-Vitro Percutaneous Absorption. *International Journal Of Pharmaceutics* 215(1), Pp. 51-56. Doi: <u>Https://Doi.Org/10.1016/S0378-5173(00)00665-7</u>

Schneider, E. And Hunke, S. 1998. Atp-Binding-Cassette (Abc) Transport Systems: Functional And Structural Aspects Of The Atp-Hydrolyzing Subunits/Domains. *Fems Microbiology Reviews* 22(1), Pp. 1-20. Doi: 10.1111/J.1574-6976.1998.Tb00358.X

Scholz, C. F. P. And Kilian, M. 2016. The Natural History Of Cutaneous Propionibacteria, And Reclassification Of Selected Species Within The Genus Propionibacterium To The Proposed Novel Genera Acidipropionibacterium Gen. Nov., Cutibacterium Gen. Nov And Pseudopropionibacterium Gen. Nov. *International Journal Of Systematic And Evolutionary Microbiology* 66, Pp. 4422-4432. Doi: 10.1099/Ijsem.0.001367

Schommer, N. N. And Gallo, R. L. 2013. Structure And Function Of The Human Skin Microbiome. *Trends Microbiol* 21(12), Pp. 660-668. Doi: 10.1016/J.Tim.2013.10.001

Schroder, K., Hertzog, P., Ravasi, T. And Hume, D. 2004. Interferon-Γ: An Overview Of Signals, Mechanisms And Functions. *Journal Of Leukocyte Biology* 75(2), Pp. 163-189. Doi: 10.1189/JIb.0603252

Schulte To Brinke, A., Mehlich, A., Doberenz, C. And Janssens-Böcker, C. 2021. Acidification Of The Skin And Maintenance Of The Physiological Skin Ph Value By Buffered Skin Care Products Formulated Around Ph 4. *Journal Of Cosmetics, Dermatological Sciences And Applications* 11, Pp. 44-57.

Schultz, C. 2016. Water Activity As Related To Microorganisms In The Manufacturing Environment. *Gen Int Med Clin Innov* 1,

Scibisz, M., Arct, J. And Pytkowska, K. 2008. Hydrolysed Proteins In Cosmetic Production, Part Ii.

Seafarers, U. 2018. Fishing For A Future.

Secchi, G. 2008. Role Of Protein In Cosmetics. *Clinics In Dermatology* 26(4), Pp. 321-325. Doi: 10.1016/J.Clindermatol.2008.04.004

Secchi, G. And Teglia, A. 1999. Proteins In Cosmetics. In: Goddard, E. And Gruber, J. Eds. *Principles Of Polymer Science And Technology In Cosmetics And Personal Care*. Vol. 1. Crc Press.

Segeritz, C.-P. And Vallier, L. 2017. Cell Culture: Growing Cells As Model Systems In Vitro. *Basic Science Methods For Clinical Researchers*, Pp. 151-172. Doi: 10.1016/B978-0-12-803077-6.00009-6

Seilie, E. S. And Bubeck Wardenburg, J. 2017. Staphylococcus Aureus Pore-Forming Toxins: The Interface Of Pathogen And Host Complexity. *Seminars In Cell & Developmental Biology* 72, Pp. 101-116. Doi: 10.1016/J.Semcdb.2017.04.003

Sen, S., Sirobhushanam, S., Johnson, S. R., Song, Y., Tefft, R., Gatto, C. And Wilkinson, B. J. 2016. Growth-Environment Dependent Modulation Of Staphylococcus Aureus Branched-Chain To Straight-Chain Fatty Acid Ratio And Incorporation Of Unsaturated Fatty Acids. *Plos One* 11(10), Pp. E0165300-E0165300. Doi: 10.1371/Journal.Pone.0165300

Sethi, A., Kaur, T., Malhotra, S. K. And Gambhir, M. L. 2016. Moisturizers: The Slippery Road. *Indian Journal Of Dermatology* 61(3), Pp. 279-287. Doi: 10.4103/0019-5154.182427

Shahrooei, M., Hira, V., Stijlemans, B., Merckx, R., Hermans Peter, W. M. And Van Eldere, J. 2009. Inhibition Of Staphylococcus Epidermidis Biofilm Formation By Rabbit Polyclonal Antibodies Against The Sesc Protein. *Infection And Immunity* 77(9), Pp. 3670-3678. Doi: 10.1128/Iai.01464-08

Shahzad, A., Knapp, M., Lang, I. And Köhler, G. 2010. Interleukin 8 (II-8) - A Universal Biomarker? *International Archives Of Medicine* 3, Pp. 11-11. Doi: 10.1186/1755-7682-3-11

Shao, Y. Et Al. 2019. Stunted Microbiota And Opportunistic Pathogen Colonization In Caesarean-Section Birth. *Nature* 574(7776), Pp. 117-121. Doi: 10.1038/S41586-019-1560-1

Sharma, D., Misba, L. And Khan, A. U. 2019. Antibiotics Versus Biofilm: An Emerging Battleground In Microbial Communities. *Antimicrobial Resistance & Infection Control* 8(1), Pp. 1-10. Doi: Doi:10.1186/S13756-019-0533-3

Shi, L. H., Balakrishnan, K., Thiagarajah, K., Mohd Ismail, N. I. And Yin, O. S. 2016. Beneficial Properties Of Probiotics. (1985-3718 (Print)),

Shida, K. 2009. The Distribution Of Genus Staphylococcus In The Oral Cavities Of Cats. *International Journal Of Oral-Medical Sciences* 8, Pp. 83-89.

Shivaji, S., Srinivas, T. N. R. And Reddy, G. S. N. 2014. The Family Planococcaceae. In: Rosenberg, E., Delong, E.F., Lory, S., Stackebrandt, E. And Thompson, F. Eds. *The Prokaryotes: Firmicutes And Tenericutes*. Berlin, Heidelberg: Springer Berlin Heidelberg, Pp. 303-351.

Shtrichman, R. And Samuel, C. E. 2001. The Role Of Gamma Interferon In Antimicrobial Immunity. *Current Opinion In Microbiology* 4(3), Pp. 251-259. Doi: <u>Https://Doi.Org/10.1016/S1369-</u> <u>5274(00)00199-5</u>

Siegart, W. 2013. Influence Of Ph On The Preservative Boosting Effect Of Chelating Agents. Available At: <u>Https://Www.Cosmeticsandtoiletries.Com/Cosmetic-</u> <u>Ingredients/Preservation/Article/21836187/Influence-Of-Ph-On-The-Preservative-Boosting-Effect-Of-Chelating-Agents</u> [Accessed: Nov 12th,].

Siemens, N., Patenge, N., Otto, J., Fiedler, T. And Kreikemeyer, B. 2011. <Em>Streptococcus Pyogenes</Em> M49 Plasminogen/Plasmin Binding Facilitates Keratinocyte Invasion Via Integrin-Integrin-Linked Kinase (Ilk) Pathways And Protects From Macrophage Killing \*<Sup></Sup>. *Journal Of Biological Chemistry* 286(24), Pp. 21612-21622. Doi: 10.1074/Jbc.M110.202671

Sieniawska, E., Swatko-Ossor, M., Sawicki, R., Skalicka-Woźniak, K. And Ginalska, G. 2017. Natural Terpenes Influence The Activity Of Antibiotics Against Isolated Mycobacterium Tuberculosis.*Med Princ Pract*. Vol. 26. Pp. 108-112.

Sigmaaldrich. 2018. Tryptic Soy Broth. In: Merck Ed.

Siliakus, M. F., Van Der Oost, J. And Kengen, S. W. M. 2017. Adaptations Of Archaeal And Bacterial Membranes To Variations In Temperature, Ph And Pressure. *Extremophiles : Life Under Extreme Conditions* 21(4), Pp. 651-670. Doi: 10.1007/S00792-017-0939-X

Silva, P. E. S. Et Al. 2018. Insights Into The Skin Microbiome Dynamics Of Leprosy Patients During Multi-Drug Therapy And In Healthy Individuals From Brazil. *Scientific Reports* 8(1), P. 8783. Doi: 10.1038/S41598-018-27074-0

Singh, A. K. 2016. Chapter 8 - Nanoparticle Ecotoxicology. *Engineered Nanoparticles*. Boston: Academic Press, Pp. 343-450.

Sip, C. G., Bhattacharjee, N. And Folch, A. 2014. Microfluidic Transwell Inserts For Generation Of Tissue Culture-Friendly Gradients In Well Plates. *Lab On A Chip* 14(2), Pp. 302-314. Doi: 10.1039/C3lc51052b

Skabytska, Y. And Biedermann, T. 2016. Staphylococcus Epidermidis Sets Things Right Again. *Journal Of Investigative Dermatology* 136(3), Pp. 559-560. Doi: <u>Https://Doi.Org/10.1016/J.Jid.2015.11.016</u>

Skowron, K. Et Al. 2021. Human Skin Microbiome: Impact Of Intrinsic And Extrinsic Factors On Skin Microbiota. *Microorganisms* 9(3), P. 543. Doi: 10.3390/Microorganisms9030543

Slifkin, M. And Pouchet, G. 1975. Growth Potential Of Cottonseed Culture Media For Various Clinically Significant Aerobic Bacteria. *Journal Of Clinical Microbiology* 1(6), Pp. 495-499. Doi: 10.1128/Jcm.1.6.495-499.1975

Sloup, R. E., Cieza, R. J., Needle, D. B., Abramovitch, R. B., Torres, A. G. And Waters, C. M. 2016. Polysorbates Prevent Biofilm Formation And Pathogenesis Of Escherichia Coli O104:H4. *Biofouling* 32(9), Pp. 1131-1140. Doi: 10.1080/08927014.2016.1230849

Smith, K. J., Neafie, R., Yeager, J. And Skelton, H. G. 1999. Micrococcus Folliculitis In Hiv-1 Disease. *Br J Dermatol* 141(3), Pp. 558-561. Doi: 10.1046/J.1365-2133.1999.03060.X

Sohn, E. 2018. Skin Microbiota's Community Effort. *Nature* 563(7732), Doi: Doi:10.1038/D41586-018-07432-8

Solabia. 2019. Potato Peptone. In: Biotech Ed.

Song, S. J. Et Al. 2013. Cohabiting Family Members Share Microbiota With One Another And With Their Dogs. *Elife* 2, P. E00458. Doi: 10.7554/Elife.00458

Sontheimer, R. 2014. Skin Is Not The Largest Organ. *The Journal Of Investigative Dermatology* 134(2), Doi: 10.1038/Jid.2013.335

Soriano, F., Ponte, C. And Galiano, M. J. 1993. Adherence Of Corynebacterium-Urealyticum (Cdc Group-D2) And Corynebacterium-Jeikeium To Intravascular And Urinary Catheters. *European Journal Of Clinical Microbiology & Infectious Diseases* 12(6), Pp. 453-456. Doi: 10.1007/Bf01967441

Soriano-Lerma, A. Et Al. 2020. Influence Of 16s Rrna Target Region On The Outcome Of Microbiome Studies In Soil And Saliva Samples. *Scientific Reports* 10(1), Pp. 13637-13637. Doi: 10.1038/S41598-020-70141-8

Sperber, W. 1983. Influence Of Water Activity On Foodborne Bacteria — A Review. *Journal Of Food Protection* 46(2), Pp. 142-150. Doi: 10.4315/0362-028x-46.2.142

Spurgeon, M. E. And Lambert, P. F. 2013. Merkel Cell Polyomavirus: A Newly Discovered Human Virus With Oncogenic Potential. *Virology* 435(1), Pp. 118-130. Doi: 10.1016/J.Virol.2012.09.029

Stackebrandt, E., Koch, C., Gvozdiak, O. And Schumann, P. 1995. Taxonomic Dissection Of The Genus Micrococcus: Kocuria Gen. Nov., Nesterenkonia Gen. Nov., Kytococcus Gen. Nov., Dermacoccus Gen. Nov., And Micrococcus Cohn 1872 Gen. Emend. *Int J Syst Bacteriol* 45(4), Pp. 682-692. Doi: 10.1099/00207713-45-4-682

Stanbury, P. F., Whitaker, A. And Hall, S. J. 2017. Chapter 2 - Microbial Growth Kinetics. *Principles Of Fermentation Technology (Third Edition)*. Oxford: Butterworth-Heinemann, Pp. 21-74.

Staudinger, T., Pipal, A. And Redl, B. 2011. Molecular Analysis Of The Prevalent Microbiota Of Human Male And Female Forehead Skin Compared To Forearm Skin And The Influence Of Make-Up. *J Appl Microbiol* 110(6), Pp. 1381-1389. Doi: 10.1111/J.1365-2672.2011.04991.X

Steenhuis, M., Ten Hagen-Jongman, C. M., Van Ulsen, P. And Luirink, J. 2020. Stress-Based High-Throughput Screening Assays To Identify Inhibitors Of Cell Envelope Biogenesis. *Antibiotics (Basel, Switzerland)* 9(11), P. 808. Doi: 10.3390/Antibiotics9110808

Stehlikova, Z. Et Al. 2019. Dysbiosis Of Skin Microbiota In Psoriatic Patients: Co-Occurrence Of Fungal And Bacterial Communities. *Frontiers In Microbiology* 10,

Steiman, C. A., Fadrosh, D., Evans, M. D., Vrtis, R. F. And Olson, B. 2018. Farm Exposure Influences Skin Microbiota In Infancy. *Allergy And Clinical Immunology* 141(2),

Stevenson, A. Et Al. 2015. Is There A Common Water-Activity Limit For The Three Domains Of Life? *The Isme Journal* 9(6), Pp. 1333-1351. Doi: 10.1038/Ismej.2014.219

Stewart, E. J., Payne, D. E., Ma, T. M., Vanepps, J. S., Boles, B. R., Younger, J. G. And Solomon, M. J. 2017. Effect Of Antimicrobial And Physical Treatments On Growth Of Multispecies Staphylococcal Biofilms. *Applied And Environmental Microbiology* 83(12), Pp. E03483-03416. Doi: 10.1128/Aem.03483-16

Stewart, P. S. And William Costerton, J. 2001. Antibiotic Resistance Of Bacteria In Biofilms. *The Lancet* 358(9276), Pp. 135-138. Doi: <u>Https://Doi.Org/10.1016/S0140-6736(01)05321-1</u>

Stojan, G. And Christopher-Stine, L. 2015. Metabolic, Drug-Induced, And Other Noninflammatory Myopathies. *Rheumatology*. Elsevier Inc, Pp. 1255-1263.

Sudagidan, M. And Aydin, A. 2009. Screening Virulence Properties Of Staphylococci Isolated From Meat And Meat Products. *Wiener Tierarztliche Monatsschrift* 96, Pp. 128-134.

Sugimoto, S., Iwamoto, T., Takada, K., Okuda, K., Tajima, A., Iwase, T. And Mizunoe, Y. 2013. Staphylococcus Epidermidis Esp Degrades Specific Proteins Associated With Staphylococcus Aureus Biofilm Formation And Host-Pathogen Interaction. *J Bacteriol* 195(8), Pp. 1645-1655. Doi: 10.1128/Jb.01672-12 Sun, J., Guo, J., Yang, Q. And Huang, J. 2019. Diluted Conventional Media Improve The Microbial Cultivability From Aquarium Seawater. *Journal Of Microbiology* 57(9), Pp. 759-768. Doi: Doi:10.1007/S12275-019-9175-7

Sun, J.-L., Zhang, S.-K., Chen, J.-Y. And Han, B.-Z. 2012. Metabolic Profiling Of Staphylococcus Aureus Cultivated Under Aerobic And Anaerobic Conditions With 1h Nmr-Based Nontargeted Analysis. *Canadian Journal Of Microbiology* 58(6), Pp. 709-718. Doi: 10.1139/W2012-046

Surewaard, B. G. Et Al. 2018. Alpha Toxin Induces Platelet Aggregation And Liver Injury During Staphylococcus Aureus Sepsis. *Cell Host Microbe* 24(2), Pp. 271-284 E273. Doi: 10.1016/J.Chom.2018.06.017

Surujballi, O. And Fackrell, H. 2021. Enzyme-Linked Immunosorbent Assay For Detection Of Staphylococcus Aureus Alpha-Toxin. *Journal Of Clinical Microbiology* 19(3),

Suzuki, H., Arshava, E., Ford, B. And Nauseef, W. 2019. Don't Let Its Name Fool You: Relapsing Thoracic Actinomycosis Caused By Pseudopropionibacterium Propionicum (Formerly Propionibacterium Propionicum). *The American Journal Of Case Reports* 20, Doi: 10.12659/Ajcr.919775

Suzuki, T., Tada, H., Sato, E. And Sagae, Y. 1996. Application Of Sweet Potato Fiber To Skin Wound In Rat. *Biological & Pharmaceutical Bulletin* 19(7), Pp. 977-983. Doi: 10.1248/Bpb.19.977

Swamy, M. K., Akhtar, M. S. And Sinniah, U. R. 2016. Antimicrobial Properties Of Plant Essential Oils Against Human Pathogens And Their Mode Of Action: An Updated Review. *Evid Based Complement Alternat Med* 2016, Doi: 10.1155/2016/3012462

Swaney, M., Kalan, L. And Richardson, A. 2021. Living In Your Skin: Microbes, Molecules, And Mechanisms. *Infection And Immunity* 89(4), Pp. E00695-00620. Doi: 10.1128/lai.00695-20

Swiatecka, D., Swiatecki, A., Kostyra, H., Marciniak-Darmochwał, K. And Kostyra, E. 2010. The Impact Of Pea Protein Hydrolysates On Bacterial Physiological Activity--An In Vitro Study. *Int J Food Microbiol* 140(2-3), Pp. 263-270. Doi: 10.1016/J.Ijfoodmicro.2010.03.015

Szpak, P. 2011. Fish Bone Chemistry And Ultrastructure: Implications For Taphonomy And Stable Isotope Analysis. *Journal Of Archaeological Science* 38(12), Pp. 3358-3372. Doi: <u>Https://Doi.Org/10.1016/J.Jas.2011.07.022</u>

Tadler, M. B., Tice, G. And Wos, S. M. 1989. Sandwich Immunoassay For The Detection Of Lipoteichoic Acid. *J Clin Lab Anal* 3(1), Pp. 21-25. Doi: 10.1002/Jcla.1860030106

Takarada, H. Et Al. 2008. Complete Genome Sequence Of The Soil Actinomycete Kocuria Rhizophila. *Journal Of Bacteriology* 190(12), Pp. 4139-4146. Doi: 10.1128/Jb.01853-07

Tanaka, N., Yonekura, H., Yamagishi, S.-I., Fujimori, H., Yamamoto, Y. And Yamamoto, H. 2000. The Receptor For Advanced Glycation End Products Is Induced By The Glycation Products Themselves

And Tumor Necrosis Factor-A Through Nuclear Factor-Kb, And By 17β-Estradiol Through Sp-1 In Human Vascular Endothelial Cells\*. *Journal Of Biological Chemistry* 275(33), Pp. 25781-25790. Doi: <u>Https://Doi.Org/10.1074/Jbc.M001235200</u>

Tang, K., Berthé, F., Nackers, F., Hanson, K., Mambula, C., Langendorf, C. And Marquer, C. 2020. Hand Hygiene Compliance And Environmental Contamination With Gram-Negative Bacilli In A Rural Hospital In Madarounfa, Niger. *Transactions Of The Royal Society Of Tropical Medicine And Hygiene* 113(12), Pp. 749-756. Doi: 10.1093/Trstmh/Trz070

Tanowitz, B. D., Solomon, E. P., Schmidt, R. R. And Adragna, P. J. 1990. *Instructor's Manual To Accompany Human Anatomy & Physiology : Second Edition, Solomon, Schmidt, Adragna<.* Philadelphia: Saunders College Publishing.

Tauch, A. Et Al. 2005. Complete Genome Sequence And Analysis Of The Multiresistant Nosocomial Pathogen Corynebacterium Jeikeium K411, A Lipid-Requiring Bacterium Of The Human Skin Flora. *J Bacteriol* 187(13), Pp. 4671-4682. Doi: 10.1128/Jb.187.13.4671-4682.2005

Taylor, C. B. 1951. The Nutritional Requirements Of The Predominant Bacterial Flora Of The Soil. *Proceedings Of The Society For Applied Bacteriology* 14(1), Pp. 101-111. Doi: <u>Https://Doi.Org/10.1111/J.1365-2672.1951.Tb01999.X</u>

Thakur, A., Clegg, A., Chauhan, A. And Willcox, M. D. P. 1997. Modulation Of Cytokine Production From An Epiocular Corneal Cell Culture Model In Response To Staphylococcus Aureus Superantigen. *Australian And New Zealand Journal Of Ophthalmology* 25(4), Pp. 43-45. Doi: <u>Https://Doi.Org/10.1111/J.1442-9071.1997.Tb01754.X</u>

Thayikkannu, A. B., Kindo, A. J. And Veeraraghavan, M. 2015. Malassezia—Can It Be Ignored?*Indian J Dermatol*. Vol. 60. Pp. 332-339.

Theresia, N. M., Aida, K., Takada, A., Iwai, N. And Wachi, M. 2018. Effects Of Egta On Cell Surface Structures Of Corynebacterium Glutamicum. *Arch Microbiol* 200(2), Pp. 281-289. Doi: 10.1007/S00203-017-1445-3

Thermofisher. 2018. Veggietones. Oxoid Ltd.

Thukral, A. K. 2017. A Review On Measurement Of Alpha Diversity In Biology. *Agricultural Research Journal* 54(1), P. 1.

Théolier, J., Hammami, R., Labelle, P., Fliss, I. And Jean, J. 2013. Isolation And Identification Of Antimicrobial Peptides Derived By Peptic Cleavage Of Whey Protein Isolate. *Journal Of Functional Foods* 5(2), Pp. 706-714. Doi: <u>Https://Doi.Org/10.1016/J.Jff.2013.01.014</u>

Timm, C. M. Et Al. 2020. Isolation And Characterization Of Diverse Microbial Representatives From The Human Skin Microbiome. *Microbiome* 8(1), P. 58. Doi: 10.1186/S40168-020-00831-Y

Tiwari, K. B., Gatto, C. And Wilkinson, B. J. 2020. Plasticity Of Coagulase-Negative Staphylococcal Membrane Fatty Acid Composition And Implications For Responses To Antimicrobial Agents. *Antibiotics* 9(5), Doi: 10.3390/Antibiotics9050214

Todar, K. 2015. Nutrition And Growth Of Bacteria. *Textbook Of Bacteriology*. University Of Wisconsin.

Trautner, B. W. And Darouiche, R. O. 2004. Catheter-Associated Infections: Pathogenesis Affects Prevention. *Archives Of Internal Medicine* 164(8), Pp. 842-850. Doi: 10.1001/Archinte.164.8.842

Treister, A. And Lio, P. 2018. Anatomy, Skin, Sudoriferous Gland. Florida: Statpearls Publishing.

Trinh, P., Zaneveld, J. R., Safranek, S. And Rabinowitz, P. M. 2018. One Health Relationships Between Human, Animal, And Environmental Microbiomes: A Mini-Review. *Front Public Health* 6, Doi: 10.3389/Fpubh.2018.00235

Troccaz, M., Gaïa, N., Beccucci, S., Schrenzel, J., Cayeux, I., Starkenmann, C. And Lazarevic, V. 2015. Mapping Axillary Microbiota Responsible For Body Odours Using A Culture-Independent Approach.*Microbiome*. Vol. 3.

Trookman, N. S., Rizer, R. L., Ford, R., Ho, E. And Gotz, V. 2009. Immediate And Long-Term Clinical Benefits Of A Topical Treatment For Facial Lines And Wrinkles. *The Journal Of Clinical And Aesthetic Dermatology* 2(3), Pp. 38-43.

Trussler, R. 2019. A Third Of Millennials Choose Jobs Based On Office Environment. Available At: <u>Https://Www.Freeofficefinder.Com/Article/A-Third-Of-Millennials-Choose-Jobs-Based-On-Office-Environment</u>.

Tuomanen, E. 2005. Microbial Inhabitants Of Humans - Their Ecology And Role In Health And Disease. *Science* 308(5722), Pp. 635-635. Doi: 10.1126/Science.1111460

Turner, E. 2021. Why Waterless Beauty Might Just Be The Future Of Cosmetics. *Glamour* 2021-07-23. Available At: <u>Https://Www.Glamourmagazine.Co.Uk/Gallery/Waterless-Beauty</u>

Uhlig, R. 2003. No One Wants To Be A Farmer Any More. *The Telegraph* 2003-02-18. Available At: <u>Https://Www.Telegraph.Co.Uk/Education/3308323/No-One-Wants-To-Be-A-Farmer-Any-More.Html</u>

Uttatree, S. And Charoenpanich, J. 2018. Purification And Characterization Of A Harsh Conditions-Resistant Protease From A New Strain Of Staphylococcus Saprophyticus. *Agriculture And Natural Resources* 52(1), Pp. 16-23. Doi: <u>Https://Doi.Org/10.1016/J.Anres.2018.05.001</u>

Vaishnavi, K. V., Safar, L. And Devi, K. 2019. Biofilm In Dermatology. *Journal Of Skin And Sexually Transmitted Diseases* 1(1), Pp. 3-7. Doi: 10.25259/Jsstd\_14\_2019

Valente, L. G. Et Al. 2021. Isolation And Characterization Of Bacteriophages From The Human Skin Microbiome That Infect Staphylococcus Epidermidis. *Fems Microbes* 2, Doi: 10.1093/Femsmc/Xtab003

Van Der Krieken, D. Et Al. 2016. An In Vitro Model For Bacterial Growth On Human Stratum Corneum. *Acta Derm Venereo* 96(7), Doi: Doi:10.2340/00015555-2401

Van Der Weyden, L., Patton, E. E., Wood, G. A., Foote, A. K., Brenn, T., Arends, M. J. And Adams, D. J. 2016. Cross-Species Models Of Human Melanoma. *J Pathol* 238(2), Pp. 152-165. Doi: 10.1002/Path.4632

Van Horn, K. G., Audette, C. D., Tucker, K. A. And Sebeck, D. 2008. Comparison Of 3 Swab Transport Systems For Direct Release And Recovery Of Aerobic And Anaerobic Bacteria. *Diagnostic Microbiology And Infectious Disease* 62(4), Pp. 471-473. Doi: <u>Https://Doi.Org/10.1016/J.Diagmicrobio.2008.08.004</u>

Van Ravenzwaay, B. And Leibold, E. 2004. A Comparison Between In Vitro Rat And Human And In Vivo Rat Skin Absorption Studies. *Human & Experimental Toxicology* 23(9), Doi: 10.1191/0960327104ht471oa

Vandegrift, R. Et Al. 2017. Cleanliness In Context: Reconciling Hygiene With A Modern Microbial Perspective. *Microbiome* 5(1), P. 76. Doi: 10.1186/S40168-017-0294-2

Vanderlelie, H. Et Al. 1995. Corynebacterium Cdc Group Jk (Corynebacterium Jeikeium) Sepsis In Haematological Patients: A Report Of Three Cases And A Systematic Literature Review. *Scandinavian Journal Of Infectious Diseases* 27(6), Pp. 581-584. Doi: 10.3109/00365549509047071

Vapniarsky, N., Arzi, B., Hu, J. C., Nolta, J. A. And Athanasiou, K. A. 2015. Concise Review: Human Dermis As An Autologous Source Of Stem Cells For Tissue Engineering And Regenerative Medicine.*Stem Cells Transl Med*. Vol. 4. Pp. 1187-1198.

Vargas, C. 2016. *Organic Acids : Characteristics, Properties And Synthesis*. Hauppauge, New York: Nova Science Publishers, Inc.

Varvaresou, A., Papageorgiou, S., Tsirivas, E., Protopapa, E., Kintziou, H., Kefala, V. And Demetzos, C. 2009. Self-Preserving Cosmetics. *International Journal Of Cosmetic Science* 31(3), Doi: 10.1111/J.1468-2494.2009.00492.X

Vary, J. C. 2015. Selected Disorders Of Skin Appendages-Acne, Alopecia, Hyperhidrosis. *Medical Clinics Of North America* 99(6), Pp. 1195-+. Doi: 10.1016/J.Mcna.2015.07.003

Ventosa, A., Nieto, J. J. And Oren, A. 1998. Biology Of Moderately Halophilic Aerobic Bacteria. *Microbiol Mol Biol Rev* 62(2), Pp. 504-544.

Vergis, J., Gokulakrishnan, P., Agarwal, R. And Kumar, A. 2015. Essential Oils As Natural Food Antimicrobial Agents: A Review. *Critical Reviews In Food Science And Nutrition* 55(10), Doi: 10.1080/10408398.2012.692127

Verzeaux, L. 2021. Focus On Enzymatic Hydrolysis. In: Silab Ed.

Vilček, J., Le, J. And Delves, P. J. 1998. Interferon F.*Encyclopedia Of Immunology (Second Edition)*. Oxford: Elsevier, Pp. 1421-1426.

Virto, R., Mañas, P., Alvarez, I., Condon, S. And Raso, J. 2005. Membrane Damage And Microbial Inactivation By Chlorine In The Absence And Presence Of A Chlorine-Demanding Substrate. *Applied And Environmental Microbiology* 71(9), Pp. 5022-5028. Doi: 10.1128/Aem.71.9.5022-5028.2005

Vylkova, S. 2017. Environmental Ph Modulation By Pathogenic Fungi As A Strategy To Conquer The Host. *Plos Pathog* 13(2), Doi: 10.1371/Journal.Ppat.1006149

Wainwright, M. 1997. Extreme Pleomorphism And The Bacterial Life Cycle: A Forgotten Controversy. *Perspectives In Biology And Medicine* 40(3), Pp. 407-414. Doi: 10.1353/Pbm.1997.0038

Walker, A. P. Et Al. 1996. Test Guidelines For Assessment Of Skin Compatibility Of Cosmetic Finished Products In Man. Task Force Of Colipa. (0278-6915 (Print)),

Walker, J. R. And Altman, E. 2005. Biotinylation Facilitates The Uptake Of Large Peptides By Escherichia Coli And Other Gram-Negative Bacteria. *Applied And Environmental Microbiology* 71(4), Pp. 1850-1855. Doi: 10.1128/Aem.71.4.1850-1855.2005

Wallen Russell, K. 2018. The Role Of Every-Day Cosmetics In Altering The Skin Microbiome: A Study Using Biodiversity.

Walsh, D. J., Livinghouse, T., Goeres, D. M., Mettler, M. And Stewart, P. S. 2019. Antimicrobial Activity Of Naturally Occurring Phenols And Derivatives Against Biofilm And Planktonic Bacteria. *Frontiers In Chemistry* 7, Pp. 653-653. Doi: 10.3389/Fchem.2019.00653

Walsh, S. E., Maillard, J. Y., Russell, A. D., Catrenich, C. E., Charbonneau, D. L. And Bartolo, R. G. 2003. Activity And Mechanisms Of Action Of Selected Biocidal Agents On Gram-Positive And - Negative Bacteria. *Journal Of Applied Microbiology* 94(2), Pp. 240-247. Doi: <u>Https://Doi.Org/10.1046/J.1365-2672.2003.01825.X</u>

Wandersman, C. 1989. Secretion, Processing And Activation Of Bacterial Extracellular Proteases. *Molecular Microbiology* 3(12), Pp. 1825-1831. Doi: <u>Https://Doi.Org/10.1111/J.1365-</u> 2958.1989.Tb00169.X

Wang, H., Chan, H. H., Ni, M. Y., Lam, W. W., Chan, W. M. M. And Pang, H. 2020. Bacteriophage Of The Skin Microbiome In Patients With Psoriasis And Healthy Family Controls. *Journal Of* 

*Investigative Dermatology* 140(1), Pp. 182-190.E185. Doi: <u>Https://Doi.Org/10.1016/J.Jid.2019.05.023</u>

Wang, J. Et Al. 2018a. In Vitro Antibacterial Activity And Mechanism Of Monocaprylin Against Escherichia Coli And Staphylococcus Aureus. *Journal Of Food Protection* 81(12), Pp. 1988-1996. Doi: 10.4315/0362-028x.Jfp-18-248

Wang, Q., Cui, S., Zhou, L., He, K., Song, L., Liang, H. And He, C. 2019. Effect Of Cosmetic Chemical Preservatives On Resident Flora Isolated From Healthy Facial Skin. *Journal Of Cosmetic Dermatology* 18(2), Doi: 10.1111/Jocd.12822

Wang, X., Koffi, P. F., English, O. F. And Lee, J. C. 2021. Staphylococcus Aureus Extracellular Vesicles: A Story Of Toxicity And The Stress Of 2020. *Toxins (Basel)* 13(2), Doi: 10.3390/Toxins13020075

Wang, X. And Lin, Y. 2008. Tumor Necrosis Factor And Cancer, Buddies Or Foes? *Acta Pharmacologica Sinica* 29(11), Pp. 1275-1288. Doi: 10.1111/J.1745-7254.2008.00889.X

Wang, Z. Et Al. 2018b. Comparison Of Fecal Collection Methods For Microbiome And Metabolomics Studies. *Front Cell Infect Microbiol* 8, Doi: 10.3389/Fcimb.2018.00301

Warming, M., Lassen, C. And Christensen, F. 2018. *Survey Of Cosmetic Products With "Probiotic" Or "Prebiotic" Claims*. Denmark:

Wassilew, S. 1989. Infections Of The Skin Caused By Gram-Negative Pathogens. Foot Infections--Wound Infections--Folliculitis. *Zeitschrift Fur Hautkrankheiten* 64(1),

Wawrik, B., Kerkhof, L., Kukor, J. And Zylstra, G. 2005. Effect Of Different Carbon Sources On Community Composition Of Bacterial Enrichments From Soil. *Applied And Environmental Microbiology* 71(11), Pp. 6776-6783. Doi: 10.1128/Aem.71.11.6776-6783.2005

Wei, S., Low, S. W., Poore, C. P., Chen, B., Gao, Y., Nilius, B. And Liao, P. 2020. Comparison Of Anti-Oncotic Effect Of Trpm4 Blocking Antibody In Neuron, Astrocyte And Vascular Endothelial Cell Under Hypoxia. *Frontiers In Cell And Developmental Biology* 8, P. 1175.

Weide, S. 2003. A New Bacteria Medium With Sericin Protein As Main Components. . Chemistry,

Weir, R. Et Al. 2008. Comparison Of Ifn-Gamma Responses To Mycobacterial Antigens As Markers Of Response To Bcg Vaccination. *Tuberculosis (Edinburgh, Scotland)* 88(1), Doi: 10.1016/J.Tube.2007.10.001

Welch, K., Cai, Y. And Strømme, M. 2012. A Method For Quantitative Determination Of Biofilm Viability. (2079-4983 (Print)),

Wertheim, H. F., Melles, D. C., Vos, M. C., Van Leeuwen, W., Van Belkum, A., Verbrugh, H. A. And Nouwen, J. L. 2005. The Role Of Nasal Carriage In Staphylococcus Aureus Infections. *The Lancet Infectious Diseases* 5(12), Pp. 751-762. Doi: 10.1016/S1473-3099(05)70295-4

Wetzels, S. U., Strachan, C. R., Conrady, B., Wagner, M., Burgener, I. A., Virányi, Z. And Selberherr, E. 2021. Wolves, Dogs And Humans In Regular Contact Can Mutually Impact Each Other's Skin Microbiota. *Scientific Reports* 11(1), P. 17106. Doi: 10.1038/S41598-021-96160-7

Weyrich, L. S. Et Al. 2019. Laboratory Contamination Over Time During Low-Biomass Sample Analysis. *Molecular Ecology Resources* 19(4), Pp. 982-996. Doi: <u>Https://Doi.Org/10.1111/1755-0998.13011</u>

White, T. C. Et Al. 2014. Fungi On The Skin: Dermatophytes And Malassezia. *Cold Spring Harbor Perspectives In Medicine* 4(8), P. A019802. Doi: 10.1101/Cshperspect.A019802

Who. 2009. Normal Bacterial Flora On Hands. *Who Guidelines On Hand Hygiene In Health Care*. Geneva: World Health Organization.

Williams, R., Urquhart, N. And Roden, K. 2018. Preservatives Used In Personal Care Products. *Australian Society Of Cosmetic Chemists*,

Willis, A. D. 2019. Rarefaction, Alpha Diversity, And Statistics. Frontiers In Microbiology 10,

Wilson, M. 2004. *Microbial Inhabitants Of Humans : Their Ecology And Role In Health And Disease*. Cambridge: Cambridge University Press.

Wilson, T. H. And Ding, P. Z. 2001. Sodium-Substrate Cotransport In Bacteria. *Biochimica Et Biophysica Acta (Bba) - Bioenergetics* 1505(1), Pp. 121-130. Doi: <u>Https://Doi.Org/10.1016/S0005-2728(00)00282-6</u>

Wishart, D. Et Al. 2015. A Comprehensive Resource For In Silico Drug Discovery And Exploration: Phenoxyethanol. Drugbank.

Wistreich, G. And Lechtman, M. 1988. Bacterial Growth And Cultivation Techniques. *Microbiology*. New York: Macmillan.

Wong, R., Geyer, S., Weninger, W. And Guimberteau, J.-C., Wong, J. 2015. The Dynamic Anatomy And Patterning Of Skin. *Experimental Dermatology* 25, Pp. 92-98. Doi: 10.1111/Exd.12832

Wu, L. Et Al. 2020a. Alphaherpesvirus Major Tegument Protein Vp22: Its Precise Function In The Viral Life Cycle. *Frontiers In Microbiology* 11,

Wu, L. Et Al. 2020b. Age-Related Variation Of Bacterial And Fungal Communities In Different Body Habitats Across The Young, Elderly, And Centenarians In Sardinia. *American Society For Microbiology Journals* 5(1), Doi: 10.1128/Msphere.00558-19 Xue, R. Et Al. 2016. Shape Changes And Interaction Mechanism Of Escherichia Coli Cells Treated With Sericin And Use Of A Sericin-Based Hydrogel For Wound Healing. *Applied And Environmental Microbiology* 82(15), Pp. 4663-4672. Doi: 10.1128/Aem.00643-16

Yang, S. Et Al. 2001. Micrococcus Luteus Teichuronic Acids Activate Human And Murine Monocytic Cells In A Cd14- And Toll-Like Receptor 4-Dependent Manner. *Infect Immun* 69(4), Pp. 2025-2030. Doi: 10.1128/Iai.69.4.2025-2030.2001

Yang, S., Wang, J., Brand, D. D. And Zheng, S. G. 2018. Role Of Tnf–Tnf Receptor 2 Signal In Regulatory T Cells And Its Therapeutic Implications. *Frontiers In Immunology* 9, P. 784.

Yarwood, J. M., Bartels, D. J., Volper, E. M. And Greenberg, E. P. 2004. Quorum Sensing In Staphylococcus Aureus Biofilms. *Journal Of Bacteriology* 186(6), Pp. 1838-1850. Doi: 10.1128/Jb.186.6.1838-1850.2004

Ying, S. Et Al. 2015. The Influence Of Age And Gender On Skin-Associated Microbial Communities In Urban And Rural Human Populations.*Plos One*. Vol. 10.

Yoshioka, S. And Newell, P. D. 2016. Disruption Of De Novo Purine Biosynthesis In Pseudomonas Fluorescens Pf0-1 Leads To Reduced Biofilm Formation And A Reduction In Cell Size Of Surface-Attached But Not Planktonic Cells. *Peerj* 4, P. E1543. Doi: 10.7717/Peerj.1543

Young, J.-A., H., Weisdorf, D. J., Bennett, J. E., Dolin, R. And Blaser, M. J. 2015. Infections In Recipients Of Hematopoietic Stem Cell Transplants.*Mandell, Douglas, And Bennett's Principles And Practice Of Infectious* 

Diseases 8ed. Philadelphia: Content Repository Only.

Younge, N. E., Araújo-Pérez, F., Brandon, D. And Seed, P. C. 2018. Early-Life Skin Microbiota In Hospitalized Preterm And Full-Term Infants. *Microbiome* 6(1), Pp. 1-11. Doi: Doi:10.1186/S40168-018-0486-4

Yousef, H., Alhajj, M. And Sharma, S. 2020. Anatomy, Skin (Integument), Epidermis. Doi: <u>Https://Www.Ncbi.Nlm.Nih.Gov/Books/Nbk470464/</u>

Yu, M., Finner, A., Shapiro, J., Lo, B., Barekatain, A. And Mcelwee, K. J. 2014. Hair Follicles And Their Role In Skin Health. <u>*Http://Dx.Doi.Org/10.1586/17469872.1.6.855*</u>, Doi: 10.1586/17469872.1.6.855

Yu, M., Guo, F., Ling, Y., Li, N. And Tan, F. 2015. Topical Skin Targeting Effect Of Penetration Modifiers On Hairless Mouse Skin, Pig Abdominal Skin And Pig Ear Skin. *Drug Delivery* 22(8), Doi: 10.3109/10717544.2013.869276

Zapata, H. And Quagliarello, V. 2015. The Microbiota And Microbiome In Aging: Potential Implications In Health And Age-Related Diseases. *American Geriatrics Society* 63(4), Doi: 10.1111/Jgs.13310

Zeeuwen, P. L. J. M. Et Al. 2012. Microbiome Dynamics Of Human Epidermis Following Skin Barrier Disruption. *Genome Biology* 13(11), Pp. R101-R101. Doi: 10.1186/Gb-2012-13-11-R101

Zhang, Y. Q. Et Al. 2003. Genome-Based Analysis Of Virulence Genes In A Non-Biofilm-Forming Staphylococcus Epidermidis Strain (Atcc 12228). *Mol Microbiol* 49(6), Pp. 1577-1593. Doi: 10.1046/J.1365-2958.2003.03671.X

Zhou, H., Shi, L., Ren, Y., Tan, X., Liu, W. And Liu, Z. 2020. Applications Of Human Skin Microbiota In The Cutaneous Disorders For Ecology-Based Therapy. *Frontiers In Cellular And Infection Microbiology* 10,

Zhou, H. Et Al. 2010. Preparation And Characterization Of A Lecithin Nanoemulsion As A Topical Delivery System. *Nanoscale Res Lett*. Vol. 5. Pp. 224-230.

Zhu, M., Cheng, C., Yi, H., Lin, L. And Wu, K. 2018. Quantitative Analysis Of The Bacteria In Blepharitis With Demodex Infestation. *Frontiers In Microbiology* 9, P. 1719.

Zhu, T. Et Al. 2019. Age And Mothers: Potent Influences Of Children's Skin Microbiota. *The Journal Of Investigative Dermatology* 139(12), Doi: 10.1016/J.Jid.2019.05.018

Zhu, Y., Weiss, E. C., Otto, M., Fey, P. D., Smeltzer, M. S. And Somerville, G. A. 2007. Staphylococcus Aureus Biofilm Metabolism And The Influence Of Arginine On Polysaccharide Intercellular Adhesin Synthesis, Biofilm Formation, And Pathogenesis. *Infection And Immunity* 75(9), Pp. 4219-4226. Doi: 10.1128/Iai.00509-07

Ziebuhr, W., Hennig, S., Eckart, M., Kränzler, H., Batzilla, C. And Kozitskaya, S. 2006. Nosocomial Infections By Staphylococcus Epidermidis: How A Commensal Bacterium Turns Into A Pathogen. *International Journal Of Antimicrobial Agents* 28, Pp. 14-20. Doi: Https://Doi.Org/10.1016/J.Ijantimicag.2006.05.012

Ziegler, U. And Groscurth, P. 2004. Morphological Features Of Cell Death. <u>*Https://Doi.Org/10.1152/Nips.01519.2004*</u> 19(3), Doi: 10.1152/Nips.01519.2004

Zomer, H. And Trentin, A. 2018. Skin Wound Healing In Humans And Mice: Challenges In Translational Research. *Journal Of Dermatological Science* 90(1), Doi: 10.1016/J.Jdermsci.2017.12.009

Zumstein, R. 1936. Fungus Growth As Affected By Varying Concentrationsof Salts. Proceedings Of The Indiana Academy Of Science.

Zwahlen, R., Walz, A., Rot, A., Richter, G. W. And Solez, K. 1993. In Vitro And In Vivo Activity And Pathophysiology Of Human Interleukin-8 And Related Peptides.*International Review Of Experimental Pathology*. Vol. 34. Academic Press, Pp. 27-42.

Zwietering, M., Jongenburger, I., Rombouts, F. And Van 'T Riet, K. 1990. Modeling Of The Bacterial Growth Curve. *Applied And Environmental Microbiology* 56(6), Pp. 1875-1881.

## 10 Appendix

The following appendix is regarding Section 3 and 7. It contains the statistical information of the minimum inhibitory concentration from Section 3.21. It also contains the complete taxa trees for all samples, the complete list of abundance of OTUs per sample and signed consent forms from Section 7.

## Appendix Contents

Appendix	xiv
MIC Tables	xv
Consent Forms	xvi
Taxonomic Trees	xviii
OTUs Abundance of all Samples	ххх

# 10.1MICTable 16 A, B and C. Minimum Inhibitory Concentration Tables for A) Staphylococcus<br/>aureus B) Staphylococcus epidermidis and C) Corynebacterium jeikeium

Α	Protein		Ik Prot Preser odium b disodiu	vatives enzoate +		Hydroavena HPO Preservatives (0.5% sodium benzoate + 0.3% potassium sorbate)					Irolacti Preser ohenoxye disodiu	vatives thanol +		(1%)	ydrosa Preser phenoxye potassiun	vatives thanol +	0.3%	(1%)	ydrosol Preser ohenoxye assium so disodiur	vatives thanol + orbate + (	0.3%	Prolevium Preservatives (1% phenoxyethanol + 0.3% potassium sorbate + 0.2% disodium EDTA)			
	Active level Min Inhibition Max Mean SD Inhibition SD			Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition			Mean SD inhibition		Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD		
	4%	99.3	100	99.7	0.33	92.5	93.6	93.2	0.51	88.9	99.6	70.5	5.36	13.4	25.1	18.6	5.96	62.3	67.7	64.6	2.80	60.7	69.6	64.9	4.48
	2%	89.4	91.4	90.3	0.88	57.7	62.7	59.4	2.28	64.6	80.2	19.3	8.44	12.5	20.0	15.2	4.19	18.4	23.4	20.8	2.51	17.6	25.7	21.6	4.05
	1%	39.7	45.4	43.5	2.60	19.1	21.2	20.2	0.93	13.5	28.0	16.3	7.65	10.5	17.0	12.9	3.54	15.7	20.4	18.1	2.35	16.5	20.1	18.2	1.82
	0.5%	13.0	17.4	15.2	2.13	12.1	13.0	12.5	0.43	12.9	22.9	14.3	5.72	7.40	15.8	11.0	4.34	10.4	18.0	15.0	4.05	11.3	18.9	14.9	3.81
	0.25%	8.04	12.9	10.6	2.12	9.83	10.1	10.0	0.13	11.6	19.2	11.4	4.23	4.40	13.5	8.93	4.55	7.9	14.5	11.8	3.48	8.9	15.8	12.9	3.58
	0.125%	3.88	7.85	3.97	6.26	7.22	8.25	7.50	0.50	9.82	14.4	6.30	2.59	1.90	10.2	5.70	4.19	5.80	10.8	8.40	2.51	5.9	9.7	7.8	1.90
	0.0625%	2.47	4.54	2.07	3.68	3.53	5.45	4.29	0.90	0.00	0.00	0.00	0.00	0.00	5.20	2.37	2.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Protein	Protein Croslik Protein Complex Preservatives (0.5% sodium benzoate + 0.01% disodium EDTA)						ena HP vatives enzoate n sorbate	+ 0.3%		phenoxye	vatives		(1%)	ydrosa Preser phenoxye potassiun	vatives thanol +	0.3%	(1%)	Preser	anum I vatives thanol + orbate + 0 m EDTA)	0.3%	Prolevium Preservatives (1% phenoxyethanol + 0.3% potassium sorbate + 0.2% disodium EDTA)			
Active level	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD
4%	100	100	100	0.00	97.7	99.1	98.3	0.62	97.4	98.3	97.7	0.50	20.5	23.3	21.6	1.50	93.9	95.6	94.7	0.84	93.5	95.9	94.3	1.39
2%	95.7	100	97.6	2.08	61.5	65.3	62.9	1.63	34.1	51.0	42.5	8.41	11.6	13.2	12.5	0.86	38.3	49.6	44.7	5.81	44.2	50.1	47.4	2.97
1%	42.3	52.1	46.3	4.16	15.0	18.3	16.9	1.42	21.4	28.8	25.3	3.72	8.34	12.3	10.4	1.97	13.9	20.4	17.8	3.48	18.7	22.2	19.9	2.03
0.5%	10.8	14.5	12.7	1.54	7.83	11.5	9.38	1.62	12.7	19.1	16.7	3.46	6.22	11.4	8.88	2.57	1.72	15.2	9.19	6.87	5.55	9.88	7.32	2.27
0.25%	3.31	6.10	4.56	1.16	3.80	5.71	4.77	0.78	11.8	15.4	13.9	1.90	4.43	10.8	8.06	3.28	0.00	9.47	3.16	5.47	1.45	4.78	3.29	1.69
0.125%	1.01	3.97	2.60	1.38	2.34	4.08	1.74	0.81	10.1	12.8	11.5	1.38	3.60	10.4	6.40	3.56	0.00	7.86	2.62	4.54	0.75	2.43	1.43	0.88
0.0625%	0.00	2.71	1.23	1.24	0.68	1.54	1.03	0.40	7.59	9.43	8.27	1.01	2.15	9.48	5.29	3.78	0.00	6.45	2.15	3.73	0.00	0.00	0.00	0.00

В

С	Protein	n Crosilk Protein Complex Preservatives (0.5% sodium benzoate + 0.01% disodium EDTA)					ydroav Preser sodium I potassiur	vatives	+ 0.3%		rolacti Preser phenoxye disodiu	vatives thanol +		(1%	lydrosa Preser phenoxye potassiur	vatives ethanol +	0.3%	(1%	phenoxye assium so	vatives ethanol +	0.3%	Prolevium Preservatives (1% phenoxyethanol + 0.3% potassium sorbate + 0.2% disodium EDTA)			
	Active level	Min Max Mean SD inhibition				Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD	Min inhibition	Max inhibition	Mean inhibition	SD
	4%	84.0	89.9	86.3	3.13	85.3	90.7	87.4	2.90	64.4	70.6	67.3	2.83	68.2	71.4	69.9	1.38	46.1	62.8	55.6	8.57	30.5	40.4	34.2	5.54
	2%	37.7	44.7	41.4	3.5	43.2	50.8	46.4	3.95	39.9	66.8	48.3	12.4	31.6	46.2	42.2	7.12	39.2	57.1	45.3	10.2	29.2	31.6	30.4	1.22
	1%	21.9	42.1	31.0	10.3	35.6	45.4	39.7	5.11	36.7	42.3	39.5	2.37	31.1	44.7	41.0	6.56	33.0	52.8	41.2	10.4	18.6	23.0	21.2	2.27
	0.5%	18.3	36.5	27.6	9.11	28.2	39.1	33.8	5.47	29.9	38.3	34.1	3.46	11.1	41.5	32.7	14.5	31.5	37.7	34.3	3.17	17.8	20.2	19.4	1.39
	0.25%	16.0	31.1	22.5	7.80	25.1	30.1	27.1	2.68	28.7	37.8	31.6	4.16	8.33	20.7	12.8	5.50	23.0	35.3	28.4	6.27	14.9	17.4	16.1	1.26
	0.125%	7.08	9.93	8.74	1.48	11.8	17.5	14.3	2.87	22.7	29.3	27.0	2.98	2.91	7.57	5.3	2.29	14.1	21.0	17.4	3.50	11.7	15.5	13.3	2.02
	0.0625%	0.00	4.81	2.28	2.41	6.11	9.69	7.96	1.79	11.1	22.7	15.2	5.37	0.35	2.97	1.56	1.15	4.63	19.3	12.2	7.34	3.15	7.90	5.91	2.45

<sup>14</sup> The red numbers indicate where the minimum inhibitory concentration had been achieved

### 10.2 Consent Forms



#### CONSENT FORM

Title of research project: Chapter in PhD Thesis Microbial Communities of Different Swab Sites

Name of Chief/Principal Investigator:	
Supervisor: Julian Marchesi	Please
PhD Candidate: Hannah Salvage	initial box

I confirm that I have understand how the research will be undertaken and how I need to HS participate.

I confirm that I have understood the information provided for the above research project HS and that I have had the opportunity to ask questions and that these have been answered satisfactorily.

I understand that my participation is voluntary, and I am free to withdraw at any time HS without giving a reason and without any adverse consequences (e.g. to medical care or legal rights, if relevant). I understand that if I withdraw, information about me that has already been obtained may be kept by Cardiff University.

I understand who will have access to personal information that I will have provided, how the data willbe stored and what will happen to the data at the end of the research project.

 [IF RELEVANT] I understand that after the research project, anonymized data may be made publicly available via a data repository and may be used for purposes not related to this research project. I understand that it will not be possible to identify me from this data that is seen and used by other researchers, for ethically approved research projects, on the understanding that confidentiality will be maintained.
 HS

 [IF RELEVANT] I consent to being audio recorded/ video recorded/ having my
 N/A

photograph taken for the purposes of the research project and I understand how it will be used in the research.

[IF RELEVANT] I understand that anonymized excerpts and/or verbatim quotes from HS my [INTERVIEW/QUESTIONNAIRE ETC] may be used as part of the research publication.

I understand how the findings and results of the research project will be written up and published.

I agree to take part in this research project.



PhD Candidate Role of person taking consent (print)

THANK YOU FOR PARTICIPATING IN OUR RESEARCH

## Figure 48. Copy of Consent Form for the Female Participant

Version xx

HS



#### CONSENT FORM

Title of research project: Chapter in PhD Thesis Microbial Communities of Different Swab Sites

Name of Chief/Principal Investigator:

Supervisor: Julian Marchesi	
PhD Candidate: Hannah Salvage	

Please initial box

I confirm that I have understand how the research will be undertaken and how I need to participate.	DT
I confirm that I have understood the information provided for the above research project and thatI have had the opportunity to ask questions and that these have been answered satisfactorily.	DT
I understand that my participation is voluntary, and I am free to withdraw at any time without giving a reason and without any adverse consequences (e.g. to medical care or legal rights, if relevant). I understand that if I withdraw, information about me that has already been obtained may be kept by Cardiff University.	DT
I understand who will have access to personal information that I will have provided, how the data willbe stored and what will happen to the data at the end of the research project.	DT
[IF RELEVANT] I understand that after the research project, anonymized data may be made publicly available via a data repository and may be used for purposes not related to this research project. I understand that it will not be possible to identify me from this data that is seen and used by other researchers, for ethically approved research projects, on the understanding that confidentiality will be maintained.	DT
[IF RELEVANT] I consent to being audio recorded/ video recorded/ having my photograph taken for the purposes of the research project and I understand how it will be used in the research.	N/A
[IF RELEVANT] I understand that anonymized excerpts and/or verbatim quotes from my [INTERVIEW/QUESTIONNAIRE ETC] may be used as part of the research publication.	DT
I understand how the findings and results of the research project will be written up and published.	DT
I agree to take part in this research project.	DT



PhD Candidate Role of person taking consent (print)

THANK YOU FOR PARTICIPATING IN OUR RESEARCH

Figure 49. Copy of Consent Form for the Male Participant

### 10.3Taxonomic Trees

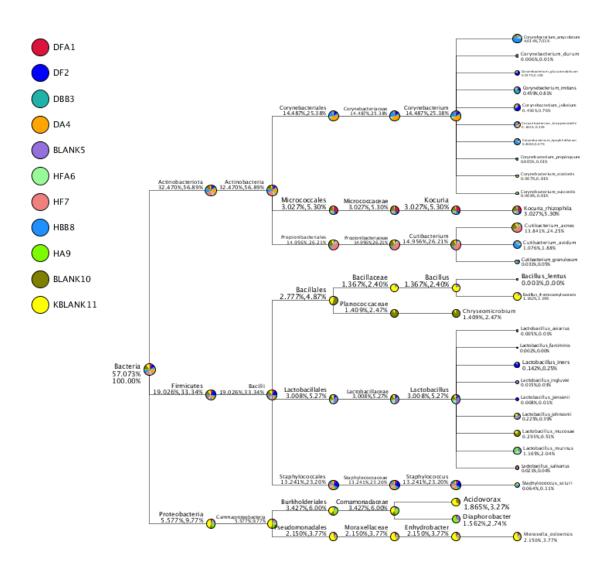


Figure 50. Taxa Tree of all Samples.

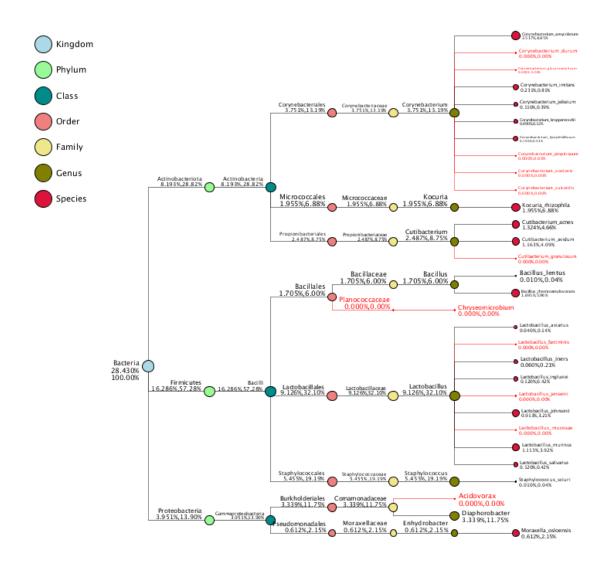


Figure 51. Taxa Tree for the Male Blank Swab Control.

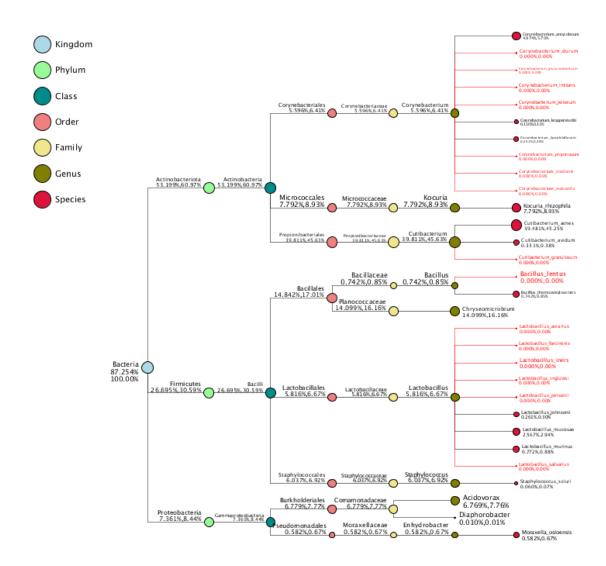


Figure 52. Taxa Tree for the Female Blank Swab Control.

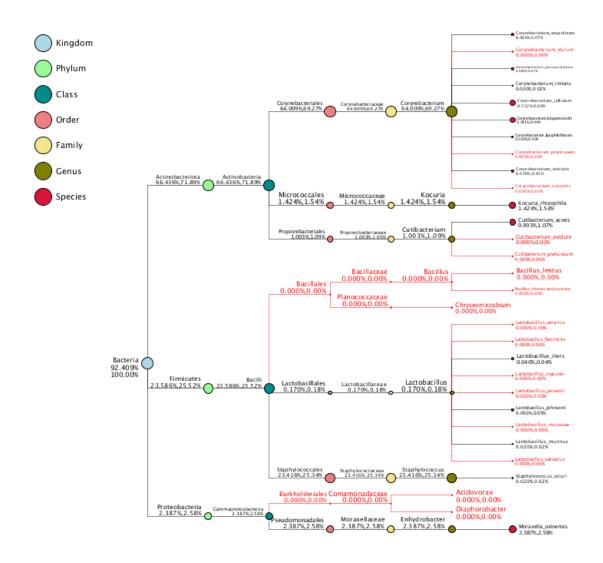


Figure 53 Taxa Tree for the Male Axilla Sample.

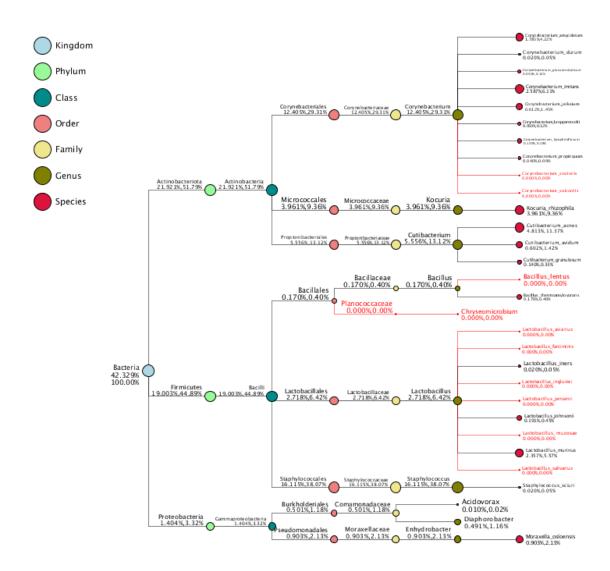


Figure 54. Taxa Tree for the Male Navel Sample.

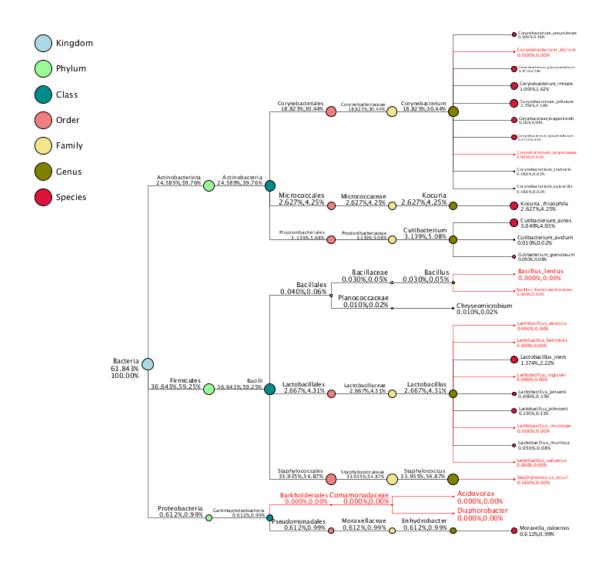


Figure 55. Taxa Tree for the Male Forehead Sample.

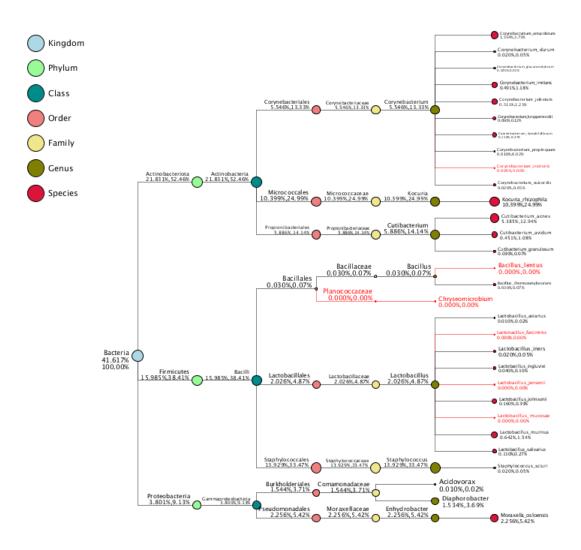


Figure 56. Taxa Tree for the Male Forearm.

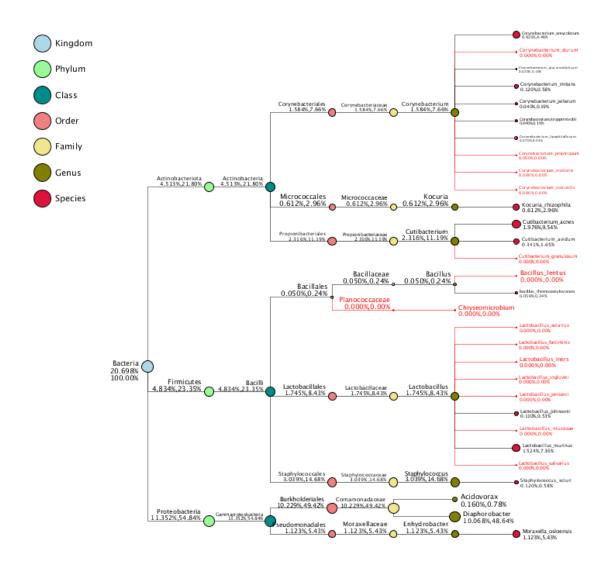


Figure 57. Taxa Tree for the Female axilla.

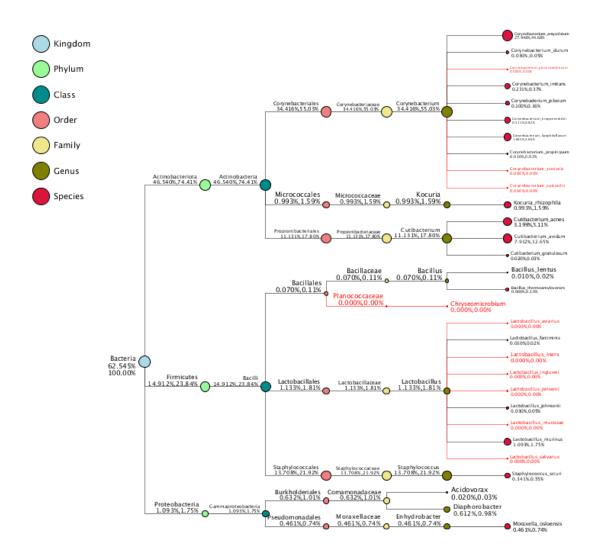


Figure 58. Taxa Tree for the Female Navel.

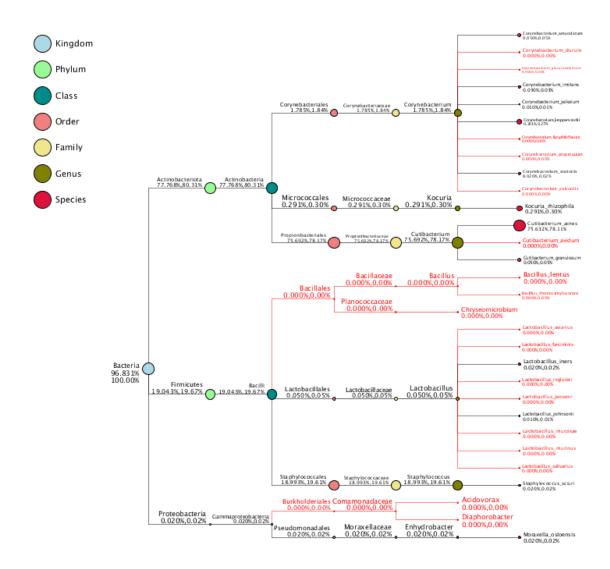


Figure 59. Taxa Tree for the Female Forehead.

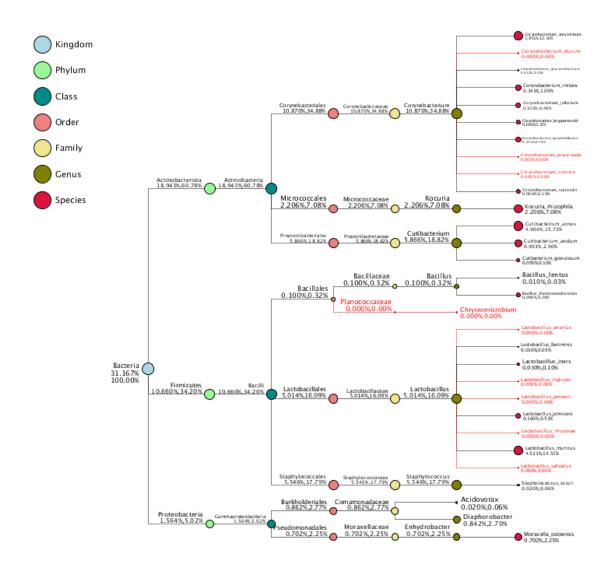


Figure 60. Taxa Tree for the Female Forearm.

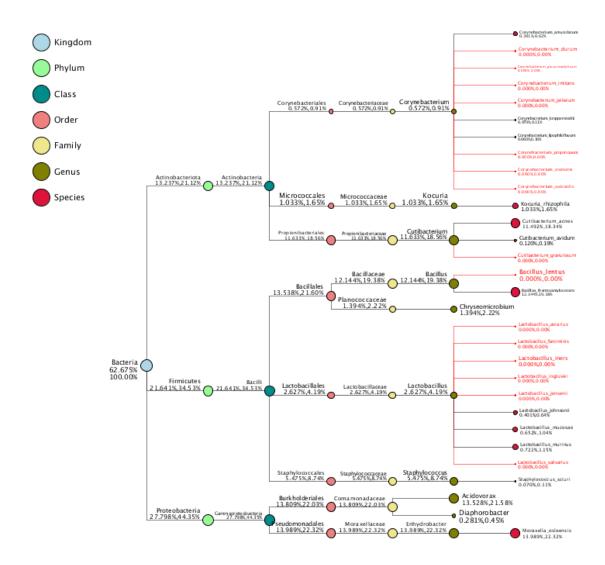


Figure 61. Taxa Tree for the Kit Blank Control.

## 10.4 OTUs Abundance of All Samples

Table 20.

											_
F	orearm	orehead		Axilla	Blank	Forearm			Axilla	Blank Ki	A Contraction of the second
	61555 1879	81474 1204	32735	83488 611	14802 805	22958	92063 641	34470 1539	64942 1405	235	10118 Total Male 106 Unqu/Female
	59661	80151	31978	82875	13997	21759	91099	32931	63536	16642	9972 Taxa Kt Blank
OTU#	15	119	6	2	0	0	323	0	0	323	0 Unclas Taxonomy
1	3215	2436 1705	1540 39	821 51307	186	1057	69149 38	1056 75	1255	6696 0	1146 k_Bacterize_Actinobacteriotoc_Actinobacterize_Propionibacterialest_Propionibacteriaceaeg_Cutibacteriums_Cutibacterism_acres 0 k facterize Actinobacteriotac Actinobacterize Commebacterizest Commebacterizeaeg Commebacterize
3	8255	27191	5129	19314	752	1186	17120	4370	1818	1015	536 k_Bacteria;p_Firmicutes;c_Bacili;o_Staphylococcales;f_Staphylococcace;g_Staphylococcus
4	929	88	570	50	353	840	55	9203	590	842	40 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Conynebacteriales;f_Conynebacteriaceac;g_Corynebacterium;s_Conynebacterium;amycolatum
5	77	12313 2116	30	326 1177	404	30 481	0	20	35	0	0 k_Bacterizp_Proteobacterizp_Gammaproteobacterizp_Bankholderialest_Neisseriaceaeg_sz_ 103 k_Bacterizp_Actinobacteriotzg_Actinobacterizp_Microaccadest_Microaccaceaeg_Kosurizy_Kosurizy/hitophila
7	6205 1293	3347	1267 1574	437	274 249	412	275	329 558	386 442	0	Ios «_inacteria;pacumulaterina;cacumulateria;pwienacuma;owienocutatura;gAtteria;cAtteria_miziopina 0 k_Bacteria;pirmicutes:c_Clostrida:oPeptostreptococcales-Tissierellale;;f_Peptostreptococcales-Tissierellale;;g_Finepoldia
8	986	0	136	0	126	215	0	186	5442	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderia!csf_N/calige naceae;g_Parapusillimonas
9	917	0	160	0	468	184	0	203	6397	3	$28 \ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Burkholderia!es; f\_Comamonadaceae; g\_Diaphorobacteria; f\_Comamonadaceae; d\_Diaphorobacteria; f\_Comamonadaceae; d\_Diaphoro$
10	1372 1349	0 499	147 288	0 2979	63 87	174	0	123	4434 711	1	0 k_Bacteriap_Protecbacteria;c_Gammaproteobacteria;o_Barkholderiales/_Comamonadaceaeg_Comamonas;c_Comamonas; _contamonas; _denitrificars 1392 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceaeg_Enhydrobacteris_Moraxella osloensis
12	1567	0	267	0	149	276	4	247	4258	0	U k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas
13	867	0	512	0	589	737	0	487	880	48	24 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;n_SAR11_clade;f_Clade_III;g_Clade_III;s_
14 15	455 310	5217 2168	187 196	405 448	18 16	38 33	37	26 28	30 25	0	0 k_Bacterixp_Actinobacteriotac_Actinobacteriap_Conynebacterialesg_Conynebacteriaceaeg_Conynebacterium 0 k_Bacteriap_Actinobacteriotac_Actinobacteriap_Conynebacterialesg_Conynebacteriaecaeg_Conynebacterium_Conynebacterium_inkeium
15	385	42	755	21	157	981	3	360	962	130	u K_sacteria,p_acinobaccerora,c_acinobaccerora,c_conynebacceria.es/
17	765	4229	2012	338	47	1153	1215	1180	276	47	$5\ k\_Bacteria;p\_Actinobacteriota;c\_Actinobacteria;o\_Corynebacteriales;f\_Corynebacteriaceae;g\_Corynebacterium$
18	1227	0	53	0	44	96	0	70	1317	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;z_Caulobacterales;f_Caulobacteracea;g_Brevundimonas
19	1860 1462	845	381 100	629 11	70 61	132 173	60 0	115 120	137 1766	23 607	225 k_Bacteriap_Actinobacteriota;c_Actinobacteriapa_Microtoccales;f_Dermacoccauce;c_Dermacoccu;s_Dermacoccu;s_0 637 k_Bacteriap_Protocoacteriacc_Gammaproteobacteriaps_Enterobacteraies;f_Enterobacteriaceae
21	4	10	0	0	D	D	0	3	0	2392	139 k_Bacterla;p_Firmicutes;c_Bacillales;f_Pilanococcaceae;g_Chryseomicrobium;s_
22	294	809	829	21	32	75	15	76	78	0	$0 \ k\_Bacteria; p\_Actinobacteriota; c\_Actinobacteria; p\_Conynebacteriales; f\_Conynebacteriace ac; \underline{u}\_Conynebacterium; \underline{u}\_Conynebacterium \_imitans action acti$
23	427	46	637	1	0	311	0	537	0	0	0 k_Bacteria;p_Protobacteria;c_Gammaprotobacteria;p_Burkholderia]es/_Burkholderia]es/_Raktonia;s_Raktonia;s_Raktotia
24	297	672 642	2 692	21	879	3 159	5	317	1	0	12 k_Bacterizp_Firmicutesc_Bacilico_Lactobacilides;f_Lactobaciliaceaeg_Lactobacilius 0 k_Bacterizp_Firmicutescz_Clostriduzo_Peptonteptoaccales:Tissierelales;f_Peptoareptoaccales:Tissierelales;g_Peptoniphilus_prossensis
26	974	0	47	0	25	61	0	48	699	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderia/csf_Alcaligenaceae;g_Bordetella
27	112	28	759	59	218	92	141	19	21	12	21 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiale;;f_Akkermansiaceae;g_Akkermansia;s_Akkermansia;muciniphila
28	289	181	123	12	47	116 58	0	56 45	1301 1230	0	0 k_Bacterixp_Protechacterizp_Gammaproteobacterizp_Preudomonadales/_Moraxellacrosy_Acinetobactery_Acinetobacter_johnsonii 0 k_Bacterixp_Actinobacteriotxy_Actinobacterizp_Microaccales/_Microaccacrosyg_Microaccasy_Microaccas_Ustrus
30	879	0	633	0	456	761	0	532	913	61	benteringactinobacteriotacactinobacteria;o_Frankialesf_Sporchthyaceae.g_hgd_clade:s
31	38	533	78	20	4	7	856	1	14	o	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Neisseriaceae;g_;s_
32	130 23	0 0	43 24	0	162	39 10	0	54 11	1076 1419	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderia/es/_Alcaigenaceae;g_Castelianielia;a_Castelianielia;defragrams
33	23	0	148	0	4	257	0	170	319	16	0 k_Sacterizp_latexibacterotaz_latexibacterotaz_latexibacterotazf_latexibacterotazg_latexibacterotaz_ 10 k_Bacterizp_Actinobacteriotac_Acidi microbiliz.o_Microbichelesf_llumatobacteriaceaeg_C1500-39_marine_group:s_
35	333 92	1269 16	488	144	70 31	76 59	1	31 35	130 2443	0	0 k_Bacteriap_Firmicutesc_Bacilico_Lactobaciliales;/_Streptococcuraezg_Streptococcus;s_Streptococcus;degalactiae 0 k_Bacteriap_Firmicutesc_Negativozaes.o_Velitoneliales-Selenomonaciales:f_Velitoneliaceae:g_Velitonelia
37	869	95	56	334	57	72	4	62	1110	o	0 k_Bacterla;p_Proteobacterla;c_Alphaproteobacterla;o_Rhodobacterale;;f_Rhodobacteraceae;g_Paracoccus
38	16	1103	7	37	7	8	16	2	1	0	0 k_Bacteria;p_Firmicutes:c_Bacilijo_Lactobaciliales;f_Lactobaciliaceae;g_Lactobacilius;s_Lactobacilius_iners
39 40	195 249	0 2050	96 164	0 58	53 16	86 31	0	82 16	2118 47	0	0 k_Bacteriap_Proteobacteriae_Gammaproteobacteriap_Xanthomenadalesef_Xanthomenadaleser_X_Stenotrophomenasx_Stenotrophomenas_acidaminiphila
40	74	34	516	0	4	265	2	373	176	7	0 k_Bacterizp_Firmicutes;c_Bacilito_Lactobacilide;;t_Streptococcaseagg_Streptococcas 6 k_Bacterizp_Protechacteria;c_Gammaprotechacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas
42	168	349	345	15	30	36	0	18	36	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidia;es;f_Prevotellaceae;g_Prevotella;s_Prevotella;disiens
43	0	83	10	1015	0	2	0	1	3	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacteriale;;f_Rhodobacteriaceaeig_Rubelimicrobium;;r_
44 45	271 89	0 346	172	0 20	149	243	0	152 22	300	25 0	20 k_Bacterizp_Actimobacteriota;c_Actimobacterizo_Frankiales;d_Sporichthyaceaeg_hgd_clades;_Candidatus_Nanopelagicus 0 k_Bacterizp_Proteobacteriz;c_Gammaproteobacterizo_Pacteurelales;d_Pacteurelaceaeg_Haemophilus
46	165	111	91	4	5	295	489	161	1	29	1 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Lawsonella;s_
47	208	90	269	8	97	145	0	1091	196	0	$0\ k\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Peptostreptococcales-Tissierellales;f\_Peptostreptococcales-Tissierellales;g\_Anaerococcus$
48	90 22	578	90 56	20 0	17 237	24 18	15 0	10 20	22	0 126	0 k_Bacteriap_Actinobacteriotac_Actinobacteriap_Micrococcoles/_Brevibacteriarceacg_Brevibacteriamy_Brevibacteriam_sp. 1211 k_Bacteriap_Firmicotesc_Baciliaces_Baciliacesc_Baciliacesc_Baciliacs_Beciliac_Internoamylovorans
49 50	326	783	289	35	33	52	7	26	34 90	0	1/11 K_skicterizp_termicutesc_Mscilico_Bsciliaest_Waciliaesterg_Bsciliuss_Bscilius_Termourtylovorans           0 k_Bacterizp_termicutesc_Clostriduso_Peptostruptococcales-Tissierelialesg_Anaerococcuss_Anaerococcus_mediterraneensis
51	135	12	56	4	220	163	2	31	184	20	8 k_Bacteria;p_Desulfobacterota;c_Desulfovbronia:o_Desulfovbronaies;f_Desulfovbronaceae;g_Desulfovbrio;s_
52	1	0	0	0	1	63	0	539	132	1	26 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Interobacteraies;f_Morganellaceae;g_Proteus
53 54	327	444	372	29 0	36 69	36 106	2	15 88	43 191	0	0 k_Sacteriap_Bacteroidotay_Bacteroidiap_Bacteroidialos/_Prevotelacoase_Prevotela;n_Prevotela_bivia 12 k_Bacteriap_Protechacteriax_Gammaprotechacteriap_Burkholderiales/_Methylophilacoaeg_Candidator_MethylopumRops_
55	202	0	144	0	92	142	0	68	195	a	8 k_Bacteriap_Bacteroidota;<_Kapabacteria)o_Kapabacteriales;f_Kapabacteriales;g_Kapabacteriales;s_
56	295	3	91	o	4	5	2	39	108	164	$\label{eq:constraint} 6\ k\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Enterobacteriae;s\_Escherichia-Singela;s\_Escherichia_collecteria;c\_Escherichia_collecteria;c\_Escherichia-Singela;s\_Esche$
57	57	128	4	146 0	8	12 518	0	7	275 140	1	8 k_Bacteria:p_Firmicutesc_Bacility_Staphylococcales;f_Staphylococcales;r_Lotypilococus;s_
58	190	237	25	8	1	518	0	14 6	140	0	21 k_Batteriap_firmicutessc_Bacilito_Bacilialest_Planococcacearg_Sporosarcinas_Sporosarcina_basteurii 0 k_Batteriap_Cyanobacteriasc_Cyanobacteriasc_Chloroplast_Chloroplast_Chloroplast
60	16	373	17	50	D	2	0	2	6	o	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium;s_Corynebacterium;glucuronolyticum
61	29	252	18	342	12	23	225	169	19	20	$7 \ k\_Bacteria; p\_Actinobacteriota; c\_Actinobacteria; a\_Corynebacteriales; f\_Corynebacteriacea; y\_Corynebacterium; s\_Corynebacterium in the second $
62 63	0	0	0 98	0	0	0 157	0	0 91	0 213	436	66 k_Battering_Firmicutessc_Bacilito_Lactobacillates;f_Lactobacillaceae;g_Lactobacilluss_Lactobacillus_mucosae 4 k_Bactering_Acidobacteriotax_Holophageso_Holophagalescj_Holophagaceae;g_marine_groups_
64	0	0	0	0	0	157	0	0	0	318	<ul> <li>aaction typ_actionation of a xAccoprologies/1Accoprologies/2armsBoutyp</li> <li>0 Unknown</li> </ul>
65	0	0	0	0	0	1	0	0	0	34	376 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Propionibacterialesf_Propionibacteriaceae
66	106	0	43	0	46	66	0	51	134	1	10 k_Bacteriago_Proteobacteriasc_Alphaproteobacteriaso_Eliteralesf_g_s_
67 68	149 309	91 5	13 26	95 14	13 15	12	0 5	5 11	34 37	0	0 k_Bacterizp_Firmicutes;c_Bacilito_Lactobaciliales;t_Aerococcaceaeg_Aerococcus;s_Aerococcus;urinaeequi 0 k_Bacterizp_Protechacteriz;c_Alphaproteobacteriz;p_Acetobacterize;f_Acetobacterize;eg_Roseonona;s_Boseonona; gilardii
69	64	328	52	154	22	11	0	11	24	o	0 k_Bacteria:p_Hrmicutes:c_Bacilito_Lactobaciliales:f_Carnobacteriaceae;g_Desemzia:s_
70	156	4	O	1	4	D	0	D	0	8	257 k_Bacteria;p_Cyanobacteria;c_Cyanobacteria;o_Chioroplast;f_Chioroplast
71	65 70	2	84 333	0	34	32 103	6 18	324	40 76	0	0 k_Bacteriap_Firmicutesc_Clostridiap_Peptostreptoroccales-Tissierellales;f_Peptostreptoroccales-Tissierellales;g_Anaerococcuss
73	3	1	9	27	441	19	0	1	322	0	21DECEMUPEnternance enterEnternances andEnternances entered enterEnternances enterEnter

230	6	4	1	0	3	12	2	0	90	1	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiracea;y_Eubacterium_aylanophilum_group;s
231	6	0	49	0	6	5	0	D	1	0	0 k_Bacteria;p_Deinococcota;c_Deinococcolo_Deinococcales;f_Deinococcaceae;g_Deinococcus
232	o	0	0	54	O	D	0	D	0	o	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bellerinckiaceae
233	2	2	20	1	0	0	2	0	53	2	3 k_Bacteria;p_firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_3_
234	15	14	1	0	0	3	0	44	2	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales:f_Actinomycetaceae;g_Actinomyces;s_Schaalia_radingae
2.35	9	0	6	0	6	9	o	13	20	1	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_FukuN57;s_
236	11	38	17	0	1	4	0	1	0	o	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Rathia;s_
237	2	0	7	0	1	95	0	0	54	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroida;o_Bacteroidale;;f_Prevotellaceae;g_Alloprevotella
238	40	8	6	26	3	1	2	1	3	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Propionibacteriale;f_Propionibacteriaceae;g_Microlunatus;s_
239	49	0	42	0	22	55	0	37	76	4	1 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_s_
240	15	0	11	0	7	19	0	9	12	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;a_Micavibrionales/_Micavibrionaceae.g_;s_
241	29	0	s	0	10	17	0	6	18	0	1 k_Bacteria;p_Acidobacteriota;x_Acidobacteriae;o_Acidobacteriae;f_Acidobacteriae;g_Paludibaculum;s_
242	32	0	8	0	25	17	0	4	18	1	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;ofig
243	18	0	31	0	0	0	0	0	0	0	0 k. Bacteriaco Protectuacteriaco Gammaproteobacteriaco Pseudomonadales/f. Moravellaceaeze Moraxella Moraxella Incolnii
244	56	0	6	0	3	2	0	4	5	0	0 k_Bacteria;p_Bdelovibrionta;c_Bdelovibrionia;o_Bdellovibrionales;1_BdellovibrionaceaegOM27_tlade;s
244	10	0	8	0	12	26	0	12	0	0	
								0			0 k_Bacteria:p_Bacteroidota:c_Bacteroida:a:o_Bacteroidales:f_Marinifilaceae;g_Odoribacter;s_
246	0 10	2 37	0	50 3	0	0	0		0	0	0 k_Bacteria;p_Brmicutes;c_Clostrida;o_Oscillospirales;f_Ruminococcaceae;g_Caproiciproducens;s_
			0		1	0	0	0		0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oucillespirales;f_Ruminococcacese;g_Subdoligrarulum;s_
248	1	16	12	62	5	6	6	4	18	0	1 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides;s_Bacteroides_acidifaciens
249	3	0	6	0	6	47	0	2	8	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroida;o_Bacteroidales;f_Muribaculaceae;g_Muribaculaceae;s_
250	63	215	41	25	21	52	3	549	49	41	5 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium;s_Corynebacterium[lipophiloflavum]
251	4	1	2	73	1	1	0	D	1	o	3 k_Bacteria;p_firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
252	18	0	22	0	10	12	0	0	0	0	2 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidiales;f_Munibaculaceae;g_Munibaculaceae;s_
253	5	43	21	0	2	2	3	4	3	0	0 k_Bacteria;p_Firmicutes;c_Bacilli,o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus_anginosus
254	33	0	3	10	D	44	0	4	0	0	0 k_Bacteria;p_firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_ruminantium_group;s
255	13	0	1	1	D	31	0	6	1	0	0 k_Bacteria;p_firmicutes;c_Clostridia;o_Clostridia_UCG-014;f_Clostridia_UCG-014;g_Clostridia_UCG-014;s
256	23	19	3	0	0	5	4	2	4	0	$0\ k\_Bacteria; p\_Proteobacteria; c\_Alphaproteobacteria; o\_Rhizobiales; f\_Beijerinckiaceae; a\_Methylobacterium-Methylorubrum Methylorubrum (Methylorubrum (Methyl))))))))))))))))$
257	0	3	0	38	0	0	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcareae;g_Caproiciproducens;s_
258	1	15	32	1	7	7	4	5	20	1	$\label{eq:lasteroide_scalar} 4 \ k\_Bacteroides;s\_Bactero$
259	1	0	5	0	38	D	0	0	1	0	0 k_Bacteria;p_Bacteraidota;c_Bacteraidia;o_Flavobacteriale;;f_Weeksellaceae;g_;s_Chryseobacterium_frigidum
260	23	37	21	3	2	4	0	4	10	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Neisseriaceae;g_Neisseria
261	0	0	2	0	1	47	0	5	40	0	0 k_Bacteria;p_firmicutes;c_Bacili;o_Lactobaciliales;f_Carnobacteriaceae;g_Atopostipes
262	21	2	6	8	40	48	3	2	11	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;s_Muribaculaceae;s_
263	77	0	56	0	1	0	0	0	0	0	2 k_Bacteria;p_Firmicute;;c_Bacili;o_Erysipelotrichales;f_Erysipelotrichaoeae;g_Allobaculum;s_
264	60	5	28	0	25	35	0	34	66	2	5 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae
265	6	3	6	1	9	9	1	24	28	0	2 k_Bacteria;p_Firmicutes;c_Clostnidia;o_Oscillospirales;f_Oscillospiraceae;g_Oscillibacter;s_
266	18	0	9	0	18	12	0	15	27	0	0 k_Bacteria;p_Bacteroidota;c_Kapabacteria;p_Kapabacteriales;f_Kapabacteriales;g_Kapabacteriales;s_
267	12	0	6	0	6	10	0	2	7	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria
268	25	0	33	0	o	4	0	D	0	o	0 k_Bacteria;p_Cyanobacteria;c_Cyanobacteria;o_Cyanobacteriales;f_Chroccoccidiopsaceae;g_Ailtereila;s_
360	11	0		0	2		0	0		4	11 Partici
269	11	0	8	0	2	13	0	9	5	1	1 L_Sectoria
270	4	49	O	5	0	D	o	9	1	o	0 k_Eacteria;p_Timicutes:c_Bacilico_Lactobaciliale;f_Aerococcaceaeg_Eremococcurs
270 271	4 12	49 75	0 0	5 4	0 0	D Z	o z	D	1 2	a a	0 k_bsterius_Tirmicutes_tisctilus_tectulosilluleisf_Arroaccaseaeg_terencoaccus_ 0 k_bsterius_Activalusteristas_Activalusterius_Activonyestaleisf_Activonyestaseaeg_Activonycess_Schaola_odorte/pta
270 271 272	4 12 41	49 75 0	0 0 22	5 4 0	0 0 17	D 2 29	0 2 0	0 33	1 2 23	0 0 1	0 k_bsteriap_trmicutes_tbiclko_bstokolluleist_Anrooccaseaeg_themococcuss_ 0 k_bsteriag_Actinductariotac_Actinductariuo_Actinomycetaleist_Actinomycetasaeeg_Actinomyceta_Sobaila_odontolytica 4 k_bsteriag_Protoclasceniasc_Gammaprotoclasteriag_Burkholderiakst/_MXH-UnPL_aquite_protp_MXH4UnPL_aquite_proup
270 271 272 273	4 12 41 33	49 75 0 1	0 0 22 1	5 4 0 2	0 0 17 6	0 2 29 0	0 2 0 10	0 33 2	1 2 23 1	0 0 1 1	0 k_BisteriusTimicutesBistlius_Lactobactivies_Annooccaceaegtrenococcuus 0 k_BisteriusActinobactoriotas_Actinobactorius_Actinomystalees_Actinomystalees_Actinomysees_Schaliu_adontolytica 4 k_BisteriusProtochactorius_Genmaporocobactorius_Biutholdoriakrd_MXHUnPL_aquitc_proupd_MXHUnPL_aquitc_proup 0 k_Bisterius_Firmicutes_Coloridus_Dovelloupiniest_BiumococcareaegRuniscoccareaeg_
270 271 272 273 274	4 12 41 33 2	49 75 0 1 0	0 0 22 1 59	5 4 0 2 0	0 0 17 6 1	0 2 29 0 0	0 2 0 10 0	0 33 2 10	1 2 23 1 3	0 0 1 1 0	0 k_Bisterius_Trimicutes_Bistliko_Listobistlivies_Anrooccaceaeg_tennococcuss_ 0 k_Bisterius_Listobistanista_Actrobisterius_Actinomyestalies_Actinomyestalies_Actinomyest_Schalia_odontolytica 4 k_Bisterius_Protochacterius_Gammaprotobacterius_Bistlobistalisty_M0044bitY_aquids_proup_M0044bitY_aquids_proup 0 k_Bisterius_Firmicuteus_Coloridaus_Ocelloginitous_Bistlobistalisty_Bistlobistanicoccaceaes_ 0 k_Bisterius_Firmicuteus_Bistliko_Bistlikouse_Coloridaese_Coloridaestus_
270 271 272 273 274 275	4 12 41 33 2 17	49 75 0 1 0 54	0 22 1 59 2	5 4 0 2 0	0 17 6 1 0	D 2 29 0 D D	0 2 0 10 0	0 33 2 10 0	1 2 23 1 3 0	0 1 1 0	0 k_bsterius_/immicates_tisctilo_tactobactilates_Annooccaseseg_inencooccus_ 0 k_bsterius_/ichicabacterista_Activabacterisa_factionnycetalatef_Activanycetasaseg_Activanyceta_Schalla_pdortclytca 4 \_bsterius_/incolonacterista_Cammaportobacterisa_Barbiotecistef_AthiCaPL_sayafi_group_I_MKHUsPL_sayafi_group 0 k_bsterius_Firmicates_Calcutida_O-Cellopi Inst/_Burnicoccustasee_Barbiotecasecasea 0 k_bsterius_Activabacterista_Barbiotecistef_Barbiotecistef_Birbiotecasec_Birbiotecasecasea
270 271 272 273 274	4 12 41 33 2	49 75 0 1 0	0 0 22 1 59	5 4 0 2 0	0 0 17 6 1	0 2 29 0 0	0 2 0 10 0	0 33 2 10	1 2 23 1 3	0 0 1 1 0	0 k_Bisterius_Trimicutes_Bistliko_Listobistlivies_Anrooccaceaeg_tennococcuss_ 0 k_Bisterius_Listobistanista_Actrobisterius_Actinomyestalies_Actinomyestalies_Actinomyees_Schalia_odontolytica 4 k_Bisterius_Protochacterius_Gammaprotobisterius_Bistlobistalisty_M0044611_eausic_proup_M004401P_aousic_proup 0 k_Bisterius_Firmicuteus_Coloridaus_Ocelloginious_Bistlobistarius_Bistlobistarius_Careeus_ 0 k_Bisterius_Firmicuteus_Bistliko_Bistlikouse_Calebisterius_Calebistus_
270 271 272 273 274 275	4 12 41 33 2 17	49 75 0 1 0 54	0 22 1 59 2	5 4 0 2 0	0 17 6 1 0	D 2 29 0 D D	0 2 0 10 0	0 33 2 10 0	1 2 23 1 3 0	0 1 1 0	0 k_bsterius_/immicates_tisctilo_tactobactilates_Annooccaseseg_inencooccus_ 0 k_bsterius_/ichicabacterista_Activabacterisa_factionnycetalatef_Activanycetasaseg_Activanyceta_Schalla_pdortclytca 4 \_bsterius_/incolonacterista_Cammaportobacterisa_Barbiotecistef_AthiCaPL_sayafi_group_I_MKHUsPL_sayafi_group 0 k_bsterius_Firmicates_Calcutida_O-Cellopi Inst/_Burnicoccustasee_Barbiotecasecasea 0 k_bsterius_Activabacterista_Barbiotecistef_Barbiotecistef_Birbiotecasec_Birbiotecasecasea
270 271 272 273 274 275 276	4 12 41 33 2 17 13	49 75 0 1 0 54 0	0 0 22 1 59 2 6	5 4 0 2 0 0 0	0 0 17 6 1 0 6	0 2 29 0 0 0 0 20	0 2 0 10 0 0	0 33 2 10 0 1	1 2 23 1 3 0 8	0 0 1 0 0	D L bateria, _ lendobateria, _ actobatiliaesf_Aerooccaseaeg_terenoccase     L bateria, _ Actobateria, _ Actobateria, _ Actobateria, _ Actoonyeataesf_Actionyeataesg_Actionyeas, _ Schalla, odortelytica     L _ Beteria, _ Freetobateria, _ Controlateria, _ Subolecia, _ Monikoffer, Jack, _ Monikoffer, _ Jack, _ J
270 271 272 273 274 275 276 277	4 12 41 33 2 17 13 20	49 75 0 1 0 54 0 0	0 0 22 1 59 2 6 5	5 4 0 2 0 0 0 0	0 0 17 6 1 0 6 8	0 29 0 0 0 0 20 12	0 2 0 10 0 0 0	0 33 2 10 0 1 17	1 2 23 1 3 0 8 21	0 1 1 0 1 1	0   bateriap_innicates_Biofilo_batobolidesi_Annooccaseseg_tennococcuss_ 0   bateriap_introducts_Biofilo_batobolidesi_Annooccaseseg_tennococcuss_ 4   bateriap_introducts_Cateriabatoriap_Antobolicniasi_MAN-MAPLapatot_protog_MAN-MAPLapatot_protog_ 0   bateriap_innicates_CateRiap_Bolidesi_Bolidesi_Bolidesiase_Cateriansee_Bolidescateriam_ 0   bateriap_innicates_CateRiap_Bolidesi_Bolidesi_Bolidescateriag_Bolidescateriap_ 0   bateriap_innicates_CateRiap_Bolidesi_Bolidesiasee_CateRiadescateriap_ 0   bateriap_innicates_Bolidia_Bolidesi_Bolidescateriag_Biologicateriap_Biologicateriam_Biologicateriam_longum 1   bateriap_interotechatoriada_Kateriada_Biologicateriag_Janthonooudistesc_Annoonesiasease_ 1   bateriap_interotechatoria_Kateriada_Biologicateriag_Janthonooudistesc_Annoonesiasease_Annoonesase_
270 271 272 273 274 275 276 277 278	4 12 41 33 2 17 13 20 9	49 75 0 1 0 54 0 0 0	0 22 1 59 2 6 5 4	5 4 0 2 0 0 0 0 0	0 17 6 1 6 8 5	0 2 29 0 0 0 20 12 16	0 2 0 10 0 0 0 0 0	0 33 2 10 0 1 17 5	1 2 3 1 3 0 8 21 7	0 1 1 0 1 1 2	D Lasteriag_Introduces_Biolito_Lastobacilidesf_Anroaccaceaeg_Internecoccuss_     Lasteriag_Actinobacteriotag_Antroductariug_Actinomycetalesf_Actinomycetaeaeg_Actinomyceta_Sobails_colontalytica     L_Bacteriag_Protoclasteriag_Coloridag_Decilidegi Intel_Summoccaceaeg_Reinforceccaceaeg_     Lasteriag_Introductariug_Decilidegi Intel_Summoccaceaeg_Reinforceccaceaeg_     Lasteriag_Introductariug_Decilidegi Intel_Summoccaceaeg_Reinforceccaceaeg_Biologuetaetaetaetaetaetaetaetaetaetaetaetaetae
270 271 272 273 274 275 276 277 278 279	4 12 41 33 2 17 13 20 9 34	49 75 0 1 0 54 0 0 0	0 22 1 59 2 6 5 4 32	5 4 0 2 0 0 0 0 0 0	0 0 17 6 1 0 6 8 5 5	0 2 29 0 0 0 20 12 16 36	0 2 0 10 0 0 0 0 0 0	0 33 2 10 0 1 17 5 19	1 23 1 3 0 8 21 7 43	0 1 1 0 1 1 2 4	0 k_baterias_firmicates_bicflo_isctabedialesf_Aerosocasese_firencosocas_ 0 k_baterias_fictioas_bretosacterias_fictionnycetalesf_Actionnycetases_Actionnycetases_Schalar_dotrolytica 4 & bisterias_firmicates_Cantidas_Oetilopi insuf_Bandosocasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Actionnycetasese_Bandosocasesese_Bandosocasesesesesesesesesesesesesesesesesesese
270 271 272 273 274 275 276 277 278 279 280	4 12 41 33 2 17 13 20 9 34 40	49 75 0 1 54 0 0 0 0 0 2	0 22 1 59 2 6 5 4 32 5	5 4 0 2 0 0 0 0 0 0 0 0	0 0 17 6 1 0 6 8 5 5 15 1	0 2 29 0 0 0 20 12 16 36 0	0 2 0 10 0 0 0 0 0 1	0 33 2 10 0 1 17 6 19 1	1 2 3 1 3 0 8 21 7 43 2	0 1 1 0 1 1 2 4 0	0 k_bsterius_/immostes_BicRio_isotokollekief_Annooccasesieg_immosoccus_ 0 k_bsterius_/ictinductoristac_Activalactorius_Activalexief_Activanyestacese_Activanyestacs_Schabla_colontelytica 4 k_bsterius_/introducts_Colontidus_Ocellapiniost_Biomacoccasese_Amerikanese_Activanyestacs_Schabla_colontelytica 0 k_bsterius_firmosters_Colontidus_Ocellapiniost_Biomacoccasesee_Biologications_ 0 k_bsterius_firmosters_Colontidus_Ocellapiniost_Biomacoccasesee_Biologications_ 0 k_bsterius_firmosters_Colontidus_Ocellapiniost_Biomacoccasesee_Biologications_ 0 k_bsterius_Activateset_Schafte_Biologications_Biologicationsee_Biologicationsee_Biologications_ 1 k_bsterius_Activateseteriose_Activatesterius_Nanthomenatalistif_Xannomenataseeeg_Activationesa. 4 k_bsterius_Activatesteriose_Activatesterius_Nanthomenatalistif_Xannomenataseeeg_Archimonasa. 4 k_bsterius_Activatesteriose_Activatesterius_Nanthomenatalistif_Xannomenataseeeg_Cologo 9g, naime_groups_ 4 k_bsterius_Activatesteriose_Activatesterius 4 k_bsterius_Activatesteriose_Activatesterius_Nanthomenatalistif_Nantalisterioseeeg_Cologo 9g, naime_groups_ 4 k_bsterius_Activatesteriose_Activatesterius
270 271 272 273 274 275 276 277 278 279 280 281	4 12 41 33 2 17 13 20 9 34 40	49 75 0 1 54 0 0 0 0 2 0	0 22 1 59 2 6 5 4 32 5 0	5 4 0 2 0 0 0 0 0 0 0 0 0 0	0 0 17 6 1 0 6 8 5 5 15 1 0	0 2 29 0 0 20 12 16 36 0 0	0 2 0 10 0 0 0 0 0 1 0	0 33 2 10 0 1 17 6 19 1	1 23 1 3 0 8 21 7 43 2 2 2	0 1 1 0 1 1 2 4 0 50 0	0 I. Jasteria, _irmicatesliscilioiscibalideid_Arrosoccasesgirenecoccus 0 I. Jasteria, _ircitobacteria, _Antonoxistaleid_Actionyetasesg_Actionyeta, _Schala, odortojtica 4 L. Jasteria, _ircitobacteria, _Gammaporcobateria, _Janiofecinez, _MmikuPi, apaid, _mupg_MMikUPL, apaid, _mupg_MikuPL, apaid,
270 271 272 273 274 275 276 277 278 279 280 281 281	4 12 41 33 27 13 20 9 34 40 0 7	49 75 0 1 0 54 0 0 0 0 2 0 0	0 22 1 59 2 6 5 4 32 5 0 31	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0	0 0 17 6 1 0 6 8 5 15 15 1 0 28	0 2 29 0 0 0 20 12 16 36 0 0 0	0 2 0 10 0 0 0 0 0 0 1 0 0 0	0 33 2 10 0 1 17 6 19 1 0 1	1 23 1 3 0 8 21 7 43 2 2 16	0 1 1 0 1 1 2 4 0 50 0	<ul> <li>b. Isaterias_Immonies_Isicking_lactobactivies_Antronoccasese_Enternococcus_</li> <li>b. Isaterias_Internolationitas_Antronoccasese_Enternococcus_</li> <li>b. Isaterias_Internolationitas_Contentionitas_Biological Antropyce Internococcus_</li> <li>b. Isaterias_Internolationitas_Biological Internociations_Antropyce Internococcus_</li> <li>b. Isaterias_Internolationitas_Antropyce Biological Internociations_Antropyce Internococcus_</li> <li>b. Isaterias_Internolationitas_Antropyce Biological Internociations_Contentions_Enternococcus_</li> <li>b. Isaterias_Internolationitas_Antropyce Biological Internociations_Contentions_Enternococcus_</li> <li>b. Isaterias_Internolationitas_Antropyce Biological Internociations_Contentions_Enternococcus_</li> <li>b. Isaterias_Antropyce Internological Internociations_Nationanous Internociations_Contentions_Enternococcus_</li> <li>b. Isaterias_Antropyce Internological Internociations_Nationanous Internociations_Antropyce</li> <li>b. Isaterias_Antropyce Internological Internociations_Nationanous Internociations_Antropyce</li> <li>b. Isaterias_Antropyce Internological Internociations_Contentions_Contentions_Contentions_Contentions_Distributed Internociations_Content</li></ul>
270 271 272 273 274 275 276 277 278 279 280 281 281	4 12 41 33 27 13 20 9 34 40 0 7	49 75 0 1 0 54 0 0 0 0 2 0 0	0 22 1 59 2 6 5 4 32 5 0 31	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0	0 0 17 6 1 0 6 8 5 15 15 1 0 28	0 2 29 0 0 0 20 12 16 36 0 0 0	0 2 0 10 0 0 0 0 0 0 1 0 0 0	0 33 2 10 0 1 17 6 19 1 0 1	1 23 1 3 0 8 21 7 43 2 2 16	0 1 1 0 1 1 2 4 0 50 0	0 k_bsterius_/immicates_bstella_istobedialeigf_Annocecceseg_internececcusAttionaryestaseg_Attionaryest_Schala_odorteyltaa 4 L_bsterius_/referebacterius_Cantidag_Deciliarias_Interlations_attionaryestaseg_Attionaryest_Schala_odorteyltaa 9 L_bsterius_/referebacterius_Cantidag_Deciliarias_Interlations_attionaryestaseg_Attionaryest_Schala_odorteyltaa 9 L_bsterius_/referebacterius_Cantidag_Deciliarias_Interlations_Cantidag_Deciliarias_Interlations_Cantidag_Deciliarias_Interlations_Cantidag_Deciliarias_Interlations_Cantidag_Deciliarias_Interlations_Cantidag_Deciliarias_Interlations_Cantidag_Deciliarias_Cantidag_Deciliariaseg_Cantidag_D
270 271 272 273 274 275 276 277 278 279 280 281 282 283 284	4 12 41 33 27 13 20 9 34 40 0 7	49 75 0 54 0 0 0 2 0 2 0 0 10 0	0 22 1 59 2 6 5 4 32 5 0 31	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 15 1 0 28 30 0	0 2 29 0 0 0 20 12 16 36 0 0 0	0 2 0 10 0 0 0 0 0 0 1 0 0 0	0 33 2 10 0 1 17 6 19 1 0 1 41 3	1 2 3 1 3 0 8 21 7 43 2 2 16 670 0	0 0 1 0 1 1 2 4 0 50 0 62 0	0 k_bsterius_/immostes_BicRio_isotabelleis_Annooccessesg_inencooccus_ 0 k_bsterius_/icrinductorista_Activalactorius_Activaleis_Activaryetboake_Activaryetboake_Activaryeta 4 L_bsterius_/icrinductorista_Controlog.commonroweductorista_Devineoccusses_Activaryetboake_Activaryetboake 0 k_bsterius_Intercess_Controlog.commonroweductorista_Devineoccussese_Activaryetboakee_Activaryetboakee 0 k_bsterius_Intercess_Controlog.commonroweductorista_Devineoccussese_Annoone 0 k_bsterius_Activates_Controlog.commonroweductorista_Devineoccussese_Annoone 0 k_bsterius_Activates_Controlog.commonroweductoriates_Devineoccussese_Annoone 1 k_bsterius_Activatesteriota_Activatesterius_Bioblacteriates_Disblacteriasese_Annoone 1 k_bsterius_Activatesteriota_Activatesterius_Bioblacteriates_Disblacteriasese_Annoone 1 k_bsterius_Activatesteriota_Activatesterius_Bioblacteriasese_Annoone 1 k_bsterius_Activatesteriota_Activatesterius_Bioblacteriasese_Annoone 1 k_bsterius_Activatesteriota_Activatesterius_Bioblacteriasese_Annoone 2 k_bsterius_Activatesteriota_Activatesterius_Bioblacteriasese_Annoone 2 k_bsterius_Activatesteriota_Activatesterius 2 k_bsterius_Activatesteriota_Activatesterius 3 k_bsterius_Activatesteriota_Activatesterius 4 k_bsterius_Activatesteriota_Activatesterius 4 k_bsterius_Activatesteriota_Activatesterius 4 k_bsterius_Activatesteriota_Activatesterius 5 k_bsterius_Nettroideteriota_Activatesterius_Monoone 5 k_bsterius_Nettroideteriota_Activatesterius_Monoone 6 k_bsterius_Nettroideterius_Batteriotiota_Monoone 5 k_bsterius_Nettroideterius 6 k_bsterius_Nettroideterius_Activatesterius_Monoone 6 k_bsterius_Nettroideterius_Activatesterius_Monoone 6 k_bsterius_Nettroideterius
270 271 273 274 275 276 277 276 277 280 281 281 283 284 285	4 12 33 2 17 13 20 9 34 40 0 7 1001 43 3	49 75 0 54 0 0 0 2 0 2 0 10 51	0 22 1 59 2 6 5 4 32 5 0 31 121 0 6	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 15 0 4	0 17 6 1 0 6 8 5 15 1 0 28 30 0 0	0 2 29 0 0 0 20 12 16 36 0 0 0	0 2 0 10 0 0 0 0 0 0 0 0 0 7 0 7 7	0 33 2 10 0 1 17 5 19 1 0 1 41 3 0	1 23 1 3 0 8 21 7 43 2 2 16 670 0 0	0 1 1 0 1 2 4 0 50 62 0 0 0 0	0   _bsteriusimmostesbicfloisotobicflokef_Annooccasesegimmosoccus 0   _bsteriusictinobicfristoActivobictristoActivobicfristo_IMMN-UMP1_space_impogMMN-UMP
270 271 273 274 275 276 277 278 279 280 281 282 283 284 285 286	4 12 41 33 2 7 33 20 9 34 40 0 7 1001 43 3 3	49 75 0 1 0 54 0 0 0 0 2 0 0 10 0 10 0 81 0	0 22 1 59 2 6 5 4 32 5 0 31 121 0 6	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 28 30 0 0 0 0 0 0	0 2 29 0 0 20 20 12 16 36 0 0 0 591 0 1	0 2 0 10 0 0 0 0 0 1 0 0 7 7 0 7 0	0 33 2 10 0 1 17 6 19 1 0 1 41 3 0 10	1 23 1 3 0 8 21 7 43 2 2 16 670 0 0 3	0 1 1 0 1 2 4 0 50 62 0 0 0 0	<ul> <li>b. Jackeriss, Jimicanes, Jackbacilleier, Annocessene g. Jimicacous, J.</li> <li>b. Jackeriss, J. Konkaksteriska, A. Konkaksteris, J. Kolinomyrekikel, A. Mikikel, Japan G. Cong, J. Mikikel, J. Sakaris, J. Resolution, G. Sakaris, J. Resolution, S. Sakaris, J. Sakaris, J. K. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. K. Sakaris, J. K. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. K. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. J. Jakaris, J. J. Jakaris, J. J. Jakaris, J. Sakaris, J. Jakaris, J. Jakaris, J. K. Sakaris, J. K. Sakaris, J. Sakaris, J. K. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. Sakaris, J. J. Jakaris, J. J. Jakaris, J. Sakaris, J. Jakaris, J. Sakaris, J. Jakaris, J. Jakaris, J. Jakaris, J. Jakaris, J. Jakaris, J. Sakaris, J. Jakaris, J. Jakaris, J. Jakari</li></ul>
270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287	4 12 41 33 27 33 20 9 34 40 0 7 1000 43 3 3 27	49 75 0 1 0 54 0 0 0 0 0 0 0 0 10 0 10 0 10	0 22 1 59 2 6 5 4 32 5 0 31 121 0 6 23 4	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 78 30 0 0 0 3	0 2 29 0 0 20 12 16 36 0 0 591 0 0 1 1	0 2 0 10 0 0 0 0 0 1 0 0 1 0 0 7 0 7 0 0 0	0 33 2 10 0 1 17 6 19 1 0 1 41 3 0 10 0 0	1 23 1 3 0 8 21 7 43 2 16 670 0 0 3 2	0 1 1 0 1 2 4 0 50 62 0 0 0 0 0 0 0 0	0   _bsterius_/immicatesbstelle_isctaballeleig_Aerosoccessegimmessecus 0   _bsteriusisctaballeleig_Actionautorusfetilonmyetabalef_Actionmyetabaleg_Actionautorus
270 271 272 273 274 275 276 277 276 280 281 282 283 284 285 286 285 286 287 288	4 12 41 33 2 17 13 20 9 34 40 0 7 1000 43 3 3 27 16	49 75 0 1 0 54 0 0 0 0 0 0 0 10 0 10 0 10 0	0 22 1 59 2 6 5 4 32 5 0 31 121 0 6 23 4 9	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 5 15 1 0 8 8 0 0 0 0 0 3 6 5	0 2 29 0 0 0 20 20 12 16 36 0 0 591 0 1 1 1	0 2 0 0 0 0 0 0 0 0 0 1 0 0 7 0 7 0 0 0 0 0	0 33 2 10 0 1 17 6 19 1 0 1 41 3 0 10 0 4	1 23 1 3 0 8 21 7 43 2 16 670 0 0 3 2 2 12	0 1 1 0 1 2 4 0 50 0 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _bsteriusimmodescbstelioisotobactimisAntioenyostalesf_Antioen
270 271 272 273 274 275 276 277 280 280 281 282 283 284 285 286 287 288 289 280	4 12 41 33 2 17 13 20 9 34 40 0 7 1000 7 1000 43 3 27 16 0 11	49 75 0 1 0 54 0 0 0 0 2 0 0 0 10 0 51 0 2 0 0 2 0 0 51	0 22 1 59 2 6 5 4 32 5 0 31 121 0 6 23 4 9 0 6	5 4 0 0 0 0 0 0 0 0 0 0 15 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 28 30 0 0 3 6 0 3 6 0 3	0 2 29 0 0 20 20 12 16 36 0 0 591 0 1 1 1 1 12 7	0 2 0 0 0 0 0 0 0 0 7 0 7 0 0 0 0 0 0 0	0 33 2 10 0 1 17 6 19 1 7 6 19 1 1 3 0 10 0 4 5	1 2 3 1 3 0 8 21 7 4 3 2 16 670 0 3 2 12 27	0 1 1 0 1 1 2 4 0 50 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackenia, J. Fondoacterida, Activalatoria, J. Attributeria et al. J. Attributeria et al. J. Schella, J</li></ul>
270 271 273 274 275 276 277 276 277 278 280 281 282 284 285 286 287 288 286 287 287 288 289 280 291	4 12 41 33 2 17 13 20 9 34 40 0 7 7 1000 43 3 3 27 16 0 11 5	49 75 0 1 0 54 0 0 0 2 0 0 10 0 51 0 51 0 2 0 0 2 0 2 0 2	0 22 1 59 2 6 5 4 32 5 0 31 121 0 6 23 4 9 0 6 23 6 0 23 6 0 23 4 9 0 6 23 4 9 0 6 23 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	5 4 0 2 0 0 0 0 0 0 0 0 15 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 28 30 0 3 6 0 3 6 0 3 10	0 2 29 0 0 20 12 16 36 0 0 591 0 0 1 1 1 1 27 16 4	0 2 0 10 0 0 0 0 0 0 0 7 0 7 0 0 0 0 0 0 0	0 33 2 10 1 17 6 19 1 1 0 1 3 0 10 0 4 5 5 1	1 2 23 1 3 0 8 21 7 43 2 16 670 0 3 2 12 27 15 0	0 1 1 0 1 1 2 4 0 50 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _bateriaimmonesbathoisobactiviaActionnycelaid_Actionalay=Actionalay
270 271 272 273 274 275 276 277 278 277 280 281 283 283 284 285 286 285 286 285 286 285 286 285 286 285 286 285 286 285 286 291	4 12 41 33 2 17 13 20 9 40 0 7 1000 43 3 7 16 0 11 5 64	49 75 0 1 0 54 0 0 0 0 0 0 0 10 0 0 10 0 10	0 22 1 59 2 6 5 4 32 5 0 31 121 0 6 23 4 9 0 6 0 7	5 4 0 2 0 0 0 0 0 0 0 0 15 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 15 10 28 0 0 0 3 6 0 3 10 29	0 2 29 0 0 20 12 16 36 0 0 0 591 0 0 1 1 1 1 27 16 4 99	0 2 0 0 0 0 0 0 0 0 0 7 0 0 0 0 0 0 0 0	0 33 2 10 0 1 17 6 19 1 41 3 0 10 0 4 5 5 1 5	1 2 23 1 3 0 8 21 7 43 2 16 670 0 3 2 12 27 15 0 78	0 1 1 0 1 1 2 4 0 50 50 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bacterias, / immicates, _ bactelos, _ lactobacterias, _ futures/excesse, _ fu</li></ul>
270 271 272 273 274 275 276 277 278 280 281 283 284 284 285 286 284 285 286 287 288 289 290 291 292 291	4 12 41 33 20 9 34 40 0 7 1001 43 3 3 27 16 0 0 11 5 64 27	49 75 0 1 0 54 0 0 0 0 0 0 0 0 0 0 0 10 0 0 10 0 2 0 0 2 5 9 0 0	0 22 1 59 2 6 5 4 32 5 0 31 1 21 0 6 23 4 9 0 6 0 7 1	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 7 8 0 0 28 0 0 3 6 0 3 10 29 0	0 2 29 0 0 20 12 16 36 0 0 591 0 0 1 1 1 1 27 16 4 99 8	0 2 0 0 0 0 0 0 0 7 0 0 0 0 0 0 0 7 1 0 0	0 33 2 10 0 1 17 6 19 1 41 3 0 10 0 4 5 5 1 5 4	1 2 23 1 3 0 8 21 7 43 2 6 7 6 70 0 3 2 12 27 15 0 78 1	0 1 1 0 1 1 2 4 0 50 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _ bateria_ / minotesc_ Backho_ Lectobelleki / Antooccesse g_ innoceccus_ 0   _ bateria_ / netrobacteria Actiobacteria Additionyretialsed / Bioblacterialsed / Additionerialsed / Bioblacterialsed / Bioblacterialsed / Additionerialsed / Additionerialsed / Bioblacterialsed / Carditorearsed / Additionerialsed / Additionerialsed / Additionerialsed / Bioblacterialsed / Carditorearsed / Additionerialsed / Additionerialsed / Additionerialsed / Additionerialsed / Bioblacterialsed / Additionerialsed / Additionerialsed / Additionerialsed / Additionerialsed / Additionerialsed / Bioblacterialsed / Additionerialsed / Addit
270 271 272 273 274 275 276 277 278 280 281 281 283 284 285 286 287 288 289 280 281 289 291 291	4 12 41 33 20 9 34 40 0 7 7 1000 43 3 27 16 0 11 5 64 27 8	49 75 0 1 0 54 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 2 6 5 4 7 31 121 0 6 23 4 9 0 6 0 7 1 8	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 28 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 29 0 0 20 20 20 20 20 20 20 0 591 0 0 1 1 1 1 27 26 4 99 8 11	0 2 0 10 0 0 0 0 1 0 7 0 7 0 0 0 7 1 0 0 7 1 0 0 1 1 0 0 1 0 0 0 0	0 33 2 10 1 1 7 6 19 1 7 6 19 1 0 1 1 0 4 5 5 1 5 4 2	1 2 23 1 3 0 8 21 7 43 2 2 6 70 0 3 2 2 7 12 27 15 0 78 1 20	0 1 1 0 1 2 4 0 50 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackenia, J. Precisia, J. Activability J. Activation (J. Activation) (Activation) (A</li></ul>
270 271 272 273 275 276 277 276 280 281 283 284 285 286 287 288 289 280 261 292 287 288 289 280 291 291 292 293	4 12 41 33 27 13 20 9 34 40 0 7 1001 43 3 3 3 27 16 0 11 5 6 4 27 8 7	49 75 0 1 0 54 0 0 0 0 0 0 0 0 0 0 0 0 0 2 0 0 0 2 5 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 2 6 5 4 2 3 1 21 0 6 23 4 9 0 6 23 6 7 1 8 5	5 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 8 5 5 5 5 1 0 28 0 0 0 3 6 0 3 6 0 3 10 29 0 1 1	0 2 29 0 0 20 12 16 36 0 0 591 1 1 1 1 1 1 27 59 1 8 4 9 9 8 1 2 2	0 2 0 0 0 0 0 0 0 7 0 7 0 0 0 0 0 7 1 0 0 0 0	0 33 2 10 1 17 6 19 1 1 1 0 1 1 0 1 1 0 1 1 5 4 2 2 2 2 2 2 2 2 2 2 2 2 2	1 23 1 3 0 8 21 7 43 2 2 16 670 0 3 2 27 15 0 78 1 20 38	0 1 1 0 1 2 4 0 50 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackenia, J. Mendeakenia, A. Acteolatoria, J. Actionary etiles (_Actionary etiles, _Actionary _Actionary, _Act</li></ul>
270 271 273 274 275 275 276 277 278 280 280 281 285 285 285 285 285 285 285 285 285 285	4 12 41 33 27 13 20 9 34 40 0 7 1001 43 3 7 1001 43 3 7 16 0 11 5 64 7 8 7 0	49 75 0 1 0 54 0 0 0 0 0 0 0 0 0 0 0 10 0 0 0 10 0 2 5 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 2 6 5 4 32 5 0 31 121 6 23 4 9 0 6 0 7 1 8 5 2	5 4 0 2 0 0 0 0 0 0 0 0 15 0 4 0 0 0 0 25 5 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 8 5 15 1 0 28 0 0 3 6 0 3 0 0 3 0 0 3 0 0 1 0 29 0 0 1 1 0 29 0 0 1 0 1 0 1 0 1 1 1 1 0 1 1 1 1 1 1	0 2 29 0 0 20 20 20 20 20 20 20 591 12 1 11 27 16 4 99 8 11 22 0	0 2 0 0 0 0 0 0 0 7 0 0 0 0 0 0 7 1 0 0 0 7 1 5 0	0 33 2 10 0 1 7 6 9 10 0 1 41 3 0 10 0 4 5 5 1 5 4 2 0	1 23 1 3 0 8 21 7 43 2 2 16 670 0 3 2 27 15 0 78 1 20 38 55	0 1 1 0 1 1 2 4 0 50 50 50 50 62 62 62 0 0 7 0 7 0 7 0 7 0 0 7 0 0 0 0 0 0 0	<ul> <li>b. bateria, _/micetesib.cliu.cliu.cliu.cliu.cliu.cliu.cliu.cliu</li></ul>
270 271 273 274 275 276 277 278 280 281 283 284 283 284 283 284 283 284 285 286 289 290 291 291 292 291 292 293 294 294 295 294 295 295 295 295 295 295 295 295 295 295	4 12 41 33 20 9 40 0 7 1001 3 3 27 1001 3 3 27 16 0 1 5 64 27 5 64 27 5 64 27 5 64 27 5 64 27 5 64 27 7 0 9	49 75 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 2 6 4 32 5 0 31 121 6 23 4 9 0 6 23 4 9 0 7 1 8 5 2 17	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 6 8 5 5 5 5 5 5 5 5 5 5 5 7 8 0 0 0 0 0 3 6 0 29 0 0 1 0 29 0 0 1 2 0 2 9 0 2 1 2 2 2 2 2 2 2 2 3 2 2 3 2 3 3 2 3	0 2 29 0 0 20 12 16 36 0 0 551 0 0 551 11 12 7 16 4 99 8 11 2 7 15 11 2 7 15 11 12 12 7 12 13 12 13 14 14 15 14 15 15 15 15 15 15 15 15 15 15 15 15 15	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 33 2 10 1 17 6 19 1 0 1 41 3 0 10 0 4 5 5 1 5 4 2 0 0	1 2 3 6 6 7 4 3 2 16 6 70 0 3 2 12 27 15 0 7 8 1 20 38 55 1	0 1 1 0 1 1 2 4 0 50 50 50 50 62 62 62 0 0 7 0 7 0 0 7 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, _irmicesc_Bickio_Lectobellect_Aerooccesse g_irmococcus_</li> <li>b. bateria, _ircicebacteria, _Actobacteria, _Actobacteria, _Antholeciebel, _Attornyetaase, _Attonnyeta, _Schala, _adotto/tha</li> <li>b. Bateria, _ircicebacteria, _ammetrobotteria, _Burbioteciebel, _Attornyetaase, _Attonnyeta, _Schala, _adotto/tha</li> <li>b. Bateria, _ircicebacteria, _ammetrobotteria, _Burbioteciebel, _Attornyeta, _Attonnyeta, _Schala, _adotto/tha</li> <li>b. Bateria, _ircicebacteria, _Burbioteciebel, _Burbioteciebel, _Attonnyeta, _Burbioteciebel, _Attonnyeta,Attonnyeta,Attonnyeta,Burbioteciebel,Attonnyeta,Burbioteciebel,Burbioteciebel,Burbioteciebel,Attonnyeta,Burbioteciebel,Burbioteciebel,Burbioteciebel,Burbioteciebel,Burbioteciebel,Attonnyeta,Burbioteciebel,Burbioteciebel,Burbioteciebel,Attonnyeta,Burbioteciebel,Attonnyeta,Burbonskin,Murbandurenez,Murbandurenez,Attonnyeta,Att</li></ul>
277 271 273 274 275 276 277 276 280 281 284 285 286 285 286 289 289 289 289 289 289 289 289 289 289	4 12 41 33 2 17 33 40 0 7 100 7 100 13 3 7 16 0 11 5 64 27 8 7 0 9 8 3	49 75 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 6 5 4 32 5 6 31 121 0 6 23 4 9 0 6 0 7 1 8 5 2 17 30	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 6 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0 2 29 0 0 20 12 16 36 0 0 561 1 1 1 1 27 16 4 99 8 11 20 19 11 20 19 11 20 19 11 20 11 21 20 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 33 2 10 17 6 19 1 41 3 0 10 4 5 5 1 5 4 2 0 0 12	1 2 3 0 8 21 7 43 2 16 670 0 3 2 12 27 15 0 78 1 20 78 1 20 38 55 1 1	0 1 1 2 4 0 50 62 0 0 2 0 7 0 7 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Laderia, J. Mindesker, J. Kolos, Ladobelleki, J. Antonycelski, J. Antonycelski, S. Kolaja, elotholytka</li> <li>c. Laderia, J. Metodakoritska, A. Konolakoritska, J. Kolosyvelski, M. Mitheli, J. Jank, G. Konolakoritska, J. Konolakoritska, J. Kolosyvelski, J. Mitheli, J. Jank, G. Konolakoritska, J. Konolak</li></ul>
270 271 273 274 275 276 277 278 280 281 283 283 284 285 286 286 286 286 286 286 286 286 286 286	4 12 41 33 20 9 40 0 7 1000 43 3 3 27 6 4 5 6 4 7 0 9 8 7 0 9 8 7 0 9 8 7 0 9 8 7 27	49 75 0 54 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 6 5 4 7 7 1 8 6 0 6 0 7 1 8 5 2 17 10 1	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 8 5 1 0 28 30 0 28 30 0 3 6 0 3 6 0 3 10 29 0 10 3 6 10 10 10 10 10 10 10 10 10 10	0 2 29 0 0 20 20 20 20 20 20 20 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 7 0 0 0 0 7 1 0 0 0 0	0 33 2 10 0 1 7 6 19 1 0 1 4 1 0 1 1 7 6 19 1 0 1 4 5 5 4 2 0 0 1 7 7 6 19 1 0 1 7 1 7 6 19 1 1 7 1 1 1 1 1 1 1 1 1 1 1 1 1	1 2 3 4 3 7 4 3 2 7 4 3 6 7 6 7 0 0 3 2 2 7 12 7 5 5 5 1 3 8 5 5 1 5 5 5 1 5 5 5 1 3 8 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0 1 1 0 1 2 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, J. minians, J. bateballeki, J. Antosacase g. J. ministrature, Ministrature, J. Ministra</li></ul>
270 271 273 274 275 276 277 278 280 281 283 284 285 285 285 285 285 285 285 285 285 285	4 12 41 33 20 9 43 40 0 7 1001 43 3 3 27 16 0 11 5 64 27 8 7 0 9 80 82 27 28	49 75 0 54 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 6 5 4 32 7 31 221 0 6 33 4 9 0 6 0 7 1 8 5 2 8 5 2 17 10 11 22	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 1 0 28 0 0 3 10 29 0 1 0 20 0 1 0 20 0 3 10 20 0 3 10 0 28 0 0 0 15 15 15 10 0 28 0 0 0 0 0 15 15 10 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 29 0 0 20 20 20 20 20 20 20 20 20 20 20 20	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 33 2 10 0 1 17 6 19 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 0 1 1 0 1 1 0 1 1 1 0 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	1 2 3 4 3 2 7 4 3 2 16 670 0 3 2 12 27 15 0 78 1 20 38 55 1 1 5 16	0 1 1 2 4 0 50 62 0 7 0 7 0 7 0 7 0 0 7 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, _irmicetes:backhotextebediefesiAerosoccessesirmicescous</li></ul>
270 271 273 274 275 276 277 276 280 281 283 284 283 284 285 286 289 280 289 289 289 289 289 289 289 289 289 289	4 22 41 33 20 9 44 40 0 7 1001 43 3 7 16 0 11 5 64 27 8 7 0 9 83 7 20 9 83 7 21 5 64 22 8 7 0 9 83 22 23	49 75 0 54 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 2 6 5 4 7 5 0 31 121 6 23 4 9 0 6 23 4 9 0 7 1 8 5 21 7 10 7 1 8 5 2 17 10 10 12 10 10 10 10 10 10 10 10 10 10 10 10 10	5 9 9 9 9 9 9 9 9 9 9 9 9 9	0 17 6 1 0 6 8 5 1 0 28 10 0 0 0 3 6 0 0 0 3 10 29 0 1 0 20 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 29 0 0 20 20 20 20 20 20 20 20 20 20 20 20	0 2 0 0 0 0 0 0 1 0 7 0 7 0 7 0 0 0 0 0 0 0	0 33 2 10 17 6 19 1 0 1 4 1 3 0 10 4 5 5 1 5 4 2 0 0 12 3 15 0	1 2 3 4 3 2 1 6 670 0 3 2 12 27 15 0 7 8 1 20 38 55 1 1 5 16 1 5 16 1 5	0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, formates, b.che, Latabelleif, Aerosaccese g. fereosacces</li> <li>b. bateria, fortabelaritz, Actobateria, Actobateria, Moltabelaitz, Mo</li></ul>
270 271 273 274 275 276 277 278 279 280 281 282 284 286 285 286 286 287 288 290 291 292 294 295 294 295 295 295 295 295 295 295 295 295 295	4 12 13 2 13 2 9 34 40 0 7 1000 43 3 27 16 0 11 5 64 7 0 8 7 0 8 2 12 13 10 10 10 10 10 10 10 10 10 10	49 75 0 54 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 6 5 6 7 1 121 6 7 1 8 7 1 8 5 2 17 10 12 3 8	5 4 0 2 0 0 0 0 0 0 15 0 4 0 0 0 2 25 5 0 6 0 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1	0 17 6 1 0 6 8 5 15 1 0 28 0 0 0 0 0 10 29 0 10 24 22 0 34 8 34 8 34 10 10 10 10 10 10 10 10 10 10	0 2 29 0 0 20 20 20 20 20 20 20 20 20 20 20 20	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 33 2 10 0 17 6 19 1 0 1 4 1 5 1 5 4 2 0 0 12 3 15 4 4 1 5 1 5 4 2 0 0 12 3 10 1 17 6 19 1 0 1 17 6 19 1 0 1 17 6 19 1 10 1 17 6 19 1 10 1 17 10 1 17 10 1 17 10 1 17 10 1 17 10 1 17 10 1 17 10 10 1 17 10 10 1 17 10 10 10 10 10 10 10 10 10 10 10 10 10	1 2 3 0 8 21 7 4 3 2 2 16 670 0 3 2 12 7 5 1 2 0 78 1 2 0 8 55 1 1 5 16 1 5 5 1 1 5 1 1 2 1 7 4 3 2 1 7 4 3 2 1 7 4 3 2 1 7 4 3 2 1 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 7 8 1 7 7 7 7 7 8 7 7 7 7 7 8 7 7 7 7	0 1 1 2 4 0 50 62 0 0 50 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Laderia, J. Forderia, C. Actrobatoria, J. Addromyredialef, Add</li></ul>
270 271 273 274 275 276 277 276 280 281 283 284 283 284 285 286 289 280 289 289 289 289 289 289 289 289 289 289	4 22 41 33 20 9 44 40 0 7 1001 43 3 7 16 0 11 5 64 27 8 7 0 9 83 7 20 9 83 7 21 5 64 22 8 7 0 9 83 22 23	49 75 0 54 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 2 6 5 4 7 5 0 31 121 6 23 4 9 0 6 23 4 9 0 7 1 8 5 21 7 10 7 1 8 5 2 17 10 10 12 10 10 10 10 10 10 10 10 10 10 10 10 10	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 28 0 0 0 3 6 0 3 10 29 0 1 0 24 22 0 3 4 8 2 2 2 3 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 2 29 0 0 20 12 16 36 0 0 0 1 1 11 27 16 4 9 9 8 11 2 0 19 11 2 7 0 19 11 2 0 0 0 11 11 37 10 0 0 0 12 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 1 0 7 0 7 0 7 0 0 0 0 0 0 0	0 33 2 10 17 6 19 1 0 1 4 1 3 0 10 4 5 5 1 5 4 2 0 0 12 3 15 0	1 2 3 0 8 21 7 4 3 2 2 16 670 0 3 2 2 7 5 1 20 7 8 1 20 8 55 1 1 5 675 1 5 5 5 1 5 5 5 1 5 5 5 5 1 5 5 5 5 5	0 1 1 2 4 0 5 0 0 0 2 0 7 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, formates, b.che, Latabelleif, Aerosaccese g. fereosacces</li> <li>b. bateria, fortabelaritz, Actobateria, Actobateria, Moltabelaitz, Mo</li></ul>
270 271 273 274 275 276 277 278 279 280 281 282 284 286 285 286 286 287 288 290 291 292 294 295 294 295 295 295 295 295 295 295 295 295 295	4 12 13 2 13 2 9 34 40 0 7 1000 43 3 27 16 0 11 5 64 7 0 8 7 0 8 2 12 13 10 10 10 10 10 10 10 10 10 10	49 75 0 54 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 6 5 6 7 1 121 6 7 1 8 7 1 8 5 2 17 10 12 3 8	5 4 0 2 0 0 0 0 0 0 15 0 4 0 0 0 2 25 5 0 6 0 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1	0 17 6 1 0 6 8 5 15 1 0 28 0 0 0 0 0 10 29 0 10 24 22 0 34 8 34 8 34 10 10 10 10 10 10 10 10 10 10	0 2 29 0 0 20 20 20 20 20 20 20 20 20 20 20 20	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 33 2 10 0 17 6 19 1 0 1 4 1 5 1 5 4 2 0 0 12 3 15 4 4 1 5 1 5 4 2 0 0 12 3 10 1 17 6 19 1 0 1 17 6 19 1 0 1 17 6 19 1 10 1 17 6 19 1 10 1 17 10 1 17 10 1 17 10 1 17 10 1 17 10 1 17 10 1 17 10 10 1 17 10 10 1 17 10 10 10 10 10 10 10 10 10 10 10 10 10	1 2 3 0 8 21 7 4 3 2 2 16 670 0 3 2 12 7 5 1 2 0 78 1 2 0 8 55 1 1 5 16 1 5 5 1 1 5 1 1 2 1 7 4 3 2 1 7 4 3 2 1 7 4 3 2 1 7 4 3 2 1 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 4 3 2 1 7 7 7 8 1 7 7 7 7 7 8 7 7 7 7 7 8 7 7 7 7	0 1 1 2 4 0 50 62 0 0 50 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Laderia, functiones, lacking, Lackabelleief, Annocessen g. Functions,</li> <li>c. Lateria, functiones, lacking, functiones, contraporteduction, functiones, functiones, schala, edotophia, edotophia, functiones, functiones,</li></ul>
270 271 273 274 275 276 277 278 280 281 283 283 283 284 285 286 286 285 286 285 286 285 286 285 291 291 291 291 291 295 296 295 296 295 295 296 295 295 295 295 295 295 295 295 295 295	4 12 41 33 2 0 9 34 40 0 7 1000 43 3 7 1000 43 3 7 1000 43 3 7 1000 43 3 7 100 11 5 64 7 0 9 83 22 12 13 13 10 0 9 10 10 10 10 10 10 10 10 10 10 10 10 10	49 75 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 5 2 6 5 4 7 1 1 2 6 5 6 7 1 8 5 2 1 1 1 1 1 1 1 1 1 1 1 1 1	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 28 0 0 0 3 6 0 3 10 29 0 1 0 24 22 0 3 4 8 2 2 2 3 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 2 29 0 0 20 12 16 36 0 0 0 1 1 11 27 16 4 9 9 8 11 2 0 19 11 2 7 0 19 11 2 0 0 0 11 11 37 10 0 0 0 12 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 33 2 10 0 1 17 6 19 1 0 1 4 5 5 1 5 4 2 0 0 12 3 5 0 12 3 5 0 12 3 5 4 2 0 0 1 17 6 19 1 0 1 17 6 19 1 0 1 1 7 6 19 1 1 1 7 6 19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 2 3 0 8 21 7 4 3 2 2 16 670 0 3 2 2 7 5 1 20 7 8 1 20 8 55 1 1 5 675 1 5 5 5 1 5 5 5 1 5 5 5 5 1 5 5 5 5 5	0 1 1 2 4 0 5 0 0 0 2 0 7 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, J. minians, J. bateria, J. Actioalizaria, J. Actioany etalset J. Actiony etalset J. Actionalizaria, J. Actioalizaria, J. Bateria, J. Actioalizaria, J. Actioalizaria, J. Actioalizaria, J. Bateria, J. Actioalizaria, J. Bateria, J. Actioalizaria, J. Contella, J. J. J. J. Bateria, J. Actioalizaria, J. J. Bateria, J. Actioalizaria, J. Actioalizaria, J. Actioalizaria, J. Actioalizaria, J. J. Bateria, J. Actioalizaria, J. Acti</li></ul>
270 271 273 274 275 276 277 278 280 281 283 284 285 286 287 288 289 281 281 285 286 287 288 289 281 292 293 294 295 295 295 295 295 295 295 295 295 295	4 12 41 13 20 9 14 40 0 7 1001 43 3 27 16 0 1 3 3 27 16 0 1 5 64 27 8 7 0 9 10 10 10 10 10 10 10 10 10 10	49 75 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 22 1 59 2 6 5 4 32 5 6 31 121 0 6 3 4 9 0 6 7 1 8 5 2 1 121 0 6 3 4 9 0 7 1 1 1 1 1 1 1 1 1 1 1 1 1	5 4 0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 8 5 15 1 0 8 5 10 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 29 0 0 20 12 16 36 0 0 5991 1 1 1 1 1 1 27 6 4 99 8 11 2 0 15 7 0 15 7 0 15 7 0 0 15 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 10 0 0 0 0 0 0 0 0 0 0 0 0 0	0 33 2 10 1 17 6 19 1 0 1 41 3 0 10 1 1 1 1 0 1 41 3 0 10 1 17 6 19 10 1 17 6 19 10 1 17 6 19 10 1 17 6 19 10 1 17 6 19 10 1 1 1 1 1 1 1 1 1 1 1 1 1	1 2 23 1 3 0 8 21 7 4 3 2 2 16 6 70 0 3 2 12 27 15 0 78 1 20 38 55 1 1 5 16 1 5 0 0 3 2 20 0 8 21 7 43 2 2 16 7 9 0 8 21 7 43 2 2 16 9 0 8 21 7 7 43 2 2 16 9 0 8 21 7 7 43 2 2 16 9 0 8 21 7 7 43 2 2 16 9 0 8 21 7 7 43 2 2 16 9 0 0 8 21 7 7 8 2 1 7 9 9 1 9 9 1 9 9 1 9 9 1 9 9 1 9 9 1 9 9 1 9 9 1 9 9 1 9 9 1 9 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 1 9 1 9 1 9 1 9 1 9 1 2 1 1 1 1	0 1 1 2 4 0 50 0 62 0 7 0 7 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, furnicates, b.tchab.ctation, b.tchabelleki, furnicaccase g. furnicates, f.tchanyesta, f.tchabeterista, furnicates, fu</li></ul>
270 271 273 274 275 276 277 278 280 281 283 284 285 286 289 280 280 280 281 284 285 286 280 280 281 284 285 286 280 280 280 281 284 285 286 280 280 280 280 281 281 283 284 285 285 285 285 285 285 285 285 285 285	4 12 41 13 20 9 14 40 0 7 1001 43 3 7 16 0 11 5 64 27 5 64 27 8 7 0 9 83 7 15 15 15 15 15 15 15 15 15 15	49 75 0 1 5 4 0 0 0 0 2 0 0 0 0 2 0 0 0 0 0 2 0 0 0 0 1 0 0 0 0	0 22 1 59 2 6 5 4 22 50 121 0 6 0 7 1 8 5 2 17 10 122 1 121 0 6 7 1 8 5 2 1 121 121 121 121 121 121	5 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 17 6 1 0 6 8 5 15 1 0 7 8 10 0 0 0 0 0 0 0 0 0 0 0 0 0	D 2 2 9 0 0 2 0 2 0 0 0 5 9 1 1 1 5 9 1 1 1 2 7 0 1 2 0 0 1 1 1 2 7 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 10 0 0 0 0 0 0 0 0 0 0 0 0 0	0 38 2 10 0 1 17 6 9 1 0 1 4 1 0 0 4 5 5 1 5 4 2 0 0 12 3 5 15 0 4 3 8 11 0 1 2 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 7 6 9 1 1 1 7 6 9 1 1 1 7 6 9 1 1 1 7 6 9 1 1 1 7 6 9 1 1 1 7 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 2 2 3 3 0 8 2 1 7 4 3 2 2 6 70 0 3 2 12 27 5 0 78 1 20 8 55 1 5 6 1 5 0 0 2 2 2 2 7 4 3 2 2 7 4 3 2 2 1 6 6 7 7 9 8 2 7 7 4 3 2 7 7 8 9 7 7 9 8 9 7 7 9 9 7 9 9 7 9 9 9 9	0 1 1 2 4 0 62 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, immanes, b.cha, Latobalderia, Antonacasse g. immacacass.</li> <li>b. bateria, introductoria, Antonacaria, Antonacaria, Antonaciasse, Antonacaria, Shaha, adotta/ta.</li> <li>b. Bateria, introduct, Cantagorota, Collapinka, J.ambaderiak, J.Mahuder, J.agan, Mikhab P., isani, grapp.</li> <li>b. bateria, introduct, Batha, Bachiad, Bachiad, Bankhaderiak, Mahuder, J.ambaderiak, Mahuder, J.ambaderiak, J.Mahuder, J.ambaderiak, J.Mahuder, J.ambaderiak, J.Mahuder, J.ambaderiak, J.Mahuder, J.ambaderiak, J.Mahuder, J.ambaderiak, J.Mahuder, J.J., J. Bateriak, J. Actobateriak, Antonacariak, J.Mahuder, J.J., J. J. Bateriak, J. Actobateriak, J.Mahuder, J.J., J.Mahuder, J.J., J. J. Bateriak, J. Actobateriak, J.Mahuder, J.Mahuder, J.J., J.J. J. J. Bateriak, J. Actobateriak, J. Constanting, J. Katabateriak, J.Mahuder, J.Mahumendek, J.Mahukenek,</li></ul>

	132	120	123	121		12	727			22	
308	11 24	0	6 26	0	4	4	0	3	14 20	1	0 k_Bacteria;p_Verucomicrobiata;c_Verucomicrobiata;c_Verucomicrobiata;o_Pedosphaeraecae;s_ 7 k_Bacteria;p_Tirmicutes;c_Clostrida;o_Occillos;i nies;f_Ruminococcase;e_s_s_
310	5	37	0	0	5	2	0	1	0	0	v K_auccentopy_nnihodosc_obstantato_obstantato_ocontropotestatesk 0 k_Bacterizyp_ActinobacteriotaxCorrobacteriales/CorrobacterialeskCollinelia.s_Collinelia.serofaciens
311	16	5	9	8	10	8	1	2	8	0	2 k_Bacteria;p_Firmicutes:c_Clostridia;o_Peptoroccales:f_Peptorocccareae;g_;s
312	0	0	34	0	6	0	0	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroida;o_Bacteroida;cs;f_Marinifilacea;;g_Odoribacter;s_
313	13	32	1	0	0	D	0	2	1	0	$0 \ k\_Bacteria; p\_Cyanobacteria; x\_Cyanobacteria; a\_Chloroplast; f\_Chloroplast g\_Chloroplast descent and the second sec$
314	0	4	2	0	14	10	1	1	46	0	$2\ k\_Bacteria; p\_firmicute; c\_clostridia; o\_Lachnospiraceae; g\_Blautias\_Lachnospiraceae\_bacterium and the state of the s$
315	56	0	1	0	0	0	2	0	27	0	1 k_Bacteria;p_Deferribacterota;c_Deferribacteres;o_Deferribacterales;f_Deferribacteraceae;g_Mucispirilum;s
316	37	8	13	13	1	6	9	3	4	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidia;s;f_Muribaculaceac;g_Muribaculaceac;s
317	16	0	5	0	3	2	0	7	11	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;/_Nitrosomonadiceae.g_GOUTA6;s
318	4	0 34	1	3 0	5	6 0	1 3	6 0	15 0	1	0 k_Bacteria;p_Frencides;c_Clostr/dup_Peptotreptococales-Tasileefales;f_Anaerovaracaose.g_tubacterium_modatum_groups 0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;p_Bicketsiales;f_Mitochondria;g_Mitochondria
320	21	0	10	0	7	10	0	3	12	6	0 k_Bacteria;p_Actinobacteriota;c_Acidenicrobia;o_Microtrichales;f_Ilumatobacteraceae;g_C1500-29_marine_group
321	1	1.3	14	2	2	3	0	1	1	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcareae
322	36	6	5	0	2	6	0	20	7	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;p_Rhizobiales;f_Xanthobacteracea;e;g_Bradyrhizobium;s_Bradyrhizobium;elkanii
323	31	0	O	1	3	5	o	9	o	o	0 k_Bacteria;p_Himicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136_group;s_Lachnospiraceae_bacterium
324	20	63	2	2	0	2	2	1	1	0	0 k_Bacteria;p_Actinobacterista;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces
325	2	0	5	0	3	8	0	11	12	0	0 k_Bacteria;p_Actinobacteriota;c_Acidimicrobila;o_IMCC26256;t_IMCC26256;g_MCC26256;a_Actinobacteria_bacterium
326	1	4	6	0	0	2	3	0	11	0	$0 \ k\_Bacteria;p\_Firmicute;;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Blautia;s\_Lachnospiraceae\_bacterium$
327	35	0	30	0	1	0	0	2	7	0	0 k_Bicteria;p_Cyanobacteria;z_Cyanobacteria;o_Cyanobacteriale;;f_Chroococcidiopsaceae;g_Alitereila;s_
328	23	0	6	0	3	22	0	10	20	0	1 k_Bacterizp_Proteobacteriac_Alphaproteobacteria.p_Acetobacteriales.f_Acetobacteriaceae
329	5	54	0 16	4	0 6	1	0 4	0 8	0 20	0 0	D k_Bacteria;p_Hrmicutes;c_Bacilito;Baciliales;f_Planococcasea;g_Sporosarcina;_Sporosarcina_psychrophila 1 k_Bacteria;p_Bacteroidota;c_Bacteroidia;p_Bacteroidia;o;f_Muhbaculacea;;g_Muribaculacea;s_
331	22	0	16	0	14	33	0	15	45	2	K
332	4	21	2	1	1	3	1	1	1	0	0 k_Bacteria;p_Actinobacterista;c_Actinobacteria;o_Conymebacteriales;f_Nocardiacea;g_Rhodococcus;s_Rhodococcus;erythropolis
333	0	47	0	3	1	D	1	D	0	o	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Adinetobacter;s_Adinetobacter_lwoffii
334	11	0	12	0	6	13	0	8	13	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;p_Burkholderiales;f_Methylophilaceae;g_;s_
335	6	0	7	0	8	9	0	13	23	0	0 k_Bacteria;p_Proteobacteria;e_Gammaproteobacteria;o_Burkholderiaks;f_TRA3-20;g_TRA3-20;s_
336	19	0	11	2	3	15	0	6	10	2	$0\ k\_Bacteria; p\_Cyanobacteria; c\_Cyanobacteria; o\_Chloroplast; f\_Chloroplast; s\_Virgulinella\_fragilis for the second s$
337	14	٥	٥	0	5	3	0	4	6	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;a_Rhizobiales;f_Rhizobiales_incertae_Sedis;g_Alsobacter;s_
338	16	0	9	0	5	18	0	14	11	1	1 k_Bacteria;p_Actinobacteriota;c_Acid microbila;o_Microtrichales;f_Ilumatobacteraceae;g_C1500-29_marine_group;s_
339	6	11	10	4	7	16	1	6	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidia!es;f_Munibaculaceae;g_Munibaculaceae;s
340	13	0	13	0 5	7	6 0	0	2	9 24	0	1 k_Bacteria;p_Acidabacteriota;z_Ckinambacteria;n_Konambacterates;t_Vcinambacteracea;sVcinambacteracea;s 0 k_Bacteria;p_Frmicates;z_Cbatrida;s_lachnospirales;t_lachnospiraceae
341	0	0	0	28	0	0	0	3	0	0	u K_skichrizp_vrmiculesc_Louribusp_istmospratesc_Latinospratese 0 k_Batterizp_WS2c_WS2jo_WS2f_WS2g_WS2s_
343	19	0	6	0	13	12	0	22	12	3	3 k Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiaks;f_Burkholderiaceae;g_Limnobacter;s
344	26	0	2	0	5	2	0	0	4	0	0 k_8acteria;p_Chloroflex;c_Ktedonobacteria;o_Ktedonobactera;cf_Ktedonobacteraceae;x_1959-1;s_
345	15	0	13	0	5	1	0	2	9	0	0 k_Bacteria;p_Bdellovibrionola;z_Bdellovibrionia;o_Bdellovibrionale;s{_Bdellovibrionaceae;g_0M27_clade;s
345	0	28	O	0	o	D	0	0	0	0	0 k_Bacteria
247	1	0	1	ä.	27	0	0		0	0	04 Buterina Statistica Chattilita Ordinaished Busicerraneur Education since energy
347 348	1 19	0	1	11 0	32 6	0 18	0	3 12	0 23	0	0 k_Sectoriag_Firmiculess_Cootridug_Docillegicalest_Burninosoccareage_Eubactorium_siteeum_progs 0 k_Dactoriagfrontcaatoriagcommapproteobactoriag_Oceanoophilalest_Peoploangellacaseg_Unitids
								3 12 6D			
348	19	0	6	o	6	18	o		23	o	0 k_Bacteria;p_Protecbacteria;c_Gammaproteobacteria;o_Oceanospirilales;t_Pseudohongrellaceae;g_8);t10;s_
348 349	19 435	0 0	6 39	0 0	6 30	18 48	0 0	60	23 1275	o o	0 I- Bacterlay_Protoclascienias_Gammaproteobacterias_Oeanoopirillaies.[_Presolotorgieliasaesg_Bly335s_ 0 Ik_Bacterlay_Protoclascienias_Gammaproteobacterias_Barholdersitesi.f_Comannovásciaseg_Comannovas, Lonsanovas, Lensterali
348 349 350	19 436 9	0 0 0	6 39 2	0 0 0	6 30 3	18 48 4	0 0 0	6D 9	23 1275 24	0 0 0	0 F_Bacterias_Protoclascterias_Gammaproteobacterias_Oceanoppribles(_Presoborogrellasaese_Bly005_ 0 k_Bacterias_Proteclascterias_Gammaproteobacterias_Barkholderales/_Comanonadaceaee_Comamonas_Comamonas_Lessesi 0 k_Bacteriag_Protoclascterias_Gammaproteobacterias_Barkholderales/_Comanonadaceaee
348 349 350 351 352 353	19 436 9 18 1 21	0 0 0 0 6	6 39 2 2 3 0	0 0 0 0 0	6 30 3 0 4 3	18 48 4 0 9	0 0 0 0 0	6D 9 0 5 0	23 1275 24 4 6 0	0 0 0 1 0	<ul> <li>b. Jasteria,Pretebacteria,Gammaproteobacteria,Gammaproteobacteria,Oreadoser,Dreadoser,Drytós,</li></ul>
348 349 350 351 352 353 354	19 436 9 18 1 21 0	0 0 0 0 6 0	6 39 2 3 0 0	0 0 0 0 0 0	6 30 3 0 4 3 1	18 48 4 9 1 0	0 0 0 0 0 0	6D 9 0 5 0 31	23 1275 24 4 6 0 2	0 0 0 1 0 9	D   Bacteriag_ Protociacteriag_ Cammaprotociacteriag_ Decasoropifilates(_Precedency # laceseg_ Comanonas, Lonamonas, Lenterial D   Bacteriag_ Protociacteriag_ Cammaprotociacteriag_Bachaderiates(_Comanonadaceae, _Comanonas, Lonamonas, Lenterial D   Bacteriag_Protociacteriag_Cammaprotociacteriag_Bachaderiates(_Comanonadaceae, _Comanonas, Lenteria) D   Bacteriag_Protociacteriag_Cammaprotociacteriag_Bachaderiates(_Comanonadaceae, _Comanonas, Lenteria) D   Bacteriag_Protociacteriag_Cammaprotociacteriag_Bachaderiates(_Comanonadaceae, _Comanonadaceae, _Comanonas, Lenteriag_Daceae, _Comanonas, Lenteriag_Daceae, _Comanonas, _Comano
348 349 350 351 353 353 354 355	19 435 9 18 1 21 0 4	0 0 0 6 0 0	6 39 2 3 0 0 5	0 0 0 0 0 0 0	6 30 3 0 4 3 1 1	18 48 4 0 9 1 0 4	0 0 0 0 0 0	6D 9 0 5 0	23 1275 24 4 6 0 2 6	0 0 0 1 9 0	D   Bacteriag_Protocolacteriag_Commonstelesteriag_Devicesteriag_Dev
348 349 350 351 352 353 354 355 356	19 436 9 18 1 21 0 4 23	0 0 0 6 0 0 17	6 39 2 3 0 5 0	0 0 0 0 0 0 0 1	6 30 3 4 3 1 1	18 48 4 0 9 1 0 4 4	0 0 0 0 0 0 0	6D 9 0 5 0 31	23 1275 24 4 6 0 2 6 0	0 0 0 1 0 9 0	<ul> <li>b. Baderia,Protechacteria,Cammporte-bacteria,Devide/org/elicaseSyt25</li> <li>b. Baderia,Protechacteria,Cammporte-bacteria,Devide/org/elicaseCommonals_Commonal_Landami</li> <li>b. Baderia,Protechacteria,Cammporte-bacteria,Devide/org/elicaseCommonalsCommonal_Landami</li> <li>b. Baderia,Protechacteria,Gammporte-bacteria,Devide/org/elicaseC_CommonalsCommonal_Landami</li> <li>b. Baderia,Protechacteria,Gammporte-bacteria,Devide/org/elicaseC_CommonalsCommonal_Landami</li> <li>b. Baderia,Protechacteria,Advance/conducteria,protechacteria</li></ul>
348 349 350 351 353 353 354 355	19 435 9 18 1 21 0 4	0 0 0 6 0 0	6 39 2 2 3 0 5 5 0	0 0 0 0 0 0 0	6 30 3 0 4 3 1 1	18 48 4 0 9 1 0 4	0 0 0 0 0 0	6D 9 0 5 0 31	23 1275 24 4 6 0 2 6 0 0 0	0 0 0 1 9 0	D   Bacteriag_Protocolacteriag_Commonstelesteriag_Devicesteriag_Dev
248 349 350 351 352 354 355 356 356	19 436 9 18 1 21 0 4 23 0	0 0 0 6 0 17 31	6 39 2 3 0 5 0	0 0 0 0 0 0 1 0	6 30 3 4 3 1 1 0	18 48 4 0 9 2 0 4 4 0	0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0	23 1275 24 4 6 0 2 6 0	0 0 1 0 9 0 0	<ul> <li>b. Jasteria,Pretechateria,Gammaprotechateria,DevaloaregaPilaied,PreedolorgeNasser,Diytös</li></ul>
248 349 350 351 352 353 354 355 356 356 358	19 435 9 18 1 21 0 4 23 0 11	0 0 0 6 0 17 31 0	6 39 2 3 0 0 5 0 0 0 0 0	0 0 0 0 0 0 1 0 0	6 30 3 4 3 1 1 0 0 10	18 48 4 0 9 1 0 4 4 5 3	0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0	23 1275 24 4 6 0 2 6 0 0 0 9	0 0 1 0 9 0 0 0	<ul> <li>b   staterisp_Protostaterisc_Gammaprotostaterisp_Decoderogialisase_Byt255_</li> <li>c   staterisp_Protostaterisc_Gammaprotostaterisp_Byt265_Constronadscase_Constronads_Constronates_Construction_Constronates_Construction_Constronates_Construction_Constraints_Constronates_Construction_Constructio</li></ul>
348 349 350 351 353 354 355 356 355 358 359	19 435 9 18 1 21 0 4 23 0 11 5	0 0 0 6 0 17 31 0 0	6 39 2 3 0 5 0 5 0 0 9	0 0 0 0 0 0 1 0 0 0	6 30 3 4 3 1 1 0 0 10 5	18 48 4 0 9 1 0 4 4 5 3 6	0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0	23 3275 24 4 6 0 2 6 0 0 9 7	0 0 1 0 0 0 0 0 0 0	<ul> <li>b   storeinsp_methoductinisc_Gammaproteoba</li></ul>
348 349 350 351 353 354 355 356 356 359 360	19 436 9 18 1 21 0 4 23 0 11 5 8	0 0 0 6 0 17 31 0 0 25	6 39 2 2 3 0 5 0 5 0 0 0 9 0	0 0 0 0 0 0 1 0 0 0 0 1	6 30 3 0 4 3 1 1 0 5 2	18 48 4 0 2 2 0 4 4 5 3 6 0	0 0 0 0 0 0 0 0 0 0 0 0	6D 9 0 5 0 31 7 3 0 5 5 3	23 1275 24 4 6 0 2 6 0 9 7 0	0 0 1 0 0 0 0 0 0 0 0	<ul> <li>b   stateling_Pretablacteria_Gammaproteblacteria_Osanoopribles(_Presoborgelisese_Byt255_</li> <li>c   stateling_Pretablacteria_Gammaproteblacteria_Osanoopribles(_Commondacese_Commonds_Commond_Larshell</li> <li>c   stateling_Pretablacteria_Gammaproteblacteria_Datablacesia(_Commondacese_Commonds_Commond_Larshell</li> <li>c   stateling_Pretablacteria_Gammaproteblacteria_Datablacesia(_Commondacese_Commonds_Commond_Larshell</li> <li>c   stateling_Gammaproteblacteria_Datablacesia(_Gammaproteblacteria_Datablacese_Commonds_Commondacese)</li> <li>c   stateling_Gammaproteblacteria_Datablacesia(_Gammaproteblacteria_Datablacese)</li> <li>c   stateling_Gammaproteblacteria_Datablacesia(_Gammaproteblacteria_Datablacese)</li> <li>c   stateling_Gammaproteblacteria_Datablacesia(_Greeningacese_Commondacese)</li> <li>c   stateling_Gammaproteblacteria_Datablacesia(_Freeningacese_Commondacese)</li> <li>c   stateling_Gammaproteblacteria_Datablacese</li> <li>c   stateling_Gammaproteblacteria_Datablacese</li> <li>c   stateling_Gammaproteblacesia_Gammaproteblacese_Gammaproteblacese</li> <li>c   stateling_Gammaproteblacesia_Gammaproteblacese</li> <li>c   stateling_Gammaproteblacesia_Gammaproteblacesesia_Gammaproteblacese</li> <li>c   stateling_Gammaproteblacesia_G</li></ul>
248 349 350 351 352 353 354 355 356 355 358 359 360 361 362 363	19 436 9 18 1 21 0 4 23 0 11 5 8	0 0 0 0 17 31 0 25 3 0 31	6 39 2 2 3 0 0 5 0 0 9 0 0 41 0	0 0 0 0 0 1 0 0 0 1 25 0 0	6 30 3 0 4 3 1 1 0 5 2	18 48 9 1 0 4 4 0 4 5 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6D 9 0 5 0 31 7 3 0 5 5 3	23 3275 24 4 6 0 2 6 0 9 7 0 9 7 0 0 0 0 0 0		<ul> <li>b. Jackeriag, Prekolacteriag, Gammaprokolacteriag, Jakhoberiaksf, Gransmonakseg, Jakhober, Jackeriag, Prekolacteriate, Gammaprokolacteriag, Jakhoberiaksf, Gransmonakseg, Gammonak, Jackeriateriateriateriateriateriateriateriat</li></ul>
348 349 350 351 353 354 355 356 355 358 359 360 361 362 363 364	19 435 9 18 1 21 0 4 23 0 11 5 8 0 1 1 5 7	0 0 0 6 0 17 31 0 0 25 3 0 31 0	6 39 2 2 3 0 0 5 0 0 0 0 0 0 0 41 0 2	0 0 0 0 0 0 0 1 0 0 1 25 0 0 0 1	6 30 4 3 1 1 0 5 2 0 0 0 0 3	18 48 4 0 5 2 0 4 4 5 6 0 0 0 0 1 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 5 3 0 0 18 5	23 1275 24 4 6 0 2 6 0 9 7 0 0 0 0 0 0 0 11	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeria, Pretokacteria, Gammaprotokacteria, Osonooprilais/, Presolvorgalizase, Psytös,</li></ul>
348 349 350 351 354 355 356 355 356 355 356 360 361 362 363 364 365	19 435 9 18 1 21 0 4 23 0 11 5 8 0 1 1 0 7 19	0 0 0 6 0 17 31 0 0 25 3 0 31 0 1	6 39 2 3 0 0 5 0 0 0 0 0 0 0 0 0 0 0 2 2 2	0 0 0 0 0 0 0 1 0 0 1 25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 3 4 3 1 1 0 5 2 0 0 0 0 3 3 3	18 48 4 0 1 0 4 4 0 4 5 6 0 0 0 1 6 0 0 0 0 0 0 0 1 6 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 5 3 0 0 18 5 1	23 1275 24 4 6 0 2 6 0 9 7 7 0 0 0 0 0 0 11 11	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackrisky_Prekadakteriak_Gammaprotekskateriak_Osanooprilaied_Preedskorgelacese_DsytSs_</li> <li>c. Jackrisky_Prekadakteriak_Gammaprotekskateriak_Commondakeseg_Commonaks_Commonak_lenterial</li> <li>c. Jackrisky_Prekadakteriak_Gammaprotekskateriak_Commondakeseg_Commonaks_Commonak_lenterial</li> <li>c. Jackrisky_Prekadakteriak_Gammaprotekskateriak_Jackriskeriak_Generalendekese</li> <li>c. Jackrisky_Prekadakteriak_Gammaprotekskateriak_Jackriskeriak_Generalendekese</li> <li>c. Jackrisky_Prekadakteriak_Gammaprotekskateriak_Jackriskeriak_Jakiseriak_Gammaprotekskateriak</li> <li>c. Jackrisky_Prekadakteriak_Abhaprotekskateriak_Jackriskeriak_Jakiseriak_Gammaprotekskateriak</li> <li>c. Jackrisky_Prekadakteriak_Abhaprotekskateriak_Jackriskeriak_Jakiseriak_Jakiseriak_Jakiseriak_Jakiseriak_Jakiseriak</li> <li>c. Jackrisky_Prekadakteriak_Abhaprotekskateriak_Johaprotekskateriak_Jakiseriak</li> <li>d. Jackrisky_Prekadakteriak_Abhaprotekskateriak_Johaprotekskateriak_Johaprotekskateriak_Jakiseriak</li> <li>d. Jackrisky_Prekadakteriak_Abhaprotekskateriak_Joh</li></ul>
348 349 350 351 353 354 355 356 359 360 361 364 364 365 366	19 436 9 18 1 21 0 4 23 7 1 5 8 0 1 1 5 8 0 1 1 7 19 12	0 0 0 0 17 31 0 25 3 0 31 0 31 0 1	6 39 2 3 3 0 0 5 0 0 0 0 0 0 0 4 1 0 2 2 8	0 0 0 0 0 0 1 0 0 0 0 1 25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 4 3 1 1 0 5 2 0 0 0 0 3	18 48 4 0 9 2 0 4 4 0 3 6 0 0 0 0 1 6 0 9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 5 3 0 0 18 5	23 1275 24 4 6 0 2 6 0 9 7 0 0 9 7 0 0 0 0 11 11 7		<ul> <li>b_lsteries_freiebacheries_beitebacheries_Deutoperliebeit_Predobergelszese_Bytös_</li> <li>b_lsteries_freiebacheries_Gammaperbebacheries_Bahbberieks_Commondeszese_Commonsk_Lententi</li> <li>b_lsteries_freiebacheries_Gammaperbebacheries_Bahbberieks_Hiebergelszese_Commonsk_Lententi</li> <li>b_lsteries_freiebacheries_Gammaperbebacheries_Bahbberieks_Hiebergelszese_Commonsk_Lententi</li> <li>b_lsteries_freiebacheries_Gammaperbebacheries_Bahbberieks_Hiebergelszese_Commonsk_Lententi</li> <li>b_lsteries_freiebacheries_Gammaperbebacheries_Bahbberieks_Hiebergese_Commonsk_Lententies</li> <li>b_lsteries_freiebacheries_AbberberbeiterSchübberbeiter_greiebacheries</li> <li>b_lsteries_freiebacheries_AbberberbeiterSchübberbeiterSchübberberbeiterBahbberbeiterSchübberbeiterBahbberbeiterSchübberbeiterSchübberbeiterSchübberbeiterSchübberbeiterBahbberbeiterSchübberbeiter</li></ul>
348 349 350 351 353 354 355 356 360 361 362 364 364 365 366 367	35 436 9 18 1 21 0 4 23 0 11 5 8 0 1 1 0 7 19 12 2	0 0 0 0 17 31 0 25 3 0 31 0 1 0 1 0	6 39 2 3 0 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 4 3 1 1 0 5 2 0 0 0 3 3 3 3 3 3 4	18 46 4 0 0 2 0 4 4 0 3 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 31 7 1 0 5 3 0 0 18 5 1 10 4	23 1275 24 4 6 0 2 6 0 9 7 0 0 0 0 10 11 11 7 6		<ul> <li>b_lsteries_freetesteries_damapertesteries_freetesteries_freetester_producting_freetesteries</li></ul>
348 349 350 351 353 354 355 356 359 360 361 364 364 365 366	19 436 9 18 1 21 0 4 23 7 1 5 8 0 1 1 5 8 0 1 1 7 19 12	0 0 0 0 17 31 0 25 3 0 31 0 31 0 1	6 39 2 3 3 0 0 5 0 0 0 0 0 0 0 4 1 0 2 2 8	0 0 0 0 0 0 1 0 0 0 0 1 25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 3 4 3 1 1 0 5 2 0 0 0 0 3 3 3	18 48 4 0 9 2 0 4 4 0 3 6 0 0 0 0 1 6 0 9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 5 3 0 0 18 5 1	23 1275 24 4 6 0 2 6 0 9 7 0 0 9 7 0 0 0 0 11 11 7		<ul> <li>b. Jackeria, Presolucturia, Gammaprotolucturia, Descolorgalizzze, Presolucturia, Commonica, Commonica</li></ul>
248 349 350 351 352 354 355 366 367 360 361 363 364 364 365 366 367 368	19 436 9 18 1 21 0 4 23 0 11 5 8 0 11 5 8 0 11 5 7 19 12 2 9	0 0 0 0 17 11 0 25 3 0 11 0 11 0 1 0	6 39 2 3 3 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 1 0 0 1 25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 3 0 4 3 1 1 0 0 0 0 0 0 0 0 3 3 3 10 4 1	18 48 4 0 1 0 4 4 0 3 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 31 7 1 0 5 5 3 0 0 18 5 1 10 4 2	23 1275 24 4 6 0 2 6 0 7 7 0 0 0 0 0 11 11 7 6 8		<ul> <li>b_lsteries_freetesteries_damapertesteries_freetesteries_freetester_producting_freetesteries</li></ul>
248 349 350 351 352 354 355 355 355 355 355 355 365 361 362 363 364 365 366 367 368 369	35 436 9 18 1 21 0 4 23 0 11 5 8 0 11 5 8 0 11 5 7 19 12 2 9 10	0 0 0 0 0 17 31 0 0 25 3 0 31 0 1 0 1 0 0 0 0 0 0 0 0	6 39 2 3 0 0 5 0 0 0 0 0 41 0 2 2 8 5 3 12	0 0 0 0 0 1 0 0 1 25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 4 3 1 1 1 0 5 2 0 0 0 3 3 10 4 10 4 10	18 48 4 0 1 0 4 4 0 3 6 0 0 0 0 1 6 0 9 0 2 4 24	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 31 7 1 0 5 3 0 0 18 5 1 10 4 2 7	23 1275 24 4 6 0 2 6 0 9 7 0 0 0 0 0 0 0 11 11 11 7 6 8 24		<ul> <li>b. Jackrisk, Prekakteria, Gammaprokekteria, Javaberiaki, Gammaprokekteria, Javaberiaki, Gammaprokekteria, Gammaprokekteriak, Gammaprokekt</li></ul>
248 349 350 351 352 355 355 357 358 359 360 361 362 363 364 365 366 366 367 368	19 436 9 18 1 1 21 0 4 23 0 11 5 8 0 11 5 8 0 11 0 7 19 12 2 9 10 0 0	0 0 0 0 17 31 0 25 3 0 0 31 0 1 0 0 1 0 0 31	6 39 2 3 0 0 5 0 0 0 0 41 0 2 2 8 5 3 12 0	0 0 0 0 0 1 0 0 1 25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 4 3 1 1 1 0 5 2 0 0 0 3 3 10 4 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	18 48 4 0 9 1 0 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 31 7 1 0 5 3 0 0 18 5 1 10 4 2 7 0	23 1275 24 4 6 0 2 6 0 0 9 7 0 0 0 0 0 0 0 11 11 7 6 8 24 0 2 2 4 0 0		<ul> <li>b_lsteries_freebacteries_Gammaprotestatries_Owanoprileies/_Presidong/aliasePryto5</li> <li>b_lsteries_freebacteries_Gammaprotestatries_larbite/size/_commondscase_Commonss_Commons_Lenteries</li> <li>b_lsteries_freebacteries_Gammaprotestatries_larbite/size/_commondscase_Commonss_Commons_Lenteries</li> <li>b_lsteries_freebacteries_Gammaprotestatries_larbite/size/_commondscase_Commonss_Commons_Lenteries</li> <li>b_lsteries_freebacteries_Gammaprotestatries_larbite/size/_lieu/size/size_Commonss_Commons_Lenteries</li> <li>b_lsteries_freebacteries_Addatatries</li></ul>
348 349 350 351 353 354 355 355 355 355 355 355 355 355	39 435 9 38 1 21 0 4 23 0 1 3 5 8 0 1 1 5 8 0 1 1 0 7 19 12 2 9 10 0 0 10	0 0 0 0 6 0 17 31 0 25 31 0 31 0 1 0 0 1 0 0 25 31 0 1 0 25 31 0 25 31 0 25 31 0 25 31 0 25 31 0 25 31 31 0 25 31 31 31 31 31 31 31 31 31 31 31 31 31	6 39 2 3 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 1 0 0 1 25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 4 3 1 1 1 0 5 7 0 0 0 0 3 3 10 4 1 0 0 9 9	18 48 4 0 9 1 0 4 4 0 3 6 0 0 1 6 0 0 1 6 0 9 9 0 4 24 0 15	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 5 3 0 0 8 5 1 10 4 2 7 0 13	23 1275 24 4 6 0 2 6 0 9 7 6 0 0 0 0 0 0 11 1 1 1 7 6 8 24 0 33		<pre>b _ istoria_ / retexturis_ Gammaprotecturisistoleristiconionationateistoleristiconionate_istolerist</pre>
248 349 350 351 353 354 355 355 355 355 355 360 360 360 360 360 366 366 366 366 366	19 436 9 18 1 21 0 4 21 0 4 21 0 1 5 8 0 1 0 7 19 10 0 7 19 12 2 9 10 0 10 0 10 0 10 2 3 10 0 11 5 8 0 11 11 11 11 11 11 11 11 11 11 11 11 1	0 0 0 0 0 17 31 0 0 31 0 31 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0	6 39 2 3 0 5 0 0 9 0 0 41 0 2 2 8 5 3 12 0 9 0 13 0	6 6 7 7 8 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	6 30 4 1 1 0 5 2 0 0 3 3 10 4 1 10 0 9 0 8 0 0 8 0 0 8 0 0 8 0 0 0 0 8 0	18 48 4 0 1 0 4 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 3 0 0 18 5 1 10 4 2 7 0 13 0 4 9	23 12275 24 4 6 0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 11 11 7 6 8 24 0 0 13 12 7 9 0 0 13 12 12 12 12 12 12 12 12 12 12 12 12 12		<pre>b _ bctories_ freideb.ctrists_Gammaproteb.ctrists_unitable/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseGammanks_Gammaproteb.ctristsintribate/sist/_commondscaseCommondscaseGammaproteb.ctristsintribate/sist/_societ/sist/_societ/sist/_societ/sist/_societ/societ/socie</pre>
248 349 350 351 353 354 355 356 359 360 361 362 363 364 365 366 365 366 365 366 367 370 371 372 374	39 436 9 18 1 21 0 4 7 7 30 10 7 9 10 22 9 10 0 30 23 4 0 11	0 0 0 0 17 31 0 25 3 0 31 0 31 0 31 0 1 0 0 21 0 0 21 0 0 0 0 21 0 0 0 0 0	6 39 2 3 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 2 2 8 5 3 12 0 9 0 0 13 0 7	6 6 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	6 30 4 1 1 0 5 2 0 0 3 3 10 4 1 0 0 8 0 8 0 8 0 2 2 2 2 2 2 2 2 2 2 2 2	18 48 4 0 9 1 4 4 0 4 0 0 0 1 5 0 9 0 4 2 4 0 15 0 15 10 15 10 15 10 15 10 15 10 15 10 15 10 15 10 10 10 10 10 10 10 10 10 10 10 10 10	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 3 0 0 18 5 1 0 4 2 7 0 13 0 4 2 7 0 13 0 4 2 7 0 13 1 2 7 1 0 5 1 2 7 1 2 7 1 7 1 7 1 7 1 7 1 7 1 7 1 7	23 1275 24 4 6 0 2 6 0 9 7 0 0 0 0 0 0 0 0 0 0 0 11 11 11 7 6 8 24 0 12 7 9 0 12 9 9 0 12 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		b. Laderba_freebacherba_clamperbeketerba_larbideristif_ereinforestatesefreebacherba. b. Laderba_freebacherba_clamperbeketerba_larbideristif_leverstateseforearonist_feramones_terterbit b. Laderba_freebacherba_clamperbeketerba_larbideristif_leverstateseconteronist_feramones_terterbit b. Laderba_freebacherba_clamperbeketerbits_larbideristif_leverstateseconteronist_feramones_terbits b. Laderba_freebacherba_freebacherba_larbideristif_leverstateseconteronist_feramones_terbits b. Laderba_freebacherba_freebacherba_larbideristif_leverstateseforebacherba b. Laderba_freebacherba_Abdebacherba_Abdebacherba_fact b. Laderba_freebacherba_Abdebacherba_
248 349 351 351 353 354 355 355 355 360 367 362 364 365 366 366 366 366 366 367 368 369 360 371 371 371 374	19 436 9 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 17 31 0 25 3 3 0 31 0 0 10 0 21 0 0 21 0 0 0 21 0 0 0 0 0	6 39 2 3 0 5 0 0 0 0 0 0 0 0 0 0 41 0 2 2 8 5 3 12 0 9 0 13 0 7 1	6 6 7 7 7 7 7 7 7 7 7 7 7 7 7	6 30 4 1 1 0 0 0 0 0 0 3 3 0 0 0 0 0 0 0 0 0 0	18 48 4 0 2 0 4 4 0 3 6 0 0 1 6 0 9 0 4 24 0 15 0 12 16 10 7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 3 0 0 18 5 1 10 4 2 7 0 13 0 4 9	23 1275 24 4 6 0 2 6 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	b. J. Jacksig, Pressbactsis, Gammprotokatsis, Johannoprikke, Johannoprikke, Gammprotokatsis, Gammprotokatsis, Johannoprikke, Johannoprikk
248 349 350 351 353 354 355 359 360 361 362 363 364 365 366 366 366 366 366 367 368 369 370 371 371 374 374 375	39 4386 9 13 1 21 0 4 23 0 1 5 8 0 1 1 5 8 0 1 1 5 7 19 10 0 10 0 10 10 10 10 10 10 10 10 10 10	0 0 0 0 17 31 0 0 25 3 3 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 39 2 3 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 7 7 7 7 7 7 7 7 7 7 7 7 7	6 30 4 3 1 0 5 7 0 0 0 3 3 10 0 9 0 8 0 9 0 8 0 9 0 8 0 2 9 0 0 9 0 9 0 9 0 9 0 9 0 9 0 9 0 9	18 48 4 0 5 1 0 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 31 7 1 0 5 5 3 0 0 18 5 1 10 4 2 7 0 13 0 4 9 11 8 3	23 1275 24 4 6 0 2 6 0 9 7 0 0 0 0 0 0 0 0 0 11 11 7 6 8 24 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b.l.bdreins_freideb.christ_Gammaprotebactristis_Gammaprotebactristis_Gammaprotebactristis_Gammaprotebactristis_Gammaproteb</pre>
248 349 351 351 353 354 355 355 355 360 367 362 364 365 366 366 366 366 366 367 368 369 360 371 371 371 374	19 436 9 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 17 31 0 25 3 3 0 31 0 0 10 0 21 0 0 21 0 0 0 21 0 0 0 0 0	6 39 2 3 0 5 0 0 0 0 0 0 0 0 0 0 41 0 2 2 8 5 3 12 0 9 0 13 0 7 1	6 6 7 7 7 7 7 7 7 7 7 7 7 7 7	6 30 4 1 1 0 0 0 0 0 0 3 3 0 0 0 0 0 0 0 0 0 0	18 48 4 0 2 0 4 4 0 3 6 0 0 1 6 0 9 0 4 24 0 15 0 12 16 10 7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 3 0 0 18 5 1 10 4 2 7 0 13 0 4 9	23 1275 24 4 6 0 2 6 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b _ bctering_ revealuctering_ commonstructure_ commonstructure_ provider commonstructure commonstructure</pre>
248 349 351 353 353 354 355 359 360 361 362 363 364 365 366 367 366 367 363 364 363 364 370 371 372 374 374 375	39 4386 9 11 21 0 4 32 0 12 5 8 0 1 30 0 12 30 0 10 13 34 0 11 5 34 34	0 0 0 0 17 11 0 12 1 0 0 11 0 0 10 0 0 0 10 0 0 0	6 39 2 3 0 5 0 9 0 0 41 0 9 0 41 0 2 8 5 3 12 0 9 0 13 0 7 1 0 7 1 0 7 1 0 7	6 6 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	6 30 4 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	18 48 4 0 1 0 4 4 0 1 6 0 1 6 0 4 4 0 1 5 0 1 5 0 1 2 4 0 1 5 0 1 0 1 0 0 4 4 0 0 1 0 4 4 0 0 0 1 0 4 4 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 1 0		60 9 0 31 7 1 0 5 5 3 0 0 18 5 1 10 4 2 7 0 13 0 4 9 11 8 3	23 1275 24 4 6 0 0 0 0 0 0 0 0 0 0 0 11 11	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b.l.bdreins_freideb.christ_Gammaprotebactristis_Gammaprotebactristis_Gammaprotebactristis_Gammaprotebactristis_Gammaproteb</pre>
248 349 351 351 353 354 355 359 361 362 361 362 364 365 366 365 366 365 366 367 366 367 370 371 372 374 375 374	39 436 9 15 1 21 0 4 7 3 7 9 10 7 19 12 2 9 10 0 10 23 4 0 11 15 13 14 2 2	0 0 0 0 0 17 1 1 0 0 17 0 0 1 0 0 0 1 0 0 0 0	6 39 2 3 0 0 5 0 0 41 0 2 8 5 3 12 0 9 0 13 0 7 1 0 7 1 0 6 0 7 1 0 1 0 1 0 1 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 7 7 7 7 7 7 7 7 7 7 7 7 7	6 30 4 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	18 48 4 0 9 1 0 4 4 0 0 0 0 1 6 0 9 0 4 2 4 0 15 0 12 16 10 7 0 6 7 1 10 1 10 10 10 10 10 10 10 10 10 10 10	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 5 5 3 1 7 1 0 5 3 0 0 18 5 10 4 2 7 0 13 0 4 9 11 8 3 6 1	23 1275 24 6 0 2 6 0 9 7 0 0 0 0 11 11 7 6 2 4 0 11 7 6 2 4 0 0 0 0 0 0 0 0 0 0 0 0 0		b. J. Jacksig, Pressbacksis, Camparotebacksis, Camparotebacksis
248 349 351 351 353 354 355 358 360 360 360 360 366 366 366 366 366 367 368 369 360 370 371 372 372 374 375 375 376 376 376	19 436 9 11 1 1 1 1 1 1 1 4 2 3 0 1 1 5 8 0 1 1 5 8 0 1 1 5 8 0 1 1 7 19 10 0 10 1 7 19 10 0 1 1 1 2 1 0 1 1 2 1 0 1 1 2 1 1 1 1 2 1	0 0 0 0 17 31 0 17 31 0 0 31 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	6 39 2 3 0 5 0 0 0 0 0 0 0 0 0 0 2 2 8 5 3 12 0 9 0 13 0 7 1 0 6 0 6	0 0 0 0 0 0 1 1 25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 30 4 1 1 0 5 2 0 0 3 3 10 4 1 0 0 9 2 8 0 9 2 2 8 0 2 9 2 2 8 8 0 2 9 2 2 8 8 9 2 2 8 8 9 2 9 2 8 8 9 9 9 9	18 48 4 0 5 1 0 4 4 0 3 6 0 0 1 6 0 0 4 4 0 12 0 12 0 12 0 12 0 12 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 5 5 31 7 1 0 5 3 7 1 0 5 3 7 1 0 5 5 3 0 0 18 5 1 0 4 2 7 0 13 0 4 9 1 8 5 1 7 1 0 5 5 3 1 7 1 0 5 5 0 31 7 1 0 5 0 31 7 1 0 5 0 31 7 1 0 5 0 31 7 1 0 5 0 31 7 1 0 5 5 0 31 7 1 0 5 5 0 31 7 1 0 5 5 0 31 7 1 0 5 5 5 3 1 7 1 0 5 5 5 3 1 0 5 5 5 5 3 1 0 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	23 3275 24 4 6 0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Laderia, Preseizentic, Gammpreseizentica, Janisolemis, Commonica, Commonica, Commonica, Lanismi</li> <li>b. Laderia, Preseizentica, Gammpreseizentica, Janisolemis, Commonica, Commonica, Lanismi</li> <li>c. Laderia, Preseizentica, Gammpreseizentica, Janisolemis, Commonica, Commonica, Lanismi</li> <li>c. Laderia, Preseizentica, Gammpreseizentica, Janisolemis, Commonica, Commonica, Lanismi</li> <li>c. Laderia, Preseizentica, Gammerseizentica, Janisolemis, Commonica, Commonica, Commonica, Lanismi, Application, Commonica, Application, Commonica, Pressi December, Commonica, Application, Commonica, Commonica, Application, Pressi December, Pressi December, Pressi December, Pressi December, Pressi December, Commonica, Application, Pressi December, Pressi Dec</li></ul>
248 349 351 351 353 354 355 359 360 361 362 363 364 365 365 366 365 366 367 370 370 370 370 370 370 370 374 375 376 377 376 377 378 379 379 379 379 379 379 379 379 379 379	19 436 9 1 1 2 1 0 4 2 0 1 5 8 0 1 0 7 19 12 2 9 10 0 10 13 14 0 11 5 15 8 0 1 9 19 12 2 9 10 0 11 5 1 1 1 0 1 1 2 1 0 1 1 1 2 1 0 1 1 1 2 1 0 1 1 2 1 0 1 1 1 2 1 0 1 1 1 2 1 0 1 1 1 1	0 0 0 0 17 11 0 0 75 3 0 11 0 0 0 0 11 0 0 0 0 0 0 0 0 0 0 0	6 39 2 3 6 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	6 30 4 3 1 1 0 5 2 0 0 3 3 10 4 1 0 9 0 8 0 2 9 0 2 8 0 9 2 2 8 0 9 2 2 8 0 9 2 8 0 9 2 8 0 9 2 8 0 9 9 2 8 0 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	18 48 4 0 5 1 0 4 4 0 5 0 0 1 6 0 9 0 4 4 0 5 0 1 1 6 0 9 0 4 4 0 5 0 1 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 7 1 0 5 5 3 0 0 18 5 1 0 4 9 11 8 3 6 1 3 0 0 12 7 0 13 1 7 1 0 5 5 3 0 0 14 7 1 0 5 5 3 1 7 1 0 5 5 0 1 7 1 7 1 0 5 5 0 1 7 1 7 1 0 5 5 0 1 7 1 7 1 0 5 5 0 1 7 1 7 1 0 5 5 5 3 1 7 1 7 1 0 5 5 5 3 1 7 1 7 1 0 5 5 5 3 1 7 1 0 5 5 5 3 1 7 1 7 1 0 5 5 5 3 1 7 1 7 1 0 5 5 5 3 1 0 0 1 1 7 1 0 5 5 5 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1	23 1275 24 6 0 9 7 0 0 0 0 11 11 7 6 3 4 0 12 11 7 6 11 12 9 0 12 12 12 12 12 12 12 12 12 12	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b.l.bdebis_freebacteris_Commonsteakteris_Lensingeriebeteris_Commonsteakteris_Commonsteakterist</pre> b.bdebiss_freebacteris_Commonsteakterist_Lensingeriebeterist_Commonsteakterist b.bdebiss_freebacteris_Commonsteakterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Densingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Densingeriebeterist_Lensingeriebet
248 349 350 351 352 353 354 355 355 355 355 360 360 360 360 360 360 360 360 360 360	19 436 9 11 0 4 23 0 12 5 8 0 1 3 7 19 12 2 9 10 0 11 5 8 0 1 7 19 12 2 9 10 0 10 12 1 1 5 8 0 1 1 1 1 1 2 1 0 4 2 3 0 1 1 5 1 1 1 1 1 2 1 1 1 1 2 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 39 2 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 10 3 4 1 1 0 0 10 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 0 10 0 0 0 0 0 0 0 0 0 0 0 0 0	18 48 4 0 9 2 0 4 4 0 3 6 0 0 0 4 4 0 5 0 2 1 6 0 9 0 4 2 4 0 5 0 2 1 6 0 9 0 4 2 0 9 0 4 4 0 9 2 0 4 4 0 9 2 0 9 2 0 9 2 0 9 0 9 1 9 0 9 0 9 0 9 0 9 0 9 0 9 0 9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 0 31 7 1 0 5 5 3 0 0 18 5 1 10 4 2 7 0 13 0 4 9 11 8 3 6 1 3 0 2 0 8	23 3275 24 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 9 0 0 0 0 0 0 0 0 1 0 0 3 0 0 0 0 0 0 0 0	b. Justiczy indexistaticzy competebatraticzy Justiczie (ammentakane justiczy indexistaticzy commentakane justiczy indexistaticzy commentakane justiczy indexistaticzy indexistaticzy Justiczy
248 349 351 351 353 354 355 359 360 361 362 363 364 365 365 366 365 366 367 370 370 370 370 370 370 370 374 375 376 377 376 377 378 379 379 379 379 379 379 379 379 379 379	39 436 9 11 21 0 4 3 7 3 9 0 10 7 19 12 7 9 10 0 10 10 10 10 10 10 10 10 10 10 10 1	0 0 0 0 17 11 0 0 75 3 0 11 0 0 0 0 11 0 0 0 0 0 0 0 0 0 0 0	6 39 2 3 6 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	6 30 4 3 1 1 0 5 2 0 0 3 3 10 4 1 0 9 0 8 0 2 9 0 2 8 0 9 2 2 8 0 9 2 2 8 0 9 2 8 0 9 2 8 0 9 2 8 0 9 9 2 8 0 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	18 48 4 0 5 1 0 4 4 0 5 0 0 1 6 0 9 0 4 4 0 5 0 1 1 6 0 9 0 4 4 0 5 0 1 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 9 0 5 7 1 0 5 5 3 0 0 18 5 1 0 4 9 11 8 3 6 1 3 0 0 12 7 0 13 1 7 1 0 5 5 3 0 0 14 7 1 0 5 5 3 1 7 1 0 5 5 0 1 7 1 7 1 0 5 5 0 1 7 1 7 1 0 5 5 0 1 7 1 7 1 0 5 5 0 1 7 1 7 1 0 5 5 5 3 1 7 1 7 1 0 5 5 5 3 1 7 1 7 1 0 5 5 5 3 1 7 1 0 5 5 5 3 1 7 1 7 1 0 5 5 5 3 1 7 1 7 1 0 5 5 5 3 1 0 0 1 1 7 1 0 5 5 5 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1	23 1275 24 6 0 9 7 0 0 0 0 11 11 7 6 3 4 0 12 11 7 6 11 12 9 0 12 12 12 12 12 12 12 12 12 12	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b.l.bdebis_freebacteris_Commonsteakteris_Lensingeriebeteris_Commonsteakteris_Commonsteakterist</pre> b.bdebiss_freebacteris_Commonsteakterist_Lensingeriebeterist_Commonsteakterist b.bdebiss_freebacteris_Commonsteakterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Densingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Lensingeriebeterist_Densingeriebeterist_Lensingeriebet

386	12	1	0	28	0	2	0	5	1	0	0 k_Bacteria;p_Myxococcota;c_Polyangia;o_Haliangiales;f_Haliangiaceae;g_Haliangium;s
387	4	0	1	0	3	8	0	5	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae
368	13	9	z	0	9	D	0	4	10	o	1 k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales-Tissierellales;f_Anaerovoracaceae;g_Eubacterium_brachy_group;s
389	13	4	0	6	4	0	0	0	7	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae; <u>z_</u> ;z_Clostridium_sp.
390	8	0	3	0	14	18	0	1	8	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG-014;f_Clostridia_UCG-014;g_Clostridia_UCG-014;s_
391	0	0	٥	0	0	D	0	D	1	14	5 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_A81;g_A81
392	15	0	1	0	11	D	o	2	0	0	0 k_Bacteria:p_Bacteroidota:c_Bacteroidia:o_Bacteroidales:f_Muribaculaceae;g_Muribaculaceae:s_
393	15	0	5	1	4	0	0	0	6	0	0 k Bacteroidota: c Bacteroidato: f Munbaculaceacig Munbaculaceacis
394	1	2	11	0	2	0	0	0	2	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UCG-002;s_
395	18	0	2	0	4	0	0		0	0	0 k_Bacteria;p_Protecbacteria;c_Gammaproteobacteria;o_Burkholderiales/_Nitrosomonadaceae.g_IS-44;s_
396	4		4	0	2	4	0	13	11	1	1 k_Bacteria;p_Protectaacteria;c_Gammaprotectaacteria;o_alteromonadale;sf_Alteromonadaceae;g_Rheinheimera;s_
397	5	0	4	0	10	3	0	0	11	0	
398	8			0	10	0	0	1		0	1 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
	21	0	0						2		0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_Chthoniobacteraceae;g_Candidatus_Udaeobacter;s_
399	28	1	1	1	0	0	0	0	0	0	4 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG-001;s_
400	0	1	3	1	0	0	0	0	21	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae;MK4A136_group;s
401	4	0	3	1	4	21	3	0	0	0	1 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidiale;f_Munbaculaceae;g_Munbaculaceae;s
402	9	0	3	0	3	15	0	3	13	0	0 k_Bacteria;p_Bdellovibrionota;c_Oligoflexia;o_0319-6620;f_0319-6620;g_0319-6620;s_
403	12	0	10	0	6	10	0	5	13	0	1 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Ga0077536;f_Ga0077536;s_Ga0077536;s_
404	1	2	3	2	2	12	1	5	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oucillospirales
405	4	0	4	0	5	7	0	3	9	0	1 k_Bacteria;p_Bdellovibrionota;c_Oligoflexia;o_0319-6620;f_0319-6620;g_0319-6620
406	7	0	7	0	4	10	0	0	4	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Sphingobacteriales;f_NS11-12_marine_group;g_NS11-12_marine_group;s_
407	0	0	17	0	0	4	0	1	10	O	$1 \ k\_Bacteria;p\_Hrmicute;;c\_Clostridia;o\_Lachnospirales;f\_Lachnospiraceae;g\_Roseburia$
408	6	1	1	0	3	2	0	4	2	0	$0 \ k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;a\_Rhizobiales;f\_Methyloligellaceae;g\_;s\_interiation and the state of the state $
409	0	0	0	0	0	1	0	0	24	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidia!es;f_Munibaculaceae;g_Munibaculaceae;s_
410	1	0	2	0	0	3	0	32	0	0	$0\ k\_Bacteria; p\_Actinobacteriota; c\_Actinobacteria; o\_PropioniBacteriales, f\_Nocardioidaceae; g\_Kribbelia; s\_Kribbelia_sp.$
411	0	0	0	0	D	D	0	26	0	0	$0\ k\_Bacteria;p\_Germatimonadota;c\_Germatimonadetes;o\_Germatimonadales;f\_Germatimonadaceae;g\_s\_$
412	2	0	4	1	1	1	0	6	4	0	$0 \ k\_Bacteria; p\_Bacteroidota; c\_Bacteroidia; o\_Bacteroidia; c\_f\_Tannerellaceac; \underline{r}arabacteroides; s\_Parabacteroides\_coldsteinii \ bacteroides; bacteroides;$
413	0	22	0	0	0	0	0	0	0	0	0 k_Bacteria
414	3	0	2	0	5	3	0	1	3	0	$0\ k\_Bacteria;p\_Dependentiae;c\_Babeliae;o\_Babeliae;f\_Babeliae;g\_Babeliae;s]$
415	8	o	9	0	5	5	0	В	9	3	$0\ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Burkholderiales; f\_Cornamona daceae; g\_Sphaerotilus; f\_Cornamona daceae; f=Cornamona $
416	17	0	0	0	1	1	0	0	4	1	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Anaerotruncus;s_
417	594	0	63	11	36	120	0	61	1334	19	21 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Pluralibacter;s_Pluralibacter_gergoviae
418	4	0	0	2	5	0	0	D	14	٥	0 k_Bacteria;p_Firmicute;c_Clostridia;o_Clostridia_vadin8860_group;(_Clostridia_vadin8860_group;e_Clostridia_vadin8860_group;s
419	9	0	5	0	2	8	o	4	12	٥	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_
420	22	0	0	0	17	D	0	D	0	o	0 k_Bacteria:p_Himicutes:c_Bacili:o_Lactobaciliales;f_Lactobaciliaceae:g_Lactobacilius:s_Lactobacilius_ingluviei
421	0	0	o	1	24	1	0	o	0	0	0 k_Bacteria;p_Hrmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136_group;s_
422	0	0	5	1	2	1	1	0	6	1	0 k_Bacteria;p_Cyanobacteria;z_Vampirivibrionia;o_Gastranaerophilales;f_Gastranaerophilales;g_Gastranaerophilales;z_
423	5	0	2	0	3	1	0	1	5	0	1 k_Bacteria;p_Bacteroidots;c_Bacteroidia;o_Cytophagales;f_Cyclobacteriaceaerg_Algoriphagus;s_
424	5	0	5	0	6	8	0	8	8	o	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;of_;g_s_
425	0	0	0	0	0	0	0	71	0	0	01 Exterior Southbetteine Alternationalistic Sciencible Complexity Description
425	0	0	0	0	0	0	0	71	0	0	0 k_Beterina_Protobacterina_Abhaprotobacterina_Bhiobhikes/_Devolaceseg_Devolaca_
425	12	0	٥	o	o	D	o	2	1	o	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Nitrosomonadaceae;g_MND1;s
425 427	12 0	0 0	0 0	0 18	0	D	0 0	2 D	1 0	o o	0 k_bsterlas_frotebucterlas_Carmoproteobacterlas_Buthablersiss/_Mitosomonaduceseg_VMD1s_ 0 k_bsterlas_Pateschoteras_Caralibacterus_Caralibitus_Perbacterlaf_Caralibitus_Perbacterlas_Candiditus_Perbacter
426 427 428	12 0 0	0 0 15	0 0 0	0 18 1	0 0 0	D D 0	0 0 0	2 0 0	1 0 0	0 0 0	0 k_lasterias_Proteioacenias_Commapotenolasterias_Burkholderales/Mitrosomonadaceseg_MRD1s_ 0 k_lasterias_Patenolasterias_Cracillasterias_Condidatus_Perilasteriad_Condidatus_Perilasterias_Candidatus_Perilasterias_ 0 k_lasterias_Turobacteriotas_Fundbacterias_Fundbacterialest_Leptontriniaceaeg_Leptotrichias_
425 427 428 429	12 0 0 0	0 0 15 0	0 0 0	0 18 1 0	0 0 0	D D 0	0 0 0	2 D 0 0	1 0 0 17	0 0 0	0 k_Bateriaa_Protokolaceteiaa_Cammupoteobateriaa_Butholderuksf_Nitrosomonaduceseg_VMD1s_ 0 k_Bateriaa_Protokolaceteriaa_Candibateriaa_Candibitua_Perisateriad_Candibitua_Perisateriag_Candibitus_Peribateriaa_ 0 k_Bateriaa_Eurobateriotaa_Fuodbateriaa_Fuodbaterialesf_Leptotrichiaeceeg_Leptotrichiaa_ 0 k_Bateriaa_Firmicutesa_Beolica_Fir93f_RF99_8F99
425 427 428 429 430	12 0 0 0	0 0 15 0 0	0 0 0 0	0 18 1 0 0	0 0 0 0	D D 0 D	0 0 0 0	2 D 0 36	1 0 17 0	0 0 0 0	0 k_Bateriag_Proteciaceriag_Communecteducteriag_Burkholderules/_Nitrosomonaduceseg_VMD1s_ 0 k_Bateriag_Palaecolacteriag_Conditacteriag_Condidatus_Perlacteriag_Condidatus_Perlacteriag_Condidatus_Perlacteriag_ 0 k_Bateriag_Eurobateriatag_Fundbateriag_Fundbaterialesf_Leptotrichiaecaeg_Leptotrichiag_ 0 k_Bateriag_Proteciacteriag_Gammuproteolacteriag_NF39
425 427 428 429 430 431	12 0 0 0 0	0 0 15 0 0 12	0 0 0 0 0	0 18 1 0 0 3	0 0 0 0	D D 0 D D	0 0 0 0	2 0 0 36 0	1 0 17 0	0 0 0 0	<ul> <li>b Lasterias_Pretechacterias_Cammaproteobacterias_Muhadérsies/_Mitosomonadaceseg_VMD1s_</li> <li>Lasterias_Pretechacterias_Canabacterias_Candidatus_Prehacterias_Candidatus_Prehacterias_Candidatus_Prehacterias_</li> <li>Lasterias_Pretechacterias_Subbacterias_Lopobacteria(cs_candidatus_Prehacterias_candidatus_Prehacterias_</li> <li>Lasterias_Pretechacterias_Subbacterias_Mitosomonadaterias_Candidatus_Prehacterias_Candidatus_Prehacterias_</li> <li>Lasterias_Pretechacterias_Pretechacterias_Subbacterias_Simplementadaterias_Simplementadaterias_Pretechacterias_Candidaterias_</li> <li>Lasterias_Pretechacterias_Candidaterias_Candidaterias_Candidateriasese_Candidaterias_</li> <li>Lasterias_Pretechacteriases_Candidaterias_Candidateriases_Atopoblem</li> </ul>
426 427 428 429 430 431 432	12 0 0 0 0 0	0 0 15 0 12 12	0 0 0 0 0 0	0 18 1 0 0 3 3	0 0 0 0 0	0 0 0 0 0 0	0 0 0 0 0 0	2 D 0 36	1 0 17 0 0	0 0 0 0 0	B   Bateriag_Protebucketriag_Granibateriag_Buthaldersist/_Mitnamonadaceseg_VMD1s_     B   Bateriag_Protectucteriag_Granibateriag_Granibateriag_Protecturing_Granibateriag_Granibateriag_Development     b   Bateriag_Protectucteriag_Granibateriag_Lingubateriag_Lingtonicitanceseg_Lingtonicitanceseg_Buthale     b   Bateriag_Protectucteriag_Granibateriag_Developmentalistics_Catediatur_Protecturing_Granibateriag_Buthale     b   Bateriag_Protectucteriag_Granibateriag_Developmentalistics_Catediatur_Protecturing_Granibateriag_Buthale     b   Bateriag_Protectucteriag_Granibateriag_Granibateriag_Developmentalistics_Catediateriag_Buthale     b   Bateriag_Protectucteriag_Granibateriag_Granibateriag_Atopobleceseg_Atopoblem     b   Bateriag_Protectucteriag_Granibateriag_Buthale     b   Bateriag_Protectucteriag_Granibateriag_Buthale     b   Bateriag_Protectucteriag_Granibateriag_Buthale     b   Bateriag_Protectucteriag_Granibateriag_Buthale     b   Bateriag_Protectucteriag_Granibateriag_Buthale     b   Bateriag_Protectucteriag_Buthale     b   Bateriag_Protect
426 427 428 429 430 431 432 433	12 0 0 0 0	0 0 15 0 12 12 12 0	0 0 0 0 0	0 18 1 0 0 3	0 0 0 0 0 1	D D 0 D D	0 0 0 0	2 0 0 36 0	1 0 17 0 0 0	0 0 0 0 0 0	b Lasterias_Protobacterias_Cammuportobacterias_Butholderolast_Mitrosomonaduceseg_VMD1s_     b Lasterias_Protobacterias_Candidatus_Peribacterias_Candidatus_Peribacterias_     b Lasterias_Frontobacterias_Fundbacterias_Londbacteriast_Londbacteriast_Londbacteriast_Candidatus_Peribacterias_     b Lasterias_Frontobacteriast_Substantias_NoteBacteriast_Londbacteriast_Londbacteriast_Candidatus_Peribacteriast_     b Lasterias_Protobacteriast_Substantias_NoteBacteriast_Candidatus_Peribacteriast_     b Lasterias_Protobacteriast_Cammuportobacterias_Kandhammudalest_Bhodanobacteriasteriast_Candidaturest_     b Lasterias_Protobacteriast_Cammuportobacteriass_Kandhammudalest_Bhodanobacteriaster
425 427 428 430 431 432 433 433	12 0 0 0 0 0	0 0 15 0 12 12 12 0 16	0 0 0 0 0 0 0 0	0 18 1 0 0 3 3 0 0	0 0 0 0 0 1	D D D D D 1 D	0 0 0 0 0 0 0 0	2 0 0 36 0 9 0	1 0 17 0 0 0 0	0 0 0 0 0 0 0	b   Bacteriag_Protocolacteriag_Cammaperotoolacteriag_Bendbacteriag_Mittage=
425 427 428 429 430 431 432 433 434 435	12 0 0 0 0 0 0 12	0 0 15 0 12 12 0 16 7	0 0 0 0 0 0 0 0 0	0 18 1 0 3 3 0 0 0	0 0 0 0 0 1 0	D D D D D 1 D 17	0 0 0 0 0 0 0 0 0	2 0 0 36 0 9 0 4	1 0 17 0 0 0 0 0	0 0 0 0 0 0 0	<ul> <li>b Lasteriaa_Pretosbacteriac_Cammapertosbacteriaa_Mitholdersiksf_Mitrosomonadceseg_VMD1s_</li> <li>b Lasteriaa_Pretosbacteriac_Gondibateriaa_Casiddau, Perbacteriad_Casiddau, Perbacteriag_Condidaus, Perbacteriag_Casiddaus, Perbacteriag_Cas</li></ul>
425 427 428 430 431 432 433 433	12 0 0 0 0 0 0 12	0 0 15 0 12 12 12 0 16	0 0 0 0 0 0 0 0	0 18 1 0 0 3 3 0 0	0 0 0 0 0 1	D D D D D 1 D	0 0 0 0 0 0 0 0	2 0 0 36 0 9 0	1 0 17 0 0 0 0	0 0 0 0 0 0 0	b   Bacteriag_Protocolacteriag_Cammaperotoolacteriag_Bendbacteriag_Mittage=
425 427 428 429 430 431 432 433 434 435	12 0 0 0 0 0 0 12 0 5	0 0 15 0 12 12 0 16 7	0 0 0 0 0 0 0 0 0	0 18 1 0 3 3 0 0 0	0 0 0 0 0 1 0	D D D D D 1 D 17	0 0 0 0 0 0 0 0 0	2 0 0 36 0 9 0 4	1 0 17 0 0 0 0 0	0 0 0 0 0 0 0	<ul> <li>b Lasteriaa_Pretosbacteriac_Cammapertosbacteriaa_Mitholdersiksf_Mitrosomonadceseg_VMD1s_</li> <li>b Lasteriaa_Pretosbacteriac_Gondibateriaa_Casiddau, Perbacteriad_Casiddau, Perbacteriag_Condidaus, Perbacteriag_Casiddaus, Perbacteriag_Cas</li></ul>
425 427 428 429 430 431 432 433 434 435 436	12 0 0 0 0 0 12 0 8 5	0 0 15 0 12 12 0 16 7 0	0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 3 3 0 0 0 0 0 0	0 0 0 0 1 0 0	D D D D D D 0 1 0 17 17	0 0 0 0 0 0 0 0 0 0 2	2 0 36 0 9 0 4 30	1 0 17 0 0 0 0 0 4 1	0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b Lasterias_Protobacterias_Gammapoteobacterias_Minbaldersias/_Minosomonadaceseg_VMD1s_</li> <li>c Lasterias_Protobacterias_Gandbacterias_Candidatus_Perbacterias{_Candidatus_PerbacteriasOddatus_Perbacterias</li></ul>
426 427 428 430 431 432 433 434 435 436 437	12 0 0 0 0 0 12 0 5 5 22	0 15 0 12 12 0 16 7 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 2	0 18 1 0 3 3 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0	D D O D D 0 1 0 17 17 8	0 0 0 0 0 0 0 0 2 0	2 0 36 0 9 0 4 30 0	1 0 17 0 0 0 0 4 1 2	0 0 0 0 0 0 0 0 0 0 0 0 1	0 I. Jacterias, Protechacterias, Carmaporteobacterias, Surbhaldersiet/ Mitosomonaduceseg_VMD1s_ 0 I. Jacterias, Protechacterias, Caralitatus, Peribacterias(Caralitatus, Peribacterias, Candidatus, Peribacterias, Candidatus, Valendado, Kandidatus, Candidatus, Ca
426 427 428 429 430 431 432 433 434 435 436 437 438	12 0 0 0 0 0 12 0 5 22 0	0 0 15 0 12 12 0 16 7 0 0 0	0 0 0 0 0 0 0 0 0 0 2 1	0 18 1 0 3 3 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0	D 0 0 0 1 0 17 1 8 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 0	1 0 17 0 0 0 0 0 4 1 2 13	0 0 0 0 0 0 0 0 0 1	<ul> <li>b   Exterlise_Protochacteriae_Cammaporteobacteriae_Mithodersiets/_Mitrosomonodoceseg_VMD15</li></ul>
426 427 428 429 430 431 432 433 434 435 436 437 438	12 0 0 0 0 0 12 0 5 22 0	0 0 15 0 12 12 0 16 7 0 0 0	0 0 0 0 0 0 0 0 0 0 2 1	0 18 1 0 3 3 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0	D 0 0 0 1 0 17 1 8 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 0	1 0 17 0 0 0 0 0 4 1 2 13	0 0 0 0 0 0 0 0 0 1	<ul> <li>b Laderbag_Protochacteriac_Commonstrativag_Burkholdersiets/_Mitrosomonadcesseg_VMD15</li></ul>
425 427 428 430 431 432 433 434 435 436 437 438 439 439 4400	12 0 0 0 0 0 12 0 5 22 0	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 2 1	0 18 1 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 2 2	D 0 0 0 1 0 17 1 8 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 0	1 0 17 0 0 0 0 4 1 2 13 8 36	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b _ bacteriafreebebacteriaGammaporteobacteriafreebebacteriafreebebacteriawhite_https://www.analytic.com/datus_pressures_pressures_pressures_pressures_white_https://www.analytic.com/datus_pressureswhite_https://www.analytic.com/datus_pressures_pressures_pressures_pressures_pressures_pressures_pressures_pressures_pressures_pressures_pressures_pr</li></ul>
425 427 428 430 431 432 433 434 435 436 437 438 439 440 441	12 0 0 0 0 0 12 0 5 22 0	0 15 0 12 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 3 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 1 0 0 0 0 0 2 0 0	D 0 0 0 1 0 17 1 8 1 4 0 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 0 36 0 9 0 4 30 0 0 4 0 1	1 0 17 0 0 0 0 4 1 2 13 8 36 17	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b Lasterias_Protobacterias_Graniportobacterias_Bubbaldersias/_Pritocomoudcases_WhD1s_</li> <li>c Lasterias_Protobacterias_Granibacterias_Candidatus_Perbacterias_Candidatus_Perbacterias_Granibacterias_Granibacterias_Candidatus_Perbacterias_Granibacteria</li></ul>
425 427 428 430 431 432 433 434 435 436 437 438 439 440 441 442	12 0 0 0 12 0 5 22 0 3 0 2 2 2 2	0 15 0 12 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 3 3 0 0 0 0 0 0 0 0 0 0 0 0 0 1	0 0 0 0 0 1 0 0 0 0 2 0 0 0 0	D 0 0 0 1 0 17 1 8 1 4 0 6 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 0 36 0 9 0 4 30 0 0 4 0 0 1	1 0 17 0 0 0 0 0 4 1 2 13 8 36 17 9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   Exterlisp_Protochacterisp_Cammaporteobacterisp_Mathodersists/_Mittosomonodicesse_VMD15</li></ul>
425 427 428 430 431 433 434 435 436 437 438 439 440 441 442 443	12 0 0 0 12 0 5 22 0 3 0 2 2 2 2	0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 22	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 0 3 0 0 0 0 0 0 0 0 0 0 0 1 3	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 1 1 8 1 4 0 6 8 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 0 36 0 9 0 4 30 0 0 4 0 0 1	1 0 17 0 0 0 0 4 1 2 18 8 13 8 56 17 9 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerias, Pretosbacterias, Canapertobacterias, Perbacterias, Canadatus, Canadatu</li></ul>
425 427 428 430 431 432 433 434 435 436 437 438 439 441 442 443 444	12 0 0 0 12 0 5 22 0 3 0 2 2 2 2	0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 22 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 1 3 0 0	0 0 0 0 1 0 0 0 2 0 0 0 0 0 0 0	0 0 0 0 1 0 17 1 8 1 4 0 6 8 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 4 0 0 4 0 1 0 1	1 0 17 0 0 0 0 4 1 2 13 8 36 17 9 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeria, Pretosbacteria, Camapeteobacteria, Perbacteria, Candidata, Candidata, Mapobacea, Mapobacea, Mapobacea, Candina, Candidata, Santhalendateria, Mapobacea, Mapobacea, Robolatorada, Candidata, Candidata, Santhalendata, Candidata, Candidata, Santhalendata, Candidata, Perbacteria, Candidata, Candidata, Santhalendaria, Candidata, Candidata, Candidata, Candidata, Candidata, Perbacteria, Candidata, Candidata, Candidata, Candidata, Candidata, Perbacteria, Candidata, Perbacteria, Candidata, Candidata, Candidata, Candidata, Perbacteria, Candidata, Candidata, Candidata, Candidata, Perbacteria, Candidata, Candidata, Candidata, Candidata, Candidata, Perbacteria, Candidata, Santhaledata, Candidata, Candidata, Candidata, Candidata, Perbacteria, Candidata, Santhaledata, Santhaledata, Candidata, Candidata, Candidata, Candidata, Candidata, Candidata, Candidata, Perbacteria, Candidata, Ca</li></ul>
425 427 428 430 431 432 433 434 435 436 437 438 439 400 401 441 442 443 444	12 0 0 0 12 0 5 22 0 3 0 2 2 2 2	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 22 0 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 13 0 0	0 18 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 17 1 8 1 4 0 6 8 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 4 0 0 4 0 1 1 0 1	1 0 17 0 0 0 0 4 1 2 13 8 36 17 9 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerias, Pretosbacterias, Canapertobacterias, Perbacterias, Canadatus, Canadatu</li></ul>
425 427 428 429 400 431 432 433 434 435 436 437 438 439 440 441 442 443 445 445	12 0 0 0 0 12 0 8 5 22 0 8 5 22 0 8 5 22 0 3 0 2 2 0 7 1 4	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0 22 0 8 0 0 8 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 8 0 1 3	0 18 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 1 1 1 1 8 1 4 0 6 8 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 4 0 0 4 0 1 1 0 1 1	1 0 17 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8		<ul> <li>b. Jackerias, Pretosbacterias, Camponetobacterias, Prebacterias, Candidatus, Candidatus, Candidatus, Candidatus, Prebacterias, Candidatus, Prebacterias, Candidatus, Candidat</li></ul>
425 427 428 429 430 431 432 433 434 435 436 437 440 441 442 443 444 445 445 447	12 0 0 0 0 12 0 8 5 22 0 3 0 7 1 4 12	0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 2 1 6 0 0 1 8 0 1 3 0 1 0	0 18 1 0 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 1 1 0 1 1 3 1 4 0 6 8 0 0 0 0 0 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 6 4 30 0 4 0 0 1 1 0 0 1 1 1 1	1 0 17 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3		<ul> <li>b. Jackerias, Pretosbacterias, Campenteobacterias, Prebacterias, Candidatus, Cand</li></ul>
425 427 428 429 430 431 432 433 434 435 439 440 441 442 443 444 455 445 444 445 445	22 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 15 0 12 12 0 16 7 0 16 7 0 0 0 0 0 0 0 0 0 12 12 12 0 15 12 12 12 0 15 12 12 12 12 12 12 12 12 12 12	0 0 0 0 0 0 0 0 0 2 1 6 0 0 13 0 13 0 0 5	0 18 1 0 3 3 0 0 0 0 0 0 0 0 0 0 0 1 3 0 1 0 0 0 0	0 0 0 0 1 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 1 1 8 1 4 0 6 8 0 0 0 0 0 2 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 6 4 30 0 4 0 0 1 1 0 0 1 1 1 0 0	1 0 17 0 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3 0		<ul> <li>b_lsteries_freeteebacteries_Campeteebacteries_Methoderskef_Mittoaronadiceseg_WRD1</li></ul>
425 427 428 429 430 431 432 433 434 435 435 436 441 442 443 444 444 443 443 444 443 445 445 445	22 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 15 0 12 12 0 16 7 0 16 7 0 0 0 0 0 0 0 0 12 12 0 15 0 12 12 0 15 0 15 12 12 0 15 12 12 12 12 12 12 12 12 12 12	0 0 0 0 0 0 0 0 0 0 1 0 0 1 3 0 0 1 3 0 0 5 1	0 18 1 0 3 0 0 0 0 0 0 0 0 0 0 0 1 3 0 1 0 1	0 0 0 0 1 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 1 1 1 8 1 4 0 6 8 0 0 0 0 0 0 0 2 4	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 4 0 1 1 0 0 1 1 1 0 0 4 5	1 0 17 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3 0 1 2 5 1		<ul> <li>b. Jackeria, Protokalacteria, Cammaportokalatteria, Sankhalderskef, Antokamonadaceseg_WHD15</li></ul>
428 427 48 429 430 431 434 433 434 435 441 442 443 444 444 445 445 445 445 445 445 445	12 0 0 0 12 0 8 5 22 0 7 1 4 12 0 7 1 4 12 0 2 8	0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 19 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 1 3 0 1 0 0 5 1 6	0 18 1 0 0 0 0 0 0 0 0 0 0 0 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 1 1 3 1 3 4 0 6 8 0 0 0 0 0 0 0 0 0 0 2 4 17	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 4 0 1 0 0 1 1 0 0 1 1 3 1 0 0 4 5 15	1 0 17 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 30 1 2 5 1 0 5		<ul> <li>b. Lateria, Presebueria, Camapeteobatria, Subhaberski, Antonomakase, WB15,</li> <li>b. Lateria, Lateria, Lateria, Cambateria, Candatur, Prebatria, Candatur, Candatur, Candatur, Candatur, Prebatria, Candatur, Prebatria, Candatur, Candatur,</li></ul>
428 427 428 429 430 431 432 433 434 435 437 438 439 400 441 444 444 444 445 446 446 446 446 446 446	12 0 0 0 0 12 0 8 5 22 0 3 0 2 2 0 7 1 4 12 0 2 2 8 7	0 15 0 12 12 12 12 16 7 0 0 0 0 0 0 0 0 0 0 19 0 1 0 19 0 1 19 0 19 19 10 10 10 10 10 10 10 10 10 10	0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0	0 18 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 1 1 8 1 4 0 6 8 0 0 0 2 0 2 2 0 2 4 17 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 4 0 1 1 0 0 1 1 1 0 0 4 5 15 3	1 0 17 0 0 4 1 2 18 8 6 17 9 0 1 2 8 30 1 2 5 1 0 5		<ul> <li>b. Jackerias, Pretesbacterias, Canabacterias, Sevidatus, Prebacterias, Candidatus, Candidatus, Paterias, Candidatus, Prebacterias, Candidatus, Candidatus, Candidature, Candidatur</li></ul>
428 427 428 429 431 432 433 434 435 437 443 449 440 441 443 444 444 444 444 444 445 446 446 446 446	12 0 0 0 12 0 8 5 22 0 7 1 4 12 0 7 1 4 12 0 2 8	0 15 0 12 12 0 16 7 0 0 0 0 0 0 22 0 8 0 19 0 19 0 19 0 19 0 19 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 1 3 0 0 1 3 0 0 1 3 0 0 1 3 0 0 1 3 0 0 0 0	0 18 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 1 1 1 8 1 8 1 8 0 0 0 0 0 2 0 2 4 1 7 5 0		2 0 36 0 9 4 30 0 4 0 4 0 1 1 30 0 4 5 15 3 6	1 0 0 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3 0 5 1 0 5 1 0 8 0 5		<ul> <li>b_lsteries_freesebacteries_Gammaperteebacteries_Methodersiets/_Metsoemondscese_WMD1s_</li> <li>b_lsteries_freesbacteries_Gambacteries_Methodersiets/_contributersese_OMD1s_</li> <li>b_lsteries_freesbacteries_Gambacteries_Services_accesteries_Gambacteries_Gambacteries_Contributerses_Contributerses_Contributerses_Contributerses_Services_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses_Bambacterieses_Gambacterieses</li> <li>b_lsteries_freenieses_Caterieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses</li> <li>b_lsteries_freenieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses</li> <li>b_lsteries_freenieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses</li> <li>b_lsteries_Freedeaterieses_Gambacterieses_Gambacterieses_Gambacterieses</li> <li>b_lsteries_freedeaterieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses</li> <li>b_lsteries_Freedeaterieses_Gambacterieses_Gambacterieses_Gambacterieses</li> <li>b_lsteries_Freedeaterieses_Gambacterieses_Gambacterieses_Gambacterieses</li> <li>b_lsteries_Freedeaterieses_Gambacterieses_Gambacterieses_Gambacterieses_Gambacterieses</li> <li>b_lsteries_Freedeaterieses_Gambacterieses_Gambacterieses_</li></ul>
425 427 428 430 431 432 434 435 436 436 437 438 439 430 442 443 444 443 444 445 445 445 445 445 445	12 0 0 0 0 12 0 8 5 22 0 3 0 2 2 0 7 1 4 12 0 2 2 8 7	0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 19 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 1 3 0 0 1 3 0 0 5 1 6 5 1 6 5 1 0	0 18 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 1 1 7 1 8 1 4 0 6 8 0 0 0 0 0 2 4 1 7 5 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 4 30 0 4 1 1 1 1 3 6 5 5 5 6	1 0 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 30 5 1 0 5 1 0 8 0 5 1 0 8 0 2 2		<ul> <li>b. Jackeria, Presebacteria, Campenteobacteria, Prebateriale, Candidatu, Prebateria, Candidatu, Candid</li></ul>
428 427 428 430 431 432 433 434 433 434 433 434 443 443 443	12 0 0 0 0 12 0 8 5 22 0 3 0 2 2 0 7 1 4 12 0 2 2 8 7	0 15 0 12 12 12 12 12 12 12 12 10 10 10 10 10 10 10 10 10 10	0 0 0 0 0 0 0 0 0 0 0 0 1 3 0 0 1 3 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 0 0	0 18 1 0 0 0 0 0 0 0 0 0 0 0 1 3 0 0 0 1 3 0 0 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 1 1 7 1 8 1 4 0 6 8 0 0 0 0 2 4 1 7 5 0 2 4 1 7 5 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 4 30 0 4 0 4 0 1 1 30 0 4 5 15 3 6	1 0 0 0 0 0 0 1 2 13 8 36 17 9 0 1 2 8 30 0 1 2 8 30 0 5 1 0 8 30 0 2 0 8 30 0 17 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b_blacksb_restebs/_freedebacksbCampapeteebacksb_p_Beblacksb_restCandidstup_PerbacksbRestLopobacksbRestLopobacksbCandidstup_PerbacksbCandidstup_PerbacksbRestLopobacksbLopobacksbRestLopob</li></ul>
428 427 428 430 431 432 433 434 435 437 438 439 430 441 443 444 444 445 446 446 446 446 446 446 446	12 0 0 0 0 12 0 8 5 22 0 3 0 2 2 0 7 1 4 12 0 2 2 8 7	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 3 0 0 1 0 0 5 1 6 5 1 0 0 5 1 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 1 7 1 8 1 4 0 6 8 0 0 0 2 0 2 4 17 5 0 2 4 17 5 0 1 0 2 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 9 0 4 30 0 4 30 0 4 0 1 1 0 0 1 1 2 0 0 4 5 5 5	1 0 0 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3 0 5 1 0 5 1 0 8 0 0 5 1 0 10 2 0 0 10 10 10 10 10 0 0 0 0 0 0		<pre>bbcterisfreesbacerisCamperteobactrisfreesbaceristfreesbaceristcampeteriobaceristfreesbaceristcampeteriobaceristfreesbaceristcampeteriobaceristfreesbaceristcampeteriobaceristfreesbaceri</pre>
428 427 428 420 431 432 433 434 435 436 437 443 444 443 444 444 445 448 448 448 448 448 448 448	12 0 0 0 0 12 0 8 5 22 0 3 0 2 2 0 7 1 4 12 0 2 2 8 7	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0	0 18 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 1 1 3 1 4 0 6 8 0 0 0 2 4 1 7 5 0 2 4 1 7 5 0 1 1 1 3 1 1 1 1 1 2 0 2 4 17 1 2 17 1 2 17 1 17 1 2 17 17 1 2 17 17 17 17 17 17 17 17 17 17 17 17 17	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 4 30 0 4 0 4 0 1 1 0 0 4 5 15 3 6 0 5 4	1 0 0 0 0 1 7 1 3 1 2 13 8 3 6 17 9 0 1 2 8 3 0 5 1 0 8 0 5 1 0 8 0 2 0 0 17 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b_lsterise_freebescherise_Communerbescherise_freebescherise_conducture_pressense_con</li></ul>
428 427 428 430 431 432 433 434 435 437 438 439 430 441 443 444 444 445 446 446 446 446 446 446 446	12 0 0 0 0 12 0 8 5 22 0 3 0 2 2 0 7 1 4 12 0 2 2 8 7	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 2 3 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 1 7 1 8 1 4 0 6 8 0 0 0 2 0 2 4 1 7 5 0 2 0 2 4 1 7 5 0 3 1 3 1 3 1 3 1 3 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 4 30 0 4 30 0 4 30 0 4 30 0 4 5 5 3 6 0 3 5 4 33	1 0 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 30 5 1 0 8 0 5 1 0 8 0 2 0 10 6 3		<ul> <li>b. Jackeria, Presebueria, Camperiobatiria, Subhabérski, Antoemondese, Wills,</li> <li>c. Jackeria, Presebueria, Grabberia, Canduberia, Prebetria, Candubit, Candubit, Candubit, Bhobbit, Candubit, Candubit, Prebetria, Candubit, Candubit,</li></ul>
428 427 428 430 431 432 433 434 433 434 433 434 433 443 443	12 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 1 1 1 4 0 6 8 0 0 0 2 0 2 4 1 7 5 0 2 4 1 7 5 0 2 4 1 7 5 0 2 0 2 0 2 0 0 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 4 30 0 4 0 4 0 1 1 0 0 4 5 15 3 6 0 0 4 13 6 0 5 4 13 0	1 0 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3 0 5 1 0 8 0 5 1 0 8 0 2 0 0 17 0 0 0 0 4 17 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>bbitelity_freebub_crists_Camupeteebubtelity_Privateriat_Anterprivateriat_conductorsy_White_Camupeteebuteriat_Privateriat_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuse</pre>
428 427 428 429 430 431 432 433 434 435 437 438 439 400 441 443 444 445 446 446 446 446 446 446 446 446	12 0 0 0 0 2 0 8 5 2 0 3 0 2 2 0 7 1 4 12 0 2 8 7 12 8 7 12 8 7 12 8 7 12 0 8 5 2 0 0 8 5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 0 12 12 0 12 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 1 7 1 8 1 4 0 6 8 0 0 0 2 0 2 4 2 7 5 0 1 0 3 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 4 30 0 4 30 0 4 30 0 4 30 0 4 5 5 3 6 0 3 5 4 33	1 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3 0 5 1 0 8 0 2 0 10 6 3 0 0 0 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>bbcterisfreedebacterisCampeterebacterisfreedebacteristfreedebacteristcanddatus_Prebacteristcanddatusinternetwistand internetwistand internetwistinte</pre>
428 427 428 430 431 432 433 434 433 434 433 434 433 443 443	12 0 0 0 0 2 0 8 5 2 0 3 0 2 2 0 7 1 4 12 0 2 8 7 12 8 7 12 8 7 12 8 7 12 0 8 5 2 0 0 8 5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 1 1 1 4 0 6 8 0 0 0 2 0 2 4 1 7 5 0 2 4 1 7 5 0 2 4 1 7 5 0 2 0 2 0 2 0 0 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 4 30 0 4 0 4 0 1 1 0 0 4 5 15 3 6 0 0 4 13 6 0 5 4 13 0	1 0 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3 0 5 1 0 8 0 5 1 0 8 0 2 0 0 17 0 0 0 0 4 17 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>bbitelity_freebub_crists_Camupeteebubtelity_Privateriat_Anterprivateriat_conductorsy_White_Camupeteebuteriat_Privateriat_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuteriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupeteebuseriateria_Camupetee</pre>
428 427 428 429 430 431 432 433 434 435 437 438 439 400 441 443 444 445 446 446 446 446 446 446 446 446	12 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 0 12 12 0 12 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 18 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 1 7 1 8 1 4 0 6 8 0 0 0 2 0 2 4 2 7 5 0 1 0 3 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 36 0 4 30 0 4 0 4 0 1 1 0 0 4 5 15 3 6 0 0 4 3 1 0 0 4 5 15 3 6 0 0 4 3 0 0 1 1 0 0 1 1 0 0 1 1 1 0 0 1 1 1 1	1 0 0 0 4 1 2 13 8 36 17 9 0 1 2 8 3 0 5 1 0 8 0 2 0 10 6 3 0 0 0 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>bbcterisfreedebacterisCampeterebacterisfreedebacteristfreedebacteristcanddatus_Prebacteristcanddatusinternetwistand internetwistand internetwistinte</pre>
428 427 428 429 431 432 433 434 433 434 433 434 443 444 443 444 443 444 443 444 443 444 443 444 445 443 444 445 445	12 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 0 12 12 0 16 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 16 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 1 1 1 8 1 4 0 6 8 0 0 0 2 4 1 7 5 0 2 4 1 7 5 0 2 1 1 0 0 0 0 0 0 0 0 0 1 1 7 1 8 1 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		2 0 0 36 0 9 0 4 0 4 0 1 1 0 0 4 5 15 3 6 0 5 4 13 6 0 5 4 13 6 0 5 4 13 6 0 5 4 13 6 0 14 0 15 15 15 15 15 15 15 15 15 15 15 15 15	1 0 0 0 4 1 2 1 8 36 1 7 9 0 1 2 8 3 0 5 1 0 8 0 2 0 0 0 6 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b_lsteries_freebescheries_Gamperbeketries_feebescheries_feebescheries_gebescheries_gebescheries_Gambeteries_feebescheries_gebe</li></ul>

464	0	24	0	0	0	0	0	0	0	0	0 k_Bacteria
465	14	0	0	0	9	6	0	D	0	0	1 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_A2;s
466	6	0	9	0	4	11	0	4	10	3	1 k_Bacteria;p_Actinobacteriota;c_Acidimicrobila;o_Microtrichales;f_llumatobacteraceae;g_CL500-29_marine_group;s_
467	31	0	6	0	10	6	0	2	2	0	$1\ k\_Bacteria; p\_Actinobacteriota; c\_Coriobacteria; o\_Coriobacteriales; f\_Eggerthellacea; g\_Enterorhabdus; s\_interorhabdus; s\_interorhabdus;$
468	1	0	1	0	10	6	0	0	0	0	$1 \ k\_Bacteria; p\_Actinobacteriota; c\_Coriobacteria; o\_Coriobacteriales; f\_Eggerthellaceae$
469	31	0	2	0	2	7	2	35	7	o	$0\ k\_Bacteria; p\_Actinobacteriota; c\_Actinobacteria; a\_Streptomycetales; f\_Streptomycetacea; g\_Streptomyces$
470	9	0	2	0	0	2	0	D	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;a_Propionibacteriales;f_Propionibacteriaceae;g_Micropruina;s
471	0	11	0	0	0	0	0	0	0	0	0 Unknown
472	0	1	0	0	0	4	0	1	8	1	1 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceac;g_;s_
473	6	1	1	1	7	10	1	0	2	0	$0\ k\_Racteria;p\_Firmicutes;c\_Clostridia;o\_Christensenellales;f\_Christensenellarea;g\_Christensenellareae_R.7\_group;s\R.7\_group;s\R.5\_group;s\R.5\_group;s\R.5\_group;s\R.5$
474	9	0	2	0	5	7	0	5	16	1	$1\ k\_Racteria;p\_Cyanobacteria;c\_Cyanobacteria;a\_Chloroplast;f\_Chloroplast;g\_Chloroplast$
475	0	14	2	0	3	0	0	1	1	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136_group
476	0	0	0	0	0	0	1	28	1	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiale;f_Rhizobiaceae;g_Allorhizobium-Neorhizobium-Pararhizobium-Rhizobi
477	7	1	1	з	1	0	0	0	7	0	1 k_Bacteria;p_Firmicutes;c_Clostridia;o_Osciltospirales;f_Ruminococcareae;g_;s_
478	4	0	3	0	7	3	0	4	2	1	0 k_Bacteria;p_Bdellovibrionota;c_Oligoflexia;o_053A03-8-DI P58;1_053A03-8-DI P58;g_053A03-8-DI P58;g_
479	13	0	O	0	o	4	0	D	7	σ	0 k_Bacteria;p_Firmicutes;c_Bacill;o_Bacillales;f_Bacillaceae;g_Urelbacillus;s_Urelbacillus_thermosphaericus
480	5	0	3	0	3	7	0	3	9	o	0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Methylacidiphilales;f_Methylacidiphilaceae;g_;s_
481	11	0	5	0	5	6	0	2	4	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Saprospiraceae;g_Candidatus_Aquirestis;s_
482	4	0	0	0	2	16	0	2	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Defluviitaleaceae;g_Defluviitaleaceae_U06-011;s_
483	1	0	10	0	0	1	4	0	3	0	0 k_Bacteria;p_Cyanobacteria;z_Cyanobacteriia;o_Chloroplast;f_Chloroplast;g_Chloroplast;s_Dryopteris_fragrans
484	11	0	o	0	6	D	0	D	0	o	0 k_Bacteria;p_Firmicutes;c_Bacili;o_Lactobaciliale;;f_Lactobaciliaceae;g_Lactobaciliu;;s_Lactobaciliu;aviarius
485	0	12	o	0	D	D	0	o	0	o	0 k_Bacteria;p_Dependentiae;c_Babeliae;o_Babeliale;;f_Vermiphilaceae;g_Vermiphilaceae;s
486	10	0	7	4	1	6	1	5	15	0	1 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroida!ex;f_Muribaculaceae;g_Muribaculaceae;s_
487	0	15	4	2	0	0	0	0	0	0	0 k_Bacteria;p_Bacterioidota;c_Bacterioidia;o_Bacterioidia!es;f_Prevotellaceae;g_Prevotella;s_Prevotella;s_Prevotella;s
488	2	0	1	0	3	2	0	3	3	2	0 k Bacteria;p Bdellovibrionota;c Oligofienia;o Sivanjgrellales;f Silvanjgrellales;f
489	6	1	0	1	0	13	0	0	0	0	
490	12	0	3	0	0	0	0	3	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadin8960_group;f_Clostridia_vadin8980_group;g_Clostridia_vadin8960_group;s_
											0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium;s_Corynebacterium_durum
491	3	9	2	0	0	1	1	3	1	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae
492	7	0	1	0	0	3	0	0	1	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Ferruginibacter;s_
493	3	2	1	0	0	D	0	4	3	0	2 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_;s_
494	9	0	0	0	0	0	0	1	3	0	0 k_Bacteria;p_Myxococcota;c_Myxococcia;o_Myxococcales;f_Anaeromyxobacteraceae;g_Anaeromyxobacter;s_
495	4	8	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Bacili;o_Erysipelotrichales;f_Erysipelotrichaceae;g_s_
496	4	0	0	0	3	4	0	1	0	0	$0\ k\_Racteria;p\_Firmicute;c\_Clostridia;o\_Christensenellales;f\_Christensenellaceae;g\_Christensenellaceae;s\_Christensenella_sp.$
497	4	0	3	0	2	5	0	7	9	1	2 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_KF-JG30-C25;f_KF-JG30-C25;g_KF-JG30-C25;s_
498	0	0	3	0	0	1	0	7	4	2	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae
499	24	8	5	0	1	3	1	5	0	0	$0\ k\_Bacteria; p\_Actinobacteriota; c\_Actinobacteria; o\_Corynebacteriales; f\_Mycobacteriaceae; g\_Mycobacterium$
500	0	0	0	0	0	59	0	7	203	10	7 k_Bacteria;p_Firmicute;;c_Bacili;p_Lactobacillales;f_Camobacteriaceae;g_Atopostipe;;s_
501	2	0	6	0	1	8	0	0	7	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria
502	4	0	1	0	15	z	0	D	14	o	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Rikenella;s_Rikenella;microfusus
503	4	0	2	0	3	2	0	4	10	0	0 }_Bettrike_Protobactorike_Germaprotobactoriao_PITA13(_PITA13e_PITA13e_
503 504	4 0	0 0	2 33	0 0	3 0	2 D	0 0	4 D	10 0	0	0 k_Bacterias_Protocolactorias_Gammaprotocolactorias_PITA135_PITA135_PITA135_ 8 k_Bacterias_Bacteroidotas_Bacteroidasa_Bacteroidaios_MannelMacsees_Oderbacters_
504	o	0	33	o	0	D	o	D	o	o	0 k_Bacterila;p_Bacteroldota;c_Bacteroldia;o_Bacteroldiales;f_Marinfiliaceae;s_Odonbacter;s_
504 505	0 12	0 0	33 3	0 0	0 1	D Z	0 0	0 2	0 0	0 0	0 k_baderiabaderoidota_baderoidoa_baderoidoined_Marrifiliceore_Odorbaders_ 0 k_baderia_Adroidateristac_Constateria_Constateria_Eggenthelisceore_Enteron1abours_
504 505 506	0 12 1	0 0 0	33 3 3	0 0 0	0 1 4	0 2 1	0 0 0	0 2 0	0 0 3	0 0 0	0 k_bsteriap_bsterioldas_bsteriolap_bsteriolap_bsteriolaiesf_MarrieNacese_Odorbacters_ 0 k_bsteriap_Actinobacteriotas_Conobacteriap_Corobacterialesf_EgentheNaceseg_triterorhabdurs_ 0 k_bsteria
504 505 506 507	0 12 1 0	0 0 0	33 3 3 1	0 0 1	0 1 4 0	0 2 1	0 0 1	0 2 0 5	0 0 3 3	0 0 0	0 k_bisteriap_lasterioldsz_Bisteriodas_Bisteriodasied_Marinfiliscenzg_Odorbisters_ 0 k_bisteriap_Actinobacteristas_Conobacteriap_Conobacterialesif_Eggentheliscenzg_Enterorhabdurs 0 k_bisteriap_Firmicutess_Colonidas_Peptostreptorocales-Takierdalest_Anservorasaceseg_Fendy_XIII_AD0011_props
504 505 506 507 508	0 12 1 0 0	0 0 0 13	33 3 3 1 0	0 0 1 2	0 1 4 0	0 2 1 1 0	0 0 1 0	0 2 0 5 0	0 0 3 3 0	0 0 0 0	0   Baderia, Baderiadota, Baderiadoa, Baderiadokief, Marrifikasee, Odorbader, 0   Baderia, Indinatoriata, Constantinta, Constantinkeif, Eggetteksaese, Internotuskuus, 0   Baderia, Finnicates, Colanda, Pantotirostanosales, Tasierdakeif, Anaerovanascese, Finnik, JULA0001, group, 0   Baderia, Finnicates, Colanda, Pantotirostanosales, Tasierdakeif, Anaerovanascese, Finnik, JULA0001, group, 0   Baderia, Finnicates, Colanda, Pantotirostanosales, Tasierdakeif, Anaerovanascese, Finnik, JULA0001, group, 0   Baderia, Finnicates, Colanda, Pantotirostanosales, Tasierdakeif, Pantet pitococaia, Tasierdakei, Anaerosocaia, Anaerosocaia, Anaerosocaia, Juliandakei, Gaderia, Josef Kalendakeit, Juliandakeita, Jenatoticateria, Pengelonbaderakeif, Jeoardokatesee, Nacardokate, Josef Kalendakeite, Ga
504 505 506 507 508 509	0 12 1 0 0 2	0 0 0 13 16	33 3 3 1 0 2	0 0 1 2 1	0 1 4 0 0	0 2 1 1 0	0 0 1 0 7	0 2 0 5 0 4	0 0 3 3 0 2	0 0 0 0 0	0 k_baderiabaderoideta_Baderoidaa_baderoidesisd_Marrifiliosese_Odorbaders_ 0 k_baderia_Dadroidaa_baderoidaa_baderoidesid_Spectralisesd_Spectralisesd_Spectralisesd_Spectralisesd_ 0 k_baderia_Timoidess_Colotidaga_Perprotestanocolon=Tasientalesid_Adaerovernacesese_Family_XILAXXXII_provas_ 0 k_baderia_Timoidess_Colotidaga_Perprotestanocolon=Tasientalesid_Perplateroprocessare=Tasientaleses_Anamoscous_Anamos
504 505 506 507 508 509 510	0 12 1 0 2 2 0	0 0 0 13 16 0	33 3 3 1 0 2 8	0 0 1 2 1 0	0 1 4 0 0 7	0 2 1 0 0 6	0 0 1 0 7 0	0 2 0 5 0 4 0	0 0 3 0 2 6	0 0 0 0	0 k_baderiabaderoiddax_Baderoidax_Baderoidaixef_Mannefiliceaez_Odorbaders 0 k_baderia_Technolacteristac_Conclusterialize_Conclusterializesf_Eggentheliceaez_Interorbadous 0 k_baderiae_Innocess_Colonidaes_PeriodirestanocalesTaisentalizesf_Anaerovonaccese_Family_UILADIOII_props 0 k_baderiae_Timicatesc_Colonidaes_PeriodirestanocalesTaisentalizesf_PeriodireptococcalesTaisentalizes_Anaerooccus_Ana
504 505 506 507 508 509 510 511 511	0 12 1 0 2 2 0	0 0 13 16 0 1 16	33 3 1 0 2 8 0 0	0 0 1 2 1 0 4 1	0 1 4 0 0 7 2	0 2 1 0 0 6 0	0 0 1 0 7 0 5 0	0 2 0 5 0 4 0	0 3 3 0 2 6 0 0	0 0 0 0 0 0 0	0   Jackrish, Jackrishes, Controlos, Bactanobied, Mannfilicese, Odorbacteris, 0   Jackrish, Lacterishes, Controlacterish, Controlacterishes, Espectifiel Jacker, Jackrishes, All, ADD J. Jackrish, Janaroscous, Jackrishes, J
504 505 506 507 508 509 510 511	0 12 1 0 2 0 1 4	0 0 0 13 16 0 1	33 3 1 0 2 8 0 0 0	0 0 1 2 1 0 4	0 1 4 0 0 7 2 0	0 2 1 0 6 0 0 5	0 0 1 7 0 5	0 2 0 5 0 4 0 0	0 3 3 0 2 6 0	0 0 0 0 0 0	<ul> <li>b. Jackeniska, Jackeniska, Jackeniska, Jackeniski, Marrifikasse, Odorbacken, J.</li> <li>b. Jackeniska, Antrodukteriska, Consbackenika, Orobackenika, Eggerthelasasse, Interohabauk, J.</li> <li>b. Jackeniska, Jernicutes, Constanting, Peptisteratoracela, Taiserbalest, Anterosoraacetez, Jaroh, XII. (2001), grups, Anterosoca, Jackeniska, Jerpisteratoracela, Taiserbalest, Anterosoca anti-Taiserbalest, Anterosoca anterosoca anti-Taiserbalest, Anterosoca anti-Taiserbalest, Antero</li></ul>
504 505 506 507 508 510 511 511 512 513	0 12 1 0 2 0 1 4 3 0	0 0 13 16 0 1 16 0 0 0	33 3 1 0 2 8 0 0 0 0 10	0 0 1 2 1 0 4 1 0 0 0	0 1 4 0 7 2 0 2 0	0 2 1 0 0 6 0 0 5 1	0 0 1 7 0 5 0 0 0	0 2 0 5 0 4 0 0 5 1	0 3 3 0 2 6 0 0 11 1	0 0 0 0 0 0 0 0 0	b   Baderia,   Baderia, Baderiada, Baderiada,   Baderiada,   Amirifakose, Odaribader,   b   Baderia,   Baderia,   Conductoria, Conductoria, Conductoriale,   Sporthalbader,   Anteroductoria,   Frenchadaderia,   Sporthalbaderia,   Sporthalbad
504 505 506 507 508 509 510 511 512 513 514 515	0 12 1 0 2 0 1 4 3	0 0 13 16 0 1 16 0 0 24	33 3 1 0 2 8 0 0 0 0 10 2	0 0 1 2 1 0 4 1 0 0 1	0 1 4 0 0 7 2 0 2 0 2 0	D 2 1 0 0 6 0 0 5 1 0	0 0 1 0 7 0 5 0 0 0 0	0 2 0 5 0 4 0 0 0 5	0 3 3 0 2 6 0 0 11 1 1	0 0 0 0 0 0 0 0 0 0 0	0   Jackreise_lackreidetac_lackreidetac_lackreidetind_Marrifikases_Odorbacters_ 0   Jackreise_lackreidetac_lackreidetac_lackreidetindet_fggerbelaceses_Intervolabilitis_ 0   Jackreise_lactionalacteristac_Controlacteristac_Controlacteristactif_Anteronomacceses_Family_NILAD0011_groups_ 0   Jackreise_lactionalacteristac_Detrolationalacteristactif_Anteronomacceses_Family_NILAD0011_groups_ 0   Jackreise_lactionalacteristac_Detrolationalacteristactif_Anteronomacceses_Family_NILAD0011_groups_ 0   Jackreise_lactionalacteristac_Detrolationalacteristactif_Anteronomacceses_Family_NILAD0011_groups_ 0   Jackreise_lactionalacteristac_Attrolatoristac_Preprohesteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactif_Anteronomacces_Intervolationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactif_Anteronomacces_Intervolationalacteristactificationalacteristactificationalacteristactificationalacteristacteristactificationalacteristactificationalacteristactificationalacteristacteristacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalacteristactificationalac
504 505 506 507 508 509 510 511 511 513 514 515 516	0 12 1 0 2 0 1 4 3 0 1 7	0 0 13 16 0 1 16 0 24 0	33 3 1 0 2 8 0 0 0 0 10 2 4	0 0 1 2 1 0 4 1 0 0 1 0	0 1 4 0 0 7 2 0 2 0 0 2 0 2	D 2 1 1 0 6 0 0 5 1 0 2	0 0 1 7 0 5 0 0 0 0 0	0 2 0 5 0 4 0 0 0 5 1 0	0 0 3 0 2 6 0 0 11 1 1 2	0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerisz, Jackeriskas, Estererőksa, Jackerskiskef, Marinfikasser, Odarbacters,</li> <li>b. Jackerisz, Antinduszteriska, Corobacteriska, Carobacteriskef, Eggethelsasser, Enterorbabius,</li> <li>b. Jackerisz, Frincieksz, Coloridus, Perjastrestarocales Tasiereläket, Asterovorsaccerez, Ferik, JULA00011, grupo,</li> <li>b. Jackerisz, Antinduszeriska, Perjastrestarocales Tasiereläket, Asterovorsaccerez, Ferik, JULA00011, grupo,</li> <li>b. Jackerisz, Christian, Antinduszeriska, Perjastrestarocales, Tasiereläket, Asterovorsaccerez, Teoriet, Julia Asterista, Antinoacteriska, Perjastrestarocales, Tasiereläket, Asterovorsaccerez, Teoriet, Julia Asterista, Antinoacteriska, Perjastrestarocales, Tasiereläket, Antinoacteriska, Feoradiodisca, Antinoacteriska, Perjastrestarocales, Tasiereläket, Antinoacteriska, Perjastrestarocales, Tasiereläket, Antinoacteriska, Teorendodes, Noordiodes, Antinoacteriska, December and Antinoacteriska, Antinoacteriska, Enterolational, Bacteriska, Antinoacteriska, Julia Asteriska, Julia Asteriska, Antinoacteriska, Julia Asteriska, Julia Asteroska, Jul</li></ul>
504 505 506 507 508 509 510 511 512 513 514 515	0 12 1 0 2 0 1 4 3 0 1 7 7	0 0 13 16 0 1 16 0 0 24	33 3 1 0 2 8 0 0 0 0 10 2	0 0 1 2 1 0 4 1 0 0 1 0 0	0 1 4 0 0 7 2 0 2 0 2 0	D 2 1 0 0 6 0 0 5 1 0	0 0 1 0 7 0 5 0 0 0 0	0 2 0 5 0 4 0 0 5 1	0 3 3 0 2 6 0 0 11 1 1	0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerise_ Jackeriskas_ Esteroidas_ Esteroidas_ Esteroidasis_ (Amrifikases_ Odorbacter,</li></ul>
504 505 506 507 508 510 511 512 513 514 515 516 517 518	0 12 1 0 2 0 1 4 3 0 1 7	0 0 13 16 0 1 16 0 24 0	33 3 1 0 2 8 0 0 0 0 0 0 0 10 2 4 0 11	0 0 1 2 1 0 4 1 0 0 1 0 0 31	0 1 4 0 0 7 2 0 2 0 0 2 0 2	D 2 1 1 0 6 0 0 5 1 0 2	0 0 1 0 5 0 0 0 0 0 0 5 5	0 2 0 5 0 4 0 0 0 5 1 0	0 3 3 0 2 6 0 0 11 1 1 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeriska, Jackeriska, Sackeriska, Jackeriskier, Marrifikasse, Oderbacker, J.</li> <li>b. Jackerisk, J. Activaluskariska, Corobackeriska, Corobackeriska, Eggerthelacese, Enterorbabatusk, J.</li> <li>b. Jackerisk, J. Frinciensk, Cabridius, Jackeriskier, J. Faierdelacet, Anserovariascense, J. Farink, J. (J. A.) 2011, group, J.</li> <li>b. Jackerisk, J. Frinciensk, Cabridius, Jackeriskier, J. (J. Sackeriskier, J. Sack</li></ul>
504 505 506 507 508 510 511 512 513 514 515 516 517 518 519	0 12 1 0 2 0 1 4 3 0 1 7 7	0 0 13 16 0 1 16 0 24 0 24 0 7 8	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 1 1	0 0 1 2 1 0 4 1 0 0 1 0 0 1 0 0 31 1	0 1 4 0 0 7 2 0 7 2 0 2 0 5 0 5	0 2 1 0 6 0 5 1 0 2 1 7 6	0 0 1 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 5 1 3 1 3	0 3 3 0 2 6 0 11 1 1 2 3 20 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeriska, Jackeriska, Sackeriska, Jackeriska, Jackeriska, Spechalase, Jackeriska, Antonikase, Contobacteriska, Personal Contobacteriska,</li></ul>
504 505 506 507 508 510 511 513 514 515 516 517 518 519 520	0 12 0 2 0 1 4 3 0 1 7 7 12 11 1 1	0 0 13 16 0 1 16 0 24 0 0 7 8 1	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 1 1	0 0 1 2 1 0 4 1 0 4 1 0 0 1 0 31 31 3	0 1 4 0 7 2 0 7 2 0 2 0 5 0 5 0 3	0 2 1 0 6 0 0 5 1 0 2 1 7 6 7	0 0 1 0 5 0 0 0 0 0 5 0 0 5 0 1	0 2 0 5 0 4 0 0 0 5 1 0	0 3 3 0 2 6 0 0 11 1 1 2 3 20 2 0 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerisz, Jackeriskas, Elstereidsz, Jackeriskisz, Amrifikasse, Odorbacteri,</li> <li>b. Jackerisz, Antobacterisz, Conducterisz, Conducterisz, Gorbacterisz, Eggethelszeset, Internahadus,</li> <li>b. Jackerisz, Frincietz, Conducterisz, Perporteriszocales Takierdizes, Anteroversacerez, Fernik, JULA00011, group,</li> <li>c. Jackerisz, Antobacterisz, Perporteriszocales Takierdizes, Anteroversacerez, Fernik, JULA00011, group,</li> <li>c. Jackerisz, Conducterisz, Conducterisz, Perporteriszocales Takierdizes, Instantizes, Neurododes, Neurosco, Juliane Conducterisz, Perporteriszocales Takierdizes, Juliane Conducterisz, Perporteriszocales, Takierdizes, Juliane Conducterisz, Neurododes, Anterioaceus, Juliane Conducterisz, Perporteriszocales, Takierdizes, Juliane Conducterisz, Jul</li></ul>
504 505 507 508 509 510 511 513 514 515 516 517 518 519 520 521	0 12 1 0 2 0 1 4 3 0 1 7 7 2 1 1 1 1 1 0	0 0 13 16 0 1 16 0 24 0 0 7 8 1 1	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 1 1 1 4 2	0 0 1 2 1 0 4 1 0 0 1 0 0 1 1 3 1 3 0 0	0 1 4 0 0 7 2 0 7 2 0 2 0 2 0 5 0 3 11	0 2 1 0 6 0 0 5 1 0 2 1 7 6 7 0	0 0 1 0 5 0 0 0 0 0 0 0 0 1 1 0	0 2 0 5 0 4 0 0 5 1 0 1 3 1 0 1 1 0	0 3 3 0 2 6 0 0 11 1 1 2 3 20 2 0 2 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_bateriabateriotaxbateriotaxbateriotaxisforebateriadependenciesdependenciesdefendenciesdefendenciesdefendenciesdefendenciesforebateriotaxisinterior bateriainterior bateria</li></ul>
504 505 507 508 509 510 511 513 514 515 516 517 518 519 520 521 522	0 12 1 0 2 0 1 4 3 0 1 7 12 11 1 1 0 5	0 0 13 16 0 1 16 0 24 0 0 7 8 1 1 1	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 1 1 1 2 8	0 0 1 2 1 0 4 1 0 0 1 0 0 3 1 1 3 0 0 0 3 1 1 3 0 0 0 0	0 1 4 0 7 2 0 7 2 0 2 0 2 0 2 0 5 0 3 11 6	0 2 1 1 0 6 0 0 5 1 0 5 1 0 2 1 7 6 7 0 11	0 0 1 0 5 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0	0 2 0 5 0 4 0 0 5 1 0 1 3 1 0 0 1 5	0 3 3 0 2 6 0 0 11 1 1 2 3 20 2 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerisz, Jackeriskas, Jackeriskas, Jackeriskis, Jackeriskiskis, Jackeriskis, Jackeriskis, Jackeriskiskiskiskiskiskiskiskiskiskis, Jackeriskiskiskis</li></ul>
504 505 507 508 509 510 511 513 514 515 516 517 518 519 520 521	0 12 1 0 2 0 1 4 3 0 1 7 7 2 1 1 1 1 1 0	0 0 13 16 0 1 16 0 24 0 0 7 8 1 1	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 1 1 1 4 2	0 0 1 2 1 0 4 1 0 0 1 0 0 1 1 3 1 3 0 0	0 1 4 0 0 7 2 0 7 2 0 2 0 2 0 5 0 3 11	0 2 1 0 6 0 0 5 1 0 2 1 7 6 7 0	0 0 1 0 5 0 0 0 0 0 0 0 0 1 1 0	0 2 0 5 0 4 0 0 5 1 0 1 3 1 0 1 1 0	0 3 3 0 2 6 0 0 11 1 1 2 3 20 2 0 2 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_bateriabateriotaxbateriotaxbateriotaxisforebateriadependenciesdependenciesdefendenciesdefendenciesdefendenciesdefendenciesforebateriotaxisinterior bateriainterior bateria</li></ul>
504 505 507 508 509 510 511 513 514 515 516 517 518 519 520 521 522	0 12 1 0 2 0 1 4 3 0 1 7 12 11 1 1 0 5	0 0 13 16 0 1 16 0 24 0 0 7 8 1 1 1	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 1 1 1 2 8	0 0 1 2 1 0 4 1 0 0 1 0 0 3 1 1 3 0 0 0 3 1 1 3 0 0 0 0	0 1 4 0 7 2 0 7 2 0 2 0 2 0 2 0 5 0 3 11 6	0 2 1 1 0 6 0 0 5 1 0 5 1 0 2 1 7 6 7 0 11	0 0 1 0 5 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0	0 2 0 5 0 4 0 0 5 1 0 1 3 1 0 0 1 5	0 3 3 0 2 6 0 0 11 1 1 2 3 20 2 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerisz, Jackeriskas, Jackeriskas, Jackeriskis, Jackeriskiskis, Jackeriskis, Jackeriskis, Jackeriskiskiskiskiskiskiskiskiskiskis, Jackeriskiskiskis</li></ul>
504 505 507 508 509 510 511 513 514 515 516 517 518 519 520 521 522 523	0 12 1 0 2 0 1 4 3 0 1 7 12 11 1 0 5 22	0 0 13 16 0 1 16 0 24 0 0 7 8 1 1 1 1 0	33 3 1 0 2 8 0 0 0 0 0 0 0 0 0 0 0 10 2 4 0 11 1 1 4 2 8 0 0 1 2 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 2 1 0 4 1 0 0 0 3 1 3 1 3 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 0 7 2 0 7 2 0 2 0 2 0 5 0 3 11 6 3	0 2 1 1 0 6 0 5 1 0 2 1 7 6 7 0 11 7	0 0 1 0 7 0 5 0 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 6 1 0 1 3 1 0 0 1 5 0 0	0 3 3 0 2 6 0 0 11 1 2 3 20 2 5 0 2 5 0 0 2 5 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, bateriota, Bateriota, Bateriota, Amerifiaces, Odorbateri,</li> <li>b. bateria, bateriota, Conductoria, Conductoria, Conductoria, Grandateriota, Grandateria, Particulationa, Conductoria, Conductoria, Conductoria, Conductoria, Conductoria, Particulation, Conductoria, Particulation, Part</li></ul>
504 505 506 507 508 500 510 511 512 513 514 515 516 517 518 519 502 521 522 523	0 12 1 0 2 0 1 4 3 0 1 7 7 2 2 1 1 1 5 22 4	0 0 13 16 0 1 156 0 24 0 0 7 8 1 1 1 1 0 0 7	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 1 1 4 2 8 0 5 5	0 0 1 2 1 0 4 1 0 0 0 0 3 1 1 3 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 7 2 0 2 0 2 0 5 0 5 0 3 11 6 3 1 1 5	0 2 1 1 0 6 0 5 1 0 2 1 7 6 7 0 11 7 1	0 0 1 0 7 0 5 0 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0	0 2 5 5 4 0 0 6 1 3 1 0 1 5 0 1 6 0 0 1 6 0 0 0 1 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 3 0 2 6 0 11 1 1 2 3 20 2 5 0 2 5 0 7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_bateries_bateriotiss_Bateriotiss_Gateriotiss_Gateriotist_Generalist</li> <li>b_bateries_bateriotiss_Catridus_Periodistraited_Generalist</li> <li>b_bateries_frictionateriotiss_Catridus_Periodistraited_Generalist</li> <li>b_bateries_frictionateriotiss_Catridus_Periodistraited_Hateriovaraaceese_Ferior/bateriotiss_Nacariotiss_Anteriococcus_Nat</li></ul>
504 505 506 507 508 510 511 512 513 514 515 516 517 518 519 520 521 522 522 523	0 12 0 2 0 1 4 3 0 1 7 7 22 11 1 5 5 22 4 1	0 0 13 16 0 1 156 0 24 0 0 7 8 1 1 1 1 0 0 0 7 8 1 1 1 0 0 0	33 3 1 0 2 8 0 0 0 10 2 4 0 11 1 1 4 2 8 0 5 4	0 0 1 2 1 0 4 1 0 0 1 0 0 1 3 1 3 0 0 0 0 0 0 0 0 0 0	0 1 4 0 0 7 2 0 7 2 0 2 0 5 0 3 11 6 3 1 4	0 2 1 0 6 0 0 5 1 7 6 7 0 11 7 8	0 0 1 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 0 5 0 4 0 0 0 5 1 0 0 1 6 0 1 6 0 1 0 1 0 1 1 0 0 1 1 0 0 5 0 1 1 0 0 5 0 0 5 0 0 5 0 0 5 0 0 0 0	0 3 3 0 2 6 0 11 1 1 2 3 20 2 5 0 2 5 0 7 0 7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_bateriabateriota;_bateriota;_bateriota;_fasteriota;_f</li></ul>
504 505 507 508 509 510 511 513 514 514 514 514 514 514 514 515 520 521 522 523 525 526	0 12 1 0 2 0 1 4 3 0 1 7 12 11 1 0 5 12 4 1 0	0 0 13 16 0 1 16 0 24 0 7 8 1 1 1 1 0 0 7 8 1 1 1 1 0 0 12	33 3 1 0 2 8 0 0 0 10 2 4 0 11 1 1 4 2 8 0 5 4 0	0 0 1 2 1 0 4 1 0 0 1 0 0 1 3 1 3 0 0 0 0 0 0 0 0 0 0	0 1 4 0 0 7 2 0 7 2 0 2 0 5 0 2 0 5 0 3 11 6 3 1 4 0	0 2 1 0 6 0 0 5 1 0 2 1 7 6 7 0 11 7 8 0	0 0 1 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 0 5 0 4 0 0 0 5 1 0 0 1 6 0 1 6 0 1 0 1 0 1 1 0 0 1 1 0 0 5 0 1 1 0 0 5 0 0 5 0 0 5 0 0 5 0 0 0 0	0 3 3 6 0 6 0 0 11 1 1 2 3 20 2 0 2 5 0 7 0 2 5 0 7 0 0 2 5 0 7 0 0 2 5 0 0 2 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_bateries_bateriotiss_Bateriotiss_Groupsateries_Gerbateries_Berbateries_Anteriotisses_Interioritisses_Anteriotiss_Gerbateries_Ge</li></ul>
504 505 507 508 510 511 512 513 515 515 515 515 515 515 515 521 522 521 522 523 524 525 526 527	0 12 1 0 2 0 1 4 3 0 1 7 2 1 1 1 5 2 2 4 1 0 5 2 4 1 0 5 2 2 4 1 0 5 2 1 1 0 0 2 0 1 1 0 0 1 1 0 0 0 1 1 0 0 0 0	0 0 13 16 0 1 16 0 24 0 7 8 1 1 1 1 0 0 7 8 1 1 1 0 0 12 0	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 1 4 2 8 0 5 4 0 1	0 0 1 2 1 0 4 1 0 0 1 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 7 2 0 2 0 2 0 2 0 2 0 5 0 3 11 6 3 1 4 0 0 2	0 2 1 0 6 0 5 1 0 7 6 7 1 7 6 7 1 8 0 5	0 0 1 0 7 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 0 6 1 0 0 1 5 0 0 1 5 0 0 1 5 0 0 1 5 0 0 0 0	0 3 3 0 2 6 0 0 11 1 1 2 3 20 2 0 2 5 0 7 0 2 5 0 7 0 0 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b laderia_ laderiadas_laderadas_laderadasis./_Marriflaces_Odorbacter b laderia_laderiadas_laderadas_laderadasis_(ggerthelacess_Interorbacter b laderia_laderadas_laderadas_laderadasis_laderadasis_Interorbacter b laderia_finicites_Cabridus_Perioderateriadsis_laderadorbacter b laderia_finicites_Cabridus_Perioderateriadsis_laderadorbacter b laderias_lateradateriads_Attendatorbacter b laderias_lateradateriads_Attendatorbacter b laderias_beneficies_Cabridus_Deverouterateriadsis_laderadorbacter b laderias_beneficies_Cabridus_Deverouterateriadsis_Manorovanaecese_Interodorbacter b laderias_beneficies_Cabridus_Deverouterateriadsis_laderadorbacter b laderias_beneficies_Cabridus_Deverouterateriadsis_Manorovanaecesec_Interodorbacter b laderias_beneficies_Cabridus_Deverouterateriad_manorovanaecesec_Interodorbacter b laderias_beneficies_Cabridus_Deverouterateriadsis_Manorovanaeces_Deverouterater b laderias_beneficies_Cabridus_Deverouterateriadsis_Manorovanaeces_Deverouteraterater b laderias_beneficies_Cabridus_Deverouterateriadsis_Chamorovanaecesec_Beneficies b laderias_beneficies_Cabridus_Deverouterater b laderias_beneficies_Cabridus_Deverouteraterater b laderias_beneficies_Cabridus_Deverouteraterater b laderias_beneficies_Cabridus_Deverouteraterateraterateraterateraterateratera</pre>
504 505 507 508 509 510 511 513 514 515 516 516 517 518 518 519 520 522 522 523 526 527 528	0 12 1 0 2 0 1 4 3 0 1 7 12 11 1 0 5 12 4 1 0 5 5 2 4 1 0 5 5 2 4 1 0 5 5 5 6 6 6 7 10 10 10 10 10 10 10 10 10 10 10 10 10	0 0 13 16 0 16 0 24 0 24 0 7 8 1 1 1 0 0 7 8 1 1 1 0 0 12 0 0	33 3 1 0 2 8 0 0 0 0 0 0 0 10 2 4 0 11 1 4 2 8 0 5 4 0 1 1 4 0 1 1 4 0 0 1 1 1 4 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 1 2 1 0 4 1 0 0 1 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 7 2 0 2 0 2 0 2 0 2 0 3 11 6 3 1 4 0 0 1 4 0 0 1	0 2 1 0 6 0 5 1 0 7 6 7 1 7 6 7 1 8 0 5 0 5 0 5 0 5	0 0 1 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 4 0 0 6 1 3 1 0 1 6 0 1 6 0 1 0 1 6 0 1 0 1 6 0 1 0 1	0 3 3 0 2 6 0 0 11 1 1 2 3 20 2 5 0 7 0 3 6		<pre>b l_bdorbisbdorbidsBisteredusBisteredukisMarinflasseOdorbidstr b l_bdorbisConobacteridsConobacteridsGreptoblessesInternohabdiss b l_bdorbisInternohasOdorbidsPeriodizetaridsed_greptoblessesInternohabdiss b l_bdorbisInternohasOdorbidsPeriodizetaridsed_AuserovariacenessInternohabdissNeuroidodesN</pre>
504 505 507 509 510 511 513 513 514 513 514 515 516 517 520 521 522 526 526 527 528 528	0 12 1 0 2 0 1 4 3 0 1 7 12 11 1 0 5 12 4 1 0 6 6	0 0 13 16 0 16 0 24 0 0 7 8 1 1 1 0 0 7 8 1 1 1 0 0 0 12 0 0 0 12 0 0	33 3 1 0 2 8 0 0 0 0 0 0 0 0 0 0 0 10 2 4 0 11 14 2 8 0 5 4 0 1 1 2 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1	0 0 1 2 1 0 4 1 0 0 1 0 0 1 3 1 3 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 7 2 0 2 0 2 0 5 0 3 11 6 3 1 4 0 0 1 2 1 2	0 2 1 0 0 0 5 1 0 2 1 7 6 7 0 11 7 8 0 5 5 1 0 2 1 7 6 7 0 1 5 1 0 2 1 1 0 6 0 0 5 1 1 0 0 6 0 0 5 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 6 1 0 1 6 0 1 0 4 3 1	0 3 3 0 2 6 0 11 1 2 3 20 2 5 0 7 0 0 3 6 7 0 0 3 5 0 7 0 7 0 2 5 0 7 1 1 1 2 3 2 0 2 5 0 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 1 1 1 1 2 3 2 0 2 1 1 1 2 3 2 0 2 0 2 0 2 1 1 1 2 3 2 0 2 0 2 0 2 1 1 2 3 2 0 2 0 2 0 2 5 0 7 7 0 0 2 0 2 5 0 7 7 0 1 2 0 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 1 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_bateries_beterietets_Betereietes_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Constantines_Proproduces_Asserts</li> <li>b_bateries_beteries_constantines_Proproducestrikes</li></ul>
504 505 507 508 509 511 512 512 513 514 515 516 517 518 519 510 521 522 521 522 521 522 522 523 524 525 526 525 526 527 525 526 527 527 527 527 527 527 527 527 527 527	0121007014001712111005124100660	0 0 13 16 0 24 0 24 0 7 8 1 1 1 0 0 12 0 0 12 0 13	33 3 1 0 2 8 0 0 0 0 0 0 0 0 0 0 10 2 4 0 11 14 2 8 0 5 4 0 5 4 0 0 11 12 2 8 0 0 10 12 2 4 0 0 0 10 10 2 2 8 0 0 10 0 10 10 10 10 10 10 10 10 10 10	0 0 1 2 1 0 4 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 7 2 0 2 0 2 0 2 0 5 3 11 6 3 1 4 0 0 1 2 0 1 2 0 0 2 0 2 0 2 0 2 0 2 0 2	0 2 1 0 6 0 5 1 0 2 1 7 6 7 0 11 7 8 0 5 0 4 0	0 0 1 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 6 1 0 1 6 0 1 0 4 1 0 4 1 0	0 3 3 6 7 6 0 11 1 1 2 3 2 0 7 0 7 0 0 3 6 7 0 7 0 7 0 7 0 7 0 7 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b l_bdreingbdreindstabdreindstabdreindstaidggrefindstasseforberbaker</pre>
504 505 507 509 510 511 512 513 514 515 516 517 518 519 520 521 522 522 523 524 525 526 526 527 528 529 529 529 529 520 520 520 520 520 520 520 520 520 520	0 12 1 0 2 0 1 4 3 0 1 7 12 1 1 0 5 12 4 1 0 0 5 2 4 1 0 0 5 2 4 1 0 0 2 0 1 2 1 1 2 1 1 2 1 2	0 0 13 16 0 24 0 24 0 7 8 1 1 1 0 0 24 0 7 8 1 1 1 0 0 0 20 0 12 0 0 12 3 0 13	33 3 1 0 2 8 0 0 0 0 0 0 0 10 2 4 0 0 11 1 14 2 8 0 5 4 0 1 1 1 2 0 1 1 2 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 2 1 0 4 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 7 2 0 7 2 0 2 0 5 0 3 11 6 3 14 0 0 1 2 0 0	0 2 1 0 0 5 1 0 2 1 7 6 7 0 1 7 8 0 5 1 8 0 5 1 8 0 5 1 8 0 5 1 0 8 0 7 8 1 0 8 1 0 8 1 0 8 1 0 8 1 0 9 6 0 9 5 1 0 9 6 9 0 9 7 1 0 9 6 9 0 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1	0 0 1 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 6 1 0 1 6 0 1 6 0 1 0 1 0 1 0 1 0 0 1 0 0 1 0 0 0 0	0 3 6 7 6 0 11 1 2 3 2 0 7 0 3 6 7 0 3 6 7 0 0 3 6 7 0 7 0 7 0 7 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b l_bdreins_lecteroids:_BdreindsBdreindsind_Marrifikase_Oderbacter b l_bdreins_lecteroids:_Bdreindsin_Corebacterialse_fgreindsicase_Interrorbakter b l_bdreins_lecteroids:_Derbacterialse_Taiseroidsicase_Interrorbakter b l_bdreins_lecteroids:_Derbacterialse_Taiseroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicase_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicasee_Neuroidsicaseee_Neuroidsicaseee_Neuroidsicaseeee_Neuroidsicaseeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee</pre>
504 505 507 508 509 510 511 512 513 515 516 516 516 516 516 516 516 516 516	0 12 1 0 2 0 1 4 3 0 1 7 12 1 1 0 5 12 4 1 0 0 5 2 4 1 0 0 5 2 4 1 0 0 2 0 1 2 1 1 2 1 1 2 1 2	0 0 13 16 0 1 16 0 24 0 0 7 8 1 1 1 0 0 0 24 0 0 12 0 0 12 0 0 12 0 0 13 0 0 13	33 3 1 0 2 8 0 0 0 0 0 10 2 4 0 11 1 14 2 8 0 5 4 0 1 1 2 0 1 2 0 1 2 2 1 2 2 1 2 2 3 1 1 0 2 2 3 1 0 2 8 0 0 0 0 1 0 1 0 1 0 2 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 2 1 0 4 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 7 2 0 2 0 2 0 2 0 2 0 2 0 2 0 3 11 6 3 1 4 0 0 1 2 0 0 2 0 2 0 2 0 2 0 2 0 2 0 0 2 0 0 2 0	0 2 3 0 6 0 5 1 7 6 7 0 11 7 8 0 5 0 12 8 0 5 0 10 10	0 0 1 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 6 1 0 1 6 0 1 6 0 1 0 1 6 0 1 0 1 0	0 3 3 0 2 6 0 11 1 2 3 20 2 5 0 7 0 3 6 7 0 0 3 6 7 0 0 1 1 1 2 3 2 0 2 5 0 0 1 1 1 2 3 0 0 1 1 1 2 3 0 0 1 1 1 2 1 2 1 1 1 2 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b.l.bacteriabacteriadasbacteriadasbacteriadasisdirectionalesi</pre>
504 505 507 508 508 511 513 513 513 513 515 516 516 517 518 516 517 512 512 512 512 512 512 512 512 512 512	0 12 1 0 2 0 1 4 0 1 7 12 1 1 0 6 6 0 1 7 7 1 1 1 0 5 12 4 1 0 6 6 0 7 7 7 1 1 1 1 0 7 1 1 1 0 7 1 1 1 0 7 1 1 1 0 7 1 1 1 0 7 1 1 1 0 7 1 1 1 0 7 1 1 1 1	0 0 13 16 0 1 16 0 24 0 0 24 0 0 7 8 1 1 1 0 0 0 24 0 0 0 24 0 0 0 12 0 0 12 0 0 0 12 13 15 15 15 15 15 15 15 15 15 15 15 15 15	33 3 3 1 0 2 8 0 0 0 0 0 10 2 4 0 11 14 2 8 0 1 1 4 0 1 1 2 0 1 2 1 2 1	0 0 1 2 1 0 4 1 0 4 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0	0 2 3 1 0 0 5 1 7 6 7 0 11 7 1 8 0 5 0 4 0 0 10 11	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 5 6 1 0 1 5 0 1 6 0 1 0 1 0 1 0 1 0 0 1 0 0 0 0 0 0	0 3 3 6 0 0 1 1 1 2 3 20 7 0 2 5 0 7 0 3 6 7 0 0 1 1 1 2 3 2 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b l_bdorbsbdorbstoxBdorbstoksBdorbstoks/Bgorbsborbstoks b l_bdorbsbdorbstoksConstantinaConstantinationGgorbsborbstoks b l_bdorbsfinitestesConstantination_Constantination_GgorbsborbstoksBdorbsborbstoks b l_bdorbsfinitestesConstantination_Preproseduetrinisting_PreproduedstoksesseInternehabitations b l_bdorbstokCharlostantination_Preproseduetrinisting_PreproduedstoksesseInternehabitationsAdvantinationations b l_bdorbstokCharlostantination_Preproseduetrinisting_PreproduedstoksesseInternehabitationsRobertsborbstokBdorbsborbstoksesseInternehabitationsRobertsborbstoksesseInternehabitationsRobertsborbstoksesseInternehabitationsRobertsborbstoksesseInternehabitationsRobertsborbstoksesseInternehabitationsRobertsborbstoksesseInternehabitationsRobertsborbstoksesseInternehabitationsRobertsborbstoksesseInternehabitationsRobertsborbstoksesseInternehabitationsRobertsborbstoksesseRobertsborbstoksesseRobertsborbstoksesseRobertsborbstoksesse_RobertsborbstoksessesseRobertsborbstoksessesseRobertsborbstoksessesseRobertsborbstoksessessessessessessessessessessessesses</pre>
504 505 507 508 509 511 512 513 514 515 516 517 518 518 519 519 521 522 521 522 523 524 525 526 529 529 530 531 532 533	01210020143017121110512410066012073	0 0 13 16 0 24 0 7 8 1 1 1 0 0 24 0 0 24 0 0 24 0 0 24 0 0 24 0 0 24 1 1 1 1 0 0 24 0 0 24 0 0 24 24 0 0 24 24 0 0 24 24 24 0 0 24 24 24 0 0 24 24 24 0 0 24 24 24 0 0 24 24 24 0 0 24 24 24 24 0 0 24 24 24 0 0 24 24 24 24 24 24 24 24 24 24 24 24 24	33 3 1 0 2 8 0 0 0 0 0 0 0 2 4 0 10 2 4 0 11 14 2 8 0 5 4 0 1 2 0 1 2 0 1 2 1 0 0 0 0 0 0 0 0 0 0	0 0 1 2 1 0 4 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 2 0 2 0 2 0 2 0 3 11 6 3 1 4 0 0 1 2 0 0 1 5 0 1 1 5 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 2 1 0 6 0 5 1 0 7 6 7 0 1 7 8 0 5 0 4 0 0 0 1 7 1 8 0 5 1 1 7 6 7 0 1 7 1 1 0 0 6 0 0 5 1 1 0 0 0 6 0 0 0 5 1 1 0 0 0 0 5 1 1 0 0 0 0 5 1 1 0 0 0 0	0 0 1 7 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 5 6 1 0 1 5 0 1 6 0 1 0 1 0 1 0 1 0 0 1 0 0 0 0 0 0	0 3 4 0 2 6 0 0 11 1 2 3 20 2 5 0 7 0 0 3 6 7 0 0 1 1 1 2 3 20 2 5 0 7 0 0 1 1 1 2 3 2 0 0 0 0 1 1 1 2 3 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b laderiay_laderiaday_laderiaday_laderiaday_dynerializase_Odorbacter;</pre>
504 505 507 508 509 511 512 513 514 514 515 517 518 517 518 517 518 519 520 521 522 521 522 523 524 530 531 533 533 533	0 12 1 0 2 0 1 4 1 0 1 7 12 11 1 0 5 12 4 1 0 0 6 0 12 0 7 8 6 0 7 8 8 7 7 12 1 0 1 7 10 1 7 10 10 10 10 10 10 10 10 10 10 10 10 10	0 0 13 16 0 1 1 16 0 24 0 24 0 7 8 1 1 1 1 0 0 22 0 0 22 0 0 1 3 0 0 1 4 1	33 3 3 1 0 2 8 0 0 0 0 0 0 2 4 0 1 1 1 4 0 1 1 4 0 5 4 0 1 1 2 0 1 2 0 1 2 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 2 1 0 4 1 0 1 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 7 2 0 7 2 0 7 2 0 7 2 0 2 0 3 11 6 3 1 4 0 0 1 2 0 1 2 0 0 1 2 0 0 1 2 0 0 1 1 2 0 0 1 1 2 0 0 1 1 2 0 0 1 1 1 2 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 2 1 0 0 6 0 0 5 1 0 7 1 7 0 1 7 7 0 1 7 8 0 5 0 4 0 0 0 1 1 7 1 8 0 5 1 1 0 0 5 1 0 7 1 0 0 0 6 0 0 0 5 1 0 0 0 0 5 1 0 0 0 0 0 0 5 1 0 0 0 0	0 0 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 0 4 0 0 6 1 0 1 6 0 0 1 6 0 0 1 0 0 0 0 1	0 3 3 0 2 6 0 11 1 2 3 0 2 5 0 7 0 0 3 6 7 0 0 1 0 0 1 0 0 1 0 1 1 2 8 0 2 5 0 7 0 1 1 1 2 8 0 0 2 6 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		<pre>b.lschrigbchrightigbchrightigbchrightigbrightightigschrightigs.</pre>
504 505 507 508 500 510 511 512 513 514 515 516 516 516 516 516 516 516 516 516	01210020143017121131051241006601207334	0 0 13 16 0 1 15 0 0 24 0 0 7 8 1 1 1 1 0 0 0 24 0 0 7 8 1 1 1 0 0 0 22 0 0 0 13 14 1 1 1 15 16 0 0 1 2 16 0 0 1 2 16 0 0 1 1 15 16 0 0 1 2 16 0 0 1 1 15 16 0 0 1 1 15 16 0 0 0 1 1 15 16 0 0 0 1 1 15 16 0 0 0 0 1 1 15 16 0 0 0 1 1 15 16 0 0 0 1 1 15 16 0 0 0 1 1 1 15 16 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	33 3 1 0 2 8 0 0 0 0 0 0 2 4 0 1 1 2 4 0 1 1 2 8 0 1 1 2 0 1 2 0 1 2 1 2 0 1 2 2 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 1 0 4 1 0 4 1 0 0 1 1 0 0 0 0 0 0	0 1 4 0 0 7 2 0 2 0 2 0 5 0 3 11 6 3 1 4 0 0 1 2 0 0 1 1 5 0 0 1 4 0 0 7 2 0 2 0 2 0 2 0 2 0 0 2 0 2 0 0 2 0 0 2 0 0 0 7 2 0 0 0 0	0 2 1 1 0 6 0 0 5 1 0 2 1 7 6 7 0 11 7 1 8 0 5 0 4 0 0 10 1 10 5 1	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 5 8 4 0 0 6 1 0 1 6 0 1 6 0 1 0 1 0 1 0 1 0 1	0 3 3 0 2 6 0 0 1 1 1 2 3 0 2 5 0 7 0 0 3 6 7 0 0 1 1 1 2 3 0 2 5 0 7 0 0 1 1 1 2 8 0 0 1 1 1 2 8 0 0 1 1 1 1 2 0 0 1 1 1 1 2 1 1 1 1 2 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b_bcterisbcteristicsbcteristicsbricksteristicstigeristicsbricksteris</pre>
904 905 907 908 909 911 913 913 913 914 915 915 916 917 917 918 919 919 919 919 919 919 919 919 919	0 22 1 0 0 2 0 1 4 3 0 1 7 12 11 1 1 0 5 22 4 1 0 0 6 6 0 12 0 7 3 3 4 1	0 0 1 1 6 0 2 4 0 7 8 1 1 1 0 0 7 8 1 1 1 1 0 0 0 2 4 0 0 1 2 0 0 0 1 2 0 0 1 1 1 1 1 1 1 1 1	33 3 3 1 0 2 8 0 0 0 0 10 2 4 0 10 2 4 0 11 1 4 2 8 0 1 1 1 2 0 1 2 1 0 1 2 3 1 2 1 2 3 1 2 3 1 1 2 2 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 1 0 4 1 0 4 1 0 0 1 0 0 0 0 0 0 0	0 1 4 0 0 7 2 0 2 0 2 0 5 0 3 1 4 0 0 1 2 0 0 1 5 0 0 1 4 0 0 0 7 2 0 2 0 0 0 2 0 0 0 0 7 2 0 0 0 0 0 0 7 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 5 1 0 2 1 7 6 7 0 11 7 1 8 0 5 0 4 0 0 10 2 1 0 5 1 0 1 5 1 0 1 5 1 0 1 5 1 1 1 1	0 0 1 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	02050400061018100160010431000013	0 3 3 0 2 6 0 0 1 1 1 2 3 20 2 5 0 7 0 0 3 6 7 0 0 1 1 1 2 3 20 2 5 0 7 0 0 1 1 1 2 3 20 2 5 0 0 1 1 1 2 3 20 2 0 0 1 1 1 2 3 20 2 0 0 0 1 1 1 2 3 20 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b_bcteries_bcteriestes_bcteriestes_briefendereties_genetiestesse_briefendereties_ b_bcteries_bcteriestes_bcteriestes_Propriefenderetiestes_propriefenderetiestes_briefenderetiestes_bcteriestesse_briefenderetiestes_bcteriestesse_bcteries</pre>
504 505 507 508 509 511 512 512 513 514 515 516 517 518 517 518 517 520 521 522 523 524 525 529 530 537 533 534 535 537 535	0 22 1 0 0 2 0 1 4 3 0 1 7 22 11 1 1 0 5 12 4 1 0 0 6 6 0 12 0 7 3 3 4 1 25	0 0 1 1 1 1 0 0 2 4 0 0 2 4 0 0 7 8 1 1 1 0 0 2 2 0 0 1 2 1 0 0 1 2 1 0 0 1 1 1 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 1 2 1 0 0 1 2 1 0 0 1 2 1 0 0 1 2 1 0 0 0 2 4 0 0 0 2 4 0 0 0 2 4 0 0 0 0 2 4 0 0 0 0	33 3 1 0 2 8 0 0 0 0 10 2 4 0 11 14 2 8 0 1 1 2 0 1 2 0 1 2 1 0 3 2 3 0 3 0 3 0 3 0 2 3 0 0 10 2 8 0 0 0 0 10 2 8 0 0 0 2 8 0 0 0 0 2 8 0 0 0 0 2 8 0 0 0 0	0 0 1 1 0 4 1 0 4 1 0 1 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 6 0 5 1 7 6 7 0 11 7 8 0 5 0 8 0 5 1 0 5 1 0 7 6 7 0 11 7 8 0 5 1 0 6 0 0 5 1 0 7 6 0 0 5 1 0 0 5 1 0 0 6 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 5 1 0 0 0 5 1 0 0 0 5 1 0 0 0 5 1 0 0 0 0	0 0 1 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 3 3 0 2 6 0 0 11 1 2 3 20 2 5 0 7 0 0 3 6 7 0 0 3 6 7 0 0 1 0 8 7 0 0 1 1 1 2 5 0 7 0 2 6 0 0 11 1 2 6 0 0 11 1 2 6 0 0 11 1 2 1 0 1 2 1 0 1 1 1 1 2 1 1 1 1		<pre>b_bcteries_bcteriedsc_bcteriedsc_bcteriedsc_figerthebcese_Cherobeteri, b_bcteries_bcteriedsc_bcteriedsc_Perporteriestoncies_Tisiereliedsc_Asserversencese_Terier/ubdates_Asserversencese_Terier/ubdates_bcareasoccus_bareroccus_bcteriedsc_beteries_figerthebceses_Interneliedsc_bcareasoccus_bareroccus_bcteriedsc_bcteri</pre>
504 505 507 508 509 511 512 513 514 514 515 516 517 518 519 520 521 520 521 520 521 520 521 522 523 524 530 531 532 532 533 534 535 537 538	0 22 1 0 2 0 1 4 3 0 1 7 12 1 1 0 5 22 4 1 0 0 6 0 12 0 7 3 8 4 1 5 2 0 1 4 3 0 1 7 12 1 0 0 2 0 1 4 3 0 17 10 10 10 10 10 10 10 10 10 10 10 10 10	0 0 13 16 0 24 0 7 8 1 1 1 0 0 0 2 7 8 1 1 1 0 0 0 2 1 0 0 1 1 1 1 0 0 0 2 1 1 1 0 0 0 2 1 1 1 1	33 3 3 1 0 2 8 0 0 0 0 0 10 2 4 0 11 14 2 8 0 11 14 2 8 0 11 14 2 8 0 11 14 2 8 0 1 1 1 1 2 8 0 0 0 0 0 0 0 0 0 2 8 0 0 0 0 0 0 0	0 0 1 1 0 4 1 0 0 1 0 0 0 0 0 0 0 0 0 0	0 1 4 0 7 2 0 2 0	0 2 1 0 6 0 5 1 0 2 1 7 6 7 0 11 7 8 0 5 0 4 0 0 10 1 10 5 1 0 2 1 7 6 0 5 1 0 2 1 7 6 0 0 5 1 0 0 0 5 1 0 0 0 5 1 0 0 0 5 1 0 0 0 5 1 0 0 0 5 1 0 0 0 5 1 0 0 0 5 1 0 0 0 0	0 0 1 7 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 3 3 4 0 0 11 1 2 3 20 2 5 0 7 0 0 3 6 7 0 0 1 1 1 2 3 20 2 5 0 7 0 0 1 1 1 2 3 20 2 5 0 0 1 1 1 2 3 2 0 2 5 0 0 1 1 1 2 3 2 0 2 5 0 0 1 1 1 2 3 2 0 2 0 0 1 1 1 2 3 2 0 2 0 0 0 1 1 1 2 3 2 0 2 0 0 0 0 1 1 1 2 3 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b_bcteries_bcteriestes_bcteriestes_briefendereties_genetiestesse_briefendereties_ b_bcteries_bcteriestes_bcteriestes_Propriefenderetiestes_propriefenderetiestes_briefenderetiestes_bcteriestesse_briefenderetiestes_bcteriestesse_bcteries</pre>

542	0	14	2	0	0	2	0	1	0	0	0 k_Bacteria;p_Actinobacteriota;c_Acidimicrobila;o_IMCC26256;f_IMCC26256;g_IMCC26256;s
543	12	0	3	0	5	6	0	3	18	1	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_;s_
544	1	0	6	0	D	4	0	1	4	o	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Frankiales;f_Sporichthyaceae;g_hgd_clade;s
545	0	12	0	0	0	0	0	0	0	0	0 k_Bacteria
546	0	12	0	1	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiale;sf_Rhizobiaceae;g_Aureimonas
547 548	23	0	3	0	2	1	0	5	4	0 0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Hydrogenophaga;s0
549	11	0	0	0	0	0	0	0	0	0	0 urknown 0 k_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Solirubrobacter;s_
550	12	0	14	0	13	19	0	12	15	4	K_parcenargActinobacteriotacInterimoterprintzo_softwareouccuratesrsoftwareouccuratesrsoftwareouccurs     K BarcenargActinobacteriotaccActinobacteria.gConverbacterialesrNocardiaceae:gRhodococcussRhodococcus_ruber
551	0	10	0	0	0	0	0	0	0	0	0 k_Bacteria
552	7	0	4	0	2	3	0	7	3	1	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Sphingobacteriales;f_NS11:12_marine_group;g_NS11:12_marine_group;s_
553	6	0	1	0	3	7	0	1	1	0	2 k_Bacteria:p_Proteobacteria:c_Gammaproteobacteria;o_Burkholderiales:f_Nitrosomonadaceae:g_;s_
554	0	7	o	1	0	0	0	o	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae.g_Bergeyella;s_
555	7	0	1	1	19	21	3	6	4	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_Muribaculaceae;s
556	4	0	2	0	2	1	0	2	3	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_KI89A_clade;f_KI89A_clade;g_KI89A_clade;s_KI89A_clade;s_
557	8	14	1	0	D	D	z	D	1	o	$0\ k\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales!s\_Sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_s\_issues:f_sutterellaceae:g\_issues:f_s$
558	6	0	2	0	2	8	0	2	4	σ	$0\ k\_Bacteria; p\_Proteobacteria; c\_Gammaproteobacteria; o\_Aeromonadales; f\_Aeromonadaceae; g\_Aeromonas; s\_Aeromonas\_veronii and set $
559	0	0	0	8	0	0	1	0	0	0	0 k_Bacteria;p_Firmicute;c_Clostridia;o_Oscillospirales;f_Ruminococcaceac;p_Ruminococcus;s_Ruminococcus_flavefaciens
560	2	0	5	2	3	3	0	1	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG-014;f_Clostridia_UCG-014;g_Clostridia_UCG-014;s_
561	7	0	1	0	2	0	0	0	1	0	$0\ k\_Bacteria; p\_Proteobacteria; c\_Alphaproteobacteria; a\_Azospirila/es; f\_Azospirila/es; g\_Stermanella; s\_f_Azospirila/es; f\_Azospirila/es; f\_Azospirila/es;$
562	2	0	0	0	1	D	0	D	0	2	10 k_Bacteria;p_Firmicutes;c_Bacili;o_Lactobaciliales;f_Listeriaceae;g_Brochothrix;s_Brochothrix_thermosphacta
563	10	0	O	0	D	D	1	D	1	o	1 k_Bacteria;p_firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Acetatifactor;s_
564	0	13	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;a_Rhizobiales;f_Rhodomicrobiaceae;g_Rhodomicrobium;s_
565	4	0	1	0	1	1	0	6	7	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;a_Reyranellales;f_Reyranellaceae;p_Reyranella;s_
566	0	14	0	3	D	D	0	D	0	0	0 k_Bacteria;p_Campilobacterota;x_Campylobacteria;o_Campylobacterale;;f_Campylobacteraceae;s_Campylobacter
567	1	0	6	0	1	1	0	1	2	0	0 k_Bacteria;p_firmicutes;c_Clostridia;o_Oscillospirales;f_Ethanoligenenaceae;g_Acetanaerobacterium;s 0 k_Bacteria;p_firmicutes;c_Bacili;o_Acholopiasmataics;f_Acholopiasmataceae;g_Aneeropiasma;s
568	9	0	0					6			
569	3	0	0	0	0	0 5	0	1	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidia;os,f_Prevotellaceae 0 k_Bacteria;p_Cyanobacteria;c_Cyanobacteria;o_Synechoococales;f_Prochlorotrichareae;g_Prochlorothrix_PCC 9006s_
571	7	0	6	0	6	3	0		3	0	b K_marketrap_systematics in mar_point and and in market and in the systematic and and interpreter and an interpreter and a systematic and an interpreter and a systematic an
572	2	0	2	0	3	2	0	5	2	0	0 k_Bacteria;p_Ovanobacteria;c_Ovanobacteria;o_Ovanobacteriales;f_Oscillatoriaceae;g_Planktothricoides_\$8001;s_
573	0	10	0	1	0	0	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
574	0	0	0	0	2	0	0	32	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;a_Sphingomonadales;f_Sphingomonadacese;g_Altererythrobacter;s_
575	3	0	2	0	3	1	0	2	3	0	2 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderialesj_TRA3-20;g_TRA3-20;s_
576	0	27	o	0	o	O	0	o	0	o	0 k_Bacteria;p_Firmicutes;c_Bacili;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Tuncibacter;s_
577	2	2	2	4	4	D	0	2	7	o	0 k_Bacteria;p_Firmicute;;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
578	8	0	0	0	0	3	0	19	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_PLTA13;f_PLTA13;g_PLTA13;s_
579	3	10	7	0	0	0	3	14	1	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;z_Marmoricola
580	5	0	z	0	1	7	0	3	1	o	$0\ k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;a\_Azospirillales;f\_Azospirillalea;g\_;s\_$
581	5	0	6	0	1	i	0	5	9	0	0 k_Bacteriap_Hydrogenedentesy_Hydrogenedentiap_Hydrogenedentialest_Hydrogenedentaceaeg_Hydrogenedentaceaes_
582	4	0	3	0	5	2	0	1	3	o	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Maninbryantia
582 583	4 95	0 18	3 3	0 0	5 6	2 11	0 0	1 10	3 81	o o	8 k_bisteriag_tirmicates<_Costraduo_Lachnospirales(_Lachnospirales(_Lachnospirales(_Mannehayatta 0 k_bisteriag_frosteolacentacc_Commisporaeolacteriao_Barkholderiales(_Maligeriaoceseg_Achronobacter
582 583 584	4 98 3	0 18 0	3 3 0	0 0 0	5 6 1	2 11 0	0 0	1 10 25	3 81 3	0 0 1	D k_Baderias_Tirmicates_Cabatralas_Lachroapitalesf_Lachroapitaeses_Mannehysatta D k_Baderias_Proteclacterias_Casimapotecladaderias_Badehalderiatesf_Nicoligenaceaeg_Adhromolacter D k_Betchias_Proteclasterias_Nahapitatealacterias_Microposalesf_Microposalecesg_ss_
582 583 584 585	4 98 3 6	0 18 0 0	3 3 0 1	0 0 1	5 6 1 2	2 11 0 9	0 0 0	1 10 25 0	3 81 3 7	0 0 1 0	0 k_bateria,p_Trimicutes_Cebatrdius_Lachroapitalesf_Lachroapitaeses_Mannehayatta 0 k_bateriap_Proteobacterias_Gammaproteobacterias_Burkholderiaksf_Ncaligeracesez_Achromobacter 0 k_beteriap_Proteobacterias_Abhaproteobacterias_Mcroposalext_Monoposalexcestsa_ 0 k_beteriap_Firmicutese_Coloridase_Oxelleopiniest_Ruminecercaceses_Burninecercaus_
582 583 584 585 586	4 98 3 6 3	0 18 0 0	3 3 0 1 2	0 0 1 0	5 6 1 2 1	2 11 0 9 2	0 0 0 0	1 1D 25 0 1	3 81 3 7 2	0 0 1 0 0	0 k_bitering_firmicutes_Coloridup_Lachnopiralesf_Lachnopiraeseg_Minnehyantia 0 k_bitering_Protoinactinic_Cammaportoihoitettaa_Barkhollerinisky_Alaigenoaaeg_k/thronobacter 0 k_bitering_Protoinactinics_Alainaportoihoitettiing_Microporalesf_Microporalesf_Li_ 0 k_bitering_Protoinactinics_Coloridage_Colorignitefs_Microporalesf_Colorogoints_ 0 k_bitering_Openotactinics_Coloridage_Onterplatef_Colorogoints_Colorogoints_
582 583 584 585 586 587	4 96 3 6 3 11	0 18 0 0 0	3 0 1 2 0	0 0 1 0	5 6 1 2 1 2	2 11 0 9 2 0	0 0 0 0	1 10 25 0 1 0	3 81 3 7 2 0	0 0 1 0 0	bitchering_firmicutes_Colorbalog_Lachnospirales{_Lachnospirales4Manehysatta     bi_Listering_freetesischering_commenseries_Manehysatta     bi_Listering_freetesischering_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_ma
582 583 584 585 586	4 98 3 6 3	0 18 0 0	3 3 0 1 2	0 0 1 0	5 6 1 2 1	2 11 0 9 2	0 0 0 0	1 1D 25 0 1	3 81 3 7 2	0 0 1 0 0	B I_Bisteriag_firmicutes_Colotriduo_Lachnospiralesf_Lachnospiralesf_LaChnospiralesf_Manehoyatta 0 I_Bisteriag_freeteisachetisc_Commisperalesf_Lachnospiralesf_Manehoyatta 0 I_Bisteriag_freeteisachetisc_Colotriduo_Docelleprinetg_Microposatestacesc 0 I_Bisteriag_freeteisachetisc_Colotriduo_Docelleprinetg_MicroposatestacescBunnieseccess
582 583 584 585 586 587 588	4 96 3 6 3 11 0	0 18 0 0 0 0 12	3 0 1 2 0	0 0 1 0 0	5 6 1 2 1 2 0	2 11 0 9 2 0 0	0 0 0 0 0	1 1D 25 0 1 0	3 81 7 2 0	0 1 0 0 0	bitchering_firmicutes_Colorbalog_Lachnospirales{_Lachnospirales4Manehysatta     bi_Listering_freetesischering_commenseries_Manehysatta     bi_Listering_freetesischering_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_manehysatta_manehysatta     bi_Listering_freetesischering_manehysatta_ma
582 583 584 585 586 587 588 589	4 96 3 6 3 11 0 6	0 18 0 0 0 12 0	3 0 1 2 0 0 4	0 0 1 0 0 0	5 1 2 1 2 0 3	2 11 0 9 2 0 0 9	0 0 0 0 0 0 2	1 10 25 0 1 0 3	3 81 3 7 2 0 9	0 1 0 0 0 1	<ul> <li>b Lasteriag. //microscCostrolaugLachnospirales/_Lachnospirales/_Mannhoyatta</li> <li>b LasteriagProtoslasteriacCammaproteobateriagBurkholderiales/_Mannhoyatta</li> <li>b LasteriagProtoslasteriacAbhaproteobateriagMicropospieles/_MicrosconacegAdhronobateri</li> <li>b LasteriagProtoslasteriacDashaproteobateriagMicrosconacescon</li> <li>b LasteriagProtoslasteriacCostrolaugDevicesconacescon</li> <li>b LasteriagControlautoriacCostrolautor_Costr</li></ul>
582 583 584 585 586 587 588 589 589	4 96 3 6 3 11 0 6 13	0 18 0 0 0 12 0 1	3 0 1 2 0 4 0	0 0 1 0 0 0 0	5 6 1 2 1 2 0 3 0	2 11 0 9 2 0 0 9 0	0 0 0 0 0 0 2 0	1 1D 25 0 1 D 0 3 2	3 81 3 7 2 0 0 9 2	0 1 0 0 1 1	b   bateriag_firmicutes_CostrolaLachooprakesf_Lachooprasesg_Mannehysrata     b   bateriag_freeteis_firedeactinis_Gammaportekotteriag_minibalerisks/Analgenoesasesg_kitemotoster     b   bateriag_freeteisactinis_Gammaportekotteriag_Memporaksf_Monoconsacesg_is_     b   bateriag_freeteisactinis_Costrolago_Occleariests_Memorecareses_Firedeactinescossa_     b   bateriag_freeteisactinis_Costrolago_Oneplatef_Olorophist_Costrolagot     b   bateriag_freeteisactinis_Costrolagot     b   bateriag_freeteisactinis_Costrolagot     b   bateriag_freeteisactinis_Costrolagot     b   bateriag_freeteisactinis_Costrolagot     b   bateriag_freeteisactinis_Oneplatef_Olorophist_Costrolagot     b   bateriag_freeteisactinis_Costrolagot     b   bateriag_
582 583 584 585 586 587 588 589 589 589	4 96 3 6 3 11 0 6 13 5	0 18 0 0 0 12 0 1 9	3 0 1 2 0 4 0	0 0 1 0 0 0 0 0	5 1 2 1 2 0 3 0 0	2 11 0 9 2 0 0 9 0 9 0	0 0 0 0 0 2 0 0	1 1D 25 0 1 0 3 2 0	3 81 3 7 2 0 0 9 2 1	0 1 0 0 1 0	b   _bisteriagfmmiotescCostnola_g_ischnolprintesf_LachnosprintestMannehysteta b   _bisteriagProtosbactmisgCammaprotobactmisgminibalienistefMalignescaseg_Achtronobactmi b   _bisteriagfmotobactmisgControlationMinisteriation_CalmaniantestasegControlation
582 583 584 585 586 588 588 589 589 589 589 589	4 96 3 11 0 6 13 5 0	0 18 0 0 0 12 0 1 9 8	3 0 1 2 0 4 0 4 0 0 0	0 0 1 0 0 0 0 0 0 0	5 6 1 2 1 2 0 3 0 0 0 0	2 11 0 9 2 0 0 9 0 1 0	0 0 0 0 0 2 0 2 0 0	1 10 25 0 1 0 3 2 0 0	3 81 7 2 0 9 9 2 1 0	0 1 0 0 1 0 1 0	<ul> <li>b. Jacketing_firmiculase_Colutiduo_Lachinospiralest_Lachinospiralest_Mainthysistla</li> <li>b. Jacketing_freetoiacchints_Cammporteobachints_Micropensect_Mainthysistla</li> <li>b. Jacketing_freetoiacchints_Colutiduo_oblicatints_Micropensect_Colutionenas_pc</li> <li>b. Jacketing_Cyclonibacterista_Colutiduo_Ordenplatet_Ordenplatet_Columpiatet_Activationenas_pc</li> <li>b. Jacketing_Cyclonibacterista_Columpiateting_Micropensect_Micropensect_Colutionenas_Collutionenas_pc</li> <li>b. Jacketing_Columbiaterista_Columpiateting_Micropensect_Columpiatet_Columpiateting_Micropensecti</li></ul>
582 583 584 585 586 587 588 589 599 590 591 592 593	4 96 3 11 0 6 13 5 0	0 18 0 0 0 12 0 1 9 8 11	3 0 1 2 0 4 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0	5 6 1 2 1 2 0 3 0 0 0 0 0 0	2 11 0 9 2 0 0 9 0 9 0 1 0 0	0 0 0 0 0 2 0 0 0 0 0	1 10 25 0 1 0 3 7 0 0 0 0	3 81 3 7 2 0 9 2 1 0 0	0 1 0 0 1 0 0 0	<ul> <li>b. Jacketing_firmicutasc_Costrolato_Lachnospiralesf_Lachnospiralest_Mannehystää</li> <li>b. Jacketing_freetoisachinks_Costrolato_Developatiesf_Lachnospiralest_Mannehystää</li> <li>b. Jacketing_freetoisachinks_Mahaproteetoisaching_Micropesaiset_Mannehystää</li> <li>b. Jacketing_freetoisachinks_Costrolato_Developatiesf_Micropesaiset_Mannehystää</li> <li>b. Jacketing_freetoisachinks_Costrolato_Developatiesf_Micropesaiset_Mannehystää</li> <li>b. Jacketing_freetoisachinks_Costrolato_Developatiesf_Micropesaiset_Mannehystää</li> <li>b. Jacketing_Costrolatorinks_Costrolator_Micropesaiset_Micropesaiset_Micropesaiset_Gelukonosas_Costrolatorina_patiesf</li> <li>b. Jacketing_Costrolatorinks_Costrolatorina_Micropesaiset_Costrolatorina_Costrolatorina_patiesf</li> <li>b. Jacketing_Costrolatorinks_Costrolatorina_Micropesaiset_Costrolatorina_Vietation</li> <li>b. Jacketing_Costrolatorinks_Costrolatorina_Micropesaiset_Oneoplast_Costrolatorina_Vietation</li> <li>b. Jacketing_Costrolatorina_Costrolatorina_Micropesaisetachina_Micropesaisetachina_Costrolatorina_Vietation</li> <li>b. Jacketing_Costrolatorina_Costrolatorina_Micropesaisetachina_Micropesaisetachina_Costrolatorina_Vietation</li> <li>b. Jacketing_Attrolatorina_Micropesaisetachina_Micropesaisetachina_Costrolatorina_Costrolatorina_Costrolatorina_Costrolatorina_Micropesaisetachina_Costrolatorina_Costrolatorina_Costrolatorina_Costrolatorina_Micropesaisetachina_Costrolatorina_Attrolatorina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Attrolatorina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Attrolatorina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_Micropesaisetachina_M</li></ul>
582 583 584 585 586 587 588 589 589 589 589 581 592 593 594	4 96 3 11 0 6 13 5 0 0 9	0 18 0 0 12 0 1 9 8 11 0	3 0 1 2 0 4 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0	5 6 1 2 1 2 0 3 0 0 0 0 0 0	2 11 0 9 2 0 9 0 9 0 1 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0	1 10 25 0 1 0 3 2 0 0 0 0 0	3 81 3 7 2 0 9 9 2 1 0 0 0 0	0 1 0 0 1 0 0 0 0	<ul> <li>b. Jacteriag, Himitotas, Cabinda g, Jachospitaser, Ladnospitaser, Minnehystä</li> <li>b. Jacteriag, Protokactinic, Gammapotokottaka, Jakihalloiniski, Malijensoase, Jakihonolaster.</li> <li>b. Jacteriag, Protokactinic, Gammapotokottaka, Jakihalloiniski, Malijensoase, Jakihonolaster.</li> <li>b. Jacteriag, Protokactinica, Oscoletari intel, Minnoveczatere, Jaine Constructiona, Gelekonona Jacker, Jakihanoteka, Minnoveczatere, Jaine Constructiona, Gelekonona, Jakihonolasteria, Jakihonolasteria, Colonoplat, Olivoplat, Olivoplat, Olivoplat, Olivoplat, Coloroplat, Olivoplat, Coloroplat, Minnoveczatere, Jaine Construction, Jakihonolasteria, Jakihonolaster, Jakihonolasteria, Jakihonolaste</li></ul>
582 583 584 585 586 588 589 590 591 592 593 594 595 596 597	4 96 3 11 0 6 13 5 0 0 9	0 18 0 0 12 0 1 9 8 11 0 10 23 7	3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 1 1 3	5 6 1 2 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 9 0 9 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 3 2 0 0 0 0 0	3 81 3 7 2 0 9 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	b) _bisteriag_fmm:datas_Coloridag_isdongprakesf_ladnosprasesg_Mannehysatta b) _bisteriag_freeteelasteriag_anneprotebatteriag_Mannehysatta b) _bisteriag_freeteelasteriag_dataspratebatteriag_Mannehysatta b) _bisteriag_freeteelasteriag_gannehesteriag_Mannehysatta b) _bisteriag_freeteelasteriag_gannehesteriag_Mannehysatta b) _bisteriag_teelasteriag_gannehesteriag_Mannehysatta b) _bisteriag_teelasteriag_gannehesteriag_Mannehysatta b) _bisteriag_teelasteriag_gannehesteriag_Mannehysatta b) _bisteriag_teelasteriag_gannehesteriag_Mannehosteriagchiroropiast b) _bisteriag_teelasteriag_gannehesteriag_freedesteriag_gannehesteriagannehest
582 583 584 585 586 588 589 590 591 592 593 594 595 596 597 598	4 96 3 11 0 6 13 5 0 0 9	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0	3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 1 1 3 0	5 6 1 2 1 2 0 3 0 0 0 0 0 0	2 11 9 2 0 9 0 9 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 3 2 0 0 0 0 0	3 81 3 7 2 0 9 9 2 1 0 0 0 0		<ul> <li>b. Jackeriag, Proceedactrice, Camagetorebacteriag, Manaparaser, Manarhysetta</li> <li>b. Jackeriag, Proceedactrice, Camagetorebacteriag, Manaparaser, Manarhysetta</li> <li>c. Jackeriag, Proceedactrice, Camagetorebacteriag, Manaparaser, Jackerosaser, Manarhysetta</li> <li>c. Jackeriag, Proceedactrice, Canadatorebag, Manaparaser, Manarhysetta</li> <li>c. Jackeriag, Canadatorebag, Oncologitariag, Manaparaser, Calandonasa, Calabonesa, Calabo</li></ul>
582 583 585 585 587 588 589 589 589 589 591 593 594 595 595 599 599	4 96 3 11 0 6 13 5 0 0 9	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0 0	3 3 1 2 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 1 1 3 0 0 0	5 6 1 2 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 25 0 1 0 3 2 0 0 0 0 0 0 0 0 0 0 2 4	3 81 7 2 0 9 2 1 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateriag_Immatase_Cabardag_Lachaoprizesf_Lachaoprizesef_Charaoprizeserg_Ammetayanta</li> <li>b. bateriag_Protosbateriag_Camaprotobateriag_Metapositesf_Malaprisesf_Malaprisesf_Manaphysista</li> <li>b. bateriag_Intereductoriag_Cabarbardag_Metapositesf_Malaprisesf_Manaphysista</li> <li>b. bateriag_transformateriag_Cabarbardag_Metapositesf_Malaprisesf_Cabarbardag_Cabarbarbardag_Cabarbardag_C</li></ul>
582 583 585 585 587 588 589 589 589 591 592 593 594 595 596 599 599 600	4 96 3 11 0 6 13 5 0 0 9	0 18 0 0 0 12 0 12 0 12 8 11 0 10 23 7 0 0 0	3 3 1 2 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 1 1 3 0 0 1 1 3 0 0 1	5 6 1 2 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 2 4 0	3 81 7 2 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacteriag_/mmcdates_Calothabu_isabinapiralesif_lachoospirasesif_Mannhoyantab</li> <li>b. bacteriag_/motosbacteriag_andeparteebacteriag_Mannhoyantab</li> <li>b. bacteriag_/motosbacteriag_andeparteebacteriag_Mannhoyantab</li> <li>b. bacteriag_/motosbacteriag_andeparteebacteriag_Mannhoyantab</li> <li>b. bacteriag_freebacteriag_andeparteebacteriag_Mannhoyantab</li> <li>b. bacteriag_freebacteriag_contexteriag_motosbacteriag_Mannhoyantab</li> <li>b. bacteriag_freebacteriag_contexteriag_Mannhoyantab</li> <li>c. bacteriag_freebacteriag_contexteriag_Mannhoyantab</li> <li>b. bacteriag_contexteriag_contexteriag_Mannhoyantab</li> <li>c. bacteriag_contexteriag_contexteriag_motosbacteriag_contexteriag_mannhoyantab</li> <li>b. bacteriag_contexteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_contexteriag_motosbacteriag_contexteriag_motosbacteriag_contexteriag_contexteriag_contexteriag_motosbacteriag_contexteriag_networteriag_netw</li></ul>
582 583 584 585 586 587 588 589 590 591 592 594 595 596 596 599 599 600	4 98 3 6 11 0 6 11 5 0 9 0 9 6 8 7	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0 0	3 3 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 1 1 3 0 0 1 1 0 0 1 0	5 6 1 2 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 25 0 1 0 3 2 0 0 0 0 0 0 0 0 0 0 2 4	3 81 3 7 2 0 9 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacteriag_fremiotase_clostrolagachinospirasesf_achinospirasesf_Manehystati</li> <li>c. bacteriag_freetosiacentisc_anneporteobacteriag_Microposasesf_Microposasesf_Achinospicases</li></ul>
582 583 584 585 587 588 589 590 593 594 595 595 596 597 598 599 600 601	4 96 3 6 3 11 0 6 13 5 0 9 6 8 7 0	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0 0 0 0 0 0 0 0 0 0	3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 1 1 3 0 0 1 1 3 0 0 1 3 0 1 3 0 1 3 1 3	5 6 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 9 2 0 9 0 9 0 1 1 0 0 0 0 0 0 0 1 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 2 0 9 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateriagInvestassCostrolagLacheoprisesf_LacheoprisessgMannehystati</li> <li>b. bateriagInvestassCostrolagLacheoprisesfMannehystati</li> <li>b. bateriagInvestasscriseAlahaproteabateriagMannehystati</li> <li>b. bateriag_InvestasscrisesAlahaproteabateriag_MannekstatisfAlaijersooraaceagin</li></ul>
542 543 544 545 547 548 549 549 549 549 549 545 545 545 545 545	4 96 3 11 0 6 13 5 0 9 6 8 7 0 4 9 6 8 7 0 10	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 1 1 3 0 0 1 0 1 0 1 0	5 6 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 9 2 0 9 0 9 0 9 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 7 2 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateriag_Immediase_Costrolog_Lochrosprisesf_Lochrosprisesey_Manehysatb</li> <li>c. bateriag_Protobacteriag_Contrological and an an</li></ul>
542 543 545 545 546 547 548 549 544 545 549 549 600 601 601 602 603 604	4 96 3 6 11 0 6 13 5 0 9 0 4 9 6 8 7 0 10 0	0 18 0 0 12 0 1 3 8 11 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 0 1 2 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 1 1 3 0 0 1 0 1 0	5 6 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 9 2 0 9 0 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 7 2 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacteriag_fremates_clostradup_ladrosprises_f_adrosprises_Manetaystati</li> <li>b. bacteriag_freetosbacteriag_annegreetosbacteriag_Manetaystats_Analgieroscascest_g_n_ b. bacteriag_freetosbacteriag_adrosprisest_manetaystats</li> <li>b. bacteriag_freetosbacteriag_Contengates_Manetaystats</li> <li>c. bacteriag_Activatostariag_Nariamatestariag_Manetaystats</li> <li>c. bacteriag_Activatostariag_Nariamatestariag_Manetaystats</li> <li>c. bacteriag_Activatostariag_Nariamatestariag_Manetaystats</li> <li>c. bacteriag_Activatostariag_Activatostariag_Manetaystats</li> <li>c. bacteriag_Activatostariag_Activatostariag_Manetaystats</li> <li>c. bacteriag_Activatostariag_Activatostariag_Manetaystats</li> <li>c. bacteriag_Activatostariag_Activatostariag_Manetaystats</li> <li>c. bacteriag_Activatostariag_Activatostariag_Manetaystats</li> <li>c. bacteriag_Activatostariag_Activatostariag_Prevotelag_P</li></ul>
542 543 544 545 546 547 549 549 544 545 545 545 545 546 547 549 600 601 602 604 604	4 96 3 11 0 6 13 5 0 9 6 8 7 0 4 9 6 8 7 0 10	0 18 0 0 12 0 1 3 8 11 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 1 2 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 1 1 3 0 0 1 1 3 0 0 1 3 0 0 1 1 3 0 0 1 1 1 1	5 6 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 9 2 0 9 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 7 2 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacteriag_frematesc_Gateriado_Laderospitasesf_Laderospitasesg_Manethystati</li> <li>b. bacteriag_freedoscateriac_Anterpotendenteriag_Manethystati</li> <li>b. bacteriag_freedoscateriac_Anterpotendenteriag_Manetocoacestes_a_</li> <li>b. bacteriag_freedoscateriac_Anterpotendenteriag_Manetocoacestes_a_</li> <li>b. bacteriag_freedoscateriac_Coartedoscateriag_Manetocoacestesg_a_</li> <li>b. bacteriag_freedoscateriac_Coartedoscateriag_Manetocoacestesg_a_</li> <li>b. bacteriag_freedoscateriac_Coartedoscateriag_Manetocoacestesg_a_Dariettescateriag_freedostariag_freed</li></ul>
542 543 545 546 546 547 548 549 549 549 549 545 545 545 545 546 545 546 601 601 603 605	4 96 3 6 11 0 6 13 5 0 9 0 4 9 6 8 7 0 10 0	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 1 1 3 0 0 1 3 0 0 1 3 0 0 1 1 0 0 1 1 0 0 1 1 1 1	5 6 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 9 2 0 9 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 7 2 0 9 7 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateriag_Immates_Catardag_Lachaaprakesf_Lachaaprakesg_Mannehysnäs</li> <li>b. bateriag_Protokachinks_Gammaponohokhatha_Jankhalkeriskisf_Afaliperasasg_Afknehoksist.</li> <li>b. bateriag_Protokachinks_Gammaponohokhatha_Jankhalkeriskisf_Afaliperasasg_Afknehoksist.</li> <li>b. bateriag_Protokachinks_Gammaponohokhatha_Jankhalkeriskisf_Afaliperasasg_Afknehoksist.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Bateriadiks_Bateriadiks_Cannehosinehosi.</li> <li>b. bateriag_Bateriadiks_Bateriadiks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Bateriadiks_Bateriadiks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Protokachinks_Cannehosinehosi.</li> <li>b. bateriag_Bateriadiks_Cannehosinehosi.</li> <li>b. bateriag_Bateriadiks_Cannehosinehosi.</li> <li>b. bateriag_Bateriadiks_Cannehosinehosi.</li> <li>b. bateriag_Bateriadiks_Cannehosinehosi.</li> <li>b. bateriag_Bateriadiks_Cannehosinehosi</li></ul>
982 983 984 985 980 980 981 983 984 985 984 985 984 985 986 989 000 001 002 003 004 003 004 005 005 005 005 005 005 005 005 005	4 96 3 6 11 6 13 5 0 9 6 8 7 0 0 9 6 8 7 0 0 5 4 0 0 5	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 1 1 3 0 0 1 0 1 0 1	5 6 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 7 0 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateriag, Immatas, Cabarda, Jachmaprikef, Ladmaprikesf, Alafaprikest, Manikyanta</li> <li>b. bateriag, Protestachnik, Anhaprotestatura, Jankalkinski M, Alafaprikaska, Minnobasteri</li> <li>b. bateriag, Immatas, Cabarda Cabarda, Maniporeskatura, Manikorszatura, Janikoroszatura, Cabarda Kabarda, Cabarda Kabarda Kabarda, Cabarda Kabarda, Cabarda Kabarda, Cabarda Kabarda Kabarda, Cabarda Kabarda Kab</li></ul>
542 543 545 546 546 547 548 549 549 549 549 545 545 545 545 546 545 546 601 601 603 605	4 96 3 6 11 0 6 13 5 0 9 0 4 9 6 8 7 0 10 0	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 1 1 3 0 0 1 3 0 0 1 3 0 0 1 1 0 0 1 1 0 0 1 1 1 1	5 6 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 9 2 0 9 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 7 2 0 9 7 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateria, _ freedebacteria, _ annegronebacteria, _ Meneparase, _ Manehyanta</li> <li>c. bateria, _ freedebacteria, _ annegronebacteria, _ Meneparase, _ Manehyanta</li> <li>c. bateria, _ freedebacteria, _ debaprotebacteria, _ Meneparase, _ Manehyanta</li> <li>c. bateria, _ freedebacteria, _ Annegronebacteria, _ Meneparase, _ Anneorease, _ Anternobacteria, _ Meneparase, _ Anternobacteria, _ Meneparase, _ Manehyanta, _ Meneparase, _ Anternobacteria, _ Meneparase, _ Anternobacteria, _ Meneparase, _ Anternobacteria, _ Meneparase, _ Calumona, _</li></ul>
982 983 985 986 987 980 983 983 983 985 985 985 985 985 985 985 989 800 801 802 803 803 804 805 805 805 805 805 805 805 805 805 805	4 96 3 6 3 11 0 6 13 5 0 9 0 4 9 6 8 7 0 10 0 5 4 0 1	0 18 0 0 1 1 9 8 11 0 10 10 10 10 10 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 1 1 3 0 0 1 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0	5 6 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 2 0 9 7 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b.batenia_Investase_Costrolog_abeneprises/_abeneprises/_Analysises_Adversebuses</li> <li>b.batenia_Investasetanis_Commercebusetanis_Memoreases_Adversebuses</li> <li>c.batenia_Investasetanis_Controlog_ContentingInvestaseta_Memoreases_Adversebuses</li> <li>c.batenia_Investasetanis_Controlog_ContentingInvestaseta_Contrologues</li> <li>c.batenia_Contrologues_Contrologue_ContentingInvestaseta_Contrologues</li> <li>c.batenia_Contrologues_Contrologues</li> <li>c.batenia_Contrologues_Contrologues</li> <li>c.batenia_Contrologues_Contrologues</li> <li>c.batenia_Contrologues</li> <li>c.batenia_Control</li></ul>
982 983 985 985 986 987 988 989 984 983 984 985 984 985 985 986 986 986 886 886 886 886 886 886 886	4 96 3 6 11 0 6 13 5 0 9 6 8 7 0 10 0 5 4 0 1 3	0 18 0 0 12 0 1 9 8 11 0 10 10 10 10 0 0 0 0 0 0 0 0 0 0	3 3 4 6 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8	6 0 1 6 0 0 0 0 0 0 0 0 1 1 3 0 1 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	5 6 1 2 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 9 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 2 0 9 7 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b.bateriag_Investas_Calandag_Lakhaparakef_Lakhaparakef_Anneparaket_Maneparaket</li> <li>b.bateriag_Investastas_Calandago technicag_anneparaket_Maneparaket_Maneparaket</li> <li>c.bateriag_Investastastas_Calandago technicag_anneparaket_Maneparaket</li> <li>c.bateriag_Investastastas_Calandago technicag_Oneparaket_Maneparaket_Environematicat</li> <li>c.bateriag_Annebacteriag_Oneparateriag_Oneparaket_Maneparaket_Environematicat</li> <li>c.bateriag_Annebacteriag_Oneparateriag_Oneparaket_Maneparaket_Environematicat</li> <li>c.bateriag_Annebacteriag_Oneparateriag_Oneparatet_Environematicaterag_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Calandaenast_Maneparatetat</li> <li>c.bateriag_Oneparateriag_Annebacteriag_Maneparatetat_Maneparatetast_Nachandaenast_Calandaenast_Calandaenastastastastastastastastastastastastasta</li></ul>
982 984 985 986 980 980 980 980 980 980 980 984 985 989 989 989 989 989 989 989 989 989	4 96 3 6 3 11 0 6 13 5 0 9 0 7 9 6 8 7 0 10 5 4 0 1 3 7	0 18 0 0 1 9 8 11 9 10 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 1 1 3 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	5 5 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 9 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b.batenia_Investase_Costrolog_abeneprises/_abeneprises/_Analysises_Adversebuses</li> <li>b.batenia_Investasetanis_Commercebusetanis_Memoreases_Adversebuses</li> <li>c.batenia_Investasetanis_Controlog_ContentingInvestaseta_Memoreases_Adversebuses</li> <li>c.batenia_Investasetanis_Controlog_ContentingInvestaseta_Contrologues</li> <li>c.batenia_Contrologues_Contrologue_ContentingInvestaseta_Contrologues</li> <li>c.batenia_Contrologues_Contrologues</li> <li>c.batenia_Contrologues_Contrologues</li> <li>c.batenia_Contrologues_Contrologues</li> <li>c.batenia_Contrologues</li> <li>c.batenia_Control</li></ul>
982 983 986 986 980 980 981 983 985 984 985 985 986 989 800 800 800 800 800 800 800 800 800	a 96 3 6 1 1 0 6 1 5 0 9 0 4 9 6 8 7 0 10 0 5 4 0 1 3 7 10	0 18 0 0 12 0 1 9 8 11 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 1 2 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 1 1 3 0 0 1 0 1 0	5 5 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 1 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 2 0 9 2 1 0 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateria, _ invastas, _ bateriada, _ bahaparaksf, _ lachospirasas, _ Manehyanti</li> <li>c. b. bateria, _ hotosbateria, _ annaportekateria, _ Manehyantik _ Malijerasas, _ Manehyanti</li> <li>c. b. bateria, _ invastacteria, _ dahaparakstaria, _ Manehospirasas, _ Manehyantik</li> <li>c. b. bateria, _ invastacteria, _ Anhaparakstaria, _ Manehospirasas, _ Manehyantik</li> <li>c. b. bateria, _ invastacteria, _ Questateria, _ Manehospirasas, _ Manehospirasa, _ Calenosoma, _ a.</li> <li>c. b. bateria, _ invastacteria, _ Anhaparakstaria, _ Manehospirasas, _ Calenosoma, _ Calenosoma, _ Gelakonosa, _ Gelakonos</li></ul>
982 983 985 986 987 980 983 983 983 985 985 985 985 985 985 985 985 985 986 807 802 803 804 805 805 805 805 805 805 805 805 805 805	a 96 3 6 1 1 0 6 1 5 0 9 0 4 9 6 8 7 0 10 0 5 4 0 1 3 7 10	0 18 0 0 1 9 1 9 1 1 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 1 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 1 0	5 5 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 2 0 9 2 1 0 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateria, freedokardia, Jachengeriekel, Jachengeriekel, Marineyenska, Marineyenska, Aktronobacker</li> <li>b. bateria, freedokardia, Aktronotobackeria, Marineyenska, Marineyenska, Aktronobacker</li> <li>b. bateria, freedokardia, Aktronotobackeria, Marineyenska, Marineyenska, Aktronobacker, J.</li> <li>b. bateria, freedokardia, Aktronotobackeria, Marineyenska, Mariney</li></ul>
982 983 985 986 987 980 981 983 984 985 984 985 986 987 989 800 801 800 801 803 805 805 805 805 805 805 805 805 805 805	a 96 3 6 1 1 0 6 1 5 0 9 0 4 9 6 8 7 0 10 0 5 4 0 1 3 7 10	0 18 0 12 0 13 8 11 0 10 10 10 10 10 10 10 10	3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 1 1 0 0 1 0 0 1 0 0 1 0 0 1 0	5 6 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 0 9 7 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		b. Jackning_Immutase_Calmatage_Ladmagnitusesi_Ladmagnitusesi_Kalmatage_Kalmanabage_Kalmanabage
<ul> <li>Sala</li> <li>Sala<td>a 96 3 6 3 11 0 6 13 5 0 0 9 0 0 4 9 6 8 7 0 10 0 5 4 0 1 3 7 16 0 3 6</td><td>0 18 0 12 0 13 14 15 10 10 10 10 10 10 10 10 10 10</td><td>3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td>0 0 0 0 0 0 0 0 0 0 0 0 1 1 3 0 0 1 0 0 1 0 0 0 1 0 0 0 0</td><td>5 6 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td>2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td>1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td>3 81 3 7 2 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td></td><td><ul> <li>b. bateria freedeactivita _ activator paralet _ activator paraet _ Anterparaet _ Anterpa</li></ul></td></li></ul>	a 96 3 6 3 11 0 6 13 5 0 0 9 0 0 4 9 6 8 7 0 10 0 5 4 0 1 3 7 16 0 3 6	0 18 0 12 0 13 14 15 10 10 10 10 10 10 10 10 10 10	3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 1 1 3 0 0 1 0 0 1 0 0 0 1 0 0 0 0	5 6 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 2 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bateria freedeactivita _ activator paralet _ activator paraet _ Anterparaet _ Anterpa</li></ul>
982 986 986 987 980 980 981 983 984 983 985 985 986 989 000 001 002 003 003 004 003 005 003 005 005 005 005 005 005 005	a 96 3 6 3 11 0 6 13 5 0 0 9 0 0 4 9 6 8 7 0 10 0 5 4 0 1 3 7 16 0 3 6	0 18 0 0 1 1 3 1 1 1 1 1 1 1 1 1 1 1 1 1	3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0	5 6 1 2 1 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 2 0 9 7 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b.bctering_introducts_Controluc_inductoring_Mathematiks_Mathematiks_Mathematiks b.bctering_introductoring_datapathematics_Mathematiks b.bctering_introductoring_datapathematics_Mathematiks b.bctering_introductoring_datapathematics_Controluctoring b.bctering_introductoring_datapathematics_Controluctoring b.bctering_databatering_datapathematics_Controluctoring b.bctering_databatering_databatering_datapathematics b.bctering_databatering_databatering_datapathematics b.bctering_databatering_databatering_datapathematics b.bctering_databatering_databatering_datapathematics b.bctering_databatering_databatering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering b.bctering_databatering_databatering_databatering b.bctering_interolog_databatering_databatering b.bctering_databatering_databatering_databatering b.bctering_faterin</pre>
982 983 985 986 987 980 983 983 984 985 984 985 984 985 986 987 989 800 801 805 806 806 806 806 806 806 806 806 806 806	a 96 3 4 5 0 9 0 4 9 6 8 7 0 10 5 4 0 1 3 7 16 0 7 6 17 4	0 18 0 1 1 9 8 11 9 8 1 1 0 10 23 7 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 0 1 2 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 6 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	10 25 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 81 3 7 2 0 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b.bctering_interacts_Charabayeraber_in_Metaperaber_K_Manapayerabe b.bctering_interactoraber_in_Metaperaber inter_Metaperabers_Metaperabers_ b.bctering_interactoraber_inter_Metaperabers_Metaperabers_Metaperabers_ b.bctering_interactorabers_Charabayerabersing_Metaperabers_Charabayeras_Charabayeras_Charabayeras_ b.bctering_interactorabersing_Metaperabersing_Charabayeras_Charabayeras_Charabayeras_ b.bctering_interactorabersing_Metaperabersing_Charabayeras_Charabayeras_Charabayeras_Charabayeras_Charabayeras b.bctering_interactorabersing_Metaperabersing_Charabayeras_Charabayeras_Charabayeras b.bctering_Activated article_Activated artic_Metaperaberg_Charabayeras_Charabayeras_Charabayeras b.bctering_Activated article_Activated article_Metaperaberga_Charabayeras_Charabayeras_Charabayeras b.bctering_Activated article_Activated article_Metaperaberga_Charabayeras_Charabayeras b.bctering_Activated article_Activated article_Metaperaberga_Charabayeras_Charabayeras b.bctering_Activated article_Activated article_Metaperaberga_Charabayeras_Charabayeras b.bctering_Activated article_Activated article_Metaperaberga_Charabayeras_Charabayeras b.bctering_Activated article_Activated article_Metaperaberga_Deaddoart b.bctering_Metaperabers_Deaters article_Metaperaberga_Deaddoart b.bctering_Interactor_Charabayeras_Charabayeras_Charabayeras_Charabayeras b.bctering_Activated article_Activated article_Activated article_Metaperated b.bctering_Activated article_Activated article_Activated article_Activated article_Activated b.bctering_Activated article_Activated Activated article_Activated article</pre>
982 983 985 985 980 981 983 983 985 985 985 985 985 985 985 985 986 987 885 885 885 885 885 885 885 885 885 8	a ma 3 6 3 11 0 6 13 5 0 0 9 0 0 4 9 6 8 7 0 10 0 5 4 0 1 3 7 16 0 2 6 17 4 0	0 18 0 0 1 9 8 11 9 8 10 13 7 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 1 0 0 1 0 0 0 1 0	5 5 1 2 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11 0 9 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 10 25 0 1 0 0 0 0 0 0 0 1 7 3 0 2 0 0 6 1 3 0 0	3 81 3 7 2 0 0 9 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		b. Jacksing _ Immakes_Cakinda _ Jackmaprices _ Landragina and _ Kainda in a set of the set of th

620	0	8	0	0	0	0	0	0	0	0	0 Unknown
621	0	0	o	0	0	12	0	1	0	0	0 k_Bacteria;p_Firmicutes;c_Bacili;o_RF39;f_RF39;g_RF39;s_
622	0	0	0	0	0	0	0	0	0	10 0	0 k_Bacterla;p_firmicutes;c_Bacilit,o_Mycoplasmataiesf_Mycoplasmataeae;g_Mycoplasmas 0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiaks;f_Nitrosporronadaceae;g_mic1.7;s_
624	19	4	0	4	2	0	0	0	0	0	0 k_parceriary_rroteoua.ceries_caminipuot.couarceriary_bannoideriarsy_ministorinareaecae_metrys_ 0 k_Bacteriary_Firmicutersc_Clostridia_cacin8660_groupsf_Clostridia_vadin8860_groupsg_Clostridia_vadin8860_groups_
625	4	0	0	0	0	D	0	1	2	٥	0 k_Bacteria;p_Actinobacteriota;c_Actionbia;o_Microtrichales
626	9	o	1	o	11	3	o	3	10	1	0 k_Bacteria;p_Protacbacteria;c_Gammaproteobacteria;o_Cellvibrionale;;f_Spongilbacteraceae;g_BD1-7_dade;s_
627	3	11	0	0	0	1	0	0	1	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Vanbaculum
628	31	0	16	0	3	7	0	36	7	0	4 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_Sphingomonas_koreensis
629	6	0	11	11	14	D	3	1	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroida;o_Bacteroidales;f_Muribaculaceae;g_Muribaculaceae;s_
630	8	1	6	0	0	3	0	2	8	٥	1 k_Bacteria;p_Firmicutes;c_Clostrida;o_Lachnospirales;f_Lachnospiraceae
631	56	0	34	0	35	37	0	31	64	8	${\tt 5 k\_Bacteria;p\_Actinobacteriotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;g\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_interiotacc\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_Actinobacteria;o\_Frankiales;f\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_Actinobacteria;o\_Frankiales;f\_Actinobacteria;o\_Frankiales;f\_Sporichthyaceae;s\_Actinobacteria;o\_Frankiales;f\_Actinobacteria;$
632	8	0	0	0	1	1	0	4	2	0	0 k_Bacteria;p_firmicutes;c_Bacill.o_Paenibacillales;f_Paenibacillaceae
633	3	0	0	0	0	1	0	5	7	0	0 k_Bacteria;p_Planctomycetota;c_OM190;c_OM190;f_OM190;a_OM190;a_
634	1	0	0	0	0	4	0	2	0	0	$0 \ k\_Bacteria; p\_Actinobacteriota; c\_Thermoleophili;; o\_Solirubrobacterales; f\_Solirubrobacteraces; e\_Conexibacter; s\_Thermoleophili; o\_Solirubrobacteraces; e\_Conexibacter; s\_Thermoleophili; o\_Solirubrobacteraces; e\_Conexibacter; s\_Thermoleophili; o\_Solirubrobacteraces; e\_Conexibacter; s\_Thermoleophili; o\_Solirubrobacteraces; e\_Solirubrobacteraces; e\_Solirubroba$
635	0	12	O	0	0	D	0	D	0	O	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotellacea;;g_Prevotella;s_Prevotella_corporis
636	0	0	1	0 3	0	2 14	0 3	1	6 0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Cellvbrionales;f_Spongibacteraceae;g_801-7_clades0 k_Bacteria;p_Firmicutex;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_3
638	å	0	2	0	1	0	0	0	0	0	1 k_Bacteria;p_Firmicutes;c_Clostridia;p_Lachnospirales;f_Lachnospiracea;g_Roseburia;s_
639	5	0	2	0	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;cGammaproteobacteria
640	4	0	o	o	3	4	0	1	7	o	0 k_Bacteria:p_Bacteroldota:c_Bacteroldia
641	6	1	o	1	5	D	0	D	z	o	0 k_Bacteria;p_Firmicutes;c_Clostrida;o_Oscillospirales;f_Ruminococcaceae;g_;s_Clostridum_leptum
642	0	0	0	15	0	0	0	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Cytophagales;f_Hymenobacteraceae;g_Pontibacter;s_Pontibacter_sp.
643	11	0	16	2	14	1	1	4	9	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroida;o_Bacteroidales;f_Muribaculaceae;g_Muribaculaceae;s_
644	4	2	1	9	3	1	1	1	4	0	0 k_Bacteria;p_Firmicutes:c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
645	0	6	0	1	D	D	0	D	0	0	$0\ k\_Bacteria;p\_Firmicutes;c\_Clostridia;o\_Peptostreptococcales-Tissiereliales;f\_Peptostreptococcales-Tissiereliales;g\_Gallicola;s\_Dallicola;s]Dallicola;s\_Dallicola;s\_Dallicola;s\_Dallicola;s\_Dallicola;s\_Dallicola;s\_Dallicola;s\_Dallicola;s]Dallicola;s\_Dallicola;s\_Dallicola;s]Dallicola;s\_Dallicola;s]Dallicola;s]Dallicola;s]Dallicola;s]Dallicola;s]Dallicola;s]Dallicola;s]Dallic$
646	6	3	3	14	2	1	1	0	1	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_ASF856;s_
647	0	0	0	0	0	0	9	0	0	0	0 Unknown
648	2	10	0	45	0	D	18	0	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium;s_Corynebacteriam_stationis
649	0	11	0	0	0	D	0	0	1	0	0 k_Bacteria;p_Firmicutes;c_Bacilito_Baciliales;t_Baciliaceae;g_Oceanobacilius;s_
650 651	0 3	0	0	0	0	0	0	9	0	0	0 k_Bacteria;p_Mixococcota;c_Polyangia;o_Polyangia(s;f_Polyangiacea:g_:s
652	3	14	0	1	5	10	0	13	15	0	0 K_sacteria;p_Hmcutetc_Ubstnas;o_Uscillopiralis;7_006-010;r_006-010;r_006-010;s_006-006-00;s_006-000;s_006-006-00;s_006-000;s_006-006-00;s_006-000;s_006-000;s_006-006-00;s_006-006-000;s_000
653	6	0	0	0	0	0	1	10	0	0	<ul> <li>b K_anctering_Criteronautering_Consolucteringprintpoint in an analyzing and an analyzing more spining units and the s</li></ul>
654	3	0	o	0	0	o	0	1	4	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Cardiobacteriales;f_Cardiobacteriaceae
655	6	0	o	0	o	D	0	D	0	o	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadale;sf_Moraxellaceae;g_Moraxella;s_
656	0	0	0	0	0	0	0	16	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas
657	0	0	4	0	3	1	0	0	3	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_40839;g_40839;a_
658	o	11	O	1	D	D	0	D	0	O	$0\ k\_Bacteria; p\_Verrucomicrobiota; c\_Verrucomicrobiae; o\_Chthoniobacterales; f\_Chthoniobacteraceae; g\_Chthoniobacter; s\_Chthoniobacter; s\_Chthoniobacter;$
659	1		3								0 k_Bacteria;p_Myxococcota;c_Polyangia;o_Blfdi19;f_Blfdi19;g_Blfdi19;g_
1220		0		0	1	2	0	0	1	0	
660	13	0	9	0	3	5	o	5	11	o	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderialesif_Nitrosomonadaceaeg_Ellin6067;s
661	13 0	0 11	9 0	0 0	3 0	5 D	0 0	5 D	11 0	0 0	0 k_Baterias_Protechaterias_Cammaprotechaterias_Barkholdersikerf_Nitrosomonadaceseg_IIIrob07s_ 0 k_Baterias_Dirmicutes_Colotindass_Neptotreptococciles=Tasieneladecf_Anaerosenacceseg_Nogbacterium_Mogbacterium_sp.
	13 0 49	0 11 4	9 0 1	0 0 0	3 0 2	5	0 0	5 D 0	11 0 20	0 0 2	0 k_Bateriap_Protechateriac_Cammaprotechateriao_Burkholderskef_Nitrosomonaticeseg_tilri0067s_ 0 k_Bateriap_Immicutes_Colutriduo_Neptotreptococcales=Tusienelalesf_Anaerosomacceseg_Nopbateriums_Mopbaterium_sp 2 k_Beteriap_Firmicutes_Colutriduo_Lachoopinalesf_Lachoopinacese_UKAA136_gmuos_
661 662	13 0	0 11	9 0	0 0	3 0	5 D 30	0 0	5 D	11 0	0 0	0 k_Bateriag_Proteobacteriac_Cammaproteobacteriao_Burkholdersikef_Nitrosomonasisceaeg_Elino567s_ 0 k_Bateriag_Immicutesi_Cbatriduo_Peptotinestacoccales-Tasienelalesf_Anaeroomacceaeg_Mogbacteriums_Mogbacterium_ 2 k_Bateriag_Emmicutesi_Cbatriduo_Tachonopinalistif_Lachonopinee.eeg_Lachonopineeae.MKA136_gmuosj_ 0 k_Bateriag_Actinobacteriatac_Actinobateriajo_Frankilass_Sportshtyaceaeg_Ngd_cladesi_Candidatus_Planitophila
661 662 663	13 0 49 7	0 11 4 0	9 0 1 5	0 0 0	3 0 2 1	5 D 30 4	0 0 0	5 D 0 1	11 0 20 11	0 0 2 0	0 k_Bateriap_Protechateriac_Cammaprotechateriao_Burkholderskef_Nitrosomonaticeseg_tilri0067s_ 0 k_Bateriap_Immicutes_Colutriduo_Neptotreptococcales=Tusienelalesf_Anaerosomacceseg_Nopbateriums_Mopbaterium_sp 2 k_Beteriap_Firmicutes_Colutriduo_Lachoopinalesf_Lachoopinacese_UKAA136_gmuos_
561. 662 663 564	13 0 49 7 2	0 11 4 0	9 0 1 5 4	0 0 0 0	3 0 2 1 1	5 D 30 4 1	0 0 0 0	5 D 0 1 2	11 0 20 11 2	0 0 2 0 0	0 k_Bateriap_Protecbateriac_Cammaproteobateriao_Burkholderiaksf_Nitrosomonatisceseg_Elino567s_ 0 k_Bateriap_Timiculesi_Colutridao_Peptotineptococcales-Tasienelalesf_Anaeroorracceseg_Wogbateriums_Mogbaterium_ 2 k_Bateriap_Fimiculesi_Colutridao_Tachonopinalosf_Lachonopinacese_Lichonopinacese_NK4A136_groups_ 0 k_Bateriap_Acinobateriatac_Acinobateriap_Franklatesf_Sportsthynosese_Ingl.clados_Candidatus_Planitophila 0 k_Bateriap_Monopinatas_Nitrospinao_Nitospiralesf_Mitrospinacese_Nitospiras_
661 662 663 664 665	13 0 49 7 2 0	0 11 4 0 0	9 0 1 5 4 0	0 0 0 0 8	3 0 2 1 1 0	5 0 30 4 1 0	0 0 0 0	5 0 1 2 0	11 9 20 11 2 9	0 2 0 0	<ul> <li>b. Escteriag_Proteebacteriag_Commaproteebacteriag_Burkholdersikef_Nitrosomonadiceexg_Eline667s_</li> <li>b. Escteriag_Proteebacteriag_Coloridag_Periodinestococalite_Intereliablesf_Anaroversaceoseg_VogBacterium_MogBacterium_pp.</li> <li>J. Escteriag_Protectacteriag_Decodersitesf_Decodersitesf_Decodersitesf_Nitrosophacese_UseAlbidig_prougs</li></ul>
661 662 663 664 665 666	13 0 49 7 2 0	0 11 4 0 0 0	9 0 1 5 4 0	0 0 0 0 8 0	3 0 2 1 1 0	5 0 30 4 1 0	0 0 0 0 0 0	5 0 1 2 0	11 0 20 11 2 0 0	0 2 0 0 5	D I _Bateriag_Protechadaritac_Cammaproteobateriao_Bathioldenialsd_Nitrosomonadaceseg_Bindboffs_ D I _Bateriag_Trendetec_Clatricita_Peptoteptacocales_Tesenelleks(_Anaerosenaceseg_VogBaterium_se_MagBaterium_sp. 2 \_Betering_Finitetec_Clatricitag_Ternialsty_Endoteptaceseg_Bathiologeneese_MAGB4_groups_ D \_Batering_Ministeric_Clatricitag_Finitetecitag_SortClathyseeseg_Natasetecitag_Ministerium_ 0 \_Batering_Ministeric_Clatricitag_Ministeric_Clarabetering_Ministericag_Micobaterium_ 0 \_Batering_Ministeric_Clatricitag_Ministeriag_Clarabetering_Ministericag_Micobaterium_ 0 \_Batering_Ministerint_Clarabetering_Complexited_Ministeric_Ministeriag_Micobaterium_ Batering_Ministering_Ministering_Ministering_Clarabetering_Ministericag_Micobaterium_ 5 \_BateringBinistering_Batering_Ministerin
661 663 664 665 666 667	13 0 49 7 2 0 0	0 11 4 0 0 0 0 0	9 0 1 5 4 0 0 8	0 0 0 0 8 0 0	3 0 2 1 0 0 0	5 0 4 2 0 1 0	0 0 0 0 0 0 0	5 0 1 2 0 0	11 0 20 11 2 0 0 6	0 2 0 0 5 0	0 I _Baterias_Protechaterias_Cammaproteobaterias_Barkholdeniasd_Nitrosomonadaceseg_Oliro8067s_ 0 k_Baterias_Drimicates_Clottridas_Peptotreptococolis=Tasienelaked_Intercompacesesg_NotQbateriums_MegBaterium_sp. 2 L_Baterias_Arinobaterias_Clottridas_Barkholdeniasd_Soverhamaprotects_NA4343_groups_ 0 k_Baterias_Arinobaterias_Clottridas_Presidentesd_Soverhamaprotects_Na4344_groups_ 0 k_Baterias_Nitrosophotac_Olirosophotacy_Entrosophots/_Barkholdeniasd_Soverhamaprotects_NA4344_groups_ 0 k_Baterias_Arinobateriasd_Arinobaterias_Ontophotski_Entrosophotecesg_Nitrosophots_ 0 k_Baterias_Nitrosophotacy_Olirosophotacy_Entrosophotski/_Barkholdeniasd_Notophotecesg_Nitrosophots_Metaberiasd_Metaberiasd_Metaberiasd_National 5 k_Baterias_Firmicatesc_Batelia_Contentiasd_Entrosophoteceseg_Notophotecesiasd_ 2 k_Baterias_Firmicatesc_Bateliasd_Lextensophotecing_Contentiasd_Firmicates_Bateriada
661 663 664 665 666 667 668 669 670	13 0 49 7 2 0 0 0 8	0 11 4 0 0 0 0 0 3 0 10	9 0 1 5 4 0 8 1 2 0	0 0 0 0 8 0 0 0 0 0	3 2 1 0 0 0 0 0	5 0 4 1 0 1 0 6 0 0	0 0 0 0 0 0 0 5 0 0	5 0 1 2 0 0 4 1 0	11 0 20 11 2 0 6 3 1 0	0 2 0 0 5 0 0 0	<ul> <li>b   bsteriag_fromotosc_Cbitridas_Peptotospisoccales_Tessenelless_Intercommodaceseg_ClineSof7s_</li> <li>b   bsteriag_fromotosc_Cbitridas_Peptotospisoccales_Tessenelless_Intercomplexeesg_ModBatteriums_MogBatterium_ps.</li> <li>2   bsteriag_fromotosc_Cbitridas_laborospisot_Lbitrospisoteset_MAI36_groups_</li> <li>b   bsteriag_Activabatteriate_Activabatteriag_Septotospisot_Bitridas_Septotospisoteset_MAI36_groups_</li> <li>b   bsteriag_Activabatteriate_Activabatteriag_Septotospisoteset_Bitridas_Septotospisoteset_MAI36_groups_</li> <li>b   bsteriag_Activabatteriate_Activabatteriag_Septotospisoteset_Bitridas_Septotospisotes_MAI36_groups_</li> <li>b   bsteriag_Nitrospitotz_MitridageNature_Activabatteriag_Septotospisoteset_Bitridas_Septotospisotes_</li> <li>b   bsteriag_Firmioatesc_Bitridas_ClineSeptotospisoteset_Bitridas_Septotospisoteset_Bitridas_Septotospisoteset_Bitridas_Septotospisoteset_Bitridas_Septotospisoteset_Bitridas_Septotospisotesetesetase_Septotospisoteset_Bitridas_Septotospisotesetasetasetasetasetasetasetasetasetase</li></ul>
661 662 663 664 665 666 667 668 669 670 671	13 0 49 7 2 0 0 0 8 2	0 11 4 0 0 0 0 0 3 0 10 9	9 0 1 5 4 0 8 1 2 0 0	0 0 0 8 0 0 0 0 0 0 0	3 2 1 0 0 0 0 0 0 0	5 0 4 1 0 1 0 6 0 0 0	0 0 0 0 0 0 5 0 0 0 0	5 0 1 2 0 0 4 1 0 0	11 0 20 11 2 0 0 6 3 1 0 0	0 2 0 0 0 5 0 0 0 0 0	<ul> <li>b _ bsteriag_ frotebacteriag_Commonotebacteriag_Batholdensisef_Nitrosomonadaceseg_BitroSofA_</li> <li>b _ bsteriag_ firmicates_Colotridus_Peptoteptococolis=Tassenbleck_Intercompaceseg_Watholg_mous_</li> <li>c _ bsteriag_firmicates_Colotridus_Peptoteptococolis=Tassenbleck_Intercompaceses_Watholg_mous</li> <li>b _ bsteriag_firmicates_Colotridus_tectoriag_firmiliates_Sonothytexeese_Lack_cluber_Colotridus_Petrosophace</li> <li>b _ bsteriag_firmicates_Colotridus_tectoriag_firmiliates_Sonothytexeese_Lack_cluber_Colotridus_Petrosophace</li> <li>b _ bsteriag_firmicates_Colotridus_tectoriag_firmiliates_Sonothytexeese_Nature</li> <li>b _ bsteriag_firmicates_Coloridus_tectoriag_firmiliates_Sonothytexeese_Nature</li> <li>b _ bsteriag_firmicates</li> <li>Coloridus_Petrosophace_Nature</li> <li>b _ bsteriag_firmicates</li> <li>Coloridus_tectoriag_firmiliates</li> <li>c _ bsteriag_firmicates</li> <li>Coloridus_tectoriag_firmiliates</li> <li>c _ bsteriag_firmicates</li> <li>Coloridus_tectoriag_firmiliates</li> <li>c _ bsteriag_firmicates</li> <li>c _ bsteriag_firmicates</li> <li>c _ bsteriag_firmicates</li> <li>c _ bsteriag_firmicates</li> <li>c _ bsteriag_firminates</li> <li< td=""></li<></ul>
561 662 663 664 665 666 667 668 669 670 671 671	13 49 7 2 0 0 8 2 0 0 8 2 0 8	0 11 4 0 0 0 0 0 3 0 10 9 1	9 0 1 5 4 0 8 1 2 0 0 0 0	0 0 0 8 0 0 0 0 0 0 0	3 2 1 0 0 0 0 0 0 0 0 0 0 0	5 0 4 1 0 6 0 0 0 0	0 0 0 0 0 0 5 0 0 0 0 0 0 0	5 D 1 2 D 0 4 1 0 0 0	11 0 20 11 2 0 6 3 1 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0	<ul> <li>b   Bateriag_ Fredebacteriag_Control bateriag_Baterial@st_financeoracide.exeg_Eline0615</li></ul>
661 662 663 664 665 666 667 668 669 670 671	13 0 49 7 2 0 0 0 8 2 0	0 11 4 0 0 0 0 0 3 0 10 9	9 0 1 5 4 0 8 1 2 0 0	0 0 0 8 0 0 0 0 0 0 0	3 2 1 0 0 0 0 0 0 0	5 0 4 1 0 1 0 6 0 0 0	0 0 0 0 0 0 5 0 0 0 0	5 0 1 2 0 0 4 1 0 0	11 0 20 11 2 0 0 6 3 1 0 0	0 2 0 0 0 5 0 0 0 0 0	<ul> <li>b _ bsteriag_ frotebacteriag_Commonotebacteriag_Batholdensisef_Nitrosomonadaceseg_BitroSofA_</li> <li>b _ bsteriag_ firmicates_Colotridus_Peptoteptococolis=Tassenbleck_Intercompaceseg_Watholg_mous_</li> <li>c _ bsteriag_firmicates_Colotridus_Peptoteptococolis=Tassenbleck_Intercompaceses_Watholg_mous</li> <li>b _ bsteriag_firmicates_Colotridus_tectoriag_firmiliates_Sonothytexeese_Lack_cluber_Colotridus_Petrosophace</li> <li>b _ bsteriag_firmicates_Colotridus_tectoriag_firmiliates_Sonothytexeese_Lack_cluber_Colotridus_Petrosophace</li> <li>b _ bsteriag_firmicates_Colotridus_tectoriag_firmiliates_Sonothytexeese_Nature</li> <li>b _ bsteriag_firmicates_Coloridus_tectoriag_firmiliates_Sonothytexeese_Nature</li> <li>b _ bsteriag_firmicates</li> <li>Coloridus_Petrosophace_Nature</li> <li>b _ bsteriag_firmicates</li> <li>Coloridus_tectoriag_firmiliates</li> <li>c _ bsteriag_firmicates</li> <li>Coloridus_tectoriag_firmiliates</li> <li>c _ bsteriag_firmicates</li> <li>Coloridus_tectoriag_firmiliates</li> <li>c _ bsteriag_firmicates</li> <li>c _ bsteriag_firmicates</li> <li>c _ bsteriag_firmicates</li> <li>c _ bsteriag_firmicates</li> <li>c _ bsteriag_firminates</li> <li< td=""></li<></ul>
661 663 664 665 666 667 668 669 670 671 673 673 673	13 49 7 2 0 0 8 2 0 0 8 2 0 8	0 11 4 0 0 0 0 0 3 0 10 9 1	9 0 1 5 4 0 8 1 2 0 0 0 0	0 0 0 8 0 0 0 0 0 0 0	3 0 2 1 1 0 0 0 0 0 0 0 0 0 3 3	5 0 4 1 0 6 0 0 0 0	0 0 0 0 0 0 5 0 0 0 0 0 0 0	5 D 1 2 D 0 4 1 0 0 0	11 0 20 11 2 0 6 3 1 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   sateriag_freedesaceriag_commercessateriag_Burkholdersisef_Nitrosomonadaceseg_cline0615_</li> <li>c   sateriag_freedesaceriag_clineoteriag_burkholdersisef_Nitrosomonadaceseg_cline0615_</li> <li>c   sateriag_freedesaceriag_clineoteriag_freedesaceriages_clineoteriages_lineoteriag_burkholdersisef_Nationaleseses_cline000000000000000000000000000000000000</li></ul>
661 662 664 665 666 667 668 667 668 670 671 671 672 673 574 575	13 0 49 7 2 0 0 0 8 2 0 0 8 2 2 1 21 5	0 11 4 0 0 0 0 0 0 0 0 1 0 1 0 7 0	9 0 1 5 4 0 0 8 1 7 0 0 0 0 5 0 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 1 1 0 0 0 0 0 0 0 3 1 1	5 0 4 1 0 1 0 5 0 0 0 0 1 1 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 7 4	5 D 1 2 D 0 4 1 0 0 0	11 0 20 11 2 0 6 3 1 0 0 0 1 2 0 1 2 0 1 1 2 0 1 1 1 2 0 0 1 1 2 0 1 1 2 0 1 1 2 0 1 1 2 0 1 1 2 0 0 1 1 1 2 0 0 0 1 1 1 2 0 0 0 1 1 1 1 2 0 0 0 1 1 1 1 2 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   stateriag_htrobeskateriag_Commapneoebasteriag_Burkholdersikef_Nitrosomonadaceseg_BirgGotA_</li> <li>b   sateriag_Introducts_Cobtridus_Peptoteptococolis=Tusienelles(_Intercorptaceses_WAB16_moustCobtridus_Pertoteptococolis=Tusienelles(_Intercorptaceses_WAB16_moustCobtridus_Pertoteptococolis=Tusienelles(_Intercorptaceses_WAB16_moustCobtridus_Pertoteptococolis=Tusienelles(_Intercorptaceses_WAB16_moustCobtridus_Pertoteptococolis=Tusienelles(_Intercorptaceses_WAB16_moustCobtridus_Pertoteptococolis=Tusienelles(_Intercorptaceses_WAB16_moustCobtridus_Pertoteptococolis=Tusienelles(_Intercorptaceses_WAB16_moustCobtridus_Pertoteptococolis=Cobtridus_Pe</li></ul>
661 663 664 665 666 667 668 669 670 671 673 673 673	13 49 7 2 0 0 8 2 0 0 8 2 0 8	0 11 4 0 0 0 0 0 3 0 10 9 1	9 0 1 5 4 0 8 1 2 0 0 0 0	0 0 0 8 0 0 0 0 0 0 0	3 0 2 1 1 0 0 0 0 0 0 0 0 0 3 3	5 0 4 1 0 6 0 0 0 0	0 0 0 0 0 0 5 0 0 0 0 0 0 0	5 D 1 2 D 0 4 1 0 0 0	11 0 20 11 2 0 6 3 1 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   sateriag_freedesaceriag_commercessateriag_Burkholdersisef_Nitrosomonadaceseg_cline0615_</li> <li>c   sateriag_freedesaceriag_clineoteriag_burkholdersisef_Nitrosomonadaceseg_cline0615_</li> <li>c   sateriag_freedesaceriag_clineoteriag_freedesaceriages_clineoteriages_lineoteriag_burkholdersisef_Nationaleseses_cline000000000000000000000000000000000000</li></ul>
661 663 664 665 666 667 668 669 670 671 672 673 674 675 675	13 0 49 7 2 0 0 0 5 2 2 1 5 0	0 11 4 0 0 0 0 0 0 0 0 1 0 1 0 7 0	9 0 1 5 4 0 8 1 7 0 8 1 7 0 0 5 0 3 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 1 1 0 0 0 0 0 0 0 0 0 0 0 1 1 1 3	5 0 4 1 0 5 0 0 0 0 0 1 1 2 3	0 0 0 0 0 0 0 0 0 0 0 0 7 4 0	5 0 1 2 0 0 0 4 1 0 0 4 4 1 2	11. 0 20 11 2 0 6 3 1 0 0 0 1 2 0 2 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   Saterlag_Tretesbacterlag_Commanneeboaterlag_Barkholdersikef_Minneomenadeceaeg_EffineOffs_</li> <li>b   Saterlag_Tretesbacterlag_ColdridsMethodersikef_Manneomenadeceaeg_Methodersikef_Manneomenadeceaeg_Methodersikef_Methodersikef_Manneomenadeceaeg_Methodersikef_Methode</li></ul>
661 663 664 665 666 667 668 669 670 671 673 674 875 676 677	13 9 49 7 2 0 0 0 0 8 2 2 1 5 0 0 0 8 2 1 5 0 0 0 0 8 2 1 5 0 0 0 0 0 0 0 0 1 7 0 0 0 0 0 0 0 0 0 0	0 11 4 0 0 0 0 0 3 0 0 1 0 9 1 0 7 0 0 9 1 0 9 1 0 9 1	9 0 1 5 4 0 8 1 7 0 8 1 7 0 0 5 0 5 0 3 2 0 3 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 4 1 0 6 0 0 0 0 1 1 2 3 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 4 1 2 0	11. 0 20 11. 2 0 6 3 1 0 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 1 2 0 1 2 0 1 2 0 1 1 2 0 1 1 2 0 1 1 2 0 1 1 2 0 1 1 2 0 1 1 2 0 1 1 2 1 1 2 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeriag, Freidebacheriag, Gammaporteobacteriag, Surbholdersikef, Mittocomonadceserg, Chiptocom, Megibacterium, June 20, Esteriag, Enricolets, Caberbain, Septembergeaccalkein, Sussenbain, Medibacterium, Megibacterium, June 20, Esteriag, Keinebacteriste, Activobacteriag, Gammaporteobacteriag, Senetheriag, Mittopireks, Mittopireks, Metabacteriag, Mittopireks, Metabacteriag, Mittopireks, Metabacteriag, Senetheriag, Mittopireks, Metabacteriag, Mittopireks, Metabacteriag, Mittopireks, Metabacteriag, Freidebacteriag, Senetheriag, Mittopireks, Metabacteriag, Mittopireks, Metabacteriag, Mittopireks, Metabacteriag, Senetheriag, Mittopireks, Metabacteriag, Metabacteriag, Metabacteriag, Metabacteriag, Metabacteriag, Mittopireks, Metabacteriag, Metabacteriag, Metabacteriag, Metabacteriag, Mittopireks, Metabacteriag, Mataacteriag, Mittopireks, Metabacteriag, Mittopireks, Metabacteriag, Mataacteriag, Mittopireks, Metabacteriag, Mataacteriag, Mittopireks, Mataacteriag, Mataacteriag,</li></ul>
661 663 664 665 666 667 668 669 670 671 673 674 675 676 677 677 678	13 9 49 7 2 0 0 0 0 8 2 2 1 5 0 0 0 8 2 1 5 0 0 0 0 8 2 1 5 0 0 0 0 0 0 0 0 1 7 0 0 0 0 0 0 0 0 0 0	0 11 4 0 0 0 0 0 3 0 0 1 0 7 0 0 9 1 0 7 0 0 9 1	9 0 1 5 4 0 8 1 7 0 8 1 7 0 0 5 0 3 2 0 8	0 0 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 4 1 0 6 0 0 0 0 1 1 2 3 0 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 0 4 1 0 0 4 4 1 2 0 1	11. 0 20 11. 2 0 6 3 1 0 0 0 0 1 2 0 0 0 1 2 0 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeria, Fredeskacheria, Cammapendeskateria, Jackholderskef, Mitteamonadaceae, J. Birderfa, J.</li> <li>b. Jackeria, J., Fredeskacheria, Cabrida, S., Peptatteptaceae, Takabaser, J. Mathada, S., Mathada, J. Mat</li></ul>
661 662 664 665 666 667 668 669 671 671 672 673 674 675 675 675 677 678 679	13 9 49 7 2 0 0 0 0 8 2 2 1 5 0 0 0 8 2 1 5 0 0 0 0 8 2 1 5 0 0 0 0 0 0 0 0 1 7 0 0 0 0 0 0 0 0 0 0	0 11 4 0 0 0 0 0 3 0 0 1 0 7 0 0 9 1 0 7 0 0 9 1	9 0 1 5 4 0 8 1 7 0 0 5 0 0 5 0 3 2 0 8 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 30 4 1 0 5 0 0 0 0 1 1 2 3 0 6 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 4 1 2 0 1 3	11. 0 20 11. 2 0 6 3 1 0 0 0 1 2 0 0 1 2 0 0 0 5 5 5 5 5 5 5 5 5 5 5 5 5	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jasterias, Proteinascherias, Cammaproteoloaterias, Juhrholdersins/, Nitroarmonalcease, Z. Birdeoffs.,</li> <li>b. Jasterias, Principase, C. Obtridas, Peptotesptococalis-Tusseeless (Anterospiceres, MAA136_groups.).</li> <li>c. Jasterias, Principase, C. Obtridas, Lachospiters (Jacknospiceres, MAA136_groups.).</li> <li>b. Jasterias, Activabacterias, Activabacterias, Secondarias, Pataliary, Modalateriary, Medalateriary, Secondary, Medalateriary, Medalateri</li></ul>
661 662 664 665 666 667 668 669 670 671 672 673 675 675 675 675 675 675 675 675	13 9 7 2 0 0 8 2 2 1 5 0 0 8 2 1 5 0 0 5 0 0 5 0 0 5 0 0 5 0 0 0 5 0 0 0 0 8 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 11 4 0 0 0 0 10 7 0 7 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 1 0 9 1 1 1 1	9 0 1 5 4 0 8 1 7 0 0 5 0 5 0 5 0 8 1 0 8 1 0 8 1 1 0 8 1 1 2 0 0 1 1 5 4 0 0 1 5 4 0 0 1 5 4 0 0 1 5 4 1 5 4 0 0 1 5 4 1 5 5 4 1 5 4 0 0 1 5 4 0 0 0 1 5 4 0 0 0 0 1 5 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 30 4 1 0 5 0 0 0 0 1 1 2 3 0 6 5 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	11 0 20 11 2 0 6 3 1 0 0 1 2 0 0 1 2 0 0 6 0 1 2 0 0 1 2 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeriag, Freiedekacheriag, Gammaporteebaateriag, Surholdersikef, Juttecomonadeceaerg, Ellineoteria,</li> <li>c. Jackeriag, Jernicolets, C. Gatridka, "epitoterbaceaaler, Taisereideks", Juttecomonadeceaerg, Jutkabil, genosis,</li> <li>c. Jackeriag, Jernicolets, C. Gatridka, "epitoterbaceaaler, "sureversaceses," Judgebacterium, Medibacterium, Junkabil, genosis,</li> <li>c. Jackeriag, Jernicolets, C. Statridka, C. Jachonspirales, J. Manoprisace, Judg. Jutka, C. Gaddatu, Janitoebila</li> <li>c. Jackeriag, Jernicolets, C. Statridka, C. Jachonspirales, J. Manoprisace, Judg. Jutka, C. Gaddatu, Janitoebila</li> <li>c. Jackeriag, Jernicolets, Statika, Gronebacteriag, Frankabilet, Jackeriag, Jutkabil, genosis,</li> <li>c. Jackeriag, Jernicolets, Jackeriag, Gronebacteriag, Tarinoprisac,</li> <li>c. Jackeriag, Jernicolets, Jackeriada, C. Statikat, Jackeriada, Jackeriad</li></ul>
661 662 664 665 667 668 669 670 671 673 674 675 675 677 678 679 680 681	13 9 7 2 0 0 8 2 2 5 0 0 8 2 2 1 5 0 0 6 0 0 6 0 0 0 8 2 0 0 0 0 8 2 0 0 0 0 0 0 0 0 0	0 11 4 0 0 0 3 0 1 0 7 0 7 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 1 1 1	9 0 1 5 4 0 8 1 7 0 0 5 0 5 0 3 2 0 8 1 0 8 1 0 8 1 0 8 1 1 2 0 8 1 1 2 0 0 1 1 5 1 1 5 1 1 5 1 1 5 1 1 5 1 1 5 1 1 5 1 1 5 1 1 5 1 1 5 1 1 5 1 1 5 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 4 1 0 6 0 0 0 0 1 1 2 3 0 6 5 0 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 0 4 1 0 0 0 4 4 1 2 0 1 3 0 1 3 0 1	11 0 20 11 2 0 6 3 1 0 0 1 2 0 0 5 0 6 0 0 5 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeria, J. Freidenkacheria, C. Sminaperdeskateria, J. Minokerskei, J. Minokerske</li></ul>
661 662 663 664 665 667 668 607 670 671 673 674 675 675 676 677 678 679 680 681 682	13 0 49 7 2 0 0 8 2 1 5 0 0 6 0 1 1	0 11 4 0 0 0 3 0 1 0 7 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 1 1 1	9 0 1 5 4 0 8 1 7 0 8 1 0 8 1 0 8 1 0 8 1 0 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 4 1 0 5 0 0 0 1 1 2 3 0 6 5 5 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 4 1 0 0 4 4 1 2 0 1 3 0 1 3 0	11 0 20 11 2 0 6 3 1 0 0 6 3 1 0 0 0 1 2 0 0 6 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeria, J. Freideia, Gammaproteolasteria, Jackholderiak, J. Nitoarnovakceae, J. Olykakteriam, J. Magiasteriam, J. J. Jackeria, J. Freideia, J. K. Schrödei, J. S</li></ul>
661 663 666 667 667 668 670 671 671 672 673 675 675 676 675 675 676 675 675 675 675	13 9 7 2 0 0 8 2 0 0 8 2 2 1 5 0 0 6 0 1 1	0 11 4 0 0 0 0 3 0 0 7 0 9 1 0 7 0 9 1 0 7 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 0 0 0	9 0 1 5 4 0 8 1 7 0 0 5 0 3 2 0 8 1 0 8 1 0 8 1 3 0 4 1 3 0 0 8 1 3 0 0 8 1 3 2 0 0 8 1 3 1 5 6 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 3 0 0 0 0 0 0 0 3 1 3 1 3 0 7 1 2 0 7 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 4 1 0 6 0 0 0 0 1 1 2 3 0 6 5 5 1 0 5 5 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 4 1 2 0 1 3 0 1 0 3 0 9	11 0 20 11 2 0 6 3 1 0 0 1 2 0 1 2 0 0 6 3 1 0 0 0 1 2 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jackeriag, Fredeskachelag, Gammapenkeskateriag, Jackhalderskaf, Jackeronaudeckerg, Ellineoff, J.</li> <li>b. J. Jackeriag, Jimmakers, Cathridag, Jenebaskeriag, Sankhalderskaf, Jackeronaudeckerg, Jelineoff, Jackeriag, Jimmakers, Jackhalderskaf, Jackeronaudeckerg, Jelineoff, Jackeriag, Jimmakers, Jackhalderskaf, Jackeronaudeckerg, Jelineoff, Jackeriag, Jimmakers, Jackeronaudeckerg, Jackeronaudeckerg</li></ul>
861 662 663 665 666 667 866 870 870 870 870 870 870 870 870 870 870	13 0 49 7 2 0 0 8 2 21 5 0 0 6 0 1 1 0 4 7 2 2 2 5 0 0 6 0 1 1 0 0 8 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1	0 11 4 0 0 0 1 0 9 1 0 7 0 9 1 0 9 1 0 9 1 0 0 9 1 0 0 0 0 0 0 0	9 0 1 5 4 0 8 1 7 0 8 1 7 0 5 7 0 8 1 0 8 1 0 8 1 1 0 4 1 3 0 0 8 1 1 5 6 9 0 0 0 5 0 5 0 0 0 1 5 0 8 1 1 5 0 8 1 1 5 0 8 1 1 5 0 8 1 1 5 0 9 1 1 5 0 9 1 1 5 0 9 1 1 5 0 9 1 1 5 0 9 1 1 5 0 9 1 1 1 5 0 1 1 1 5 0 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 1 0 0 0 0 0 0 0 0 0 0 0 1 1 1 3 0 7 1 0 7 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 4 1 0 5 0 0 0 1 2 3 0 6 5 5 5 1 0 0 6 5 5 5 1 0 0 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 4 1 2 0 1 3 0 1 3 0 9 1	11 0 20 11 7 0 6 3 1 0 0 6 3 1 0 0 1 2 0 0 6 3 1 0 0 6 3 1 0 0 6 3 1 0 0 6 3 1 0 0 0 6 3 1 0 0 0 6 3 1 0 0 0 6 3 1 0 0 0 6 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>bbiteling_freebeakeriesfermanerebeakeriesBeakheldersiesInterconnacteursfinesofis</pre>
60.1 60.2 60.6 60.6 60.7 60.6 60.7 60.7 60.7 60.7	13 0 49 7 2 0 0 8 2 1 0 0 8 2 21 5 0 0 6 0 1 1 0 4 1 1 0 0 8 2 1 1 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 11 4 0 0 0 3 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 0 9 1 0 0 0 9 1 0 0 0 0	9 1 5 4 0 8 1 7 0 5 7 0 5 7 0 5 7 0 8 1 0 8 1 0 8 1 0 8 1 0 8 1 0 9 6 0 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 1 0 0 0 0 0 0 0 0 0 3 1 1 3 1 3 0 7 1 0 2 0 0 0 0 0 0 0 1	5 0 4 1 0 6 0 0 1 2 3 0 6 5 5 5 1 0 0 6 5 5 5 0 0 6 0 0 0 0 0 0 1 2 3 0 6 0 0 0 0 1 1 0 0 1 1 1 0 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 4 1 2 0 1 3 0 9 1 0 9 1 0	11 0 20 11 2 0 6 3 1 0 6 3 1 0 0 0 1 2 0 0 6 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>bbcteriafreedealceticsfermaproteedealceticsfermationalcetesfilesopris</pre>
861 662 663 665 667 666 670 670 670 670 677 673 675 675 675 675 675 675 675 675 681 683 684 685 686 685 685 685 685 685 685 685 685	13 0 49 7 2 0 0 8 2 21 5 0 0 6 0 1 1 0 4 7 2 2 2 5 0 0 6 0 1 1 0 0 8 2 2 2 5 0 0 0 8 2 0 0 0 8 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 11 4 0 0 1 0 1 0 7 0 9 1 0 7 0 9 1 0 9 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 0 1 5 4 0 8 1 7 0 0 5 0 0 5 0 0 5 0 0 3 2 0 8 1 0 4 1 3 0 0 8 1 0 0 0 8 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 3 0 0 0 0 0 0 0 0 0 0 1 2 1 3 0 7 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 4 1 0 5 0 0 0 1 1 2 3 0 6 5 5 1 0 0 6 5 5 1 0 0 6 0 0 0 0 1 2 3 0 0 0 0 1 0 0 0 1 0 0 0 1 0 1 0 0 1 0 1 0 0 1 0 0 1 0 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 1 2 0 1 3 0 1 0 9 1 0 0 0 0 0 4 1 0 0 0 0 0 0 0 0 1 2 0 0 0 0 1 0 0 0 0	11 0 20 11 2 0 6 3 1 0 0 0 1 2 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeriag, Freiedekacheka, Gemmapnekeekataka, Janhadersker, Janneoranzekaser, Jehneoran, Jehneoran</li></ul>
61 62 63 64 65 66 67 67 70 87 87 87 87 87 87 87 87 87 87 87 87 87	13 49 7 0 0 8 2 11 5 0 0 5 0 1 1 0 4 5 0 1 1 0 4 5 7 7 0 0 8 2 1 1 1 1 1 1 1 1 1 1 1 1 1	0 11 4 0 0 0 1 0 7 0 9 1 0 7 0 9 1 0 6 0 0 0 8 0 0 0 0 8 0 0 0 0 0 7 0 0 0 0 7 0 0 0 0	9 0 1 5 4 0 8 1 7 0 0 5 0 0 5 0 0 5 0 0 5 0 0 8 1 0 0 4 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 9 1 1 0 0 0 0 0 0 0 0 0 0 0 1 2 1 0 0 0 0	5 0 4 1 0 5 0 0 0 0 1 2 3 0 5 5 5 0 6 5 5 1 0 0 6 5 5 1 0 0 6 0 0 1 2 3 1 0 1 2 3 1 0 1 1 1 1 1 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 4 1 2 0 1 0 3 0 9 1 0 0 0 0 4 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	11 0 20 11 2 0 6 3 1 0 0 1 2 0 0 1 2 0 0 1 2 0 0 1 2 0 0 1 2 0 0 6 3 1 0 0 0 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>bbcteriesfreedeebacteriesdenergeebacteriesdenergeeraesudebacteriesMediateries bbcteriesfreedeebacteriesfreedeebacteriesgeeraesudebacteriesMediateriesMediateries bbcteriesfreedeebacteriesfreedeebacteriesget_debacteries_UdebacteriesMediateries_ bbcteriesfreedeebacteriesfreedeebacteriesfreedeebacteriesget_debacteriesMediateries_ bbcteriesfreedeebacteriesfreedeebacteriesfreedeebacteriesget_debacteriesMediateries_ bbcteriesketiedeabacteriesactivabacteriesfreedeebacteriesMediateriesaesMediateriesaes_Mediateriesae bbcteriesfreedeebacteriesactivabacteriesfreedeebacteriesMediateriesaesMediateriesaes_Mediateriesae_Mediateriesae bbcteriesfreedeebacteriesaeinteriedeebacteriesaeMediateriesaesMediateriesaesMediateriesae ActivatesketiedeabacteriesaeinteriedeebacteriesaesMediate</pre>
861 662 663 665 667 670 671 674 673 674 675 675 675 675 675 675 675 675 675 675	13 0 49 7 2 0 0 8 2 1 0 0 8 2 21 5 0 0 6 0 1 1 0 4 1 1 0 0 8 2 1 1 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 11 4 0 0 0 2 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 0 9 1 0 0 9 1 0 0 9 1 0 0 0 0	9 0 1 5 4 0 8 1 7 0 5 0 7 0 5 0 7 0 8 1 0 6 8 1 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 3 0 0 0 0 0 0 0 0 0 0 1 2 1 3 0 7 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 30 4 1 0 6 0 0 0 1 2 3 0 6 5 5 1 0 6 0 0 0 2 3 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 1 2 0 1 3 0 1 0 9 1 0 0 0 0 0 4 1 0 0 0 0 0 0 0 0 1 2 0 0 0 0 1 0 0 0 0	11 0 20 11 2 0 6 3 1 0 0 0 1 2 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	b. Lateria, Freiebacheta, Cammaneteebacheta, Butholderskef, Mitteomondecker, Ellineoff, S. Karlins, Freiebacheta, S. Karlins, Karlinsker, Karlinsker, S. Karlins, Karlinsker, Karlinsker, S. Karlinsker, Karlinsker, Karlinsker, S. Karlinsker, Kar
61 62 63 64 65 66 67 67 70 87 87 87 87 87 87 87 87 87 87 87 87 87	13 49 7 0 0 8 2 11 5 0 0 5 0 1 1 0 4 5 0 1 1 0 4 5 7 7 0 0 8 2 1 1 1 1 1 1 1 1 1 1 1 1 1	0 11 4 0 0 0 1 0 7 0 9 1 0 7 0 9 1 0 6 0 0 0 8 0 0 0 0 8 0 0 0 0 0 7 0 0 0 0 7 0 0 0 0	9 0 1 5 4 0 8 1 7 0 0 5 0 0 5 0 0 5 0 0 5 0 0 8 1 0 0 4 1 3 0 0 8 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 9 1 1 0 0 0 0 0 0 0 0 0 0 0 1 2 1 0 0 0 0	5 0 4 1 0 5 0 0 0 0 1 2 3 0 5 5 5 0 6 5 5 1 0 0 6 5 5 1 0 0 6 0 0 1 2 3 1 0 1 2 3 1 0 1 1 1 1 1 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 4 1 2 0 1 0 3 0 9 1 0 0 0 0 4 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	11 0 20 11 2 0 6 3 1 0 0 1 2 0 0 1 2 0 0 1 2 0 0 1 2 0 0 1 2 0 0 6 3 1 0 0 0 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	b. Lateria, Freiebacheta, Cammaprotestateria, Butholdersist, Introamoudcater, Ellinoopies, Mediateriam, Mediateriam, P. 2 J. Bateria, J. Freiebachetriate, Catributeria, J. Frainier, Scoreithyraes, J. (ediateriam, Scoreithyraes, J. (ediateriam), Mediateriam, P. 3 J. Bateria, J. Freiebachetriate, Aktrobateria, Scoreithyraes, J. (ediateria, Catributeria, J. (ediateriam), Mediateriam, Mediateriam, Mediateriam, Mediateriam, Mediateriam, Mediateriam, Mediateriam, Mediateriam, J. (ediateria, J. (ediateria, J. (ediateriam), Mediateriam,
60.1 60.2 60.6 60.6 60.7 60.6 60.7 60.7 60.7 60.7	13 49 7 0 0 8 2 11 5 0 0 5 0 1 1 0 4 5 0 1 1 0 4 5 7 7 0 0 8 2 1 1 1 1 1 1 1 1 1 1 1 1 1	0 11 4 0 0 0 0 10 9 1 0 7 0 9 1 0 7 0 0 9 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 0 1 5 4 0 8 1 7 0 0 5 7 0 0 5 7 0 8 1 3 2 0 8 1 3 0 0 8 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 1 0 0 0 0 0 0 0 0 0 1 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 10 1 0 1 0 0 0 0 1 1 2 3 0 6 5 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 2 0 0 4 1 0 0 4 4 1 2 0 1 0 3 0 9 1 0 0 0 0 4 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	11 0 20 11 2 0 6 3 1 0 0 1 2 0 0 1 2 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>bbctelse_freedestarisfreedestarisseturbalecturisfutureareauducese_clifteeEff</pre>
861 662 663 665 667 666 677 666 670 870 873 874 875 875 875 875 875 875 875 875 875 875	13 0 49 7 2 0 0 8 2 0 0 8 2 1 5 0 0 6 0 1 1 0 0 4 5 7 2 0 0 8 2 15 0 0 8 2 15 0 0 8 2 0 0 8 2 0 0 0 8 7 2 0 0 0 0 8 7 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0	0 11 4 0 0 0 0 7 0 9 1 0 7 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 9 1 0 0 0 0	9 0 1 5 4 0 8 1 7 0 0 5 0 3 2 0 8 1 0 4 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 3 0 0 0 0 0 0 1 1 1 0 2 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 30 4 1 0 5 0 0 0 1 1 2 3 0 5 5 1 0 0 6 0 2 0 0 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 1 2 0 0 4 1 0 0 0 4 4 1 2 0 1 3 0 1 0 3 0 9 1 0 0 0 1 2	11 0 20 11 2 0 6 3 1 0 0 0 1 2 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0		b. Lateria, Freiebacheta, Cammaprotestateria, Butholdersist, Introamoudcater, Ellinoopies, Mediateriam, Mediateriam, P. 2 J. Bateria, J. Freiebachetriate, Catributeria, J. Frainier, Scoreithyraes, J. (ediateriam, Scoreithyraes, J. (ediateriam), Mediateriam, P. 3 J. Bateria, J. Freiebachetriate, Aktrobateria, Scoreithyraes, J. (ediateria, Catributeria, J. (ediateriam), Mediateriam, Mediateriam, Mediateriam, Mediateriam, Mediateriam, Mediateriam, Mediateriam, Mediateriam, J. (ediateria, J. (ediateria, J. (ediateriam), Mediateriam,
81 62 63 64 65 66 67 85 85 87 87 87 87 87 87 87 87 87 87 87 87 87	13 0 49 7 2 0 0 8 2 0 0 8 2 1 5 0 0 6 0 1 1 0 0 4 5 7 2 0 0 8 2 15 0 0 8 2 15 0 0 8 2 0 0 8 2 0 0 0 8 7 2 0 0 0 0 8 7 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0	0 11 4 0 0 0 0 1 0 7 0 9 1 0 7 0 9 1 0 9 1 0 9 1 0 0 0 0 8 0 0 0 0 7 0 0 0 7 0 0 9 1 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 0 1 5 6 0 8 1 7 0 0 5 0 7 0 8 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 10 1 0 1 0 0 0 1 1 2 3 0 6 5 5 1 0 6 0 0 0 0 1 2 3 0 6 5 5 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 1 2 0 0 4 1 0 0 0 4 4 1 2 0 1 3 0 1 0 3 0 9 1 0 0 0 1 2 1	11 0 20 11 2 0 0 6 3 1 0 0 0 1 2 0 0 0 1 2 0 0 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>bbcteriesresearcecontractcontracted_sseturatestatestintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontractedintercontractedcontracted_intercontractedcontracted_intercontractedcontracted_intercontractedcontracted_intercontracted_contractedintercontractedcontracted_intercontractedcontracted_intercontractedcontracted_intercontractedcontracted_intercontracted_contractedintercontracted_contractedintercontracted_contractedcontracted_intercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_contractedintercontracted_intercontractedintercontrac</pre>
861 662 663 665 667 670 671 674 673 674 675 677 675 677 675 677 678 673 684 685 681 682 681 682 683 684 685 685 685 685 685 685 685 685 685 685	13 0 49 7 2 0 0 8 2 0 0 8 2 1 5 0 0 6 0 1 1 0 0 4 5 7 2 0 0 8 2 15 0 0 8 2 15 0 0 8 2 0 0 8 2 0 0 8 7 2 0 0 0 8 7 2 0 0 0 8 7 2 0 0 0 8 7 0 0 8 7 0 0 0 0 0 0 0 0 0 0 0	0 11 4 0 0 0 1 0 7 0 9 1 0 7 0 9 1 0 9 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 0 1 5 4 0 8 1 7 0 0 5 0 7 0 7 0 8 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 30 4 1 0 1 0 6 0 0 0 1 1 2 3 0 6 5 1 0 6 0 0 2 0 0 0 1 2 3 0 6 5 5 1 0 0 6 0 0 0 1 2 3 0 6 5 5 1 0 6 0 0 0 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 1 2 0 0 4 4 1 2 0 1 3 0 1 0 3 0 9 1 0 0 0 1 2 1 2	11 0 20 11 7 0 0 6 1 2 0 0 1 2 0 0 1 2 0 0 1 2 0 0 0 1 2 0 0 0 1 2 0 0 0 0 1 2 0 0 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b _ b.teritag_ freedeelactingChampendeelactingBathaldersingManoremackes_gMediatrymmMediatersimp. 2 _ b.teritingimmediateChampendeelactingImmediates_g_MediatrymmMediatersimp. 2 _ b.teritingimmediatesChampendeelactingImmediates_g_MediatrymmMediatersimp. 3 / b.teritingimmediatesManopendeelactingImmediates_g_Mediatersimp_Mediatersimp. 4 / b.teritingMinopenderManopendeelactingImmediates_g_Mediatersimp_Medi</pre>
861 662 663 665 667 670 671 673 674 675 676 677 678 676 677 678 676 678 678 679 680 681 683 684 685 686 686 685 680 681 682 683 685 685 685 685 685 685 685 685 685 685	11 0 49 7 2 0 0 8 2 21 5 0 0 6 0 0 1 1 0 0 4 15 0 4 0 4 3 4 1 0	0 11 4 0 0 0 1 0 7 0 0 9 1 0 7 0 0 9 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 0 1 3 4 0 8 1 7 0 8 1 7 0 8 1 7 0 8 1 3 2 0 8 1 3 2 0 8 1 3 2 0 0 8 1 3 2 0 0 8 1 3 2 0 0 8 1 3 2 0 0 8 1 3 2 0 0 8 1 3 2 0 0 8 1 3 2 0 0 8 1 3 2 0 0 8 1 3 2 0 0 8 1 3 1 3 2 0 0 0 8 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 30 4 1 0 6 0 0 0 1 2 3 0 6 5 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 1 2 0 0 4 1 0 0 0 4 4 1 2 0 1 3 0 1 0 3 0 9 1 0 0 0 1 2 2 0	11 0 20 0 6 1 0 0 0 1 2 0 0 6 3 0 0 1 2 0 0 6 3 0 0 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	b. Lateria, Protein, Catrino, Catrino, Septemportestation, Buthelderial, Mitteamonalacear, Sinteeter, Mediaterian, Schwarterian, Schwarterian, Mediaterian, Mediaterian, Mediaterian, Mediaterian, Schwarterian, Mediaterian, M

698	5	0	2	0	1	0	0	9	5	0	$0\ k\_Bacteria;p\_Proteobacteria;c\_Gamma proteobacteria;o\_Burkholderia!esf\_Comamonadaceae$
699	0	10	0	0	0	D	0	D	0	0	0 k_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales;f_67-14;g_67-14;s_
700	1	0	1	0	2	4	0	1	2	0	2 k_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Galellales;f_;g_;s_
701	4	0	0	0	1	1	0	3	2	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Kilonicllales;f_Fodinicurvataceae;g_;s_
702	0	9	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium;s
703	4	0	3	0	1	5	0	7	0	٥	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG-014;f_Clostridia_UCG-014;g_Clostridia_UCG-014;s_
704	1	0	1	0	0	3	0	D	4	0	0 k_Bacteria;p_Armatimonadota;c_Fimbri imonadia;o_Fimbri imonadales;f_Fimbri imonadaceae;g_Fimbri imonadaceae;s_
705	0	0	0	2	5	1	0	0	1	0	$1\ k\_Bacteria; p\_Cyanobacteria; c\_Vampirivibrionia; o\_Gastranaerophilales; f\_Gastranaerophilales; g\_Gastranaerophilales; s\_f=f=f=f=f=f=f=f=f=f=f=f=f=f=f=f=f=f=f=$
706	23	2	8	5	6	9	0	1	25	1	$2\ k\_Bacteria:p\_firmicutes:c\_Clostridia:o\_Oscillospirales;f\_Ruminococcaceae;g\_Incertae\_Sedis:s\_Clostridium\_sp.$
707	1	0	2	0	1	3	0	0	4	0	0 k_Bacteria;p_Planctomycetota;c_Planctomycete;;o_Gemmatale;;f_Gemmataceae;g_
708	٥	14	O	0	٥	D	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
709	0	3	0	1	3	3	0	0	2	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum_group;s
710	3	2	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales-Tissierellales;f_Peptostreptococcales-Tissierellales;g_Murdochiella;s_Murdochiella_asaccharolytica
711	1	0	0	0	0	18	0	0	0	z	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
712	2	0	1	0	0	0	0	0	3	0	0 k_Bacteria;p_Myxococota;x_Polyangia;o_Haliangiales;f_Haliangiaoeae;g_Haliangium;s
713	11	0	17	0	O	2	0	D	1	0	0 k_Bacteria;p_Cyanobacteria;c_Cyanobacteriale;f_Chroococcidiopsaceae;g_;s_
714	5	0	U	0	1	D	0	D	0	0	$0\ k\_Bacteria; p\_Firmicutes; c\_Clostridia; o\_Christensenellales; f\_Christensenellaceae; g\_Christensenella; s\_Christensenella_minuta = 0.0000000000000000000000000000000000$
715	1	0	3	0	5	5	0	7	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Nitrosomonadaceae;g_MND1;z_
716	1	0	2	0	2	4	0	1	1	0	0 k_Bacteria;p_Actinobacteriota;c_Actidimicrobila
717	5	0	0	0	0	1	0	0	0	0	0 k_Bacteria;p_Chloroflexi;c_Anaerofineae;p_SIA:15;f_SIA:15;g_SIA:15;s_
718	0	0	0	0	0	D	0	D	5	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriale;;f_Crocinitomicaceae;g_Fluviicola;s
719	0	0	σ	12	0	D	0	0	0	0	0 k_Bacteria;p_Hrmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Haloimpatiens;s_bacterium_NLAE-zl-C463
720	7	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Gemmatimonadota;x_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;a_Gemmatimonas;s_
721	1	7	0	0	0	0	0	3	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceac;g_Nocardioides
722	12	14	0	3	D	15	1	0	3	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Conynebacteriales;f_Conynebacteriaceae;g_Conynebacterium;s_Conynebacterium_sukcordis
723	0	8	0	1	o	D	0	0	0	0	0 k_Bacteria;p_Actinobacteriata;c_Actinobacteria;o_Franklales;f_Acidothermaceae;g_Acidothermus;s
724	89	67	222	1	16	13	0	12	14	0	0 kBacteria;pCyanobacteria;cCyanobacteria;oChloroplast;fChloroplast;gChloroplast
725	0	8	0	0	0	0	0	0	0	0	0 k_Bacteria;p_firmicutes
726	0	0	0	0	0	0	0	10	0	.0	0 k_Racteria;p_Actinobacterista;c_Acidimicrobila;o_Actinomarinales
727	5	10	0	0	0	D	0	D	1	0	0 k_Bacteria;p_Firmicute;;c_Bacili;o_Baciliale;;f_Baciliaceae;g_Geobacilius
728	2	10	1	1	0	0	0	0	2	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Micrococcales;f_intrasporangiaceae;g_Omithinibacter;s
729	0	5	0	0	0	0	0	0	0	0	0 k_Bactoria
730	3	0	0	0	3	2	0	3	1	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales/_Nitrosomonadaceae;g_MND1;s_
731	4	0	n	0	0	2	0	0	0	0	0 k_Racteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Oscillibacter;s_Oscillibacter_sp,
732	2	0	7	0	2	0	0	1	5	0	0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Pedosphaerales;f_Pedosphaeraceae;g_SH3-11:s_
733	0	1	2	0	ı	1	0	4	2	0	0 k_Bacteria;p_Firmicutes;c_Bacilli;o_RF30;f_RF30;g_RF30;s
734	4	0	1	0	0	1	0	0	2	0	$0 \ k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;a\_Ferrovibrionales;f\_Ferrovibrionales = 0 \ k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;a\_Ferrovibrionales = 0 \ k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;a\_Ferrovibrionales = 0 \ k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;a\_Ferrovibrionales = 0 \ k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;a\_Ferrovibrionales = 0 \ k\_Bacteria;p\_Bacteria;c\_Alphaproteobacteria;a\_Ferrovibrionales = 0 \ k\_Bacteria;a\_Bacteria;a\_Bacteria;a\_Bacteria;a\_Ferrovibrionales = 0 \ k\_Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a=Bacteria;a$
735	4	0	2	0	3	0	0	1	3	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;p_Cytophagales;f_Microscilacea;;g_Ohtaekwangia;s_
735	0	1	O	0	D	3	0	1	3	0	0 k_Bacteria;p_Actinobacteriota;c_Coriobacteriale;o_Coriobacteriale;f_Eggerthellaceae;g_Enterorhabdu;;s
737	7	0	1	0	0	1	0	0	0	0	0 k_Bacteriag_Firmicutesc_Clostridiusp_Occillospin lest_Oscillospinaesaeg_UG6405;5
737 738	7 0	0 0	1 0	0	0	1 0	0 0	0 5	0 0	0 0	0 k_Berteriusp_Firmiculessc_Clostridiusp_Orcilleopiraleosf_Orcilleopiraceseg_UG6-0055_ 0 k_Butteriusp_Opandiazteriusz_Serkiptodromatiusg_Serkiptodromatiug_Serkiptodromatiug_Serkiptodromatiuss_
738	o	0	٥	0	o	D	o	5	o	o	D k_Bacteria;p_Cyanobacteria;c_Serkytodrromatia;o_Serkytodrromatia;f_Serkytodrromatia;g_Serkytochromatia;s_
738 739	0 11	0 0	o o	0 0	0	D	0 0	5 D	0 0	o o	0   Esteriza_Cyanolacturla<_Serkytochromatiza_Serkytochromatiza_Serkytochromatiza_Serkytochromatiza_ 0   Esteriza_Dezinfolacterota;_Dezutfordhroniza_Dezutforktronalesf_Dezutforkhrossceze_Dezutfordhros_Dezutforkhro
738 739 740	0 11 7	0 0 0	0 0 0	0 0 0	0 0 0	0 0 0	0 0 0	5 D 1	0 0 0	0 0 0	0   _bsterize_Cyanobacturize_Serioptodromatize_Serioptodromatize_Serioptodromatize_Serioptodromatize_ 0   _bsterize_Cezifobacterotze_Decutedovbronize_Decutedovbronosceaeg_Decutedovbros_Decutedovbros_tarheldencis 0   _bsterize_Sectemidotze_Bacteroidze_Chtephageletf_Hmonobacteroceaeg_Hmonobacter
738 739 740 741	0 11 7 0	0 0 7	0 0 0	0 0 0	0 0 0	D D O O	0 0 0	5 D 1 0	0 0 0	0 0 0	0 k_bsterice_Cyanobacterize_Serieptodromatize_Serieptodromatizi_Serieptodromatize_Serieptodromatas_ 0 k_bsterice_Deculfobacteristz_Deculfobarinize_Deculforbironized_Deculforbironscence_Deculfobarios_Deculfobarios 0 k_bsterice_Bacteriolotze_Bacteriolize_Cytophagaiesf_Hemonobacteriscence_Hemonobacter 0 k_bsterice
738 739 740 741 742	0 11 7 0 0	0 0 7 7	0 0 0 0	0 0 0 0	0 0 0 0	0 0 0 0	0 0 0 0	5 0 1 0	0 0 0 0	0 0 0 0	0 k_bsterickCyanobacterisz_Sericytochromatiza_Sericytochromatizd_Sericytochromatiza_Sericytochromatass_ 0 k_bsterickDecultobacteristz_Decultorobronisa_Decultorbronicesf_Decultorbroniceserg_Decultorbrois_Decultorbro_tariteldensis 0 k_BesterickBesteroidexc_Besteroidexo_Cytophagaicsf_Hemenobacterisceserg_Hemenobacter 0 k_Besterick
738 739 740 741 742 743	0 11 7 0 0 2	0 0 7 7 3	0 0 0 0	0 0 0 0 0	0 0 0 0	D D O O D	0 0 0 0 0	5 0 1 0 0	0 0 0 0	0 0 0 0	0 )_bidelayCyansbacteria_Serkytoderanatiao_Serkytoderanatia_Serkytoderanatia_ 0 k_bidelay_Devalfabacterotax_Devalfowbraniaa_Devalfowbranatisef_Devalfowbraceseag_Devalfavbrace_Devalfavbrace 0 \_bideriaa_Becteroidaac_Cytophagiest_Henronobactericeseg_Henronobacteri 0 k_bidelia 0 k_bideliap_Timiculeus_Colotrabus_Lachnospiraceseg_Lachnospiraceseg_NKA136_groups_
738 739 740 741 742 743 744	0 11 7 0 0 2 4	0 0 7 7 3 0	0 0 0 0 0 0	0 0 0 0 0 0	0 0 0 0 0	D D O D D D O	0 0 0 0 0 0	5 0 1 0 0 0 0	0 0 0 0 0 2	0 0 0 0 0	0   Escheriza_Cyanobacturiax_Serkytochromatiza_Serkytochromatiza_Serkytochromatiza_Serkytochromatiza_ 0   Escheriza_Dezinfobacterotax_Dezutforohroniza_Dezutforktronatesf_Dezutforktronatese_Dezutforktron_Dezutforktron_tariteldenus 0   Escheriza_Becteroidexa_Chrophigalesf_Humonobactericese_Humonobacter 0   Escheriza 0   Escheriza 0   Escheriza_Promodecs_Colutions_Lachnoophraesese_Lachnoophraeses_MK4135_groups_ 0   Escheriza_Protochereniza_Alongor oteobacteria
738 739 740 741 742 743 744 744	0 11 7 0 0 2 4 0	0 0 7 3 0 7	0 0 0 0 0 0 0	0 0 0 0 0 0 0	0 0 0 0 0 0	D D D D D D 0	0 0 0 0 0 0 0	5 0 1 0 0 0 0	0 0 0 0 0 2 0	0 0 0 0 0 0	0   Esclerize_Cyanobacturius_Serkytochromatizesses_NK4134_groups_ 0 & Esclerizes_Protochromatice_Serkytochromatizesses_Licknoophaceses_NK4134_groups_ 0 & Esclerizes_Protochromatice_Serkytochromatizesses_Serkytochromatizesses_Conclubactorss_
738 739 740 741 742 743 744 745 745	0 11 7 0 2 4 0 0	0 0 7 3 0 7 0	0 0 0 0 0 0 0 0	0 0 0 0 0 0 0	0 0 0 0 0 0 0	D D D D D D 0 0	0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 0 6	0 0 0 0 0 2 0 0	0 0 0 0 0 0 0	0 & Lacteriza_Cyanobacteriza_Serkytochromataa_Serkytochromatisd_Serkytochromatisd_Serkytochromatisa_ 0 & Lacteriza_Desalfobacterista_Desalforbhroniza_Desalforbhronized_Desalforbhronizeaeag_Desalforbhros_Desalforbhros_fairfeldensis 0 & Lacteriza_Bacterisdesa_Bacterisdea_Cytophagaket_Himonobacteriseaeag_Himonobacteriseaeag_Himonobacteriseaeag 0 & Lacteriza 0 & Lacteriza_Pacterisdesa_Costrikus_Lachnosphalest_Lachnosphaceaeag_Lachnosphaceaeag_NK41136_groups
738 739 740 741 742 743 744 745 745 745	0 11 7 0 2 4 0 5	0 0 7 3 0 7 0 0	0 0 0 0 0 0 0 0 6	0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 5	D D 0 D D 0 0 0 0 4	0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 6 5	0 0 0 0 0 2 0 0 10	0 0 0 0 0 0 0 0	0 ) _bideliaCyanisacteriaSerkytodevanatao_Serkytodevanatao_Serkytodevanatao_Serkytodevanatao_ 0 \_bidelia_Destructions_DestructiveServiceSerkytodevanatao_Serkytodevanatao_DestructiveSerky_D
738 739 740 741 742 743 744 745 746 747 748	0 11 7 0 0 2 4 0 5 0	0 0 7 3 0 7 0 0 0	0 0 0 0 0 0 0 0 0 6 2	0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 5 2	D D O D D O O O 0 4 3	0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 5 1	0 0 0 0 2 0 10 3		0   _bsteria
738 739 740 741 742 743 744 745 746 746 747 748 749	0 11 7 0 0 2 4 0 5 0	0 0 7 3 0 7 0 0 0 0 20	0 0 0 0 0 0 0 0 6 2 0	0 0 0 0 0 0 0 0 3	0 0 0 0 0 0 0 5 2 0	D D D D D D 0 0 4 3 0	0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 5 1	0 0 0 0 2 0 10 3 0	0 0 0 0 0 0 0 0 0 0 0	0 & _lacterizeCyanobactorizeSerkytochromatizeSerkytochromatizeSerkytochromatizeSerkytochromatize_ 0 & _bacterizeDesulfoobstorstor_C_BacteridezeChrophagiestHomenobactorizesezLichhosophizosezeHomenobactorizesezConsubactorizesezRomenobactorizesezServicesezezServicesezezezezezezezezezezezezezezezezezeze
738 739 740 741 742 743 744 745 746 746 747 748 749 750	0 11 7 0 2 4 0 6 0 6 0 0 3	0 0 7 3 0 7 0 0 20 0	0 0 0 0 0 0 0 6 2 0 1	0 0 0 0 0 0 0 0 3 0	0 0 0 0 0 0 0 0 5 2 0	D D D D D D 0 0 0 4 3 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 5 1 1 3	0 0 0 0 2 0 10 3 0 0		0   Lacteria, _ Cynobacteria, _ Serkytodromata,
738 739 740 741 742 743 744 745 746 746 747 748 749 750	0 11 7 0 2 4 0 6 0 6 0 0 3	0 0 7 3 0 7 0 0 20 0	0 0 0 0 0 0 0 6 2 0 1	0 0 0 0 0 0 0 0 3 0	0 0 0 0 0 0 0 0 5 2 0	D D O D D O O D 0 4 3 0 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 5 1 1 3	0 0 0 0 2 0 10 3 0 0		0 ) _ bickrisCysobiactria_Serkytodromatiac_Serkytodromatiac_Serkytodromatia_ 0 \_ bickrisDevelopedromatiac_Serkytodromatiac_Serkytodromatiac_Serkytodromatia_ 0 \_ bickrisDestromations_Batteridae_Cystophagicsf_Hermonbacteriscese_Hermonbacteriscese_Hermonbacteriscese_Controlses_Controlses_Controlses_Controlses 0 \_ bickris_ 0 \_ bickrisProtocolactriac_Absorbedeets 0 \_ bickrisProtocolactriac_Absorbedeets 0 \_ bickrisProtocolactriac_Absorbedeets 0 \_ bickrisProtocolactriac_Controlses_Controlses_Controlses_Controlses 0 \_ bickrisProtocolactriac_Controlses_Lindrosprotocolactriac_Serviceses 0 \_ bickris_Protocolactriac_Controlses_Controlses_Controlses 0 \_ bickris_Protocolactriac_Controlses_Protocolactrias_Controlses 0 \_ bickris_Protocolactriac_Controlses_Protocolactrias_Protocolactriacs 0 \_ bickris_Protocolactriac_Controlses_Protocolactrias_Protocolactriacs 0 \_ bickris_Protocolactriac_Controlses_Controlses_Protocolactrias_Protocolactrias_Protocolactrias_Protocolactrias_Protocolactrias_Protocolactrias_Protocolactrias_Controlses 0 \_ bickris_Protocolactrias_Controlses_Controlses_Protocolactrias_Protocolactr
738 739 740 741 743 744 745 746 745 746 749 750 751 751	0 11 7 0 2 4 0 6 0 6 0 0 3	0 0 7 3 0 7 0 0 20 0 0 0	0 0 0 0 0 0 0 6 2 0 1	0 0 0 0 0 0 0 0 3 0	0 0 0 0 0 0 0 0 5 2 0	D D O D D O O D 0 4 3 0 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 5 1 1 3 0 0	0 0 0 0 2 0 10 3 0 0		0 k_baterias_Cyanobacterias_Serkytodevonatas_Serkytodevonatas_Serkytodevonatas_Bendfordeross_Desuffordeross_Desufforderossses_Desuffordeross_Desuffordeross_Desufforderosssesses_Desuffordeross=Researce_Herenobactericssase_Herenobactericssase_Herenobactericssase_Desuffordeross_Desuffordeross_Desuffordeross=Researce_Herenobactericssase_Herenobactericssase_Herenobactericssase_MontalBig_groups 0 k_bateris_Researce_Desufforderos_Lachonophacese_Lachonophacese_Consubactery 0 k_bateris_Activatess_Abstraterics_Desufforderosteross=0 (indebusterossases_Desubertory
738 739 740 741 743 744 745 746 745 746 749 750 751 751 752 753	0 11 7 0 2 4 0 6 0 6 0 0 3	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 6 2 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 0 D D 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 5 1 1 3 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 k_ladekias_Cyunoladurluk_Sekkydorumataka_Sektytokuronataks_Sektytokuronataka_Sektytokuronataka_ 0 k_ladekias_Deurifubaterotak_Deurifubytonataa_Deurifubutronatest_Deurifubutronakaese_Deurifubutrons_Deurifubutrons_Deurifubutronakaese_ 0 k_ladekias_Deurifubaterotaka_Chitaphagekist_Humonobackinacese_Humonobackinacese_Humonobackinacese_ 0 k_ladekias_Timmicatesc_Costrindus_Ladmosphalest_Ladmosphaceseg_Lachnopphacese_MAAI36_groups_ 0 k_ladekias_Protoclaateriase_Admosphalest_Ladmosphaceseg_Lachnopphacese_Consubaters_ 0 k_ladekias_Protoclaateriase_Admosphalest_Ladmosphaceseg_Lachnopphacese_Consubaters_ 0 k_ladekias_Protoclaateriase_Costrindus_Sectorateriase_Softworbeckeracese_Consubaters_ 0 k_ladekias_Protoclaateriase_Costrindus_Sectorateriase_Softworbeckeracese 0 k_ladekinss_Protoclaateriase_Costrinduses_Kenthamonotakese_Costrinduseaese 0 k_ladekinss_Protoclaateriase_Genompotenteriase_Kenthamonotakesese 0 k_ladekinss_Protoclaateriase_Bedilosesi_Bedilosest_Bedilosese_Bedilose 0 k_ladekinss_Protoclaateriase_Bedilosesi_Bedilosest_Bedilosese_Bedilose 0 k_ladekinss_Protoclaateriase_Bedilosest_Bedilosese_Bedilos 0 k_ladekinss_Protoclaateriase_Bedilosest_Bedilosese_Bedilose 0 k_ladekinss_Protoclaateriase_Bedilosest_Bedilosest_Bedilose 0 k_ladekinss_Finitesese_Bedilosest_Bedilosest_Bedilosest_Bediloses 0 k_ladekinss_Costrindusedekinstersise_Protoclaateriase_Bedilosest_Bediloses
738 740 741 742 743 744 745 746 746 747 748 749 750 751 752 753 754	0 11 7 0 2 4 0 6 0 8 1 1 0 2	0 0 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 6 2 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 0 D 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 5 1 1 3 0 0 0 17	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0   Laderia,Vandaduria,Serkytodramata,Serkytodramata,Serkytodramata, 0   Laderia,
738 740 741 742 743 744 745 746 746 747 748 749 750 751 752 753 754	0 11 7 0 2 4 0 8 0 3 1 1 0 2 0	0 0 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 1 0 1 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 0 D 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 5 1 1 3 0 0 17 11	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. backetiagdynaksiacteriagdenoidation</li></ul>
738 740 741 742 743 744 745 745 745 745 745 745 751 751 752 753 755 756	0 11 7 0 2 4 0 0 6 0 0 6 0 0 3 1 1 0 2 0 29	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D 0 0 0 1 1 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 5 1 1 3 0 0 17 11 1	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacteriasCysobiactorius_Serkytodromatias_Serkytodromatias_SerkytodromatiasBenghodromatiasDesufforkorius_Desu</li></ul>
738 740 741 742 743 744 745 746 746 746 749 750 751 752 753 754 755 755 756 757	0 11 7 0 0 2 4 0 0 5 0 0 3 1 1 0 2 0 29 2 2	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 6 2 0 1 0 1 0 1 0 0 1 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D 0 0 0 1 1 1 0 0 0 5 5 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 0 6 5 1 1 3 0 0 17 11 1 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. lacteria,</li></ul>
738 740 741 743 744 745 746 746 746 749 750 751 752 753 754 755 755 755 755	0 11 7 0 2 4 0 5 0 5 0 3 1 1 0 2 9 2 0 29 2 0	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 6 2 0 1 0 1 0 1 0 0 1 3 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D 0 0 0 0 0 0 0 1 1 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. hadreinsCysekskateriac_Serkytederenation_Serkytederenation_Serkytederenation_Serkytederenation_</li> <li>b. hadreinsDeutlicheteretac_Deutlicheterenation_DeutlicheterenationHernobeteter</li> <li>b. hadreinsBesterreidenc_Bestereiden_ChernobeteterenationHernobeteterenation</li> <li>b. hadreinsBesterreidenc_Bestereiden_ChernobeteterenationHernobeteter</li> <li>b. hadreinsTerreicheteretac_ChernobeteterenationHernobeteterenation</li> <li>b. hadreinsTerreicheteretac_DeutlicheterenationHernobeteterenation</li> <li>b. hadreinsTerreicheteretac_Deutlicheterenation</li> <li>b. hadreinsTerreicheteretac_Ablageratebesterena</li> <li>b. hadreinsTerreicheteretac_DeutlicheteretaceConsubaterenations</li> <li>b. hadreinsTerreicheteretace_Ablageratebesterena</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenaLosthoosphaceses_Consubaterenations</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenaLosthoosphaceses_Consubaterenations</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenationConsubaterenations</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenaLosthoosphacesesConsubaterenations</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenaLosthoosphacesesLosthoosphaceses</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenaLosthoosphacesesLesthoosphaceses</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenasLesthoosphacesesLesthoosphacesLesthoosphaceses</li> <li>b. hadreinsTerreicheteretace_ConsubaterenasLesthoosphacesesLesthoosphaceses</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenasLesthoosphacesesLesthoosphaceses</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenasLesthoosphacesesLesthoosphaceses</li> <li>b. hadreinsTerreicheteretace_AblageratebesterenasLesthoosphacesesMethoosphaceses</li> <li>b. hadreinsTerreicheteretaceLesthoosphacesesStrephacesesesLesthoosphaceses</li> <li>b. hadreinsTerreicheteretace_AblageratebesteretaceLesthoosphacesesMethoosphaceses<!--</td--></li></ul>
738 740 741 742 743 744 745 746 749 749 749 750 751 753 754 755 755 755 755 755 759	0 11 7 0 2 4 0 5 0 3 1 1 0 29 2 0 7	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 1 0 1 0 1 3 0 0 1 3 0 0 1 3 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 10 3 0 0 5 3 0 1 0 12 0 12 0 12 0 12 0 12 0 12 0 1		<ul> <li>b. backetias</li></ul>
738 740 741 742 743 744 745 746 746 747 748 749 750 751 752 755 755 755 755 755 755 755 755 755	0 11 7 0 2 4 0 5 0 3 1 1 0 29 2 0 7	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 1 0 1 0 0 1 3 0 0 0 0 1 3 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacterias</li></ul>
738 749 741 742 743 744 746 746 746 746 746 746 746 750 751 752 755 756 757 756 759 760 760 761	0 11 7 0 2 4 0 0 6 0 0 3 1 1 0 2 0 2 9 2 0 7 0 7 0 7	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 1 0 1 0 1 0 0 1 3 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 2 0 0 0 3 0 0 5 3 0 1 0 5 3 0 1 0 1 0 1 0 4		<ul> <li>b. laderia,</li></ul>
738 739 740 741 741 743 744 745 746 746 746 746 746 746 746 750 751 755 755 755 755 755 755 755 755 755	0 11 7 0 2 4 0 6 0 3 1 1 0 2 9 2 0 7 0 7 0 7 0 7	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 1 0 1 0 0 1 3 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 6 5 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 2 0 0 0 3 0 0 5 3 0 1 0 1 0 1 0 1 0 4 0		<ul> <li>b. hadenia,</li></ul>
738 740 741 743 743 744 746 747 748 747 748 747 748 755 755 755 755 755 755 755 755 755 75	0 11 7 0 2 4 0 0 6 0 3 1 1 0 2 9 2 0 7 0 7 0 7 0 7 0 7	0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 0 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. backetas</li></ul>
738 739 741 743 744 744 746 746 746 746 746 746 751 752 753 755 755 755 755 755 755 755 755 755	0 11 7 0 2 4 0 0 8 0 2 8 2 0 7 0 7 0 7 0 2 8 2 0 7 0 7 0 2 8 2 0 7 0 2 8 2 0 7 0 2 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 1 0 1 0 0 1 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. backetise</li></ul>
738 749 741 743 744 745 746 746 746 746 746 746 746 746 755 756 756 756 756 756 756 756 756 75	0 11 7 0 2 4 0 0 8 0 2 8 2 0 7 0 7 0 7 0 2 8 2 0 7 0 7 0 2 8 2 0 7 0 2 8 2 0 7 0 2 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 1 0 1 0 0 1 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 0 0 0 0 0 0 0 1 1 0 0 0 0 1 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 1 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 0 0 0 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 2 0 0 10 3 0 0 5 3 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0		<ul> <li>b. bateria,</li></ul>
738 740 741 741 743 744 746 746 746 746 750 751 755 755 755 755 755 755 755 755 755	0 11 7 0 2 4 0 0 8 0 2 8 2 0 7 0 7 0 7 0 2 8 2 0 7 0 7 0 2 8 2 0 7 0 2 8 2 0 7 0 2 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 7 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0 5 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 6 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 3 0	0 0 0 0 2 0 0 10 3 0 0 5 3 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0		<pre>b laderia</pre>
733 739 741 741 741 741 741 741 741 741 755 755 755 755 755 755 755 755 755 75	0 11 7 0 0 2 4 0 0 6 0 3 1 1 0 2 0 2 7 0 7 0 7 0 2 4 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 3 1 1 7 0 0 2 7 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 6 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 a 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b ladeniabeneriabenericationbeneficientesiste/_beneficientesistebeneficiente</pre>
738 739 741 743 743 744 746 747 748 749 749 755 756 757 750 740 741 744 744 744 744 745 745 755 756 757 750 744 744 744 745 745 745 745 745 745 745	0 11 7 0 0 2 4 0 0 6 0 3 1 1 0 2 0 2 7 0 7 0 7 0 2 4 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 3 1 1 7 0 0 2 7 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 a 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>0 1_bideiusCynabiadariaBertandour_Bertandourbacking_BertandourbackBertandourbackDerudiourbackDerudiourbackingBertandourbackDerudiourbackingBertandourbackingBerta</pre>
733 739 741 743 744 745 746 747 746 747 746 747 746 747 746 747 746 746	0 11 7 0 0 2 4 0 0 6 0 3 1 1 0 2 0 2 7 0 7 0 7 0 2 4 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 3 1 1 7 0 0 2 7 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 7 7 3 0 7 0 0 20 0 20 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 6 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 3 0 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. backets,</li></ul>
738 739 741 741 743 744 745 746 746 747 748 746 755 755 755 755 755 755 755 755 755 75	0 11 7 0 0 2 4 0 0 6 0 3 1 1 0 2 0 2 7 0 7 0 7 0 2 4 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 3 1 1 7 0 0 2 7 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 0 7 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 6 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 3 0 1 0 1 0 1	0 0 0 0 0 2 0 0 10 3 0 0 5 3 0 1 0 10 4 0 0 4 0 0 15 2 0		<pre>b laderiacyasisteriaservjeterianitse_servjeterianitse_servjeterianitse_benefactorianitse_bene</pre>
733 739 741 743 743 743 743 743 743 743 743 743 743	0 11 7 0 0 2 4 0 0 6 0 3 1 1 0 2 0 2 7 0 7 0 7 0 2 4 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 3 1 1 7 0 0 2 7 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 0 7 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 6 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 3 0 1 0 1 0 1	0 0 0 0 0 2 0 0 10 3 0 0 5 3 0 1 0 10 2 0 0 1 0 4 0 0 4 0 0 1 5 2 0 1 5 3 0 10 10 10 10 10 10 10 10 10 10 10 10 1		<ul> <li>b. b. b</li></ul>
738 749 741 741 741 741 741 745 755 757 757 757 757 757 757 757 757	0 11 7 0 0 2 4 0 0 6 0 3 1 1 0 2 0 2 7 0 7 0 7 0 2 4 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 3 1 1 7 0 0 2 7 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 0 7 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 5 2 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 6 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 3 0 1 0 0 1 1 1	0 0 0 0 0 2 0 0 10 3 0 0 5 3 0 1 0 12 0 0 1 0 4 0 0 4 0 0 1 5 2 0 1 2		<pre>b ladenia</pre>
738 739 741 743 744 745 746 746 747 748 749 749 740 741 745 745 745 745 745 745 745 745 745 745	0 11 7 0 0 2 4 0 0 6 0 3 1 1 0 2 0 2 7 0 7 0 7 0 2 4 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 4 0 0 2 3 1 1 7 0 0 2 7 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 0 7 7 3 0 20 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 0 1 0 0 0 0 6 5 1 1 3 0 0 0 17 11 1 0 0 0 0 0 0 0 0 3 0 1 0 1 1 2 0	0 0 0 0 0 2 0 0 10 3 0 0 5 3 0 1 0 12 0 0 1 0 4 0 0 4 0 0 1 5 2 0 1 2 0		<pre>b laderias_Cynabiadrius_Serkytodromatas_Serkytodromatas_Serkytodromatas_Deudforbroks_Deudfo</pre>

776	13	0	1	0	0	3	0	1	1	0	0 k_Bacteria
777	0	1	4	1	1	D	0	0	1	0	0 k_Bacteria;p_Bacteroldota;c_Bacterolda:es,f_Murlbaculaceae;g_Murlbaculaceae;s_
778	9	0	O	0	0	D	0	D	1	o	0 k_Bacteria;p_Actinobacteriotac_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_CBricoccus;s_Oltricoccus;sp,
779	0	7	0	0	0	0	0	0	0	0	0 k_Bacteria
780	2	0	0	0	3	0	0	0	0	0	0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiac;o_f_;p_;s_
781	0	0	0	0	0	10	0	o	0	o	0 k_Bacteria;p_Campilobacterota;x_Campylobacteria;o_Campylobacterale;sf_Campylobacteraceae;g_Campylobacter;s_Campylobacter_hominis
782	0	0	0	0	D	5	0	5	0	0	
											0 k_Bacteria;p_Bacteroidiota;c_Bacteroidia;a_Bacteroidia;es_f_Marinifilaceae;g_Odoribacter;s
783	0	5	0	1	0	0	0	0	0	0	0 k_Bacteria;p_Firmicute;sc_Clostridia;o_Clostridia;f_Hungateiclostridiaceae;g_Fastidiosipila;s_Fastidiosipila;sanguinis
784	0	5	0	0	0	0	0	0	0	0	0 k_Batteria
785	8	0	5	0	6	5	0	2	3	0	0 k_Bacteria;p_S4R324_clade(Marine_group_B);c_S4R324_clade(Marine_group_B);o_S4R324_clade(Marine_group_B);d_S4R324_clade(Marine_group_B);c_S4R324_clade(Mar
786	0	10	0	0	0	D	0	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroida;p_Cytophaga!es/_Hymenobacteraceae;g_Hymenobacter;s_
787	0	0	0	6	0	0	0	0	0	0	0 k. Bacteria
								5			0 k Bacteria;o Chloroflexic Chloroflexia;f Rozeiflexaceae.g ;s_
788	0	0	0	0	0	0	0		0	0	
789	5	0	1	0	2	0	0	0	3	0	0 k_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_GaieBale;sf_;z_;s_
790	0	0	1	1	1	2	0	2	2	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;p_Bacteroidates;f_Marihaculaceae;g_Marihaculaceae;s
791	3	0	0	0	0	1	0	D	3	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderialesf_Nitrosomonadaceae;g_MND1;s_
792	4	0	5	0	0	4	0	0	4	0	0 k_Bacteria;p_Bacterioidota;c_Bacterioida;o_Chtiinophagales;f_Chtiinophagaceae
793	1	0	1	4	2	0	0	0	0	0	0 k_Barteria;p_Firmicutes;c_Clostridia;o_Oscillespirales;f_Butyricicoscaceaeg_UCG-009
794				0		5	0	0	8	1	
794	1	0	5		2				8		0 k_Bacteria;p_Firmicutes;c_Clostridia;p_Oscillospirales;f_Oscillospiraceae
795	1	0	0	0	0	0	0	0	3	0	0 k_Bacteria;p_Bdellovibrionota;c_Bdellovibrionaia;o_Bdellovibrionalee;t_Bdellovibrionaceae;g_OM27_tlade;x_
796	2	0	2	0	2	5	0	1	1	1	1 k_Bacteria;p_Acidobacteriota;c_Blastocatella;o_Blastocatella;es;f_Blastocatellaceae
797	7	0	3	0	1	1	0	2	9	σ	$1\ k\_$ Bacteria;p $\_$ Gemmatimonadota;z $\_$ Gemmatimonadates;a $\_$ Gemmatimonadates;d $\_$ Gemmatimonadacea; $\underline{s}\_$ ,z $\_$
798	9	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaleea;g_Photobacterium;s_Photobacterium;phosphoreum
799	37	21	90	2	1	0	1	27	12	0	0 k_Bacteria;pActinobacteriota;cActinobacteria;oMicrococcales;fMicrococcaceae
			2			0		2	12		0 K_parcentypncinobaccentocncinobaccentyp_mini-occurresand-occurres
800	1	0		0	1		0			0	
801	0	7	0	1	D	D	0	0	0	0	0 k_Bacteria;p_Bacteroldota;c_Bacteroldia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Sphingobacterium;s_Sphingobacterium_hotanense
802	0	0	0	0	0	0	0	5	0	0	0 k_Bacteria;p_Chloroflexic_OLB14;p_OLB14;f_OLB14;g_OLB14;s_
803	0	9	0	0	0	0	0	0	1	0	0 k_Bacteria;p_Chloroflexic_KD4:96;o_KD4:96;f_KD4:96;g_KD4:96;s
804	6	0	0	0	0	1	0	0	1	0	0 k_Bacteria;p_Bdellovibrionota;c_Bdellovibrionia;o_Bdellovibrionale;;f_Bdellovibrionaceaeg_Bdellovibria;s_
	0		2			D	0	0	3	0	0 k_Bacteria;p_Germatimonadotax_Germatimonadetas;o_Germatimonadales;f_Germatimonadaceae;g_s_
805		0		0	0						
806	1	0	0	0	3	0	0	2	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirilaies;f_Magnetospiraceae;g_;s_
807	0	0	0	0	0	0	7	0	0	0	0 k_Bacteria;p_Actinobacteriotac_Acidimicrobila;o_IMCC26256;f_IMCC26256;g_IMCC26256;s_
808	0	0	3	0	0	0	0	0	4	0	0 k_Bacteria;p_Firmicute;c_Clostrida;p_Lachnospirales;f_Lachnospiraceaeg_>_
809	6	2	1	0	0	0	0	0	2	0	0 k_Bacteriacp_Actinobacteriotacc_Actinobacteriaco_Propionibacteriales;f_Propionibacteriaceae
810	2	0	1	0	o	4	0	o	4	0	0 k_Bacteria:p_Bacteroidota:c_Bacteroidia:o_Chitinophagales:f_Saprospiraceae:g_;s_
811	2	0	3	0	6	3	0	D	3	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Sphingobacteriales;f_NS11-12_marine_group;g_NS11-12_marine_group;s_
812	3	0	0	0	1	1	0	1	0	0	0 k_Bacteria;p_Bdellovibrionota;c_Bdellovibrionaia;o_Bdellovibrionales;{_Bdellovibrionaceae.g_OM27_thate;s_
813	4	0	0	0	0	2	0	0	0	0	0 k_Bacteria;p_Actinobacteriotax_Actinobacteria;o_Frantiales;f_Acidothermaceae;z_Acidothermus
814	84	8	27	19	14	62	5	17	151	3	12 k_Bacteria;p_firmicutes;c_Clostridu.o_Oscillospirales;f_Oscillospiraceae;g_s_Clostridium_sp.
815	12	0	0	0	0	0	0	0	0	5	0 L_SectringFirmiculessClost/dosp_lathmospiless_Lathmospileses
816	5	0	٥	0	o	D	0	2	0	o	0 k_Excterizp_Protecbacterizc_Gammaproteobacterizo_Xanthomonadalesf_Rhodanobacterzceaeg_PseudofuWimonass_
				0 0			0 0		0 0	o o	0 k_Bacteriag_Proteclascherias_Gammaproteobacterias_Tenthomonadales/_Rhodonobacteriscease_Presidorlahmonass_ 0 k_Bacteriag_Proteclascherias_Gammaproteobacterias_Berholderales
816	5	0	٥	0	o	D	0	2	0	o	0 k_Excterizp_Protecbacterizc_Gammaproteobacterizo_Xanthomonadalesf_Rhodanobacterzceaeg_PseudofuWimonass_
816 817	5 2	0 0	0 1	0 0	0 0	D 4	0 0	2 4	0 0	o o	0 k_Bacteriag_Proteclascherias_Gammaproteobacterias_Tenthomonadales/_Rhodonobacteriscease_Presidorlahmonass_ 0 k_Bacteriag_Proteclascherias_Gammaproteobacterias_Berholderales
815 817 818	5 2 0	0 0 0	0 1 0	0 0 0	0 0 0	D 4 1	0 0	2 4 1	0 0 2	0 0 0	0 K_Bisteriap_Proteclasteriac_Gammaproteobacteriap_Tanthomonudalesf_Rhodowolasteriaceaeg_Preudofulormonass_ 0 K_Bisteriap_Proteclasteriac_Gammaproteobacteriap_Tantholder-lake 0 K_Bisteriap_Firmicutesc_Costridap_Ocelloginalesf_Bammococcasese
816 817 818 819 820	5 2 0 7 1	0 0 0 0	0 1 0 1 0	0 0 0 0	0 0 2 3	0 4 1 6 3	0 0 0 0	2 4 1 2 2	0 0 2 14 0	0 0 0 0	0 k_Bisterlag_Proteclasterlag_Gammaproteobacterlag_Tatotomonudalksf_Rhodonobacteraceaeg_Peesdofubirmonass_ 0 k_Bisterlag_Proteclasterlag_Gammaproteobacterlag_Devilopinessf_Biumnooccacceae 0 k_Bisterlag_Proteclasterlag_Gammaproteobacterlag_Biumnooccacceae 0 k_Bisterlag_Proteclasterlag_Gammaproteobacterlag_Bist_Gates_At-G344sAt-G344s
816 817 818 819 820 821	5 2 0 7 1 2	0 0 0 0 0	0 1 0 1 0 2	0 0 0 0 0	0 0 2 3 4	D 4 1 6 3 2	0 0 0 0 0	2 4 1 2 2 0	0 0 2 14 0	0 0 0 0	0 I_Bisteriag_Pretextuateria_Cammaproteobacteriag_Barbomonadales/_Infodorobacteriage_Presidorlahmonass_ 0 k_Bisteriag_Pretextuateriag_Cammaproteobacteriag_Barboldersiaks 0 k_Bisteriag_Pretextuateriag_Control of the standard stan
816 817 818 819 820 821 822	5 2 0 7 1 2 6	0 0 0 0 0 0	0 1 0 1 0 2 3	0 0 0 0 0 0	0 0 2 3 4 2	0 4 1 6 3 2 1	0 0 0 0 0 0	2 4 1 2 2 0 1	0 2 14 0 4	0 0 0 0 0	0 I _BacteriagProteclascheriag_CasmaproteobacteriagBacteriage_Bacteriage_Presodork/emonass_ 0 k_BacteriagProteclascheriag_Casmaproteobacteriag_Barholderales 0 k_BacteriagFronteobacteriag_Casmaproteobacteriag_Barholderales 0 k_Bacteriag_Proteclascheriag_Bacheriaget_Barholderales 0 k_Bacteriag_Proteclascheriag_Bacheriaget_Bacheriaget_Bacheriaget_Linnobacters_ 0 k_Bacteriag_Proteclascheriag_Casmaproteobacteriag_Casheriaget_Bacheriaget_Linnobacters_ 0 k_Bacteriag_Proteclascheriag_Casmaproteobacteriag_Casheriaget_Bacheriaget_District_Gasmaproteobacteriag_Casheriaget_Bacheriaget_Linnobacters_ 0 k_Bacteriag_Proteclascheriag_Casheriaget_Bacheriaget_Bacheriaget_District_Gasmaproteobacteriag_Casheriaget_Districture_Casheriaget_District
816 817 818 819 820 821	5 2 0 7 1 2	0 0 0 0 0	0 1 0 1 0 2	0 0 0 0 0	0 0 2 3 4	D 4 1 6 3 2	0 0 0 0 0	2 4 1 2 2 0	0 0 2 14 0	0 0 0 0	0 I_Bacteriag_Protectacteriag_Cammaproteobacteriag_Bacteriag_Bacteriage_Facedorlubrenorass_ 0 k_Bacteriag_Protectacteriag_Cammaproteobacteriag_Bacteriageset 0 k_Bacteriag_Protectacteriag_Control of the stand strategy and the strate
816 817 818 819 820 821 822	5 2 0 7 1 2 6	0 0 0 0 0 0	0 1 0 1 0 2 3	0 0 0 0 0 0	0 0 2 3 4 2	0 4 1 6 3 2 1	0 0 0 0 0 0	2 4 1 2 2 0 1	0 2 14 0 4	0 0 0 0 0	0 I _BacteriagProteclascheriag_CasmaproteobacteriagBackgoonglasteriagBackgoonglasteriag_Backgoonglaste
816 817 818 819 820 821 822 823	5 2 0 7 1 2 6 0	0 0 0 0 0 0 0	0 1 0 1 2 3 0	0 0 0 0 0 0 0	0 0 2 3 4 2 0	0 4 1 6 3 2 1 0	0 0 0 0 0 0	2 4 2 2 0 1 0	0 2 14 0 4 4	0 0 0 0 0 0	0   Jacteriag_Protectacteriag_Cammaproteobacteriag_Tarthamenudales/_Produrobacterizeese_Presiderlawmenass_ 0   Jacteriag_Protectacteriag_Cammaproteobacteriag_Tarthademiales 0   Jacteriag_Protectacteriag_Cammaproteobacteriag_Tarthademiales 0   Jacteriag_Protectacteriag_Cammaproteobacteriag_Tartialedemiales 0   Jacteriag_Protectacteriag_Cammaproteobacteriag_Tartialedemiales 0   Jacteriag_Protectacteriag_Cammaproteobacteriag_Catrialedemiales 0   Jacteriag_Protectacteriag_Catrialege_Catrialedemiales 0   Jacteriag_Protectacteriag_Catrialege_Catrialege_Catrialedemialesse_DDi7_citedes_ 0   Jacteriag_Protectacteriag_Catrialege=Catrialege_Catrialege_DDi7_tides_ 0   Jacteriag_Activateriag_Catrialege=Catrialege=Catrialege=DDi7_tides_
816 817 818 819 820 821 822 823 823 824	5 2 7 1 2 6 9	0 0 0 0 0 0 0 0	0 1 0 1 2 3 0	0 0 0 0 0 0 0	0 0 2 3 4 2 0	D 4 1 6 3 2 1 0 1	0 0 0 0 0 0 0	2 4 2 2 0 1 0	0 2 14 0 4 4 0	0 0 0 0 0 0 0	0   _BicteriagProtectacteriagGammaproteobacteriagTantiamenudakisfRodonobacteriagesg_Pseudorlukmenass 0   _BicteriagProtectacteriagGammaproteobacteriagBinnocorcasese 0   _BisteriagProtectacteriagGammaproteobacteriag_Binnocorcasese 0   _BisteriagProtectacteriag_Gammaproteobacteriag_Binnocorcasese 0   _Bisteriag_Protectacteriag_Gammaproteobacteriag_Binnocorcasese 0   _Bisteriag_Protectacteriag_Gammaproteobacteriag_Gammaproteobacteriag_Binnocorcasese 0   _Bisteriag_Protectacteriag_Gammaproteobacteriag_Gammaproteobacteriag_Binnocorcasese 0   _Bisteriag_Protectacteriag_Gammaproteobacteriag_Gammaproteobacteriag_Binnocorcasese 0   _Bisteriag_Protectacteriag_Gammaproteobacteriag_Gammaproteobacteriage_Gammaproteobacteriag
816 817 818 819 820 821 823 824 825 825	5 2 7 1 2 6 0 9 1 1	0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 3	0 0 2 3 4 2 0 0 0 1	D 4 1 6 3 2 1 0 1 0 1 0 2		2 4 2 2 0 1 0 0 1 0	0 2 14 0 4 4 0 6 0	0 0 0 0 0 0 0 1	0   _BicteriaProtectacteriaGammaproteobacteriaBarbooksteriaBetworksteriaFieldeburgeness 0 k_BicteriaFindebacteriaGammaproteobacteria_Barbooksterias 0 k_BicteriaFindebacteriaGammaproteobacterias_Barbooksterias(_Barbooksterse= 0 k_Bicteria_Protectacterias_Gammaproteobacterias_Barbooksterias(_Barbooksterse= 0 k_Bicterias_Protectacterias_Gammaproteobacterias_GABrbooksterias(_Barbooksterse= 0 k_Bicterias_Control = Control
816 817 818 819 820 821 823 824 823 824 825 826 827	5 2 0 7 1 2 6 0 9 1 1 2	0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 3 3	0 0 2 3 4 2 0 0 0 1 3	D 4 1 6 2 1 0 1 0 2 5		2 4 1 2 7 0 1 0 1 0 1	0 2 14 0 4 4 4 0 5 0 1	0 0 0 0 0 0 0 0 0	0 I_Bateriag_Pretexbateriac_Gammapertexbateriag_Bendbookstriag_Bendbookstriag_Pretexbateriag_Bendbookstriag_Control = 1 - Bendbookstriag_Bend
816 817 818 819 820 821 823 824 823 824 825 826 827 828	5 2 0 7 1 2 6 0 9 1 1 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 3 0 1	0 0 2 3 4 2 0 0 1 3 0	D 4 1 6 3 2 1 0 1 0 1 0 2 5 0		2 4 2 2 0 1 0 0 1 0 1 0	0 2 14 0 4 4 0 6 0 1 0	0 0 0 0 0 0 1 0 0 0	0
816 817 818 819 820 821 822 823 824 825 826 827 828 829	5 2 0 7 1 2 6 0 9 1 1 2	0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 3 3	0 0 2 3 4 2 0 0 0 1 3	D 4 1 6 2 1 0 1 0 2 5		2 4 2 2 0 1 0 0 1 0 1 0 0	0 2 14 0 4 4 4 0 5 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1_lstoretisg_Protocolsterisg_Cammaprotocolsterisg_Darkhonorstakled_Photocolsterisceet_Phetodoklemonss_         0 1_lstoretisg_Protocolsterisg_Cammaprotocolsterisg_Darkhonorstakled_Photocolsterisceet_Phetodoklemonss_         0 1_lstoretisg_Protocolsterisg_Control         0 1_lstoretisg_Protocolsterisg_Control         0 1_lstoretisg_Protocolsterisg_Control         0 1_lstoretisg_Protocolsterisg_Darkhonorsteriet         0 1_lstoretisg_Protocolsterisg_Control         0 1_lstoretisg_Decompositisg_Control         0 1_lstoretisg_Control         0 1_lstoretisg_Co
816 817 818 819 820 821 823 824 823 824 825 826 827 828	5 2 0 7 1 2 6 0 9 1 1 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 3 0 1	0 0 2 3 4 2 0 0 1 3 0	D 4 1 6 3 2 1 0 1 0 1 0 2 5 0		2 4 2 2 0 1 0 0 1 0 1 0	0 2 14 0 4 4 0 6 0 1	0 0 0 0 0 0 1 0 0 0	0
816 817 818 819 820 821 822 823 824 825 826 827 828 829	5 2 0 7 1 2 6 0 9 1 1 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 3 0 1	0 0 2 3 4 2 0 0 1 3 0	D 4 1 6 3 2 1 0 1 0 1 0 2 5 0		2 4 2 2 0 1 0 0 1 0 1 0 0	0 2 14 0 4 4 0 6 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1_lstoretisg_Protocolsterisg_Cammaprotocolsterisg_Darkhonorstakled_Photocolsterisceet_Phetodoklemonss_         0 1_lstoretisg_Protocolsterisg_Cammaprotocolsterisg_Darkhonorstakled_Photocolsterisceet_Phetodoklemonss_         0 1_lstoretisg_Protocolsterisg_Control         0 1_lstoretisg_Protocolsterisg_Control         0 1_lstoretisg_Protocolsterisg_Control         0 1_lstoretisg_Protocolsterisg_Darkhonorsteriet         0 1_lstoretisg_Protocolsterisg_Control         0 1_lstoretisg_Decompositisg_Control         0 1_lstoretisg_Control         0 1_lstoretisg_Co
816 817 818 819 820 821 822 823 824 825 826 827 828 829 830	5 2 0 7 1 2 6 0 9 1 1 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 3 0 1	0 0 2 3 4 2 0 0 1 3 0	D 4 1 6 3 2 1 0 1 0 1 0 2 5 0		2 4 2 2 0 1 0 0 1 0 1 0 0	0 2 14 0 4 4 0 6 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 i _istorius_Protestactritac_Gammaproteobactritas_Technomodalist_Photoebactriscest_Presidolubrinosus_ 0 k_istorius_Protestactritac_Gammaproteobactritas_Technomotaceree 0 k_istorius_Protestactritac_Gammaproteobactritas_Barbioleciasts 0 k_istorius_Protestactritac_Gammaproteobactritas_Barbioleciasts 0 k_istorius_Protestactritac_Gammaproteobactritas_Calibritaciast_Barbioleciascest_Distributions 0 k_istorius_Protestactritac_Gammaproteobactritas_Calibritaciast_Barbioleciascest_Distributions 0 k_istorius_Protestactritac_Gammaproteobactritas_Calibritaciast_Barbioleciascest_Distributions 0 k_istorius_Protestactritac_Gammaproteobactritas_Calibritaciast_Barbioleciascest_Distributions 0 k_istorius_Protestactritac_Astrobactritas_Calibritaciast_Socialbritanescest_Distributions 0 k_istorius_Astrobactritations 0 k_istorius_Calibritaciastritations 0 k_istorius_Calibritations 0
816 817 818 819 820 821 823 823 824 825 826 827 828 829 830 831	5 2 7 1 2 6 9 1 2 0 6 2 9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 3 0 1	0 0 2 3 4 2 0 0 1 3 0	D 4 1 6 3 2 1 0 1 0 1 0 2 5 0		2 4 1 2 0 1 0 0 1 0 1 0 1 0 2 0 2 0 3	0 2 14 0 4 4 0 6 0 1 0 7 0 7		0   _lsterisreletisfreetes_freetes_freetessampeteebsterislandooresteretesfreetesbetters 0   _lsterisfreetesbetterissampeteebsterislandooresteretes 0   _lsterisfreetesbetterissampeteebsterislandooresteretes 0   _lsterisfreetesbetterissampeteebsteris_
816 817 818 820 821 824 823 824 825 826 827 828 829 830 831 832 833	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0	D 4 1 6 3 2 1 0 1 0 1 0 2 5 0		2 4 1 2 2 0 1 0 1 0 1 0 1 0 1 0 2 0 3 16	0 2 14 0 4 4 0 6 0 1 0 7 0 1 0 7		b L Jacteria, Pretokateria, Gammapetokoteria, Jachobernik, Hodorobaterizeez, Presobildemonas, b L Jacteria, Pretokateria, Gammapetokoteria, Jachobernik, Hodorobaterizeez, Presobildemonas, b L Jacteria, Pretokateria, Cammapetokoteria, Jachobernik, Hodorobaterizeez, Honobertra, b L Jacteria, Pretokateria, Gammapetokoteria, Jachobernik, Jachobernik, Jachobernik, Jackobertra, b Lateria, Pretokateria, Gammapetokoteria, Jachobernik, Jachobernik, Jackobernik, Ja
816 817 818 820 821 823 824 825 826 827 828 829 830 831 832 833 834	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0	0 4 1 6 3 2 1 0 1 0 1 0 2 5 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 6 3 2 1 1 0 1 1 1 6 3 2 1 1 0 1 1 1 6 3 2 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		2 4 1 2 2 0 1 0 1 0 1 0 1 0 1 0 2 0 3 16 1	0 2 14 0 4 4 0 5 0 1 0 7 0 1 0 3		0 I_Bidrelia_Pretokolacteria_Cammaperkebacteria_Cammaperkebacteria_Cammaperkebacteria_Fielderiaces 0 I_Bidrelia_Pretokolacteria_Cammaperkebacteria_Cammaperkebacteriace_Cammaperkebacteriaces 0 I_Bidrelia_Pretokolacteriac_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriac_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriacese_DEVI14s_ 0 I_Bidrelia_Pretokolacteriace_Antenbacteriace_Camberopacketeriacese_DEVI14s_ 0 I_Bidrelia_Deteriadeseteriaceseteriace_FinaliatesE_Societabareacese_DEVI14s_ 0 I_Bidrelia_Deteriadeseteriace_Cammaperkebacteriace_Camberopacketeriaceseteriace
816 817 818 820 821 824 823 824 825 826 827 828 829 830 831 832 833	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0	D 4 1 6 3 2 1 0 1 0 1 0 2 5 0		2 4 1 2 2 0 1 0 1 0 1 0 1 0 1 0 2 0 3 16	0 2 14 0 4 4 0 6 0 1 0 7 0 1 0 7		b L Jacteria, Pretokateria, Gammapetokoteria, Jachobernik, Hodorobaterizeez, Presobildemonas, b L Jacteria, Pretokateria, Gammapetokoteria, Jachobernik, Hodorobaterizeez, Presobildemonas, b L Jacteria, Pretokateria, Cammapetokoteria, Jachobernik, Hodorobaterizeez, Honobertra, b L Jacteria, Pretokateria, Gammapetokoteria, Jachobernik, Jachobernik, Jachobernik, Jackobertra, b Lateria, Pretokateria, Gammapetokoteria, Jachobernik, Jachobernik, Jackobernik, Ja
816 817 818 820 821 823 824 825 826 827 828 829 830 831 832 833 834	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0	0 4 1 6 3 2 1 0 1 0 1 0 2 5 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 6 3 2 1 1 0 1 1 1 6 3 2 1 1 0 1 1 1 6 3 2 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		2 4 1 2 2 0 1 0 1 0 1 0 1 0 1 0 2 0 3 16 1	0 2 14 0 4 4 0 5 0 1 0 7 0 1 0 3		0 I_Bidrelia_Pretokolacteria_Cammaperkebacteria_Cammaperkebacteria_Cammaperkebacteria_Fielderiaces 0 I_Bidrelia_Pretokolacteria_Cammaperkebacteria_Cammaperkebacteriace_Cammaperkebacteriaces 0 I_Bidrelia_Pretokolacteriac_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriac_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriaces 0 I_Bidrelia_Pretokolacteriace_Cammaperkebacteriace_Camberopacketeriacese_DEVI14s_ 0 I_Bidrelia_Pretokolacteriace_Antenbacteriace_Camberopacketeriacese_DEVI14s_ 0 I_Bidrelia_Deteriadeseteriaceseteriace_FinaliatesE_Societabareacese_DEVI14s_ 0 I_Bidrelia_Deteriadeseteriace_Cammaperkebacteriace_Camberopacketeriaceseteriace
816 817 818 820 821 823 824 825 826 826 827 828 829 830 831 831 833 834 834	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0 3 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 0 0 0 1 3 0 0 1 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 1 0 2 5 0 0 0 0 1 1 1 1 1 0 0 1 1 0 0 1 1 0 1 0 1 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0		2 4 1 2 2 0 1 0 0 1 0 0 1 0 0 2 0 3 16 1 0 0 2 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0	0 2 14 0 4 4 0 5 0 1 0 7 0 1 0 3 2		0 I. Jackerise_Pretextuateria_Gammaproteobacterias_Landonomabiled_Photobacterizese_Prezedultemonas_         0 I. Jackerise_Pretextuateria_Gammaproteobacterias_Landonomabiled_Photobacterizese_Prezedultemonas_         0 I. Jackerise_Pretextuateria_Gammaproteobacterias_Landonomabiled_Photobacterizese         0 I. Jackerise_Pretextuaterias_Gammaproteobacterias_Landonomabiled_Photobacterizese_Univoluterize_         0 I. Jackerise_Pretextuaterias_Gammaproteobacterize_Sandonomabiled_Photobacterizese_Univoluterize_         0 I. Jackerise_Pretextuateriase_Gammaproteobacterizes_Calverbacterizese_Gammaproteobacterize_Calverbacterizese         0 I. Jackerise_Pretextuateriase_Gammaproteobacterizes_Calverbacterizese_Gammaproteobacterizese         0 I. Jackerise_Definition_Definition_Gammaproteobacterizes_Calverbacterizese         0 I. Jackerise_Definition_Gammaproteobacterizese_Calverbacterizese         0 I. Jackerise_Definition_Gammaproteobacterizese_Networkser_Gammaproteobacterizese         0 I. Jackerise_Definition_Gammaproteobacterizese         0 I. Jackerise
818 817 818 819 820 821 823 824 825 825 826 827 828 830 831 832 833 833 833	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 9 3 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 0 0 1 3 0 0 1 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 1 5 0 0 0 0 1 1 1 1 0 0 0 0 0 0		2 4 1 2 2 0 1 0 0 1 0 0 1 0 0 2 0 3 16 1 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 14 0 4 4 0 6 0 1 0 7 0 1 0 3 2 6		<ul> <li>b. Jackrise_Prekolactrike_Cammaprotobactrike_Darbhomoudaled_Notobactricese_Prekoladvirmouss_</li> <li>b. Jackrise_Freidouctrike_Cammaprotobactrike_Darbhomoudaled_Notobactricese_Prekoladvirmouss_</li> <li>b. Jackrise_Freidouctrike_Cammaprotobactrike_Darbhomoudaled_Notobactricese_Prekoladvirmouss_</li> <li>b. Jackrise_Preidouctrike_Cammaprotobactrike_Darbhomoutarese</li> <li>b. Jackrise_Preidouctrike_Cammaprotobactrike_Darbhomoutarese</li> <li>b. Jackrise_Preidouctrike_Cammaprotobactrike_Darbhomoutarese</li> <li>b. Jackrise_Preidouctrike_Cammaprotobactrike_Darbhomoutarese</li> <li>b. Jackrise_Preidouctrike_Cammaprotobactrike_Cambardined_Socialse_Darbhomoutarese</li> <li>b. Jackrise_Preidouctrike_Cammaprotobactrike_Cambardined_Socialse_Darbhomoutarese</li> <li>b. Jackrise_Preidouctrike_Cammaprotobactrike_Cambardined_Socialse_Darbhomoutarese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardined_Socialse_Darbhomoutarese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardined_Socialse_Darbhomoutarese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cambardinese_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cambardinese_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cammaprotobactrike_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cambardinese_Cambardinese</li> <li>b. Jackrise_Lammaprotobactrike_Cambardinese</li></ul>
818 817 818 820 821 824 824 825 826 827 828 829 829 829 829 823 829 823 823 834 834 834 835 835 835	5 7 0 7 1 7 6 0 9 1 1 7 0 6 7 9 0 0 8 1 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 7 7 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0	0 4 6 7 1 0 1 0 1 7 0 0 0 0 1 1 1 1 0 0 0 0 0		2 4 2 2 0 1 0 1 0 1 0 2 0 3 16 1 0 0 2 0 3 16 1 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 14 0 4 4 0 5 0 1 0 7 0 1 0 7 0 1 0 3 2 6 2 1		<ul> <li>b. Jackeria, _/reteksizeria,innicest Calmaperteksizeria,innikationinn</li></ul>
81.8 81.7 81.8 81.9 82.0 82.0 82.0 82.0 82.0 82.0 83.0 83.0 83.0 83.0 83.0 83.0 83.0 83	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0 3 1 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 1 0 2 5 0 0 0 0 0 1 1 1 0 0 0 0 0 0 1 1 0		2 4 1 2 0 1 0 0 1 0 1 0 0 2 0 3 16 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 14 0 4 4 0 1 0 7 0 1 0 7 0 1 0 3 2 6 2 1 0		<ul> <li>b. Jackeria,freidebacteria,famineteebacteria,famineteebacteria,famineteebacteria,famineteee,faminetee,faminetee,faminetee,fam</li></ul>
818 817 818 820 821 824 824 825 826 827 828 829 829 829 829 823 829 823 823 834 834 834 835 835 835	5 7 0 7 1 7 6 0 9 1 1 7 0 6 7 9 0 0 8 1 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 7 7 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 2 1 0 1 0 2 5 0 0 0 0 1 1 1 0 0 2 0 0 0 0 2 0 0 0 2 0 0 0 0		2 4 2 2 0 1 0 1 0 1 0 2 0 3 16 1 0 0 2 0 3 16 1 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 14 0 4 4 0 6 0 1 0 7 0 1 0 3 2 1 0 1 0 1 0 1 0 1 0 1 1 0 1 1 0 1 1 0 1 1 1 1 0 1		<ul> <li>b. Lacteria, Pretextacteria, Cammaproteobacteria, Janhanomakike/ Hodonobacterisce / Preschickmonaus_</li> <li>b. Lacteria, Pretextacteria, Cammaproteobacteria, Janhanomakike/ Hodonobacterisce / Preschickmonaus_</li> <li>b. Lacteria, Pretextacteria, Cammaproteobacteria, Janhanomakike/ Hodonobacterisce / Innobecterisc.</li> <li>b. Lacteria, Pretextacteria, Cammaproteobacteria, Janhanomakie/ Janhano</li></ul>
81.8 81.7 81.8 81.9 82.0 82.0 82.0 82.0 82.0 82.0 83.0 83.0 83.0 83.0 83.0 83.0 83.0 83	5 7 0 7 1 7 6 0 9 1 1 7 0 6 7 9 0 0 8 1 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 1 0 2 5 0 0 0 0 0 1 1 1 0 0 0 0 0 0 1 1 0		2 4 1 2 0 1 0 0 1 0 1 0 0 2 0 3 16 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 14 0 4 4 0 1 0 7 0 1 0 7 0 1 0 3 2 6 2 1 0		<ul> <li>b. Jackeria,freidebacteria,famineteebacteria,famineteebacteria,famineteebacteria,famineteee,faminetee,faminetee,faminetee,fam</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.9</li> <li>B.20</li> <li>B.21</li> <li>B.22</li> <li>B.24</li> <li>B.25</li> <li>B.26</li> <li>B.26</li> <li>B.27</li> <li>B.27</li> <li>B.26</li> <li>B.27</li> <li>B.26</li> <li>B.27</li> <li>B.26</li> <li>B.27</li> <li>B.26</li> <li>B.27</li> <li>B.27</li> <li>B.26</li> &lt;</ul>	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0 3 1 1 0 0 7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 2 1 0 1 0 2 5 0 0 0 0 1 1 1 0 0 2 0 0 0 0 2 0 0 0 2 0 0 0 0		2 4 1 2 0 1 0 0 1 0 1 0 2 0 3 16 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 14 0 4 4 0 6 0 1 0 7 0 1 0 3 2 1 0 1 0 1 0 1 0 1 0 1 1 0 1 1 0 1 1 0 1 1 1 1 0 1		<ul> <li>b. Lacteria, Pretextacteria, Cammaproteobacteria, Janhanomakike/ Hodonobacterisce / Preschickmonaus_</li> <li>b. Lacteria, Pretextacteria, Cammaproteobacteria, Janhanomakike/ Hodonobacterisce / Preschickmonaus_</li> <li>b. Lacteria, Pretextacteria, Cammaproteobacteria, Janhanomakike/ Hodonobacterisce / Innobecterisc.</li> <li>b. Lacteria, Pretextacteria, Cammaproteobacteria, Janhanomakie/ Janhano</li></ul>
818 817 818 819 820 821 823 824 824 825 825 825 825 825 825 825 825 833 844 833 844 835 845 845 845	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0 3 1 1 0 0 0 7 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 2 5 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0		2 4 1 2 2 0 1 0 0 1 0 0 2 0 3 16 1 0 0 0 0 0 0 0 3	0 2 14 0 4 4 0 6 0 1 0 7 0 1 0 3 2 6 2 1 0 1 7 7		<ul> <li>b. Lacteria, Pretokacteria, Cammapotobacteria, Jachaberais</li> <li>b. Lacteria, Pretokacteria, Cammapotobacteria, Jachaberais, Ja</li></ul>
81.8 81.7 81.9 82.0 82.1 82.0 82.0 82.0 82.0 82.0 82.0 82.0 83.0 83.0 83.0 83.0 83.0 83.0 83.0 83	5 2 0 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0 3 1 1 0 0 0 7 2 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 2 1 0 1 0 2 5 0 0 0 1 1 1 0 2 5 0 0 0 1 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2412201001002031610000310	0 2 14 0 0 4 4 0 6 0 1 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5		<ul> <li>b. Lacteria, _ freedotacteria, _ cammupote bacteria, _ landbacteria (_ floodbacterizese _ jest dot kinnous,</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.9</li> <li>B.20</li> <li>B.21</li> <li>B.22</li> <li>B.24</li> <li>B.25</li> <li>B.26</li> <li>B.27</li> <li>B.26</li> &lt;</ul>	5 2 6 7 1 2 6 8 1 1 2 0 6 2 9 0 0 3 1 1 0 0 7 2 0 1 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 2 1 0 1 0 2 5 0 0 0 1 1 1 0 2 5 0 0 0 1 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2412201001002031610000031000	0 2 14 0 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0		<ul> <li>b. Lacteria, Pretexacteria, Gammaproteobacteria, Javiabalerais</li> <li>b. Lacteria, Pretexacteria, Gammaproteobacteria, Javiabalerais, Javiabalera</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.7</li> <li>B.7</li> <li>B.7</li> <li>B.4</li> <li>B.7</li> <li>B.6</li> <li>B.7</li> <li>B.6</li> <li>B.7</li> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.7</li> <li>B.6</li> <li>B.7</li> <li>B.7</li></ul>	5 2 6 7 1 2 6 6 9 1 1 2 0 6 2 9 0 0 3 1 1 0 0 0 7 2 0 1 3 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 3 4 2 0 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 2 5 0 0 0 1 1 1 0 2 5 0 0 0 1 1 5 0 0 0 1 1 0 2 5 0 0 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 0 2 0 3 16 1 0 0 0 0 0 3 1 0 0 0 0 0 0 0 3 1 0 0 0 0	0 2 34 0 4 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0 0		<ul> <li>b. Lacteria, Pretokacteria, Cammapotokacteria, Jarobanenakik/ Piodokokterscenz _ Paskdokkeronas, _</li> <li>b. Lacteria, Pretokacteria, Cammapotokacteria, Jarobanenakik/ Piodokokterscenz _ Paskdokkeronas, _</li> <li>b. Lacteria, Pretokacteria, Cammapotokateria, JArobak/Lak/Aro</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.9</li> <li>B.20</li> <li>B.21</li> <li>B.22</li> <li>B.24</li> <li>B.25</li> <li>B.26</li> <li>B.27</li> <li>B.26</li> &lt;</ul>	5 2 6 7 1 2 6 8 1 1 2 0 6 2 9 0 0 3 1 1 0 0 7 2 0 1 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 1 3 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 2 1 0 1 0 2 5 0 0 0 1 1 1 0 2 5 0 0 0 1 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2412201001002031610000031000	0 2 14 0 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0		<ul> <li>b. Laderia, Pretokachria, Gamaprotobachria, Jachbolerski, Hodsebachrisse "Paskdolamous,</li> <li>c. Laderia, Pretokachria, Gamaprotobachria, Jachbolerski,</li> <li>c. Laderia, Pretokachria, Gamaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Pretokachria, Gamaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Pretokachria, Gamaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Pretokachria, Krinoberria, Freinkist, Sorochhyraet</li> <li>c. Laderia, Mennomirabita, Vennomirabita, Sahbolerski, Pretokachria, Gabaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Mennomirabita, Vennomirabita, Sahbolerski, Pretokachria, Gabaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Mennomirabita, Sahbolerski, Pretokachria, Gabaprotobachria, Gabaprotobachria, Pretokachria, Sahbolerski, Pretokachria, Pretokachria, Sahbolerski, Pretokachria, Pretokachria, Sahbolerski, Pretokachria, Pretokachria, Sahbolerski, Pretokachria, Pretokachria, Pretokachria, Sahbolerski, Pretokachria, Pretoka</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.7</li> <li>B.7</li> <li>B.7</li> <li>B.4</li> <li>B.7</li> <li>B.6</li> <li>B.7</li> <li>B.6</li> <li>B.7</li> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.7</li> <li>B.6</li> <li>B.7</li> <li>B.7</li></ul>	5 2 6 7 1 2 6 6 9 1 1 2 0 6 2 9 0 0 3 1 1 0 0 0 7 2 0 1 3 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 3 4 2 0 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 2 5 0 0 0 1 1 1 0 2 5 0 0 0 1 1 5 0 0 0 1 1 0 2 5 0 0 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 0 2 0 3 16 1 0 0 0 0 0 3 1 0 0 0 0 0 0 0 3 1 0 0 0 0	0 2 34 0 4 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0 0		<ul> <li>b. Lacteria, Pretokacteria, Cammapotokacteria, Jarobanenakik/ Piodokokterscenz _ Paskdokkeronas, _</li> <li>b. Lacteria, Pretokacteria, Cammapotokacteria, Jarobanenakik/ Piodokokterscenz _ Paskdokkeronas, _</li> <li>b. Lacteria, Pretokacteria, Cammapotokateria, JArobak/Lak/Aro</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.9</li> <li>B.2</li> <li>B.2</li> <li>B.2</li> <li>B.4</li> <li>B.5</li> <li>B.4</li> <li>B.4</li></ul>	5 2 6 7 1 2 6 0 9 1 1 2 0 6 2 9 0 0 3 1 1 0 0 0 7 2 0 1 3 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 3 4 2 0 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 1 0 0 2 0 3 16 1 0 0 0 0 0 3 1 0 0 0 0	0 2 34 0 0 4 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0 3		<ul> <li>b. Laderia, Pretokachria, Gamaprotobachria, Jachbolerski, Hodsebachrisse "Paskdolamous,</li> <li>c. Laderia, Pretokachria, Gamaprotobachria, Jachbolerski,</li> <li>c. Laderia, Pretokachria, Gamaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Pretokachria, Gamaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Pretokachria, Gamaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Pretokachria, Krinoberria, Freinkist, Sorochhyraet</li> <li>c. Laderia, Mennomirabita, Vennomirabita, Sahbolerski, Pretokachria, Gabaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Mennomirabita, Vennomirabita, Sahbolerski, Pretokachria, Gabaprotobachria, Sahbolerski, Pretokachria,</li> <li>c. Laderia, Mennomirabita, Sahbolerski, Pretokachria, Gabaprotobachria, Gabaprotobachria, Pretokachria, Sahbolerski, Pretokachria, Pretokachria, Sahbolerski, Pretokachria, Pretokachria, Sahbolerski, Pretokachria, Pretokachria, Sahbolerski, Pretokachria, Pretokachria, Pretokachria, Sahbolerski, Pretokachria, Pretoka</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.9</li> <li>B.2</li> <li>B.2</li> <li>B.3</li> <li>B.4</li> <li>B.4</li></ul>		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 3 4 2 0 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 a 2 1 0 1 0 2 5 0 0 0 1 1 1 0 0 0 2 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 0 1 1 0 0 0 0 1 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 0 2 0 3 16 1 0 0 0 0 0 3 1 0 0 0 3	0 0 2 14 0 0 4 4 0 6 0 1 0 0 7 0 1 0 8 2 6 2 1 0 1 7 0 5 0 0 3 1		<ul> <li>b. Lateria, Pretokateria, Gamaprokobatiria, Jacobaenakir, Notokobatiracea, Paskdolamonas,</li> <li>b. Lateria, Pretokateria, Gamaprokobatiria, Jacobaenaki, Jacobaenakira, Jacoba</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.9</li> <li>B.7</li> <li>B.2</li> <li>B.4</li> <li>B.5</li> <li>B.4</li> <li>B.5</li> <li>B.4</li> <li>B.5</li> <li>B.6</li> <li>B.6</li></ul>		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 3 4 2 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 2 5 0 0 0 1 1 1 0 0 0 2 0 0 0 1 1 0 0 0 6 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 1 0 2 0 3 16 1 0 0 0 0 0 3 1 0 0 0 3 17 0	0 0 2 14 0 0 4 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0 0 3 1 1 0		<ul> <li>b. Laderia, Pretokachia, Gamaprotokachia, Jarbahanakki, Piodokokirszeez, Jakabahanaus,</li> <li>b. Laderia, Pretokachia, Gamaprotokachia, Jarbahanak, Piodokokirszeez, Piesköhlemous,</li> <li>b. Bateria, Pretokachia, Ampartakateria, Art 44, Art 34, 4rt 344,</li> <li>b. Bateria, Pretokachia, Ampartakateria, Art 44, Art 34, 4rt 344,</li> <li>b. Bateria, Pretokachia, Ampartakateria, Art 44, Art 34, 4rt 344,</li> <li>b. Bateria, Pretokachia, Ampartakateria, Art 44, Art 34, 4rt 344,</li> <li>b. Bateria, Pretokachia, Ampartakateria, Art 44, Art 34, 4rt 344,</li> <li>b. Bateria, Pretokachia, Ampartakateria, Art 44, Art 34, 4rt 344,</li> <li>b. Bateria, Antonokachia, Antonokaria, Pretokachia, Gamaprotokatira, Sorthyszee</li> <li>b. Bateria, Antonokachida, Benenokaphila, Saintokachia, Gata, 714, 51, 41, 41, 51,</li></ul>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.9</li> <li>B.2</li> <li>B.2</li> <li>B.2</li> <li>B.2</li> <li>B.2</li> <li>B.2</li> <li>B.2</li> <li>B.3</li> <li>B.3</li> <li>B.3</li> <li>B.3</li> <li>B.4</li> <li>B.3</li> <li>B.4</li> <li>B.4</li></ul>		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 4 2 0 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 2 5 0 0 0 1 1 1 0 0 0 2 0 0 0 1 1 0 0 0 6 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 1 0 2 0 3 16 1 0 0 0 0 0 3 1 0 0 0 3 17 0 1	0 0 2 14 0 0 4 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0 0 3 1 1 0 7		<ul> <li>b. Laderia, Predeskeria, Gammaprotokstrika, Jachstenstrike, Moderskarterszer, Jackstrikelinersze, Cammaprotokstrika, Jackstenstrike, Moderskarterszeri, Mode</li></ul>
818 817 818 819 821 821 823 824 825 824 825 826 827 838 839 839 839 839 839 839 839 839 839		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 1 4 2 0 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 2 5 0 0 0 1 1 1 0 0 0 2 0 0 0 1 1 0 0 6 0 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 1 0 0 2 0 3 16 1 0 0 0 0 0 0 3 1 0 0 0 3 17 0 1 8	0 0 2 14 0 0 4 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0 0 3 1 1 0 7 0		<pre>b _ bcteris_ restais_firmates:_ Gammapotebsterisinstableris: b _ baterisinvestacionis Gammapotebsteris Frainistateris: b _ baterisinvestacionis Gammapotebsteris Frainistateris: b _ baterisinvestacionis Cammapotebsteris Frainistateris: b _ baterisinvestacionis Cammapotebsteris Frainistateris: b _ baterisinvestacionis Cammapotebsteris Frainistateris: b _ baterisinvestacionis Cammapotebsteris Frainistateris_ Sorthhyses b _ baterisinvestacionis bateristateris Frainistateris Sorthhyses b _ baterisinvestacionis Calmadoteris Frainistateris Sorthhyses b _ baterisinvestacionis Calmadoteris Frainistateris Calmapotebsteris Calmadoteris. b _ baterisinvestacionis bateristateris Calmadoteris Calmadoteris. b _ baterisinvestacionis Dateristateris Frainistateris Calmadoteris Calmadoteris. b _ bateris Prestacionis Bateristateris Calmadoteris. b _ bateris Investacionis Gammapotebstering Antimazoalexi _ Calmadoteris. b _ bateris Investacionis Gammapotebstering Antimazoalexi _ Calmadoteris. b _ bateris Investacionis Gammapotebstering Calmadoteris. b _ bateris Investacionis Gammapotebstering Antimazoalexi _ Calmadoteris. b _ bateris Investacionis Gammapotebstering Calmadoteris. b _ bateris Investacionis Gammapotebstering Calmadoteris. b _ bateris Investacionis Gammapotebstering Calmadoteris. b _ bateris Investacionis Calmadoteris Manmapotebstering Calmadoteris. b _ bateris Investacionis Calmadoteris Calmadoteris. b _ bateris Investacionis Calmadoteris Calmadoteris. b _ bateris Investacionis Calm</pre>
<ul> <li>B.8</li> <li>B.7</li> <li>B.8</li> <li>B.9</li> <li>B.20</li> <li>B.21</li> <li>B.22</li> <li>B.24</li> <li>B.25</li> <li>B.26</li> <li>B.27</li> <li>B.26</li> <li>B.26</li> <li>B.26</li> <li>B.26</li> <li>B.26</li> <li>B.26</li> <li>B.26</li> <li>B.26</li> <li>B.26</li> <li>B.27</li> <li>B.26</li> <li>B.27</li> <li>B.26</li> <li>B.27</li> &lt;</ul>		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 4 2 0 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 2 5 0 0 0 1 1 1 0 0 0 2 0 0 0 1 1 0 0 0 6 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 1 0 2 0 3 16 1 0 0 0 0 0 3 1 0 0 0 3 17 0 1	0 0 2 4 0 0 4 4 0 6 0 1 0 0 7 0 1 0 8 2 6 2 1 0 1 7 0 5 0 0 8 1 1 0 7 0 1		<ul> <li>b. Ludrita, francisc, annapartekskativa, Jarkhannakakat, fladarbaktaturaser, j. kuddekinanus, j.</li> <li>b. Ludrita, franciska, c. Cardia, D. Ochonizita, Janhaderika, Jarkhaderika, Jarkhad</li></ul>
818 817 818 819 821 821 823 824 825 824 825 826 827 838 839 839 839 839 839 839 839 839 839		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 1 4 2 0 0 0 1 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 6 3 2 1 0 1 0 2 5 0 0 0 1 1 1 0 0 0 2 0 0 0 1 1 0 0 6 0 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 4 1 2 2 0 1 0 0 1 0 1 0 0 2 0 3 16 1 0 0 0 0 0 0 3 1 0 0 0 3 17 0 1 8	0 0 2 14 0 0 4 4 0 6 0 1 0 0 7 0 1 0 3 2 6 2 1 0 1 7 0 5 0 0 3 1 1 0 7 0		<pre>b _ bcteris_ restais_firmates:_ Gammapotebsterisinstableris: b _ baterisinvestacionis Gammapotebsteris Frainistateris: b _ baterisinvestacionis Gammapotebsteris Frainistateris: b _ baterisinvestacionis Cammapotebsteris Frainistateris: b _ baterisinvestacionis Cammapotebsteris Frainistateris: b _ baterisinvestacionis Cammapotebsteris Frainistateris: b _ baterisinvestacionis Cammapotebsteris Frainistateris_ Sorthhyses b _ baterisinvestacionis bateristateris Frainistateris Sorthhyses b _ baterisinvestacionis Calmadoteris Frainistateris Sorthhyses b _ baterisinvestacionis Calmadoteris Frainistateris Calmapotebsteris Calmadoteris. b _ baterisinvestacionis bateristateris Calmadoteris Calmadoteris. b _ baterisinvestacionis Dateristateris Frainistateris Calmadoteris Calmadoteris. b _ bateris Prestacionis Bateristateris Calmadoteris. b _ bateris Investacionis Gammapotebstering Antimazoalexi _ Calmadoteris. b _ bateris Investacionis Gammapotebstering Antimazoalexi _ Calmadoteris. b _ bateris Investacionis Gammapotebstering Calmadoteris. b _ bateris Investacionis Gammapotebstering Antimazoalexi _ Calmadoteris. b _ bateris Investacionis Gammapotebstering Calmadoteris. b _ bateris Investacionis Gammapotebstering Calmadoteris. b _ bateris Investacionis Gammapotebstering Calmadoteris. b _ bateris Investacionis Calmadoteris Manmapotebstering Calmadoteris. b _ bateris Investacionis Calmadoteris Calmadoteris. b _ bateris Investacionis Calmadoteris Calmadoteris. b _ bateris Investacionis Calm</pre>

854	2	0	2	0	18	0	0	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_Muribaculaceae;s_
855	6	0	2	0	1	D	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
855		0 6	2	0	1	2	0	0 2	0	0	0 k_Bacteria;p_latescibacterota;c_Latescibacterota;o_latescibacterota;f_latescibacterota;g_latescibacterota;s_
857	1	0	0	0	3	3	1	6	4	1	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Propionibacteriale;sf_Nocardioidaceae; <u>x</u> _Nocardioides
859	4	0	0	0	1	D	0	D	0	0	0 k_Bacteria;p_Protocobacteria;c_Gammaprotocobacteria;o_Burkholdoriales;f_Comamonadaceae;g_Leptothrin;s_ 0 k_Bacteria
860	0	7	0	0	0	D	0	D	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;a_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides
861	0	0	0	0	0	1	0	29	0	0	0 k_Bacteria;o_Proteobacteria;c_Gammaproteobacteria;o_Gammaproteobacteria_Incertae_Sedis;f_Unknown_Family;g_Acidibacter;s_
862	6	1	0	0	7	4	0	0	1	0	0 k_Bacteria;p_Firmicutes:c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;gs
863	1	0	o	0	1	3	0	5	3	0	1 k_Bacteria;p_Profeobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_TR43-20;g_TR43-20;s_
864	1	0	1	1	2	2	0	1	1	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales-Tissierellales;f_Peptostreptococcales-Tissierellales;g_Peptoniphilus;s_Peptoniphilus_lacrimalis
865	0	4	o	0	o	0	0	0	0	0	0 Unknown
866	9	0	0	0	0	0	0	9	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_CCD24;f_CCD24;g_CCD24;s_
867	0	0	0	0	0	1	0	2	1	0	0 k_Bacteria;p_Gemmatimonadota;x_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadacese;g_;s_
868	2	0	2	1	2	1	2	0	4	0	0 k_Bacteria;p_Firmicutes;c_Clostridis;o_Lachnospirales;f_Lachnospiraceae
869	2	0	2	0	2	D	0	3	Б	o	0 k_Bacteria;p_Acidobacteriota;s_Vicinamibacteria;o_Vicinamibacterales;f_Vicinamibacteraceae;g_Vicinamibacteraceae;s_
870	4	0	U	0	1	1	0	1	1	0	0 k_Bacteria;p_Actinobacteriota;c_Acidimicrobila;o_Microtrichales;f_Microtrichaceae;g_s_
871	6	0	3	0	1	7	0	10	10	0	$0 \ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Burkholderia les f\_Comamonadaceae$
872	5	1	0	1	0	1	0	0	0	0	$0\ k\_Bacteria;p\_Firmicute;c\_Clostridia;o\_Lachnospirale;;f\_Lachnospiraceae;g\_n\_Clostridium\_sp.$
873	0	9	0	1	0	0	0	0	0	0	$0\ k\_Bacteria; p\_Cyanobacteria; z\_Cyanobacteria; o\_Chloroplast; f\_Chloroplast; g\_Chloroplast; s\_Pseudomuriella_schumacherensis and the set of the set of$
874	2	0	2	0	2	2	0	D	0	0	0 k_Bacteria;p_Chlaroflext;c_KD4-96;s_KD4-96;f_KD4-96;g_KO4-96;s
875	7	0	6	0	2	4	0	4	7	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Methylophilaceae.g_Methylotenera;s
876	0	0	0	0	0	0	0	7	0	0	$0\ k\_Bacteria; p\_Actinobacteriota; c\_Actinobacteria; o\_Streptosporangiales; f\_Streptosporangiaceae; g\_Nonomuraeaacteria; bacteria; bac$
877	1	0	0	0	0	7	0	0	0	0	$0\ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Burkholderia; esf\_Sutterellaceae; a\_Parasutterella; s\_rellaceae; a\_Parasutterellaceae; a\_Parasutterellaceae; a\_Parasutterellaceae; a\_Parasutterellaceae; a\_Parasutterellaceae; s\_rellaceae; a\_Parasutterellaceae; a\_Parasuterellaceae; a\_Parasutterellaceae; a\_Parasutterellaceae; a\_Paras$
878	5	0	0	0	0	D	0	9	2	0	0 k_Bacteria;p_Protecibacteria;c_Gammaproteobacteria;o_Burkholderialesf_Nitrosomonaciaceae;g_Ellin6067;s_
879	0	0	7	0	1	1	0	D	0	0	0 k_Bacteria;p_Chloroflexk;c_SI56_marine_group;o_SI:56_marine_group;f_SI:56_marine_group;g_SI:56_marine_group;s_
880	5	0	1	0	0	3	0	0	1	0	0 k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g_Solibacillus
881	2	5	0	0	1	3	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
882	1	0	0	0	0	1	0	5	1	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderia/es;f_Comamonadaceaeg_Curvibacter;s_
883	4	9	0	0	0	3	1	0 9	0	0	0 k_Bacteria;p_Firmicutes;c_Bacili;o_Lactobaciliales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus_urinalis
885	ž	1	0	0	1	2	0 3	0	0	0	0 k_Batteriacp_Proteolasteriacc_Gammaproteobatteria.o_Xanthomonadalesf_Rhodanobatteraceaeg_Dokdonella;s0
896	0	0	0	0	0	0	0	14	0	0	0 k. Bacteria;p. Sectoroloces, Sacteroloado Sacteroloados, ministruarces;g. Munistruarces;s
887	0	3	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;p_Seudonocardiale;sf_Pseudonocardiacea;z_Saccharopolyspora;s_
888	0	0	0	0	0	3	0	2	0	0	0 k_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriae;f_Acidobacteriae;g_Paludibaculum;s_
889	0	0	o	0	0	D	0	7	0	0	0 k_Bacteria;p_Actinobacterista;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Solirubrobacter;s_
890	1	0	1	0	1	1	0	2	2	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Cytophagales;f_Spirosomaceae;g_Pseudarcicella;s_
891	4	0	0	0	0	2	0	3	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g>_
892	4	0	o	0	o	D	0	D	0	o	0 k_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Galellales;f_;g_;s_
893	2	0	5	0	3	3	0	15	8	0	$0 \ k\_Bscterise\_Acidsbacteriotax\_Vcinamibacterise\_Vcinamibacteralesd\_Vcinamibacteraceaex=Vcinamibaceaex=Vcinamibacteraceaex\_Vcinamibaceaex\_Vcinamibaceaex\_Vcinamibac$
893 894	2	0 0	5 0	0 0	3 0	3 D	0 0	15 0	8 3	0	0 k_Bacterixg_Acidobacteriotz_Vicinamibacterixg_Vicinamibactericg_Vicinamibactericeae:g_Vicinamibactericeae;g_ 0 k_Bacterixg_Wyorococotis_Polyingbac_Polyingbacf_Birlikl;g_Birlikl;s_
			0 0				0 0				0 k_Bisteriag_Mysocococtsz_Polyingiaso_Polyingialesf_Birl41.g_ 0 k_Bisteriag_Protocolacterias_Cammaportobacterias_Patterrelibest_Factorrelibease.g_frederiksena.s_
894 895 896	1	0 1 0	0 0 0	0 0 0	0	D D 0	0 0 0	D D 4	3 0 0	0 0 0	0 k_Bateriag_Mynotococtss_Poylangilao_Poylangilesf_Birl41s_ 0 k_Bateriag_Protoblacteriag_Cammaprotoblacteriag_Patererillesf_Pattererillesasg_frederiksenias_ 0 k_Bateriag_Acidoblecterious_Acidobacterice_PAUC26ff_PAUC26fg_PAUC26fg_
894 895 896 897	1 3 0	0 1 0	0 0 0 1	0 0 0	0 0 3	D D 0 1	0 0 0	0 0 4 1	3 0 0	0 0 0	0 k_Bacteriap_Mynococcotas_Poylangilao_Poylangilaesf_BINRISg_BINRIS_ 0 k_Bacteriap_Proteobacterias_Cammaponteobacteriao_Parteurellaesf_Parteurellaceaeg_InteGerkentias_ 0 k_Bacteriap_Acdobacteriotas_Acdobacteriaes_PAUC266f_PAUC266g_PAUC266s_ 0 k_Bacteriap_Proteobacteriae_Gammaponteobacteriao_Buchholderiaksf_Nitrosorromadaceaeg_Nitrosorpira
894 895 896 897 898	1 3 0 0	0 1 0 0	0 0 1 0	0 0 0 0	0 0 0	0 0 1 0	0 0 0 0	0 0 4 1	3 0 0 3	0 0 0 0	0 k_Bisteriap_Mysococostsz_Polyangiaso_Polyangialesf_BINRISg_BINRIS_ 0 k_Bisteriap_Proteobacterias_Cammaposteobacterias_Parteurellaiesf_Parteurellaceaeg_Prederikaenias_ 0 k_Bisteriap_Acidobacteriosp_Acidobacteriaco_PaVC26f_PAVC26fg_PAVC26fs_ 0 k_Bisteriap_Proteobacteriac_Gammaposteobacterias_Bistholdenialssf_Nitrosorromadiceaeg_Witersorpina 0 k_Bisteriap_Proteobacteriac_Gammaposteobacterias_Bistholdenialssf_Nitrosorromadiceaeg_WiterSp_
894 895 896 897 898 898	1 3 0 0 0	0 1 0 0 0	0 0 1 0	0 0 0 0 0	0 0 3 0	D D D 1 D D	0 0 0 0	0 0 4 1 3	3 0 0 3 0	0 0 0 0	<ul> <li>Bisteriap_Mysococotsz_Polyangales_Binitisg_Dirikts_Dirikts_</li> <li>Listeriap_Proteckaceriac_Commoproteckateriac_Proteinelides_Tature tilesasg_Tederilseniag_</li> <li>Listerias_Proteckaceriac_Commoproteckateriac_PiNC06/F_MUC06/E_MUC065_</li> <li>Listerias_Proteckaceriac_Commoproteckaterias_Dirikteriateriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriateriag_ministeriateriateriag_ministeriateriag_ministeriateriag_ministeriateriateriag_ministeriateriateriag_ministeriateriateriag_ministeriateriag_ministeriateriag_ministeriateriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriag_ministeriateriateriag_ministeriateriateriag_ministeriateriateriag_ministeriateriateriag_ministeriateriateriag_ministeriateriateriag_ministeriateriateriateriateriateriateriateria</li></ul>
894 895 896 897 898 899 900	1 0 0 0 0	0 1 0 0 0 0	0 0 1 0 0	0 0 0 0 0 0	0 0 3 0 0	D D 1 D D 0	0 0 0 0 4	D 4 1 3 0	3 0 0 3 0 0	0 0 0 0 0	D I _BacteriagMysocococtsz_Teviyragiasg_Polyangialesf_Bin4i1_gBin4i1_s D I _BacteriagProtocolaceriag_C_anomporteolaceriagPatrovelilesed_Factorevilleseasg_frederikaensa D I _BacteriagProtocolaceriagAnodesacteriagPAVC26ffPAVC26fgPAVC26fs D I _Bacteriag_Protocolaceriag_CanomporteolaceriagPavlicaeriag_Pavlicaeriag_meteriage_ D _ LaberiagProtocolaceriagAnodesacteriagMicroarinolaceriag_meteriag_ D _ Laberiag_ActinolaceriategAnodemicrobiasg_Microarinolalesid_g_g_ D I _Bacteriag_Actinolaceriateg_Acidemicrobiasg_Microarinolalesid_g_g_ D I _Bacteriag_Actinolaceriateg_Acidemicrobiasg_Microarinolalesid_g_g_ D Unknows
894 895 896 897 898 898 899 900 901	1 0 0 0 0 0	0 1 0 0 0 0 0	0 0 1 0 0 0	0 0 0 0 0 0 0	0 0 3 0 0 0	0 0 1 0 0 0	0 0 0 0 4 0	0 0 4 1 3 0 3	3 0 0 3 0 0 1	0 0 0 0 0 0	0 k_Bisteriag_Mysococots_Polyanglaso_Polyanglalesf_Birl41.g_ 0 k_Bisteriag_Protocoloceting_Commonstrations_Patterialblesf_Patterialbase_frederilsentas_ 0 k_Bisteriag_Protocoloceting_Commonstrations_Birl41028/fg_PAU/28/fg_PAU/28/fg_PAU/28/fg_ 0 k_Bisteriag_Protocoloceting_Commonstrations_Birl41048/er18/fg_PAU/28/fg_
894 895 896 897 898 899 900 900 901	1 0 0 0 0 0 0	0 1 0 0 0 0 0	0 0 1 0 0 0 0	0 0 0 0 0 0 0 0	0 0 3 0 0 0	D D 1 D 0 0 0 0	0 0 0 0 4 0	0 4 1 3 0 3 4	3 0 0 3 0 0 1 0	0 0 0 0 0 0 0	<ul> <li>b Lacteria,Proteclacetta,Gammperterbattatia,Partervilleterattur titesaagInderitaaniaattur titesaagInderitaaniaattur titesaagInderitaaniaattur titesaagInderitaaniag</li></ul>
894 895 896 897 898 899 900 900 901 900 901 902 903	1 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0	D D 1 D 0 0 0 0	0 0 0 0 4 0 0	D 4 1 3 0 3 4 0	3 0 0 3 0 1 0	0 0 0 0 0 0 0 0	<ul> <li>b Lasteriag_Mysococotas_Polyangales_Bulkst_Binkit_Binkits_</li> <li>c Lasteriag_Protocolacteriag_Componentialsateriag_Protocolacteriag_Polyangales_Binkits_Bi</li></ul>
894 895 896 897 898 899 900 901 901 903 903	1 0 0 0 0 0 0 0 4 0	0 1 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0	0 0 1 0 0 0 0 0 0	0 0 0 4 0 0 0	0 4 1 3 0 3 4 0 14	3 0 0 3 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0	<ul> <li>b   Isateriap_Mysocacetas_Polyangiaes_Bolyangiales_Bin4ii.g_Din4ii.s_</li> <li>b   Isateriap_Protechacetriac_Commoprotechateriao_Particurelless_Faturellessag_Inderitaenias_</li> <li>b   Isateriap_Actobacteriac_Commoprotechateriao_Particurelless_Faturellessag_Inderitaenias_</li> <li>b   Isateriap_Netochateriac_Commoprotechateriao_Particurelless_Faturellessag_Inderitaenias_</li> <li>b   Isateriap_Netochateriac_Commoprotechateriao_Bolyangiaes_Bin4ii.g_Particurellessag_Inderitaenias_</li> <li>b   Isateriap_Netochateriac_Acid microbiae_Microbacteriao_g</li></ul>
894 895 896 897 898 899 900 901 900 901 903 904 905	1 0 0 0 0 0 4 0	0 1 0 0 0 0 0 0 0 0 3	0 0 1 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0	D D 1 D 0 0 0 0 0 0 0 0	0 0 0 0 4 0 0 0 0	D 4 1 3 0 3 4 0 14 0	3 0 0 3 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b _ lacteriag_ Mysoaccetts_ Polyanglais_BinkitBinkitBinkit</li> <li>b _ lacteriagProtoclacetriac_Gammaporteolacteriag_Physicalitest_BinkitBinkit_BinkitBinkit_Binkit_BinkitBinkitBinkit_Binkit_BinkitB</li></ul>
894 895 896 897 898 899 900 901 901 903 903	1 0 0 0 0 0 0 0 4 0	0 1 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0	0 0 1 0 0 0 0 0 0	0 0 0 4 0 0 0	0 4 1 3 0 3 4 0 14	3 0 0 3 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0	<ul> <li>b   Isateriap_Mysocacetas_Polyangiaes_Bolyangiales_Bin4ii.g_Din4ii.s_</li> <li>b   Isateriap_Protechacetriac_Commoprotechateriao_Particurelless_Faturellessag_Inderitaenias_</li> <li>b   Isateriap_Actobacteriac_Commoprotechateriao_Particurelless_Faturellessag_Inderitaenias_</li> <li>b   Isateriap_Netochateriac_Commoprotechateriao_Particurelless_Faturellessag_Inderitaenias_</li> <li>b   Isateriap_Netochateriac_Commoprotechateriao_Bolyangiaes_Bin4ii.g_Particurellessag_Inderitaenias_</li> <li>b   Isateriap_Netochateriac_Acid microbiae_Microbacteriao_g</li></ul>
894 895 896 897 898 899 900 901 900 901 903 904 905 906	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 3 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0	D D 1 D D 0 0 0 0 0 0 0 0	0 0 0 0 4 0 0 0 0 0	D 4 1 3 0 3 4 0 14 0	3 0 0 3 0 1 0 0 0 0 3		<ul> <li>b   stateriag_Mysotocotts:_Objergias_Polyargiales_BH412_DH415_</li> <li>c   stateriag_Protocolocits:_Cammporteolocitrico_Partnerilles(</li></ul>
894 895 896 897 898 899 900 901 901 902 903 904 905 906 907	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 3 0 3 0 5	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0	D 4 1 3 0 3 4 0 14 0	3 0 0 3 0 1 0 0 0 3 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerisp_Mysococotsz_Oniyangasa_Polyangales(_BHRLS_BHRLS_BHRLS_BHRLS_BHRLS_BHRLS_BHRLS_BHRLS_CARANGPORESALTING_PARCHASE_TABLE PARCHASE_TABLE PA</li></ul>
894 895 896 897 898 899 900 901 901 903 904 905 906 906 907 908	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 3 0 3 0 5	0 0 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0	D 4 1 3 0 3 4 0 14 0	3 0 0 3 0 1 0 0 0 3 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   stateriap_Mysococots_Polyangiae_Polyangiaes_Bin41.s</li></ul>
854 895 897 858 859 900 901 901 903 904 905 906 907 905 906	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 3 0 3 0 5	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 4 1 3 0 3 4 0 14 0	3 0 0 3 0 1 0 0 0 3 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b  sateriap_Mysoaccets_De/regise_Pelyarpiales_BH41s_BH41s_</li> <li>c  sateriap_Protoclasteriac_Commonprotoclasteria_Protocellest_Pation/licess_finderiaess_finderiaess_</li> <li>c  sateriap_Protoclasteriac_Commonprotoclasteria_Pation/licessess_finderiaes_finderiaess_finder</li></ul>
854 895 897 888 899 900 901 903 904 905 906 907 906 907 908 909 910	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 3 0 5 0 0 4	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 1 D D 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 3 0 3 4 0 14 0 0 0 3 3 0 0	3 0 0 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerish,Protechacettis,Gammpertechattish,Partervilleter,Tatkur vilcesa,Inderitsenta,</li> <li>b. Jackerish,Protechacettish,Gammpertechattish,Partervilleter,AUCASS,</li></ul>
884 895 897 868 869 900 901 903 903 904 905 905 905 905 905 905 909 910 911	1 0 0 0 0 4 0 0 0 0 1 0 0 1 0 4	0 1 0 0 0 0 0 0 0 0 0 0 0 3 0 0 3 0 0 4 0 0 4 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 1 D D 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 3 0 3 4 0 14 0 0 0 3 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 3 0 1 0 0 0 0 3 0 0 4 2 0 0		<ul> <li>b. Jackeria,Poteskacetric,Sammpereisbattrita,Potestellet,Dirita,</li></ul>
884 895 896 897 888 889 900 901 900 901 904 905 906 905 906 905 906 909 910 911 911	1 3 0 0 0 0 4 0 0 0 0 0 0 0 0 0 0 1 0 0 1 1 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 3 0 3 4 0 0 3 4 0 0 3 3 0 0 3 3 0 0 7 7	3 0 0 3 0 1 0 0 0 0 3 0 0 3 0 4 2 0 0 2		<ul> <li>b. Jasteria, _/retealactrika, _ forjangalas_forjangalas_f_BHALSEMHALS</li> <li>b. Jasteria, _/retealactrika,anterpetrebalatrikaantervellakasantervellakasantervellakasantervellakasantervellakasantervellakasantervellakasantervellakasantervellakasantervellakasAntervellakasAntervellakasAntervellakasantervellakasantervellakasAntervellakasAntervellakasAntervellakasantervellakasantervellakasAntervellakas</li></ul>
894 895 896 897 888 899 900 900 900 900 900 905 906 906 909 910 911 912 913	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 3 0 3 4 0 0 3 4 0 0 3 3 0 0 3 3 0 0 7 7	3 0 0 3 0 0 1 0 0 0 0 3 0 0 3 0 4 2 0 0 2 3		<ul> <li>b. Jasteria,hostoscotis,hosingsiesBojangsiesf_Birki,gDirki,s</li> <li>b. Jasteria,ghostoscotis,AndesterincoParteurilleisfPatieurilleisegInderilsenta</li> <li>b. Jasteria,ghostoscotis,AndesterincoParteurilleisfPatieurilleisegInderilsenta</li> <li>b. Jasteria,ghostoscotisc,AndesterincoBakubaleriakegPatieurilleisegmit175</li> <li>b. Jasteriaghostoscotisc,AndesterincoBakubaleriakegBirkitagmit175</li> <li>b. Jasteriaghostoscotisc,AndesterincoBakubaleriakegBirkitagmit175</li> <li>b. Jasteriaghostoscotisc,Andesterindo,BakubaleriakegBirkitagmit175</li> <li>b. JasteriagbakutenidetzBakteriada,Spingobateriaker,Stitab.zumaine,mangH51142_maine, groups</li> <li>b. Jasteriagbakteriadetz,Andesteriada,Spingobateriaker,Stitab.zumaine,mangH51142_maine, groups</li> <li>b. Jasteriagbakteriadetz,Andesteriada,Subabaterialer,Savabateriaceae</li> <li>b. Jasteriaghostoscotisco,AlphaprotosbateriagAssitubaterialer,Savabateriaceae</li> <li>b. Jasteriaghostoscotisco,AlphaprotosbateriagAssitubaterialer,Savabateriaceae</li> <li>b. Jasteriaghostoscotisco,AlphaprotosbateriagAssitubaterialer,Savabateriaceae</li> <li>b. Jasteriaghostoscotisco,AlphaprotosbateriagAssitubaterialer,Savabateriaceae</li> <li>b. JasteriagKeindoscotisco,AlphaprotosbateriagAssitubaterialer,Savabateriaceae</li> <li>b. JasteriagKeindoscotisco,AlphaprotosbateriagNativativativaceaegSove996_maine_groups</li></ul>
894 895 896 897 888 899 900 901 900 900 900 900 900 905 905 905 905 909 911 912 913 913	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 3 0 3 4 0 0 3 4 0 0 3 3 0 0 3 3 0 0 7 7	3 0 0 3 0 0 1 0 0 0 0 0 3 0 0 3 0 0 2 3 2 2 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerish,Protechacterish,ParkangkestBritist, Protechalterish, Protechacterish, Protechacterish, Protechalterish, Protechalterish,Protech</li></ul>
894 895 896 897 888 899 900 900 900 900 900 900 900 900	1 3 0 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 1 3 4 0 3 4 0 0 3 3 0 0 7 0 7 0 1 0	3 0 0 3 0 0 1 0 0 0 0 3 0 0 4 2 0 0 2 3 2 0		<ul> <li>b. Jackeria,Protokacetar,PolyangakesBirkitDirkit</li> <li>c. Jackeria,Protokacetar,Gammportokaturia,PartervilleketPathor MicessaInderitarna,</li> <li>d. Lackeria,Protokacetaria,Andrometokaturia,Andrometokaturia,AndrometokacetarNitroopia</li> <li>c. Lackeria,Protokacetaria,andrometokaturia,AndrometokacetarNitroopia</li> <li>c. Lackeria,Andrometokaturia,Andrometokacetaria,Nitroopia</li> <li>d. Lackeria,Andrometokaturia,Andrometokacetaria,Nitroopia</li> <li>d. Lackeria,Andrometokaturia,Andrometokacetaria,</li></ul>
894 895 896 897 809 900 900 900 900 900 900 900 904 905 906 900 911 912 911 912 915 916	1 3 0 0 0 0 4 0 0 0 0 0 0 0 1 1 0 0 1 1 0 0 1 1 1 0 0 0 1 1 0	0 1 0 0 0 0 0 0 3 0 0 3 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 1 3 0 3 4 0 0 3 4 0 0 3 3 0 7 0 3 3 0 0 7 0 2 2 2	3 0 0 3 0 1 0 0 0 3 0 4 2 0 0 2 3 2 0 0 2 3 2 0 0		<ul> <li>b. Jackeria,hotocaccts.chotyangalesBirkit.giniti.s</li> <li>c. Jackeria,hotocaccts.cGommporteebacteria.ghotochelHotocateria.ginderikaenta.g.</li> <li>d. Jackeria,hotochecteria.ghotochecteria.ghotochelHotocateria.giniti.s</li> <li>d. Jackeria,hotochecteria.ghotochecteria.ghotochecteria.ghotochecteria.giniti.s</li> <li>d. Jackeria,hotochecteria.ghotochec</li></ul>
894 895 896 897 898 900 901 903 905 905 905 905 905 905 905 905 905 905	1 3 0 0 0 0 0 0 0 0 0 0 1 0 4 1 0 0 1 0 1 3	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D	0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 1 3 0 3 4 0 3 4 0 0 3 3 0 0 7 0 1 2 3 0 2 3	3 0 0 3 0 1 0 0 3 0 4 2 0 0 2 3 2 0 0 0 2 3 2 0 0 0 0 2 3 0 0 0 0		<ul> <li>b. Jackeria,ketenia,keteniator,keteniato</li></ul>
884 885 886 888 889 900 901 902 903 904 904 905 905 906 901 911 912 913 913 915 916 918	1 3 0 0 0 0 0 0 0 0 0 0 1 0 4 1 0 0 1 0 1 3	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 1 3 0 3 4 0 3 4 0 0 3 3 0 0 7 0 1 2 3 0 2 3	3 0 3 0 1 0 0 1 0 0 3 0 0 3 0 0 2 3 2 0 0 0 2 3 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerisa, Protokacetisz, Goirnegotes/Letitaisa, Parkerilleki, Britki, B. Br</li></ul>
894 895 896 907 900 900 900 900 900 900 900 904 905 906 900 910 911 912 913 914 915 915 916	1 3 0 0 0 0 0 0 0 0 0 0 1 0 4 1 0 0 1 0 1 3	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 1 3 0 3 4 0 3 4 0 0 3 3 0 0 7 0 1 2 3 0 2 3	3 0 3 0 1 0 0 1 0 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jackeria,Protokaceta,Animprotokaceta,Marki,</li></ul>
884 895 896 907 900 900 900 900 900 900 910 910 910 910	1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 3 0 3 4 0 34 0 0 3 3 0 0 7 0 1 0 2 3 4 5 0 0	3 0 0 3 0 1 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>bbiderbybyoaccestsbyingbabyingbedBHBLBHBLS</pre>
884 865 867 868 868 860 900 900 900 900 900 900 911 912 913 915 916 915 915 915 915 915 915 915 915 915 915	1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 1 3 4 0 3 4 0 0 0 3 0 0 7 0 1 0 2 3 4 5 0 0 1 1 0 3 4 0 0 1 1 1 0 3 4 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b  _blocksbMysolocotissMysolocotissMysolocotissMACS#EMACS#ESaturationsasInderkanas b  _blocksbredeblockstrissAddblockstrissMACS#EMACS#EAddCS#EMACS#E b  _blocksbredeblockstrissAddblockstrissMACS#EMACS#E b  _blocksbredeblockstristsMacMacS#E_MACS#E b  _blocksbdtorbackstristsMacMacS#E_MACS#E b  _blocksbdtorbackstristsMacMacS#E_MACS#E b  _blocksbdtorbackstristsMacMacS#E_MACS#E b  _blocksbdtorbackstristsMacMacS#E_MACS#E b  _blocksbdtorbackstristsMacMacS#E_MACS#E b  _blocksbdtorbackstristsMacMacS#E_MACS#E b  _blocksbdtorbackstristsMacMacS#E_MACS#E b  _blocksbblockstristsBlockstristsMacMacS#E_MACS#E b  _blocksbdtorbackstristsMacMacMacS#E_MACS#E_MACS#E b  _blocksbAddresstristsMacMatS#E_MACS</pre>
884 865 867 868 869 900 901 903 900 903 904 905 900 911 913 913 913 914 915 915 916 917 913 915 916 917 913 915 916 917 915 916 917 915 916 917 917 917 917 917 917 917 917 917 917	1 3 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 3 0 3 4 0 34 0 0 3 3 0 0 7 0 1 0 2 3 4 5 0 0	3 0 0 3 0 1 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ bateria/vectoacetar/overgaaPolyargales/_BHALSDAHALS</pre>
884 865 867 868 869 900 901 904 905 900 900 900 900 910 911 912 913 914 915 916 917 918 916 917 918 916 917 918 910 917 918 910 917 918 918 917 918 918 918 919 918 919 919 919 919 919	1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 1 1 0 3 4 0 14 0 0 0 3 3 0 0 7 0 1 0 2 3 4 5 0 0 0 1 0 1	3 0 0 0 3 0 1 0 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 4 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b _ bsterisp_ brokeskets:_ polyangukebinkisinterventionsinterventionsintervisess</pre>
884 895 896 907 900 900 900 900 900 900 910 910 910 910	1 3 0 0 0 0 4 0 0 0 4 0 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 1 2 0 3 4 0 4 0 0 3 3 0 0 7 0 1 0 2 3 4 5 0 0 0 1 0 1 3	3 0 0 0 3 0 0 1 0 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 0 4 0 1 0		<pre>b _bdotba_/byookcottsboyongote_bdotbaisproteoriesintervelues_intervelues_interveluesintervelue</pre>
884 885 887 888 888 900 900 900 900 900 900 900 911 910 911 911	1 3 0 0 0 0 4 0 0 0 4 0 0 0 1 0 0 1 3 0 0 0 0 4 0 0 0 5 0 0 0 1 3 0 0 0 0 5 0 0 0 0 5 0 0 0 5 0 0 0 0 5 0 0 0 0 5 0 0 0 0 0 5 0		0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 1 3 0 3 4 0 4 0 0 0 3 3 0 0 7 0 1 0 2 3 4 5 0 0 1 1 0 1 3 2 0 1 0 1 3 0 0 1 3 0 0 7 0 1 0 2 3 4 5 0 0 1 1 0 1 3 3 0 0 1 1 0 1 3 3 0 0 1 1 0 1 1 0 1 3 3 0 0 1 1	3 0 0 3 0 1 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 4 0 1 0 0		<pre>b _ bateria/vectoacetasfo/argubsfo/argubsBitAisEntits</pre> c _ bateria/c deductoriasc AndobestraissMACAFEMACAFEAntocetassreferiessassContentiessassContentiessassContentiessassContentiessassContentiessassContentiessassContentiessassContentiessassContentiessassContentiessassContentiessassContentiessassContentiessassassassassassassassassassassassassa
884 865 867 868 869 900 901 903 903 903 903 910 910 910 911 913 913 913 913 913 913 913 914 915 916 817 813 915 916 817 813 915 916 812 915 916 917 917 917 917 917 917 917 917 917 917	1 3 0 0 0 0 4 0 0 0 4 0 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 1 2 0 3 4 0 4 0 0 3 3 0 0 7 0 1 0 2 3 4 5 0 0 0 1 0 1 3	3 0 0 0 3 0 0 1 0 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 0 4 0 1 0		<pre>b _ buderba_/wyootcotta_/byingba_/byingba/_byingba/_binktintertion_/activalitation_/act</pre>
884 865 867 868 869 900 901 904 905 900 900 900 900 910 910 911 912 913 914 915 916 917 918 916 917 918 910 910 910 911 912 913 914 915 916 917 917 916 917 917 916 917 917 917 917 917 917 917 917 917 917	1 3 0 0 0 0 4 0 0 0 4 0 0 0 1 0 0 1 3 0 0 0 0 4 0 0 0 5 0 0 0 1 3 0 0 0 0 5 0 0 0 0 5 0 0 0 5 0 0 0 0 5 0 0 0 0 5 0 0 0 0 0 5 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 3 0 3 4 0 3 0 0 3 3 0 0 7 0 1 0 2 3 4 5 0 0 0 1 0 1 3 0 0 1	3 0 0 0 3 0 0 1 0 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 0 4 0 1 0 0 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b _ bsterios_ / vocacets_ / vorangenetes/bsterios_ / variane/bsterios_ / variane/</pre>
884 865 867 868 869 900 901 903 903 903 903 910 910 910 911 913 913 913 913 913 913 913 914 915 916 817 813 915 916 817 813 915 916 812 915 916 917 917 917 917 917 917 917 917 917 917	1 3 0 0 0 0 4 0 0 0 4 0 0 0 1 0 0 1 3 0 0 0 0 4 0 0 0 5 0 0 0 1 3 0 0 0 0 5 0 0 0 0 5 0 0 0 5 0 0 0 0 5 0 0 0 0 5 0 0 0 0 0 5 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 1 1 1 3 0 3 4 0 4 0 0 0 3 3 0 0 7 0 1 0 2 3 4 5 0 0 1 1 0 1 3 2 0 1 0 1 3 0 0 1 3 0 0 7 0 1 0 2 3 4 5 0 0 1 1 0 1 3 3 0 0 1 1 0 1 3 3 0 0 1 1 0 1 1 0 1 3 3 0 0 1 1	3 0 0 3 0 1 0 0 3 0 4 2 0 0 2 3 2 0 0 0 0 0 0 4 0 1 0 0		<pre>b _ buderba_/wyootcotta_/byingba_/byingba/_byingba/_binktintertion_/activalitation_/act</pre>

932	6	0	3	0	ă.	0	0	4	0	0	1 k_Bacterixp_Verucomicrobiotax_Verucomicrobiota;o_Othtoniobacterales;f_Chthoniobacteraceaeg_Chthoniobactera_
933	0	0	0	0	0	z	1	D	3	0	3 k_batteriap_teriadonicionada,_teriadonicionecto_cniconada de alega_cantonicionecenación y
934	o	o	3	0	o	D	0	D	0	o	0 k_Bacteria
935	0	0	4	0	0	0	0	0	0	0	0 k_Batteria;p_Sva0485;c_Sva0485;d_Sva0485;f_Sva0485;s
936	0	0	4	0	0	1	0	2	0	0	0 k_Bacteria:p_Proteobacteria:c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae:g_Vibrio
937	0	0	٥	0	0	D	0	6	0	0	0 k_Bacterix;p_Accidobacteriota;x_Blastocatellaço_Blastocatellace;f_Blastocatellaceaeg_;s_
938	0	0	0	0	0	D	0	7	0	0	0 k_Bacterizp_Proteobacterizc_Alphaproteobacteriz;p_Rhizobiales;f_Bejerinckizeeae;g_Bosea
939 940	0	0	0	0	0	0	0	3	0 3	0	0 k_Bateriap_Actinobateriotac_Actinobateriap_Micromenosporalesf_Micromenosporacearg_Phytomenosporas_Phytomenospora_endophytica 0 k_Bateriap_Firmicutesc_Clostridap_Orcillospiralesf_Reminococcacearg_s_
941	0	0	0	0	1	0	0	2	0	0	
942	o	3	o	0	0	D	0	D	0	0	0 k_Bacteria
943	12	7	o	0	o	2	2	1	0	0	0 k_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Burkholderiales:f_Dkalobacteraceae;g_Massilia:s
944	2	0	0	0	1	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;p_Tistrellale;;f_Gerninicoccaceae;g_Gerninicoccu;;s
945	0	0	0	2	1	0	6	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroida;o_Bacteroidales;f_Munbaculacese;g_Munbaculacese;s
946	0	2	0	1	0	0	0	0	0	0	0 k_Bacteria;p_Firmicute;s_Clostridu.p_Ouilloopirales;f_Ruminocoscareae;g_Caproiciproducens;s_
947 948	0 5	0	0	0	0	o o	0	8	0	o o	0 k_Batteria;p_Actinobacteriotac_Acidimicrobia;o_IMCC26256;f_IMCC26256;f_IMCC26256;f_
949	0	0	0	0	0	1	0	0	3	0	0 k_Bateriap_Cyanobacteriaz_Cyanobacteriazo_Chioroplast_Chioroplasts_Chioroplasts_Myrmedia_traellensis 0 k_Bateriap_Firmicutesc_Clostridipo_Oticilospi ness/_Rvminoscoccarceste_x_
950	0	4	0	0	0	0	0	0	0	0	0 Unknown
951	0	4	0	0	0	0	0	0	0	0	0 k_Bacteriixp_Bacteroiidota;c_Bacteroiidaies,d_Porphyromonadaceae:g_Porphyromonas;s_Porphyromonas_endodontalis
952	0	0	o	0	o	D	0	3	0	o	0 k_Bacteria;p_Gemmatimonadota;c_Gemmatimonadete;;o_Gemmatimonadale;f_Gemmatimonadaceae;g_
953	13	0	20	0	5	6	0	4	12	0	1 k_Bacteria;p_Bacteroidota;c_Bacteroidia.o_Chitinophagales;f_Chitinophagaceae;g_Dinghulbacter;s
954	3	0	0	0	2	0	0	0	0	0	0 k_Bacteria:p_SAR324_clade(Marine_group_B);c_SAR324_clade(Marine_group_B);o_SAR324_clade(Marine_group_B);f_SAR324_clade(Marine_group_B);z_SAR324_clade(Marine_group_B);x_bacterium,
955	3	0	0	0	0	1	0	0	0	0	0 k_Bacteriap_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Dinghuibacter;a_
956	2	0	2	0	0	B	0	10	8	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;p_Microaccales;f_Microbacteriaces;e_Candidate_Planitoluna;c_ 0 k_Bacteria;p_Germatimonadota;c_Germatimonadela;s_Germatimonadales;f_Germatimonadacea;e_Germatimonas
958	3	0	0	0	0	0	0	0	0	0	
959	1	2	0	0	0	0	0	0	3	0	0 k_Bacteriap_Firmicutesc_Clostridia;o_Lachnospiralestf_Lachnospiraecae;z_s_
960	2	1	٥	2	3	2	1	0	8	0	1 k_Bacteria;p_Bacternidota;c_Bacternida;o_Bacternida;es/_Murbaculaceaeg_Murbaculaceae;s
961	0	0	٥	0	2	1	0	D	0	0	$0 \ k\_Bacteria;p\_Actinobacteriota;c\_Coriobacteria;o\_Coriobacteriales;f\_Eggerthellaceae$
962	3	0	0	0	1	0	0	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Cytophagale;f_Spirosomaceae;g_Huanghella;s_Huanghella, arctica
963	4	0	1	0	1	0	0	2	3	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagacea;g_Dinghuibacter;s
964	0	0	1	0	0	1	0	2	1	0	0 k_Bacterizp_Proteobacterizc_Gammaproteobacterizp_Bunkholderizles/_Mitrosorronadaceseg_MND1;s
965 966	5	0 76	1	0 8	1	2	0	1	6 0	1	3 k_Bacteriago_Protectacteriag_Aphaprofestatoriag_Acetatacteriag_Acetatacteriage_Enceptional and a second as
967	0	0	0	0	0	3	0	0	0	0	0 k_Bacteria;p_Chlorofloxic_Anaerolineae;a_Caldilinea(s;f_Caldilineae;ae;g_;s_
968	3	0	0	0	1	0	0	0	0	0	0 k_Bacteriap_Firmicutess_Clostridapp_Lachnospiraless_f_Lachnospiraceaeg_Roseburiap_
969	0	0	0	0	0	0	0	4	0	0	0 k_Bacteria;p_Myxxxxxxxxia;c_Polyangia;co_Polyangialex;t_Bhii41;x_Bhii41;x_
970	o	0	O	0	D	D	0	3	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia.o_Chitinophagales;f_Chitinophagaceae;g_Chitinophaga_s_Chitinophaga_japonensis
971	0	0	0	0	0	0	0		0	0	0.1 Buttering Arielekusteriatur Veienenkustering Veienenkusteriadur <sup>2</sup> or a
971 972	0	0	0	0 0	0	0	0	3 2	0	0	0 k_Bacterixp_Acidabacteriotax_Voinamibacterixo_Voinamibacteralosf_xz_n_ 0 k_Bacterixp_Verucomicrobitac_Verucomicrobitaco_Pedospharealesf_Pedosphareaceaeg_st_
											0 k_Baterinka_Acidabaterotax_Verhamibateraka_Verhamibateraka;f_;g_m_ 8 k_Batering_Vernutomitotabitac_Vernutomitotabitac_Bedoghamaka;f_Hedoghamitotaeg_is_ 0 k_Baterinka_Germatimotodotac_Germatimonodeka:_Germatimonodoka;f_Germatimonodocea;g_Germatimonotacs_
972	o	0	٥	0	0	D	0		1	o	0 k_Batterlap_Verrucomicrobletas_Verrucomicroblae.o_Pedosphaerales.f_Pedosphaeraceaes_js_
972 973	0 0	0 0	0 0	0 0	0 0	D	0 0	2 5	1 0	o o	0 k_listerisp_Verucomicrobiotac_Verucomicrobiotac_Pedosphareakest_Pedosphareaceaeg_si_ 0 k_listerisp_Germatimonadotac_Germatimonadeteso_Germatimonadolesf_Germatimonaticeaeg_Germatimonasis_
972 973 974 975 976	0 0 6 0 3	0 0 2 3 0	0 0 12 0 1	0 0 0 0	0 0 32 0 4	0 0 26 0 3	0 0 2 0 0	2 5	1 0 35 0 2	0 0 0 0	0 k_bsterisp_Verucomkrobiotac_Verucomkrobiotac_Fedosphareales(_Fedospharealesg_si_ 0 k_bsterisp_Germatimonadotac_Germatimonadesc_germatimonadies(_Germatimonadaceaeg_Germatimonada_ 2 k_Bateriap_Firmicutesc_Clostifiap_Oxelloppinies_Oxelloppiniceaeg_Coldentibactors_ 0 k_Bateriap_Firmicutesc_Negativicateso_Vellondiales-Scientromadaksf_Vellonellaceseg_Vellonellas_Vellonellas_0. 0 k_Bateria
972 973 974 975 976 977	0 6 0 3 0	0 0 2 3 0	0 0 12 0 1 0	0 0 0 0 0	0 32 0 4	D 26 0 3 0	0 2 0 0	2 5 8 0 1 4	1 0 35 0 2 0	0 0 0 0	0 k_bisterisp_Verrusomicrobiotac_Verrusomicrobiotac_Tedosphareaket_Pedosphareaketg_si_ 0 k_bisterisp_Germatimocsdotac_Germatimocsdotac_Germatimocsdotac_g_Germatimocsas_ 2 k_bisterisp_Firmicitesc_Cobindip.g_Oxellexpinesct_Coblempinesct_Cobletorbiotory_ 0 k_bisterisp_Protectacterisp_Firmicitesc_Negativators_Vellondiacsdotacters_Vellondiac_Vellondiac_Vellondiacs_ 0 k_bisterisp_Protectacterisp_Approtectatorsf_z_s_
972 973 974 975 976 977 978	0 6 0 3 0	0 0 2 3 0 0 3	0 12 1 1 0 1 0	0 0 0 0 0 0	0 0 32 0 4 0	D D 26 0 3 D 0	0 2 0 0 0	2 5 8 0 1	1 0 35 0 2 0 0	0 0 0 0 0	0 k_listerisp_Verucomicrobiotac_Verucomicrobiotac_Pedosphareaket_Pedosphareaketg_si_ 0 k_listerisp_Germatimonadotac_Germatimonadeteso_Germatimonadotest_Germatimonaticase_Germatimonatics_ 2 k_listerisp_Firmicatesc_Costriduo_Oxelleopintest_Oxelleopintesc_Coldensitivationatics= 0 k_listerisp_Firmicatesc_Negativiantes_Velloordiaets/Sectomonadiets/_Velloordiaccesg_Velloordias_Velloordia_p. 0 k_listerisp_Firmicatesc_Negativianteso_Velloordiaets/Sectomonadiets/_Velloordiaccesg_Velloordias_Velloordia_p. 0 k_listerisp_Fireideaterisp_firm_s
972 973 974 975 976 977	0 6 0 3 0 0	0 2 3 0 3 3 0	0 12 0 1 0 0 1	0 0 0 0 0 0 0	0 32 0 4 0 0	D D 26 0 3 D 0 3 3	0 2 0 0 0 0	2 5 8 0 1 4	1 0 35 0 2 0 0 1	0 0 0 0 0 0	0 k_bisteriap_Verrusomicrobiotac_Verrusomicrobiotac_Generationandalesf_Generationandaceaeg_sc_ 0 k_bisteriap_Generationandetias_Generationandetias_Generationandalesf_Generationandaceaeg_Generationands_ 2 k_barteriap_Firmicatesc_Verbindup_Oxillogianlesf_Oxillogianlesf_Oxillogianlescesg_Verbindetias_Verbindetias_Verbindetias_0 0 k_barteriap_Firmicatesc_Verbindup_oxillogianlesf_oxillogianlesf_Verbindeticesg_Verbindetias_Verbindetias_Verbindetias_0 0 k_barteriap_Firmicatesc_Apphaproteobatteriag_f_g_s_ 0 k_barteriap_Fortestaateriag_Apphaproteobatteriag_f_g_s_ 0 k_barteriap_Generationandetias_Generationandalesf_Generationandaceaeg_Generationanas_
972 973 974 975 976 977 978	0 6 0 3 0	0 0 2 3 0 0 3	0 12 1 1 0 1 0	0 0 0 0 0 0	0 0 32 0 4 0	D D 26 0 3 D 0	0 2 0 0 0	2 5 8 0 1 4	1 0 35 0 2 0 0	0 0 0 0 0	0 k_listerisp_Verucomicrobiotac_Verucomicrobiotac_Pedosphareaket_Pedosphareaketg_si_ 0 k_listerisp_Germatimonadotac_Germatimonadeteso_Germatimonadotest_Germatimonaticase_Germatimonatics_ 2 k_listerisp_Firmicatesc_Costriduo_Oxelleopintest_Oxelleopintesc_Coldensitivationatics= 0 k_listerisp_Firmicatesc_Negativiantes_Velloordiaets/Sectomonadiets/_Velloordiaccesg_Velloordias_Velloordia_p. 0 k_listerisp_Firmicatesc_Negativianteso_Velloordiaets/Sectomonadiets/_Velloordiaccesg_Velloordias_Velloordia_p. 0 k_listerisp_Fireideaterisp_firm_s
972 973 974 975 976 977 978 979 980	0 6 0 3 0 0 0	0 2 3 0 3 0 3 0 0	0 0 12 0 1 0 1 0	0 0 0 0 0 0 0 0	0 32 0 4 0 0 0 1	D 26 0 3 0 3 0 3 0	0 2 0 0 0 0 0	2 5 0 1 4 0 1 0	1 0 35 0 2 0 0 1 3	0 0 0 0 0 0 0	0 & _itsterizeVerucomicrobitezVerucomicrobitesSemmatinonadelesGermatinonadoceaeSe
972 973 974 975 976 977 978 979 980 981	0 6 0 8 0 0 0 0	0 2 3 0 3 0 3 0 0 7	0 12 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 1	0 32 0 4 0 0 1	D D 26 0 3 D 0 3 0 3 0 0	0 2 0 0 0 0 0 0	2 5 0 1 4 0 1 0	1 35 0 2 0 1 3 0	0 0 0 0 0 0 0 0	0 k_bisterisVernzomicrobiotaVernzomicrobia.es_Deologiparabels(_Pedospharabels
972 973 974 975 976 977 978 979 960 961 962	0 6 0 0 0 0 0 0	0 2 3 0 3 0 3 0 7 0	0 12 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 1	0 32 0 4 0 0 1 1 0	D D 26 0 3 D 0 3 D 0 3 0 2	0 2 0 0 0 0 0 0 0 0 0	2 5 0 1 4 0 1 0 0 2	1 35 0 2 0 1 3 0 3	0 0 0 0 0 0 0 0 0	0 k_listeriusVerrusomicrobiotac_Verrusomicrobiae.0_Pedosphareades;Pedosphareadeseg_is_ 0 k_listeriusEmmotimosadotac_Germatimonadeles.0_Germatimonadeles/_Germatimonadaceae_Germatimonads. 2 k_listeriusEmmotimosadotac_Germatimonadeles.0_ColleopineexesCollectebectors 0 k_listerius_Termicutes:_Ntrativioutes.0_Vellondiles.5cbernomadales.f_Vellondiles.Vellondiles_Vellondile.go. 0 k_listerius_Termicutes:_Attrativioutes.0_Vellondiles.5cbernomadales.f_Germatimonadaceae_Germatimonage. 0 k_listeriusPretexbacterius_Germatimonadeles.g_Germatimonadales.f_Germatimonage.commatimonage. 0 k_listerius_Germatimonadots_Germatimonadeles.g_Germatimonadales.f_Germatimonage.commatimonage. 0 k_listerius_Germatimonadots_Germatimonadeles.g_Germatimonadales.f_Germatimonage.commatimonage. 0 k_listerius_Methodotarenze.org.Oligofinales.g_Digofinales.g_Oligofinaes.g_Nendobacterum.
972 973 974 975 976 977 978 979 960 961 962	0 6 0 0 0 0 0 0	0 2 3 0 3 0 0 7 0 0 0 0	0 12 0 1 0 1 0 1 3 0 0	0 0 0 0 0 0 0 0 1 0 0 4 0	0 32 0 4 0 0 1 0 0 0 0 0 0 0	D D 26 0 3 D 0 3 0 3 0 2 1 0	0 2 0 0 0 0 0 0 0 0 0	2 5 0 1 4 0 1 0 0 2	1 0 35 0 2 0 1 3 0 3 3	0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. laderia,Veracemicrobia.cVeracemicrobia.e.oPedespharabet;Pedespharabet</li></ul>
972 973 974 975 976 977 978 979 960 961 962	0 6 0 0 0 0 0 0	0 2 3 0 3 0 7 0 7 0 0 0	0 12 0 1 0 1 0 1 0 1 3 0	0 0 0 0 0 0 0 0 1 0 0 4	0 32 0 4 0 0 1 0 0 0 0 0	D 26 0 3 0 3 0 3 0 2 1 2	0 2 0 0 0 0 0 0 0 0 0 0 1	2 5 0 1 4 0 1 0 0 2	1 0 35 0 2 0 1 3 3 3 3 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Istorius,iveruzomirototetac_veruzomicotetace,ivedosphareaketivedosphareaketaceis</li></ul>
972 974 975 976 977 978 979 960 961 962 983 964 965 966 966 967	0 6 0 0 0 0 0 0	0 2 3 0 3 0 7 0 7 0 0 0 0 0 0 0 1 4	0 12 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 1 0 0 0 4 0 0 0 4 0 0 0	0 32 0 4 0 0 1 0 0 0 0 0 0 0	D D 26 0 3 D 0 3 0 3 0 2 1 0	0 2 0 0 0 0 0 0 0 0 0 0 1 0 1 0	2 5 0 1 4 0 1 0 0 2	1 0 35 0 2 0 1 3 0 3 3 0 2 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>0 1_bitderisp_VerucomicrobitesVerucomicrobitesPedosphareadest</pre>
972 973 974 975 976 977 978 979 960 961 962	0 6 0 0 0 0 0 0	0 2 3 0 3 0 7 0 7 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 1 0 0 0 0 0 0 0 0 0 0	D D 26 0 3 D 0 3 0 3 0 2 1 0	0 2 0 0 0 0 0 0 0 0 0 0 1	2 5 0 1 4 0 1 0 0 2	1 0 35 0 2 0 1 3 3 3 3 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>0 1_biterityVerucomicrobitesVerucomicrobitesSedosphareaket_Pedosphareaketg_si</pre>
972 974 975 976 977 978 979 980 981 982 984 985 986 986 985 986 987	0 6 0 0 0 0 0 0	0 2 3 0 3 0 7 0 7 0 0 0 0 0 0 0 1 4	0 12 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 1 0 0 0 4 0 0 0 4 0 0 0	0 32 0 4 0 0 1 0 0 0 0 0 0 0 0	0 26 0 3 0 3 0 2 1 0 1 0 1 0 0 1 0 0	0 2 0 0 0 0 0 0 0 0 1 0 1 0 1 0	2 5 0 1 4 0 1 0 0 2	1 0 35 0 2 0 1 3 0 3 3 0 2 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. laderia,Wenzonicolatez,Venzonicolates,Pedospharaket;Pedospharaketzg_i</li></ul>
972 974 975 976 977 978 979 980 981 982 984 985 986 986 985 986 987	0 6 0 0 0 0 0 3 0 2 1 0 2 5	0 2 3 0 3 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 1 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 3 0 2 1 0 1 0 1 0 0 1 0 0	0 2 0 0 0 0 0 0 0 0 1 0 1 0 1 0	2 5 0 1 4 0 1 0 0 2	1 0 35 0 2 0 1 3 0 3 3 0 2 1 0		<pre>0 1_biterityVerucomicrobitesVerucomicrobitesSedosphareaket_Pedosphareaketg_si</pre>
972 974 975 976 977 978 979 980 981 982 983 984 985 986 985 986 989 969	0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 3 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 0 1 0 0 0 0 0 0 0 0 0 0 2 0 2 0 2 0	0 26 0 3 0 3 0 2 1 0 1 0 1 0 4 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0	2 5 0 1 4 0 1 0 0 2	1 0 35 0 2 0 1 3 0 3 0 2 1 0 2 0 0 2 0 2 0 2 0 2 0 2 0 2 0 0 2 0 2 0 2 0 2 0 2 0 0 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Istorius</li></ul>
972 974 975 976 977 983 983 984 985 985 985 986 985 986 985 986 985 989 990	0 6 7 0 0 0 0 0 0 0 0 0 0 1 0 2 5 0 0	0 2 3 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 12 0 1 0 1 0 1 0 0 0 0 2 0 2 0 4	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 26 0 0 0 0 0 0 0 0 2 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0 1 0	0 2 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0	2 5 8 0 1 4 0 1 0 0 0 0 0 0 0 0 0 0 2 3 5 1	1 0 35 0 2 0 1 3 0 3 3 0 2 1 0 0 2 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 2 0 0 2 0 0 0 1 3 5 0 0 1 5 0 0 0 0 1 5 0 0 0 0 0 0 0 0 0		<pre>b lstdriks_Verucomicrobites_Verucomicrobites_Pelosphareadet_Pelosphareadetesi b lstdriksCermatimonadetsCermatimonadetes_Cermatimonatetes_Cermatimonatetes_Cermatimonadetes_Cermatimo</pre>
972 973 976 976 977 978 979 980 983 984 983 984 989 980 980 991 993 994	0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 3 0 3 0 7 0 0 0 0 0 0 0 1 0 0 1 0 0 0	0 12 0 1 0 1 0 1 0 0 0 0 0 0 0 0 2 0 0 4 2 0 0 4 2 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 0 0 0 0 0 0 2 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 1 0 0 1 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0	0 2 0 0 0 0 0 0 0 1 0 0 1 0 0 0 1 0 0 0 0	2 5 8 0 1 4 0 1 0 0 0 0 0 0 0 0 0 0 2 3 5 1	1 0 35 0 2 0 1 3 0 3 3 0 2 1 0 0 2 0 0 1 0 0 2 0 0 1 0 0 2 0 0 1 3 3 0 2 0 0 1 3 3 0 0 2 0 0 1 5 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0		<pre>b laderiaverucomicrobiacs_CerrotimonodessCeleophareadestideophareadesti</pre>
972 973 974 975 976 977 978 977 979 980 981 983 984 988 988 988 989 980 991 993 994 985	0 6 7 7 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0 2 3 0 3 0 7 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 0 2 1 0 1 0 0 4 0 1 1 0 0 2 1 0 0 0 4 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 1 0 0 1 0 0 0 1 0 0 0 0	2 5 8 0 1 4 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 2 0 1 3 0 2 0 2 0 0 2 0 1 0 2 0 1 0 2 0 1 0 2 0 1 3 0 2 0 1 3 0 2 0 1 3 0 2 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1		<pre>b lstdriks_Veruomicrobitste_Veruomicrobitste_Debophersheld_Pebophersheld_j: b lstdriks_Cermatinoouddiks_Germatinoouddiks_Germatinoouddiksf_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Cellberks_p. b lstdriks_Firmicess_Cellberhouts_Vellberksess_Germatinooudskess_Vellberks_Vellberks_Vellberks_p. b lstdriks_Firmicess_Germatinooudskess_Cellberksess b _ lstdriksVeruomicrobateks_Cellberksess_Gerberbaseaces b _ lstdriksVeruomicrobateks_Cellberbaseaces b _ lstdriks_Proteouscentino_Germatinooudskesf_Manophaseaces b _ lstdriksNeuromicrobateks_Cellberbaseaces b _ lstdriksNeuromicrobateksAthenophaseaces b _ lstdriksNeuromicrobateksAthenophaseacesNeurophasea b _ lstdriksNeuromicrobateksAthenophaseacesNeurophaseaces b _ lstdriksNeuromicrobateksAthenophaseacesNeurophaseaces b _ lstdriksNeurophaseacesStderwikessStderwikessStderwikess b _ lstdriksNeurophaseaces, _ lstdriksfortanaCellbergers b _ lstdriksNeurophaseaces, _ lstdriksfortanaStderwikessStderwik</pre>
972 973 975 976 977 978 978 978 978 984 983 984 985 980 981 981 985 985	0 6 0 7 0 0 0 0 7 1 0 2 5 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0	0 2 3 0 3 0 7 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 1 0	0 12 0 1 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 0 3 0 1 0 0 1 0 0 4 0 1 1 0 0 0 4 0 0 0 1 1 0 0 0 0	0 2 0 0 0 0 0 0 0 1 0 0 1 0 0 0 1 0 0 0 0	2 5 8 0 1 4 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 2 0 1 3 0 2 0 2 0 0 1 0 2 0 1 0 2 0 1 0 2 0 1 0 2 0 1 3 0 2 0 1 3 0 2 0 1 0 0 1 0 1 0 1 0 0 1 0 1 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b laderia_/emailmostadata_/emailmostadesa_feedopheraket_feedopheraketg_i= c laderia_fermitimostadata_fermitimostadesa_fermitimostadesa_fermitimostatesa_f</pre>
972 973 974 975 976 977 978 977 979 980 981 983 984 988 988 988 989 980 991 993 994 985	0 6 7 7 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0 2 3 0 3 0 7 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 0 2 1 0 1 0 0 1 0 0 4 0 1 1 0 0 0 2 1 0 0 0 0 0 1 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 1 0 0 1 0 0 0 1 0 0 0 0	2 5 8 0 1 4 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 2 0 1 3 0 2 0 2 0 0 2 0 1 0 2 0 1 0 2 0 1 0 2 0 1 3 0 2 0 1 3 0 2 0 1 3 0 2 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1		<pre>b lstdriks_Veruomicrobitste_Veruomicrobitste_Debophersheld_Pebophersheld_j: b lstdriks_Cermatinoouddiks_Germatinoouddiks_Germatinoouddiksf_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Germatinooudskess_Cellberks_p. b lstdriks_Firmicess_Cellberhouts_Vellberksess_Germatinooudskess_Vellberks_Vellberks_Vellberks_p. b lstdriks_Firmicess_Germatinooudskess_Cerbateriess_ b lstdriks_Veruomicrobateriess_Germatinooudskess_Gerbateriess_Germatinooudskess_Germatinooudskess_Gerbateriess b lstdriks_Proteoudskeriess_Germatinooudskess_Gerbateriess_Gerbateriess b lstdriks_Proteoudskeries_Germatinooudskess_Gerbateriess_Gerbateriess b lstdriks_Proteoudskeries_Germatinooudskess_Gerbateriess_Firefoldskeriess b lstdriks_Proteoudskeries_Germatinooudskess_Gerbateriess b lstdriks_Proteoudskeries_Germatinooudskess_Gerbateriess_Firefoldskeriess b lstdriks_Proteoudskeriess_Germatinooudskess_Gerbateriess_Firefoldskeriess b lstdriks_Proteoudskeriess_Gerbateriess_Gerbateriess_Gerbateriess_Gerbateriess b lstdriks_Methoditeriess_Gerbateriess_Gerbateriess_Gerbateriess_Methoditeriess_Methoditeriess b lstdriks_Methoditeries_Gerbateriess_Gerbateriess_Gerbateriess_Methoditeriess b lstdriks_Methoditeries_Gerbateriess_Gerbateriess_Gerbateriess_Firefoldskeriess_Methoditeriess b lstdriks_Gerbateries_Gerbateriess_Gerbateriess_Gerbateriess_Gerbateriess_Gerbateriess_Gerbateriess b lstdriks_Methoditeries_Gerbateriess_Gerbateriess_Gerbateriess_G</pre>
972 973 976 976 977 978 977 978 977 978 977 978 980 881 884 885 885 885 989 900 1812 993 994 993 994 905 977	0 6 0 3 0 0 0 0 3 0 2 1 0 2 5 0 0 0 2 3 3	0 2 3 0 3 0 7 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0	0 12 0 1 0 1 0 0 1 3 0 0 0 0 2 0 4 2 0 0 2 0 4 2 0 0 1 0 0 1 0 0 2 0 1 0 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 0 2 1 0 2 1 0 0 0 2 1 0 0 0 1 2 0 0 0 1 0 0 0 0	0 2 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0	2 5 8 0 1 4 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 1 3 0 1 0 2 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b laderiawernomicrobitatvernomicrobitatfedopharabetyfedopharabety c lateriafermitinosidatfermitinosidatfermitinosidatfermitinosidat_afermitinosit_a 2 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosidat_afermitinosidat_afermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_afermitinosidat_afermitinosit_afermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_afermitinosidat_afermitinosit_afermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosidat_afermitinosit_afermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosidat_a_fermitinosit_afermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosidat_a_fermitinosit_afermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosidat_a_fermitinosit_afermitinosit_a 4 l_ateriafereiosit_ateria_ 4 l_ateriafereiosit_fermitinosidat_a_fermitinosidat_a_fermitinosit_a 4 l_ateriafereiosit_fermitinosidat_a_fermitinosidat_a_fermitinosit_a_fermitinosit_a 4 l_ateriafereiosit_fermitinosidat_a_fermitinosidat_a_fermitinosit_a_fermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosit_fermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosit_a 4 l_ateriafermitinosidat_a_fermitinosidat_a_fermitinosit_a 4 l_ateriafermitinosidateriafermitinosidat_a_fermitinosit_a 4 l_ateriafermitinosidateriafermitinosidat_a_fermitinosit_a 4 l_ateriafermitinosidateriafermitinosidat_afermitinositfermitinosit_a 4 l_ateriafermitinosidateriafermitinosidateriafermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinositfermitinos</pre>
972 973 976 976 977 978 979 960 961 963 964 964 964 964 964 964 965 964 965 965	0 6 0 3 0 0 0 0 3 0 7 1 0 2 5 0 0 0 0 7 0 3 0	0 2 3 0 0 7 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0	0 12 0 1 0 1 0 1 3 0 0 0 2 0 0 2 0 0 2 0 0 2 0 0 1 0 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 2 3 0 2 1 0 0 2 1 0 0 0 1 1 0 0 0 1 1 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 2 0 1 3 0 2 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b laderiaveruponitorbitzveruponitorbitzfermatinonadiksiGermatinonadiksi</pre>
972 973 975 976 977 978 979 980 984 985 985 990 985 985 990 991 995 995 995 995 995 995 995	0 6 8 8 0 0 0 0 0 2 1 0 2 5 0 0 0 2 0 3 0 2 1 0 2 5 0 0 0 0 2 0 3 0 2 1 0 2 5 0 0 0 0 2 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 3 0 0 7 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 1 0	0 12 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 2 3 0 2 1 0 2 1 0 2 1 0 0 4 0 2 1 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 2 0 1 3 0 2 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lsderisversonirotiotesversonirotiotesfeedophereisesi</pre>
972 973 976 976 977 978 980 984 984 985 986 990 991 993 994 995 995 995 995 995 995 995 995 995	0 0 6 0 3 0 0 0 0 3 0 2 1 0 2 5 0 0 0 0 3 0 3 0 0 0	0 2 3 0 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 32 0 4 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 2 3 0 2 1 0 2 1 0 2 1 0 0 4 0 2 1 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 2 0 1 3 0 2 0 1 3 0 2 0 0 1 0 0 2 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 2 0 0 1 3 0 2 0 2 0 0 1 3 0 0 2 0 0 1 3 0 0 2 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 1 0		<pre>b laderia_/emailmonadotaemailmonadotasemailmonadotasi_educatoriangi</pre>
972 973 975 976 977 978 979 980 981 983 984 985 985 985 985 985 985 985 985 985 985	0 0 6 0 3 0 0 0 0 0 3 0 2 1 0 2 5 0 0 0 0 2 0 3 0 0 0 0 1	0 2 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0		0 32 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 0 2 1 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 2 0 1 3 0 2 1 0 2 0 1 0 2 0 1 0 2 0 1 3 0 2 0 1 3 0 2 0 1 3 0 2 0 0 1 3 0 2 0 0 1 3 0 0 1 3 0 0 1 3 0 0 1 3 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lsteris_/evencemicrobieserencemicrobieseleminitronables/_eleminitronablessGenerationauss 2 lsterisfrinciencsContradioOctoprints/_DelonginesseColorbiebetory 0 lsterisfrinciencsContradioOctoprints/_DelonginesseColorbiebetory 0 lsterisfrinciencsContradioOctoprints/_DelonginesseColorbiebetory 0 lsteris 0 lsterisfrinciencsContradioOctoprints/_DelonginesseColorbiebetory 0 lsteris 0 lsterisfrinciencsContradio_Octoprints/_DelonginesseColorbiebetory 0 lsterisContradio_Octoprints/_DelonginesseColorbiebetory 0 lsterisContradio_Octoprints/_DelonginesseColorbiebetory 0 lsterisContradio_Octoprints/_DelonginesseColorbiebetory 0 lsterisContradio_Octoprints/_DelonginesseColorbiebetory 0 lsterisContradio_Octoprints/_DelonginesseColorbiebetory 0 lsterisContradio_Colorbiebetory 0 lsteris 0 lsteris 0 lsteris</pre>
972 973 976 976 976 976 977 978 980 984 984 985 986 990 991 993 994 995 995 995 995 995 995 995 995 995	0 0 6 0 3 0 0 0 0 0 3 0 2 1 0 2 5 0 0 0 0 2 0 3 0 0 0 0 1 1	0 2 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0		0 32 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 2 1 0 1 0 0 2 1 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 1 0 0 0 0 0 0 0 0 0 0 2 3 5 1 0 4 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 2 0 1 3 0 2 1 0 0 1 0 0 1 0 0 1 0 0 1 3 0 0 1 3 0 0 1 3 0 0 1 3 0 0 0 1 3 0 0 0 1 3 0 0 0 1 3 0 0 0 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lsteris_/wrucentrobatewrucencobiesiedeopheraketiedeopheraketsiemutinoosisiiiiiiiiiiiiiiiiiiiiiiiiiiiii</pre>
972 973 976 976 977 978 980 981 984 984 985 985 985 985 985 985 985 985 985 985		0 2 3 0 7 0 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 26 0 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 1 0 0 2 0 0 0 0 0 2 3 5 1 0 4 0 1 0 0 0 0 0 0 0 0 3	1 0 55 0 2 0 0 1 3 0 2 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 8 0 0 1 3 5 0 2 0 0 1 3 5 0 2 0 0 1 3 5 0 0 2 0 0 1 3 5 0 0 2 0 0 1 3 5 0 0 1 3 5 0 0 1 3 5 0 0 1 3 1 0 0 1 3 1 0 0 1 3 1 0 0 1 1 1 0 0 1 1 1 0 1 1 1 1		<pre>b lstdrig_termininskitswincenicobles_Pidephashel_PidephashelsGemminioablesGemminioablesGemminioablesGemminioablesGemminioablesCelemminioablesCelemminioablesCelemminioablesCelemminioablesCelemminioables_CelemminioablesVelocebas_Velocebas_Velocebas_QelemminioablesVelocebas_CelemminioablesVelocebas_CelemminioablesVelocebas_CelemminioablesVelocebas_Velocebas_QelemminioablesVelocebas_CelemminioablesVelocebas_CelemminioablesVelocebas_Velocebas_Velocebas_QelemminioablesVelocebas_CelemminioablesVelocebas_Velocebas_Velocebas_QelemminioablesVelocebas_Velocebas_QelemminioablesGemminioablesGemminioablesQue_GeminioablesQue_GemminioablesQue_GemminioablesQue_GemminioablesQu</pre>
972 973 976 976 976 976 977 978 980 984 984 985 986 990 991 993 994 995 995 995 995 995 995 995 995 995	0 0 6 0 3 0 0 0 0 0 3 0 2 1 0 2 5 0 0 0 0 2 0 3 0 0 0 0 1 1	0 2 3 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0		0 32 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 2 1 0 1 0 0 2 1 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 1 0 0 0 0 0 0 0 0 0 0 2 3 5 1 0 4 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 35 0 2 0 1 3 0 2 1 0 0 1 0 0 1 0 0 1 0 0 1 3 0 0 1 3 0 0 1 3 0 0 1 3 0 0 0 1 3 0 0 0 1 3 0 0 0 1 3 0 0 0 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lsteris_/wrucentrobatewrucencobiesiedeopheraketiedeopheraketsiemutinoosisiiiiiiiiiiiiiiiiiiiiiiiiiiiii</pre>
972 973 976 976 977 978 980 981 983 984 985 986 987 988 989 980 981 984 985 989 980 991 993 993 993 995 997 995 997 905 907 905 907 905 907 905 907 905 907 905 905 905 905 905 905 905 905 905 905		0 2 3 0 7 0 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		22 24 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 3 0 0 2 1 0 2 1 0 0 2 1 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 1 0 0 2 0 0 0 0 2 3 5 1 0 4 0 1 0 0 0 0 0 0 0 0 3 1	1 0 35 0 2 0 1 3 0 2 0 0 1 0 0 2 0 0 1 0 0 1 0 0 1 0 0 1 8 0 0 1 3 0 0 2 0 0 1 3 0 0 1 3 0 0 1 3 0 0 1 3 0 0 0 1 3 0 0 0 0		<pre>b l.bdrbistermonicondetsfedorphasehet_pdophasehetsdophasensesi b l.bdrbisfermonicondetsGermonicondetsContemptronetalistGermonicondetsVelocetasVelocet</pre>
972 973 974 975 976 977 980 981 983 984 985 985 990 991 992 994 993 994 995 994 995 994 995 995 996 997 998 997 998 997 998 997 998 997 997		0 2 3 0 7 0 0 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 12 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		0 32 0 0 0 0 0 0 0 0 0 0 0 0 0	0 26 0 1 0 2 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 8 0 1 4 0 1 0 0 2 0 0 0 0 2 3 5 1 0 4 0 1 0 0 0 0 0 0 0 3 1 6	1 0 55 0 2 0 0 1 3 0 2 1 0 0 2 0 0 1 0 0 1 0 0 0 3 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 0 0 1 8 1 1 8 0 1 8 1 1 8 1 1 8 1 1 1 1		<pre>b b.btmiskmutonizzkiekskmutonizzkiesknowe betweekskiewstweeksekscannet investeeksekcannet investeeksekcannet investeeksekscannet investeeksekscannet investeeksekscannet investeeksekscannet investeeksekscannet investeeksekskiewstweekseksekskiewstweekseksekskiewstweekseksekskiewstweekseksekskiewstweekseksekskiewstweeksekseksekseksekseksekseksekseksekseks</pre>

00000											
1010	0	0	3	0	0	0	0	0	3	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_Muribaculaceae;s_
1011	1	0	4	0	1	4	0	1	9	o	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Cytophagales;f_Microscillaceae
1012	0	0	O	0	0	D	0	3	0	o	0 k_Bacteria;p_Acidobacteriota;c_Blastocatellia;o_Blastocatellales;f_Blastocatellaceae
1013	2	0	0	0	2	1	0	0	3	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Reyranellales;f_Reyranellaceac;g_;s_
1014	2	0	0	0	2	0	0	0	0	0	0 k_Bacteria;p_Acidobacteriota;c_Vicinamibacteria;o_Vicinamibacterales;f_Vicinamibacteraceac;g_Vicinamibacteraceac;s_
1015	0	0	3	0	0	D	0	o	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria
1016	0	0	0	0	2	D	0	1	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidiales;f_Muribaculaceae;g_Muribaculaceae;s_
1017	1	0	5	0	1	0	0	2	0	0	
											0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitutales;f_Opitutaceae;g_IMCC26134;s_
1018	6	0	0	0	0	0	1	13	1	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiale;;f_Hyphomicrobiaceae;g_Hyphomicrobium
1019	а	0	0	0	1	0	0	2	0	0	$0\ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Xan thomonadale; sf\_Xan thomonadaceae; g\_Thermomonas and the standard standar$
1020	1	0	0	0	0	2	2	б	2	0	0 k_Bacteria;p_Protecbacteria;c_Alphaproteobacteria;o_Reyranellales;f_Reyranellaceae;g_Reyranella;s_
1021	1	0	1	0	0	0	0	5	0	0	$0\ k\_acteria; p\_Actinobacteriota; c\_Actinobacteria; o\_Propionibacteriale; f\_Nocardioidaceae; g\_Nocardioides actinobacteria; backgroup and actinobacteria; backgroup actinoba$
1022	0	0	0	0	0	0	0	0	3	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes
1023	26	7	11	0	10	19	3	16	10	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG-014;t_Clostridia_UCG-014;g_Clostridia_UCG-014;s_
1024	0	3	0	0	0	0	0	0	0	0	0 k_Bacteria
1025	o	0	O	0	o	3	0	D	0	σ	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Cytophagales:f_Spirosomaceae;g_Pseudarcicella;s_
1025	0	0	1	0	0	0	0	0	3	o	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadin8860_group;f_Clostridia_vadin8860_group;g_Clostridia_vadin8860_group;s_
1027	0	0	0	2	0	0	0	10	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Streptosporangiales;f_Thermomonosporaceae;g_Actinomadura;s_Actinomadura_sp.
1028	0	0	0	0	0	0	0	5	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Diplorickettsiales;f_Diplorickettsiaceae;g_Aquicella;s
1029	1	0	0	0	0	1	0	3	2	0	0 k_Bacteria;p_Chloroflexi;r_KD4:96;a_KD4:96;f_KD4:96;z_KD4:96;s_
1030	0	0	0	0	0	D	0	6	0	o	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Kanthobacteraceae;g_Pseudolabrys;s_
1031	2	0	1	0	0	1	1	D	0	a	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Pseudonocardiale;;f_Pseudonocardiaceae;g_Actinomycetospora;s_
1032	2	0	0	0	1	0	0	0	2	0	0 k_Bacteria;p_Firmicutes;c_Bacili;o_Erysipelotrichales;f_Erysipelotrichaceae
1033	0	0	0	0	0	0	0	4	3	0	0 k_Bacteria;p_Gemmatimonadota;x_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae; <u>z_</u> 3_
1034	0	2	0	0	0	0	0	15	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Pedomicrobium;s
1035	0	0	0	0	0	D	0	7	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizoblales;f_Devosiaceae;g_Devosia
1036	3	0	0	0	0	1	0	0	2	0	0 k_Bacteria;p_Bdellovibrionota;c_Oligoflexia;o_0319-6620;f_0319-6620;g_0319-6620;g_
1037	0	0	0	0	0	0	0	19	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiaics;f_Xanthobacteraceac;g_;s_
1038	0	0	0	0	0	D	0	3	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Edaphobaculum;s_
1039	4	0	0	0	0	D	0	1	0	0	0 k_Bacteria;p_Desulfobacterota;c_Desulfovibrionia;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio
1040	0	0	0	0	8	1	0	0	2	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
1041	0	0	0	0	0	0	0	0	4	0	0 k_Bactoria
1042	4	0	1	0	0	1	0	1	0	0	0 k_Bacteria;p_Bacternidota;c_Bacternidia;o_Cytophagales/_Microssillaceae
1043									1		
	3	0	۵	0	0		0	0		0	0 k_Bacteria;p_Bacteriaidata;c_Bacteriaidia;p_Cytophagales/_Hymenobacteraceae;g_Hymenobacter;s_Hymenobacter_nivis
1044	1	0	O	0	1	0	0	2	5	O	0 k_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Saccharimonadales;g_Saccharimonadales;s_
1045	0	0	0	0	0	1	0	0	6	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales-Tissierellales;f_Anaerovoracaceae;g_Eubacterium_brachy_group;s
1046	2	0	0	0	1	2	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae; <u>x_</u> Legionella;s_
1047	2	0	0	0	3	1	0	2	0	0	0 k_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Microtrichales;f_Humatobacteraceae;g_Cl500-29_marine_group;s_
1048	15	z	7	15	10	1	1	D	2	o	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_GCA-900066575;s
1049	2	0	0	0	3	0	0	0	2	0	0 k_Bacteria;p_MBNT15;c_MBNT15;p_MBNT15;f_MBNT15;g_MBNT15
1050	0	0	0	0	0	D	0	D	4	o	0 k_Bacteria;p_Chloroflextc_Chloroflexia;o_Chloroflexiales;f_Rosetflexaceae;g_;s_
1051	0	0	O	0	0	D	4	D	0	o	0 Unknown
						0	4	0	0	0	0 k_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Saccharimonadales;g_Saccharimonadales;s_
1052	0	0	0	0	0					0	0 k_Bacteriarp_Acidobacteriotaxc_AT-s3-28.0_AT-s3-28.f_AT-s3-28.sc_AT-s3-28.sc_
1052		0	0	0	0	0	0	0	2		
1053	0 0	0	0	0	0	0	0	0	3		0 k. Basterians, Brotachastarians, Alekaansterians, Bistachisler f. Bellarinskinsenaur, Statiudohastarium Mathularuhrum
1053 1054		0 0	0 0	0 0	0 0	1	3	D	4	٥	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;p_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium-Methylorubrum
1053 1054 1055	0 8 9	0 0 0	0 0 0	0 0 2	0 0 0	1 5	a o	0 1	4 0	0 1	1 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceaeg_Oscillibacter;s_
1053 1054 1055 1056	0 8 9 0	0 0 0	0 0 0	0 0 2 6	0 0 0	1 5 0	3 0 0	D 1 0	4 0 0	0 1 0	1 k_Bacteriox_Tirricutes_Cbatrduo_Occilopinius_Coccilopinaeaeg_Occilliaaters_ 0 k_Bacterniae_Bacternidetac_Bacternideae_Ohtirophagalesf_Ohtirophageseaeg_Feruginbacters_
1053 1054 1055 1056 1057	0 8 9	0 0 0	0 0 0	0 0 2 6 0	0 0 0	1 5	a o	0 1	4 0 0	0 1 0 0	3 k_Barterlay_Terrelatesc_Cohtriduo_Coldiografied_docillogianaaag_Coldillasters
1053 1054 1055 1056	0 8 9 0	0 0 0	0 0 0	0 0 2 6	0 0 0	1 5 0	3 0 0	D 1 0	4 0 0	0 1 0	1 k_Bacteriox_Tirricutes_Cbatrduo_Occilopinius_Coccilopinaeaeg_Occilliaaters_ 0 k_Bacterniae_Bacternidetac_Bacternideae_Ohtirophagalesf_Ohtirophageseaeg_Feruginbacters_
1053 1054 1055 1056 1057	0 8 9 0	0 0 0 0	0 0 0 0	0 0 2 6 0	0 0 0 0	1 5 0 0	3 0 0	D 1 0 3	4 0 0	0 1 0 0	3 k_Barterlay_Terrelatesc_Cohtriduo_Coldiografied_docillogianaaag_Coldillasters
1053 1054 1055 1056 1057 1058	0 8 9 0 4	0 0 0 0 0	0 0 0 0 0	0 0 2 6 0	0 0 0 0	1 5 0 0	a 0 0 0	D 1 0 3 0	4 0 0 0	0 1 0 0	3 k_Bateriap_Terricutesc_Cohtriduo_Cociliopinalesf_Onciliopinaoaeg_Cociliasters 0 k_Bateriao_Baterinidotac_Baterioidao_Chidrophagricaf_Chitriophagacaeg_Foruginibacters 0 k_Bateriap_Terotobacteriac_Gammaprotobacteriao_Gammaprotobacteria_Incertae_Soliuf_Uninown_Familyg_AddBacters 0 k_Bateriap_Devalidobacteriato_Devalidoviteriato_Commissionalesf_Devalidovitericanceeg_Devalidoviterics
1053 1054 1055 1056 1057 1058 1059	0 8 9 0 4 0	0 0 0 0 0 0	0 0 0 0 0	0 2 6 0 0	0 0 0 0 0	1 5 0 0 0	3 0 0 0 0	D 1 0 3 0	4 0 0 0 0	0 1 0 0	3 k_Bateriag_Terricoless_Cohtridus_Cociliopiniesf_Onciliopinaoaeg_Cociliasters_ 0 k_Bateriag_Baterridotasc_Bateridiaa_Chikirophagnicaf_Chikirophagaceaeg_Foruginibaters_ 0 k_Bateriag_Protobacteriag_Cammaportobateriaa_Gammaportobateria_Incertae_Soligf_Uninown_Familyg_Addibaters_ 0 k_Bateriag_Desultabaterists_Desultobaterinaa_Gammaportobateria_Desultobiriosaceaeg_Desultobirios_ 0 k_Bateriag_Baterinidotsc_Bateriodiaa_Bateriodiams_Bateria_Jonalisticriag_Desultobirios_
1053 1054 1055 1056 1057 1058 1059 1060	0 9 0 4 0	0 0 0 0 0 0 0	0 0 0 0 0 0 0	0 2 6 0 0 0	0 0 0 0 0 6	1 5 0 0 0 0 0	3 0 0 0 0 0	0 1 3 0 5	4 0 0 0 0	0 1 0 0 0 0	1 k_Bateriay_Terricolecs_Cohtriduo_Ooclooprises_Oocloopriseseg_Ooclibacters_ 0 k_Bateriay_Bateriorisettic isc_Gannaperotobatticao_Gannaperotobatticao_Territoria_Distributoria_ 0 k_Bateriay_Deschoolectic_Gannaperotobatticao_Gannaperotobatticao.com 0 k_Bateriay_Deschoolecticao_Deschoolecticao_Gannaperotobatticao.com 0 k_Bateriay_Deschoolecticao_Deschoolecticao_Gannaperotobatticao.com 0 k_Bateriay_Deschoolecticao_Deschoolecticao_Gannaperotobatticao.com 0 k_Bateriay_Deschoolecticao_Deschoolecticao_Gannaperotobatticao.com 0 k_Bateriay_Deschoolecticao_Deschoolecticao_Gannaperotobatticao.com 0 k_Bateriay_Deschoolecticao_Deschoolecticao_Gannaperotobatticao.com 0 k_Bateriay_Deschoolecticao_Deschoolecticao_Gannaperotobatticao.com 0 k_Bateriay_Deschoolecticao_Holoobagees_Subgrapo_74_Subgrapo_74_Subgrapo_74_
1053 1054 1055 1056 1057 1058 1059 1060 1061	0 9 0 4 0 0	0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0	0 0 0 0 5 0 0	1 5 0 0 0 0 0 0	3 0 0 0 0 0 0	D 1 0 3 0 0 6 3	4 0 0 0 0 0	0 1 0 0 0 0 0	1 k_Bacteriay_Territorbes_Cohtridus_Cokologinises_Dicologinaosag_Cokolisaters_ 0 k_Bacteriag_Bacteriolotise_Bacteriolotise_Cohtriophagelest_Chriticophageraseg_Terruginbacters_ 0 k_Bacteriag_Petrobacteriag_Ganual contents_Ganuagerotobacteria_Contents_Con
1053 1054 1055 1056 1057 1058 1059 1060 1061 1061	0 9 0 4 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0	0 0 0 0 0 5 0 0 0 2	1 5 0 0 0 0 0 0 0	a 0 0 0 0 0 0 0 0	D 1 3 0 5 3 1	4 0 0 0 0 0 3	0 1 0 0 0 0 0	1 i _Bacteriag_Terricolecc_Cohtriduo_Cokcloginised_Oxiclioginiaeaeg_Cokclinaters_  0 k_Bacteriag_Bacterioidatac_Bacterioidazo_Chitrophagalesf_Chitrophagescaeg_Terruginibacters_  0 k_Bacteriag_Testeobacterize_Genutrophagescaeg_Desutheriaeaeg_Desutheriaeg_Desutheriaeg_Desutheriaeaeg_Desutheriaeg_Desutheriaeg_Desutheriaeg_Desutheriaeaeg
1053 1054 1055 1056 1057 1058 1059 1060 1061 1061	0 9 0 4 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0	0 0 0 0 0 5 0 0 0 2	1 5 0 0 0 0 0 0 0	a 0 0 0 0 0 0 0 0	D 1 3 0 5 3 1	4 0 0 0 0 0 3	0 1 0 0 0 0 0	<ol> <li>Jactericz, Pirotochastrika, Santorobastrika, Gonielaide, Biofelaide, Jionielaide, Tagesz,</li> <li>Lastericz, Jorechastrika, Santorobastrika, Santorobastrika, Controphagesz, Jornajhasterz,</li> <li>Lastericz, Brotochastrika, Santorobastrika, Santorobastrika, Incerte, Seldif, Ushroon, Family, Addbasterz,</li> <li>Lastericz, Bestoriodza, Bacteriodza, Deutlowbronze, Deutlowbroze, Bestorier, Bestorier, Bestoriodza, Bacteriodza, Bacteriodza, Bestoriodza, Bestoriodza, Bestoriodza, Bacteriodza, Bestorier, Santorobastrika, Schorper, Jr.,</li> <li>Lastericz, Monopientz, Thermotesufewicz, Bachadorona, J., Santorobasteria, Jonefallowbrozed, Tagezz,</li> <li>Lastericz, Monopientz, Thermotesufewicz, Bachadorona, J., Santorobasteria, Jacobastericz, Jackerski, Monopientz, Thermotesufewicz, Bachadorona, J., Zunielaidz, Bactericz, Jackerski, Jackerski,</li></ol>
1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064	0 9 0 4 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0	0 0 0 0 0 5 0 0 0 2	1 5 0 0 0 0 0 0 0	a 0 0 0 0 0 0 0 0	D 1 3 0 5 3 1	4 0 0 0 0 0 3	0 0 0 0 0 0 0 0 0	<ul> <li>1 Lasterias, Introduces_Chatridus_Occilospirales_Occilospirales_CoccilospiralesCoccil</li></ul>
1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065	0 9 0 4 0 0 0 0 0 2 2 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 2 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0	a 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 5 3 1 0 0 0	4 0 0 0 0 0 3 0 2 0	0 0 0 0 0 0 0 0 0	<ul> <li>1 f_batteliag_Timicalesc_Cohtriduo_Occilopinios/_Occilopinaosag_Occilioaters_</li> <li>0 k_batteliag_Timicalesc_Cohtriduo_Occilopinios/_Occilopinaosag_Occilioaters_</li> <li>0 k_batteliag_Textobatteliag_GenerativeS_DestructionCommercicioaterbattelia_cortex_Config_University_Addibatters_</li> <li>0 k_batteliag_Textobatteliag_DestructureS_DestructiveS_S_Statevoe_Dfs</li> <li>0 L_batteriag_DestructiveS_DestructiveS_DestructiveS_DestructiveS_DestructiveS_S_Statevoe_Dfs</li> <li>0 L_batteriag_DestructiveS_CommerciveSectiveS_DestructiveS_DestructiveSectiveS_DestructiveSectiveS_S_Statevoe_S_S_</li> <li>0 L_batteriag_CommerciveSectiveS</li></ul>
1053 1054 1055 1056 1057 1058 1060 1061 1062 1063 1064 1065 1066 1067	8 9 0 4 0 0 0 0 2 2 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 3 0 3 0 4	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 1	0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 5 3 0 5 3 1 0 0 0 0 0	4 0 0 0 0 0 3 0 2 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>1 Lasteria, Intrinstes, Charinka, Dacklopinske, Oscillopinske, Charinebagene, Conflicators,</li> <li>1 Lasteria, Intrinstes, Carteriodas, Chinophagine, Chinophag</li></ul>
1053 1054 1055 1056 1057 1058 1060 1061 1062 1063 1064 1065 1066 1067	8 9 0 4 0 0 0 0 2 2 0 0 1	0 0 0 0 0 0 0 9 0 3 0 4 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 5 3 0 0 0 0 0 0	4 0 0 0 0 0 0 3 0 0 2 0 0 0 3 3	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>1 [acterias]. Terricolacci, Cabrirduo, Oxclooprises[_Oxclooprisesae_Oxclooprisesae_Oxclooprisesae=_Ox</li></ul>
1053 1054 1055 1056 1057 1058 1060 1061 1063 1064 1065 1066 1065	0 8 9 0 4 0 0 0 2 2 0 0 1 2 0 1 2 0 1 2 205	0 0 0 0 0 0 0 9 0 3 0 4 0 25	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 1 0 1 0 23	0 0 0 0 0 0 0 0 0 0 0 0 1 9	1 5 0 0 0 0 0 0 0 0 0 0 19	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0 0 3	D 1 0 5 1 0 0 0 0 0 7	4 0 0 0 0 0 3 0 2 0 0 3 3 3 3	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>1 f_bateriay_Terricolecs_Cobriduo_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises</li> <li>0 Lateriay_Bateria/Setting_Developrises_Occleoprises/Occl</li></ul>
1053 1054 1055 1056 1057 1058 1059 1060 1061 1063 1064 1065 1066 1067 1068 1069	0 8 9 0 4 0 0 0 2 2 0 0 1 205 3	0 0 0 0 0 0 0 0 3 0 3 0 4 0 26 0 26	0 0 0 0 0 0 0 0 0 0 0 0 0 0 39 0 0	0 2 6 0 0 0 0 0 0 0 0 1 0 23 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 19 0	3 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0 3 0 0 3	D 1 0 5 1 0 0 0 7 0 7 0	4 0 0 0 0 0 3 0 2 0 0 0 3 1 3 0 0 13 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>1 f_akteriang_Territoteks_Cabtridus_Oxclooprinsesfeeff_Oxclooprinsesfeeff_Oxclooprinsesfeeffeeffeeffeeffeeffeeffeeffeeffeef</li></ul>
1053 1054 1055 1056 1057 1058 1060 1061 1063 1064 1065 1066 1065	0 8 9 0 4 0 0 0 2 2 0 0 1 2 0 1 2 0 1 2 205	0 0 0 0 0 0 0 9 0 3 0 4 0 25	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 1 0 1 0 23	0 0 0 0 0 0 0 0 0 0 0 1 9	1 5 0 0 0 0 0 0 0 0 0 0 19	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0 0 3	D 1 0 5 1 0 0 0 0 0 7	4 0 0 0 0 0 3 0 2 0 0 3 3 3 3	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>1 f_bateriay_Terricolecs_Cobriduo_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises</li> <li>0 Lateriay_Bateria/Setting_Developrises_Occleoprises_Occleoprises</li> <li>0 Lateriay_Developrises_Developrises_Occleoprises</li> <li>0 Lateriay_Developrises_Occleoprises_Occleoprises</li> <li>0 Lateriay_Occleoprises_Occleoprises_Occleoprises</li> <li>0 Lateriay_Occleoprises_Occleoprises_Occleoprises</li> <li>0 Lateriay_Occleoprises_Occleoprises_Occleoprises</li> <li>0 Lateriay_Occleoprises_Occleoprises_Occleoprises</li> <li>0 Lateriay_Occleoprises</li> <li>0 Lateriay_Occleoprises&lt;</li></ul>
1053 1054 1055 1056 1057 1058 1059 1060 1061 1063 1064 1065 1066 1067 1068 1069	0 8 9 0 4 0 0 0 2 2 0 0 1 205 3	0 0 0 0 0 0 0 0 3 0 3 0 4 0 26 0 26	0 0 0 0 0 0 0 0 0 0 0 0 0 0 39 0 0	0 2 6 0 0 0 0 0 0 0 0 1 0 23 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 19 0	3 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0 3 0 0 3	D 1 0 5 1 0 0 0 7 0 7 0	4 0 0 0 0 0 3 0 2 0 0 0 3 1 3 0 0 13 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>1 f_akteriang_Territoteks_Cabtridus_Oxclooprinsesfeeff_Oxclooprinsesfeeff_Oxclooprinsesfeeffeeffeeffeeffeeffeeffeeffeeffeef</li></ul>
1053 1054 1055 1056 1057 1058 1060 1061 1063 1064 1065 1066 1066 1067 1068 1069 1070	0 8 9 0 4 0 0 0 2 2 2 0 0 1 205 3 1	0 0 0 0 0 0 0 0 0 3 0 3 0 4 0 25 0 26 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 1 0 23 0 0 23 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 19 0 19	a 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0 0 0 3 0	0 9 0 5 1 0 0 0 0 7 0 2	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		1 f_bateriay_Terricolecs_Cobirduo_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises 0 L_bateriay_Bateria/Stric_Sammeretobateria_Commeretobateria_Devaluations_Commercesses_Courses 0 L_bateriay_Devaluations 0 L_bateriay_Proteobateriay_Overlaiders 0 L_bateriay_Proteobateriay_Overlaiders 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Proteobateriay_Overlaiders 0 Lateriay_Devaluations 0 L_bateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders<
1053 1054 1055 1056 1057 1058 1050 1061 1063 1064 1065 1066 1066 1066 1069 1070 1071	0 8 9 0 4 0 0 0 0 2 2 0 0 0 1 205 3 1 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 26 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 1 0 0 23 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 19 0 1 1 0	a 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 6 3 1 0 0 0 0 0 0 7 0 0 0 7 0 0 0 0 0 0 0 0	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>1 Lacteria, Enternistics_Extendes_Childraines_Colloginates_Colloginates_Colloginates_</li> <li>1 Lacteria, Extendes_Extendes_Childraines_Colloginates_Colloginates_Colloginates_</li> <li>2 Lacteria, Extendestrics_Commenterobacteria_Commenterobacteria_Extendestria_Enternistics_Colloginates</li> <li>Colloginates_Colloginates_Colloginates_Colloginates_Colloginates</li> <li>Colloginates_Colloginates_Colloginates_Colloginates</li> <li>Colloginates_Colloginates_Colloginates</li> <li>Colloginates_Colloginates_Colloginates</li> <li>Colloginates_Colloginates_Colloginates</li> <li>Colloginates_Colloginates_Colloginates</li> <li>Colloginates_Colloginates_Colloginates</li> <li>Colloginates</li></ul>
1053 1054 1055 1056 1057 1060 1061 1062 1064 1065 1066 1067 1068 1069 1070 1071	0 8 9 0 4 0 0 0 0 2 2 0 0 0 1 205 3 1 5	0 0 0 0 0 0 0 0 0 0 0 0 0 26 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 1 0 0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 19 0 1 1 0	a 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 6 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		1 f_bateriay_Terricolecs_Cobirduo_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises_Occleoprises 0 L_bateriay_Bateria/Stric_Sammeretobateria_Commeretobateria_Devaluations_Commercesses_Courses 0 L_bateriay_Devaluations 0 L_bateriay_Proteobateriay_Overlaiders 0 L_bateriay_Proteobateriay_Overlaiders 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Devaluations 0 L_bateriay_Proteobateriay_Overlaiders 0 Lateriay_Devaluations 0 L_bateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders 0 Lateriay_Proteobateriay_Overlaiders<
1053 1054 1055 1056 1057 1058 1059 1050 1051 1050 1051 1055 1056 1057 1059 1057 1059 1057 1057 1057 1057	0 8 9 0 4 0 0 0 0 2 2 0 0 0 1 205 3 1 5	0 0 0 0 0 0 0 0 0 3 0 3 0 4 0 26 0 0 0 4 0 0 4 0 0 0 4 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 1 0 23 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 9 0 0 1 0 0 0 0	a 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 6 3 1 0 0 0 0 7 0 0 7 0 0 0 0 0 0 0 0 0 0 0	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>1 _ lacteria, _ Intricates Catricia Controprises Occiloprisesag Occilopris</li></ul>
1053 1054 1055 1057 1057 1059 1059 1060 1064 1069 1064 1067 1068 1066 1067 1068 1067 1068 1067 1071 1072	0 8 9 0 4 0 0 0 2 2 0 0 1 206 3 1 5 0 0 0 1 5 0 0 0	0 0 0 0 0 0 0 0 0 3 0 3 0 4 0 26 0 0 0 4 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 1 0 0 23 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 1 9 0 0 1 0 0 0 1 0 0 0 1 3 3	a 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 0 6 3 1 0 0 0 0 7 0 0 7 0 0 0 7 0 0 0 1 1	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		3 L_Bateria,_Beteriotes_Cetridus_Octooprises_Qoctoopriseseq_Octoopris
1053 1054 1055 1055 1057 1057 1059 1069 1069 1069 1069 1069 1069 1069 106	8 9 0 4 0 0 0 2 0 2 0 1 2 06 3 1 5 0 0 2 2 5 0 0 2 2 2 2 2 2 2 2 2 2 2 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	a 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 9 0 6 3 1 0 0 0 0 7 0 0 0 0 1 0	4 0 0 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>1 _ Bateriag_Terricolacs_Chatridus_Occilosprises_Coccilosprisess_Coccilosprisess_Coccilosprisess_Coccilosprisess_Coccilosprisess_Cocciliosprisessa_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisessa_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprisess_Cocciliosprises_Cocciliosprisess_Cocciliosprisess_Cocciliosprises_Cocciliosprises_Cocciliosprises_Cocciliosprisesse_Cocciliosprises_Cocciliosprises_Cocciliosprises_Cocc</li></ul>
1053 1054 1055 1056 1057 1057 1057 1057 1058 1057 1058 1057 1058 1057 1057 1057 1057 1057	8 9 0 4 0 0 0 2 2 0 0 1 2 205 3 1 5 0 0 2 2 0 2 0 2 2 0 2 2 0 2 2 0 2 2 0 2 2 0 2 2 2 0 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	a 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 9 0 6 3 1 0 0 0 7 0 0 0 1 0 1 0	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>1   Lateriay_Terricolacci, Catricolus_Occilospinase/_Occilospinases_Occilosoters_</li> <li>0   Lateriay_Lecteristics_Exteriods_Occilospinase/c_Occilospinases_Occilosoters_</li> <li>0   Lateriay_Lecteristics_Catricolus_Occilospinase/c_Occilospinases_Occilosoters_</li> <li>0   Lateriay_Lecteristics_Occilosoteriay_Devolutiversity_Devolutiversity_Occilospinasesey_Devolutivers_</li> <li>0   Lateriay_Devolutiversity_Devolutiversity_Devolutiversity_Occilospinasesey_Devolutivers_</li> <li>0   Lateriay_Devolutiversity_Devolutiversity_Devolutiversity_Occilospinasesey_Devolutivers_</li> <li>0   Lateriay_Devolutiversity_Devolutiversity_Devolutiversity_Operativersity_Operativersity_Devolutivers_</li> <li>0   Lateriay_Devolutiversity_Devolutiversity_J_T_Subgrup_J_Subgrup_J_L_Subgrup_J_L_Subgrup_J_L_</li> <li>0   Lateriay_Devolutiversity_Headvirosity_J</li></ul>
1053 1054 1055 1055 1057 1057 1058 1060 1060 1060 1060 1066 1067 1066 1067 1066 1067 1066 1067 1070 1071 1075 1076	8 9 0 4 0 0 0 2 2 0 0 1 2 205 3 1 5 0 0 2 2 0 2 0 2 2 0 2 2 0 2 2 0 2 2 0 2 2 0 2 2 2 0 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	a 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 0 0 0 0 0 3 0 0 0 0 3 0 0 0 0 0 0 0 0		1 Lateria, Intrinse, Catridus, Oxforginise, Oxforginise, Oxforginise, Chinophages, Chinophage
1053 1054 1055 1056 1057 1058 1060 1060 1060 1060 1067 1066 1067 1066 1067 1067	8 9 0 4 0 0 0 2 2 0 0 1 2 205 3 1 5 0 0 2 2 0 2 0 2 2 0 2 2 0 2 2 0 2 2 0 2 2 0 2 2 2 0 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>1 Lateriag_InviroidesChatridus_Occilosprises/_Occilosprisese_Occilosofers 2 Lateriag_LaternidetsExtendedsChinophage(stChinophage(stEnglishettrs 2 Lateriag_LaternidetsStateriads_Chinophage(stChinophage(stEnglishettrs 2 Lateriag_LaternidetsStateriads_Chinophage(stChinophage(stEnglishettrs 2 Lateriag_LaternidetsStateriads_Chinophage(stEnglishettrs 2 Lateriag_LaternidetsLaternidetsLaternidetsStateriad_Internet_ 2 Lateriag_LaternidetsNaturationsOcc_Lateriag_Laternidets_Chinophage(stEnglishettrs 2 Lateriag_LaternidetsNaturations_Occ_LaternidetsStaternidets_Chinophage(stEnglishettrs 2 Laternidg_LaternidetsNaturations_Occ_LaternidetsStaternidetsCaternidets_Chinophage(stEnglishettra_2) 2 Laternidg_LaternidetsAbhardrobadetsGaternidetsBathardians</pre>
1053 1854 1855 1957 1858 1869 1860 1861 1865 1866 1867 1866 1867 1869 1967 1971 1972 1973 1972 1973 1974 1975 1975 1975	0 8 9 0 0 0 2 2 0 0 0 1 2 20 0 1 2 20 0 1 2 5 0 0 2 0 0 2 0 0 2 0 0 1 2 2 0 0 0 0 0 2 2 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>1 f_biteling_Terricolesc_Costridus_Occilosprises(_Occilospriseseg_Occiliosters_ 0 L_biteling_Exectomistric_Esteroids_Occilionphagics(_Chirinophagics(_Chi</pre>
2053 2054 2055 2056 2057 2057 2057 2056 2057 2056 2057 2056 2057 2057 2057 2057 2057 2057 2057 2057	0 8 9 0 4 0 0 0 0 2 2 0 0 0 1 205 3 1 5 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 1 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>1 _ isterias_ invisions</pre>
2053 1054 1057 1057 1057 1057 1050 1060 1061 1063 1066 1067 1068 1066 1067 1068 1069 1070 1071 1072 1075 1075 1077 1075 1077 1077 1077 1079 1080 1081 1081	0 8 9 0 0 0 2 2 0 0 0 1 2 20 0 1 2 20 0 1 2 5 0 0 2 0 0 2 0 0 2 0 0 1 2 2 0 0 0 0 0 2 2 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>1 _ Lateria, _ IntriodesChardusOncloaprises/_OncloaprisesOncloaprisesOncloaprises 0 _ Lateria, _ IntroduscCarmaneorebakeria, _ CharabaperisesIntributeris. 0 - Lateria, _ Interbakeria, _ Carmaneorebakeria, _ Enterprises. 0 - Lateria, _ Interbakeria, _ Charabaperises, _ Nature, _ Interbakeria, _ Constructionaneore, _ Oncloaprises, _ Oncloaprises, _ Interbakeria, _ Carmaneorebakeria, _ Enterprise, _ Interbakeria, _ Carmaneorebakeria, _ Enterprise, _ Interbakeria, _ Carmaneorebakeria, _ Enterbakeria, _ Carmaneorebakeria, _ Enterbakeria, _ Carmaneorebakeria, _ Enterbakeria, _ Carmaneorebakeria, _ Enterbakeria, _ Contrabateria, _ Enterbakeria, _ Ent</pre>
2053 2054 2057 2057 2057 2057 2057 2063 2064 2064 2064 2065 2070 2071 2071 2070 2070 2070 2070 2070	0 8 9 0 4 0 0 0 0 2 2 0 0 0 1 205 3 1 5 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 1 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0		3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>1 Lateriag_Invirolates_Catridus_Oncloquinise_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises</pre>
1053 1054 1057 1057 1057 1057 1058 1060 1061 1063 1065 1066 1067 1066 1067 1070 1071 1072 1070 1071 1072 1070 1071 1072 1070 1071 1070 1071 1070 1071 1072 1075 1075 1075 1075 1075 1075 1075 1075	0 8 9 0 0 0 0 2 2 0 0 0 2 2 0 0 0 1 2005 3 1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0		1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 9 0 0 0 0 0 7 0 2 0 0 1 0 1 0 0 0 0 9 1	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>1 Lateriay_Inviolates_Catridus_Oncleaprises_Oncleaprises_Oncleaprises_Oncleaprises_ 0 Lateriay_Extension: Extensions_Catridus Catridus Catridu</pre>
2053 2054 2057 2057 2057 2057 2057 2063 2064 2064 2064 2065 2070 2071 2071 2070 2070 2070 2070 2070	0 8 9 0 4 0 0 0 0 2 2 0 0 0 1 205 3 1 5 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 1 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>1 Lateriag_Invirolates_Catridus_Oncloquinise_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises_Oncloquinises</pre>
1053 1054 1057 1057 1057 1057 1058 1060 1061 1063 1065 1066 1067 1066 1067 1070 1071 1072 1070 1071 1072 1070 1071 1072 1070 1071 1070 1071 1070 1071 1072 1075 1075 1075 1075 1075 1075 1075 1075	0 8 9 0 0 0 0 2 2 0 0 0 2 2 0 0 0 1 2005 3 1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 6 0 0 0 0 0 0 0 0 0 0 0 0 0		1 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 9 0 0 0 0 0 7 0 2 0 0 1 0 1 0 0 0 0 9 1	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>1 Lateriay_Inviolates_Catridus_Oncleaprises_Oncleaprises_Oncleaprises_Oncleaprises_ 0 Lateriay_Extension: Extensions_Catridus Catridus Catridu</pre>

1088	4	0	0	0	0	0	0	0	0	0	$0 \ k\_Bacteria; p\_Actinobacteriota; c\_Actinobacteria; a\_Streptosporangiales; f\_Thermomonosporaceae; g\_Actinomadura and the streptosporangiales; f\_Thermomonosporaceae; streptosporangiales; streptosporangiales; streptosporaceae; streptosporaceae; streptosporangiales; streptosporaceae; streptosporaceae; streptosporangiales; streptosporaceae; streptosporaceae; streptosporangiales; streptosporaceae; streptospora$
1089	4	0	0	0	0	D	0	D	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_B1-785;g_B1-785;s_
1090	o	5	0	0	D	D	10	D	1	o	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Propionibacteriale;;f_Nocardioidaceae;g_Marmoricola;s
1091	2	0	4	0	0	1	0	2	3	0	0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiac;o_Chthoniobacterale;;f_Chthoniobacteraceae;g_Chthoniobacter;s_
1092	0	0	1	0	4	4	0	0	0	0	0 k_Bacteria;p_Firmicutes:c_Clostridia;o_Clostridia_UCG-014;f_Clostridia_UCG-014;g_Clostridia_UCG-014;s_
1093	1	0	2	0	0	D	0	D	3	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Holosporales;f_Holosporaceae;g_;s_
1094	0	0	٥	8	0	D	0	D	0	0	0 k_Bacteria;p_Firmicute;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
1095	\$	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Acetobacteriales;f_Acetobacteriaceae;g_Acidiphilium;s
1096	3	0	1	0	1	3	0	0	2	0	0 k_Bacteria;p_Acidobacteriota;x_Subgroup_22;o_Subgroup_22;f_Subgroup_22;g_Subgroup_22;s_
1097	0	0	0	0	0	0	0	3	0	0	0 k_Bacteria;p_Chloroflexi;c_TK10;a_TK10;f_TK10;g_TK10;s_
1098	0	0	O	0	٥	D	1	0	2	0	0 k_Bacteria;p_Firmicutes;c_Clostrida;o_Oscillospirales;t_Ruminococcacea;g_Anaerotruncus;c_Anaerotruncus_colhominis
1099	0	0	0	0	0	0	0	2	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia vadin8860_group;f_Clostridia vadin8860_group;g_Clostridia vadin8860_group;g_
1100	0	0 4	0	0	0	0	0	0	2	0	0 k_Bacteria;p_Cyanobacteria;z_Cyanobacteria;zo_Phormide;miale;sf_Nodosilineaceae;j_Nodosilinea_PCC-7104;s_Nodosilinea_sp.
1101			1		0	1	0	0			0 k_Bacteriap_Bacteroidota;c_Bacteroidiap_Sphingobacteriales;f_Sphingobacteriaceae 2 k_Bacteriap_Cyanobacteriax_Cyanobacteria;p_Cyanobacteriales;f_Microcystaceaeg_Microcystis_PCC:78(4;s_Microcystis_aeruginosa
1102	° 0	0	0	0	2	D	0	D	1	0	
1103	1	0	o	0	0	2	0	3	0	0	0 k_Bacteria;p_Myxococcota;c_Myxococcia;o_Myxococcale;f_Anaeromyxobacteraceae;g_Anaeromyxobacter
1105	,	0	0	0	1	2	0	0	0	0	0 k_Bacteria;p_Bdellovibrionota;c_Bdellovibrionia;o_Bdellovibrionales;f_Bdellovibrionaceaeg_OM27_dades; 0 k_Bacteria;p_Protechacteria;c_Gammaprotechacteria;o_PITA13;t
1106	С 0	33	1	27	0	4	3	2	25	1	5 k_Bacteria;p_Firmicutex;c_Clostrida;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136_group;s_
1100	1	0	0	0	0	4 0	0	1	0	0	b C_exteringminuturesobstitutesoktionogeneticscalumogeneticscalumogeneticse_meeticse_groups 0 k_BacteringCyanobacteringCyanobacteringChloroplast/ChloroplastChloroplast
1108	0	0	1	0	0	z	0	D	6	o o	0 K_Bacteria;p_Cyalicoacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae
1109	1	0		0	o	1	0	D	0	0	0 k_aacteria;p_rrotebaacteria;oanningsbeeboacteria;obakhabeebines;onianondoactee 0 k_Bacteria;p_firmicutes;c_Clostrida;o_Docllospirale;f_Ruminococcaceae;g_;s
1110	;	0	0	0	0	0	0	0	2	0	0 k_Bacteria;p_Bacteroidota;c_Capabacteria;p_Kapabacteriale;s_Kapabacteriale;sKapabacteriale;s
1111	0	0	0	0	0	2	0	0	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria
1112	0	0	0	0	0	1	0	1	4	0	0 k_Bacteria;p_MBNT15;c_MBNT15;c_MBNT15;c_MBNT15;g_MBNT15;s_
1113	1	0	1	0	3	D	0	0	4	0	0 k_aucustasy_numrtasy_numrtasy_numrtasy_numrtasy_numrtasy_ 0 k_Bacteria:p_Cyanobacteria:c_Cyanobacteria:sa_Cyanobacteriale:r_Nostocaceae.g_Cuspidothnx_IMECYA_163:s_Cuspidothnx_Issatschenkol
1114	0	0	0	0	3	0	0	0	0	0	0 k_Bacteria;p_Cyanobacteria;c_Vampirivibrionia;o_Obscuribactera/es_f_Obscuribactera/esacsac;p_Obscuribactera/esacsac;s_
1115	6	0	2	o	1	1	0	0	3	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;p_Rhodobacterale;s_Ahodobacteraceae
1116	ō	83	1	2	1	0	3	0	0	0	0 k_akteria;p_Atlinobacteriota;c_Atlinobacteria;o_Micrococcales;f_Dermabacteriaceae;g_Brachybacterium
1117	1	1	1	1	1	D	0	0	0	0	0 k Bacteria;p Firmicute;c Clostridigo Lachnospirales/ Lachnospiracee;g 3
1118	0	0	0	0	0	0	0	0	0	3	0 k_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales
1119	1	0	0	0	2	0	0	0	0	0	0 k_Bacteria;p_Nitrospirota;c_Thermodesulfovibrioniaso;f;g;s
1120	0	0	0	0	2	0	0	0	0	0	0 k_Bacteria;p_Chloroflex;c_AnaeroTimea;p_AnaeroTimeales;f_AnaeroTimeaceae
1121	0	0	o	0	1	1	0	0	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_legionellales;f_legionellaceseg_legionella;s_
1122	3	0	o	0	o	0	0	0	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Streptosporangiales;f_Streptosporangiaceae;g_Thermopolyspora;s_Streptosporangiaceae_str.
1123	2	0	0	0	o	D	0	0	0	0	0 k_Bacteria;p_IXIA-33;c_IXIA-33;c_IXIA-33;f_IXIA-33;g_IXIA-33;;
1124	3	0	1	0	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;p_Rhizobiales;f_Rhizobiaceae;g_Aureimonas;s_Aureimonas;sp.
1125	0	0	0	0	0	0	0	3	0	0	0 k_Bacteria;p_Firmicutes;c_Bacill;c_Staphylococcates;f_Staphylococcacese;p_Nosocomiicoccus;
1125	o	0	o	0	D	D	0	D	3	o	0 k_Bacteria;p_Proteclaacteria;c_Gammaproteobacteria
1127	0	2	0	0	0	0	0	0	0	0	0 k_Bacteria
1128	1	0	2	0	0	1	0	4	1	o	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Hyphomonadaceae;g_SWB02;s_
1128 1129	1 0	0 0	2 0	0 0	0	1 3	0 0	4 D		o o	0 k_Bacteria;p_Froteobacteria;c_Aphaproteobacteria;p_Caudobacteria;es_Hyphomonadaceaeg_SWH02;s_ 0 k_Bacteria;p_Actinobactericta;c_Actinobacteria;p_Trankiale;f_Sponchtlyaceaeg_hgd_clude;s_
									1		
1129	o	0	O	0	o	3	o	D	1	o	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Frankiales;f_Sporichthyaceae;g_hgd_clade;s_
1129 1130	0 2	0 0	0 0	0 0	0 0	3 0	0 0	D 0	1 1 0	a O	0 k_bacteriuskctmobacteriotaxkctmobacteriusirranitalesf_Sporchthysoaseirgg_ctades 0 k_bacteria
1129 1130 1131	0 2 0	0 0 1	0 0 0	0 0 0	0 0 0	3 0 2	0 0 0	D 0 0	1 1 0 0	0 0 0	0 k_bacterias_hchinobacterias_Activobacterias_Irankialesf_5porchthysoaaeg_hogi_clades_ 0 k_bacteria 0 k_bacterias_Ovanobacterias_Cyanobacterias_Perudanabacnalesf_Perudanabacenaceaeg_Perudanabacena_PCC-7439
1129 1130 1131 1132	0 2 0	0 0 1 0	0 0 0	0 0 0	0 0 0	3 0 2 D	0 0 0	D 0 0 3	1 0 0 1	0 0 0	0 k_baterias_Attinobateridas_Attinobaterias_frankialesf_Sporchthysoaesg_hod_clades_ 0 k_bateria 0 k_baterias_Ovanchaterias_Covanobaterias_Perudarabaenaiesf_Perudanabaenaceasg_Perudanabaena_PCC7429 0 k_bateriasp_Protechateriasc_Cammuproteobateriaso_iogionelbias;f_uegionellaceasg_togionellass_
1129 1130 1131 1132 1133	0 2 0 0	0 0 1 0	0 0 0 2	0 0 0 0	0 0 0 0	3 0 2 D D	0 0 0 0	0 0 3 0	1 0 0 1 2	0 0 0 0	0 k_bsterius_htmobactariotac_Actrobactarius_frankialesf_Sporchthysoaaeg_hgd_clades
1129 1130 1131 1132 1133 1134	0 2 0 0 65	0 0 1 0 0	0 0 0 2 12	0 0 0 0 0	0 0 0 0 5	3 0 2 D 0 19	0 0 0 0 0	0 0 3 0 9	1 0 0 1 2 180	0 0 0 0 0	0 k_bateriusLetinobateriotacActinobateriusinaniuled_SportdHysaase_jigd_doks_ 0 k_baterius 0 k_bateriusOvenobateriusPeedanabaenetest_Peedanabaenetest_E-Peedanabaene_PCC7429 0 k_baterius_Protecobaterius_Gammuporteobateriuslegionelluises_Legionelluiseslegionelluises_ 1 k_baterius_Protecobaterius_Gammuporteobaterius_UMM/beccentest_Methylococcusess_ 0 k_baterius_Protecobaterius_Gammuporteobaterius_Peedanabaenetals_Peedanabaenetaleeneleeidomona
1129 1130 1131 1132 1133 1134 1135	0 2 0 0 65 0	0 0 1 0 0 0	0 0 0 2 12 2	0 0 0 0 0 0	0 0 0 0 5 0	3 0 2 0 19 0	0 0 0 0 0 0	0 0 3 9 0	1 0 1 2 180 0	0 0 0 0 0 0	0 k_bacteriusictinobacteriotac_Actmobacteriusirankiules(_sportchthysaese_jregi_dades
1129 1130 1131 1132 1133 1134 1135 1136	0 2 0 0 65 0 0	0 0 1 0 0 0 0	0 0 0 2 12 2 1	0 0 0 0 0 0	0 0 0 0 5 0	3 0 2 0 19 0 0	0 0 0 0 0 0	0 0 3 0 9 0	1 0 0 1 2 180 0 2	0 0 0 0 0 0	0 k_bsteriusictinobacteriosictinobacteriusirankialesf_sportchthysoaseg_logi_clades
1129 1130 1131 1132 1133 1134 1135 1136 1137	0 2 0 0 65 0 0 0	0 0 1 0 0 0 0 0 0	0 0 0 2 12 2 1 0	0 0 0 0 0 0 0	0 0 0 0 5 0 0	3 0 2 0 19 0 0 0	0 0 0 0 0 0 0	D 0 3 D 9 0 0 2	1 0 1 2 180 0 2 0	0 0 0 0 0 0 0	0 k_bsteriusActinobacteriusActinobacteriusinantialesf_Sporthitysoaseg_logi_dalesr
1129 1130 1131 1132 1133 1134 1135 1136 1137 1138	0 2 0 0 65 0 0 0	0 1 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0	0 0 0 0 0 0 0 0 0	0 0 0 0 5 0 0 0	3 0 2 0 19 0 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 3 9 0 0 2 0	1 0 1 2 180 0 2 0 2	0 0 0 0 0 0 0 0	b   bacterius _ Letinobacteriotatetinobacteriustransibled_Sportdbhysasse_jetit_doks b   bacterius
1129 1130 1131 1133 1134 1135 1136 1137 1138 1139	0 2 0 0 65 0 0 0	0 1 0 0 0 0 0 0 0 0	0 0 2 12 1 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 0 0 5 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 3 0 9 0 2 0 2 0	1 0 0 1 2 180 0 2 0 2 0 2 0	0 0 0 0 0 0 0 0 0	<ul> <li>b. Jacteriag _ ActinobacteriotacActinobacteriag_ republicled_Sporteblypasseg_jegd_cloke</li> <li>b. Jacteriag _ AntinobacteriagCareboacteriagPrevious basenatestPrevious basenatestRCG7429</li> <li>b. JacteriagProtechacteriagcommonstretebacteriagproducting_legonalitiestlegonalitiesteregonalitiester</li></ul>
1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140	0 0 0 65 0 0 0 0 2 0	0 1 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 0 5 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 2 0 0 2 0 0 2 2	1 0 0 1 2 180 0 2 0 2 0 2 0 0	0 0 0 0 0 0 0 0 0 0 0	0 k_bateriusictinobaterintacActrobaterintarankluksi_sportethiyaaseg_jegi_daksi_ 0 k_bateriustechnobaterintacConnobaterintac_Prevdanabasenaleseg_Provdanabasena_PSC7429 8 k_bateriustechnobaterintacCommuparteobaterintacteqionelbanesequinelbane 1 k_baterintactechnobaterintacdommuparteobaterintacteqionelbanesequinelbanesequinelbanes 0 k_baterintactechnobaterintacdommuparteobaterintactechnobaterintac_technobaterintacenterpointeobaterintac
1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140	0 0 0 65 0 0 0 0 2 0	0 1 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 0 5 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 2 0 0 2 0 0 2 2	1 0 0 1 2 180 0 2 0 2 0 2 0 0	0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jacteriag _ ActinobacteriotacActinobacteriag_ republicled_Sporteblypasseg_jegd_cloke</li> <li>b. Jacteriag _ AntinobacteriagCareboacteriagPrevious basenatestPrevious basenatestRCG7429</li> <li>b. JacteriagProtechacteriagcommonstretebacteriagproducting_legonalitiestlegonalitiesteregonalitiester</li></ul>
1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1141	0 0 0 65 0 0 0 0 2 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 5 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 2 0 0 2 0 0 2 2	1 0 1 2 180 0 2 0 2 0 0 0 0 0 0 0		<ul> <li>b  saterius_letinobacterios_archibasterios_ronklinesd_sporthtypases_jegi_daks_</li> <li>b  saterius_letinobacterios_Querobacterios_ronklinesd_sporthtypases_jegi_daks_</li> <li>b  saterius_Proteobacterios_Guerobacterios_ronklinesd_sporthtypases_jegi_daks_</li> <li>b  saterius_Proteobacterios_Guerobacterios_ronklinesd_sporthtypases_jegi_daks_</li> <li>b  saterius_Proteobacterios_Guerobacterios_ronklinesd_sporthtypases_jegi_daks_</li> <li>b  saterius_Proteobacterios_Guerobacterios_ronklinesd_sporthtypases_jegi_daks_</li> <li>b  saterius_Proteobacterios_Guerobacterios_ronklinesd_sporthtypases_Proteobacterios_ronklinesd_sporthtypases</li> <li>b  saterius_Descriptions_guerobacterios_proteobacterios_Proteobacterios_Ronklinesd_sporthtypases</li> <li>b  saterius_Proteobacterios_Abordios_Showparesky_Holdsportherg_Brotebacterios_</li> <li>b  saterius_Proteobacterios_Abordios_Babeliderd_UAN2009_UBA12409</li> <li>b  saterius_Proteobacterios_Abordios_Babeliderd_UAN2009_UBA12409</li> <li>b  saterius_Proteobacterios_Abordiosecterios_Babeliderd_Brotebacterios_Ronklinesd_sporthy_Brotebacterios_</li> <li>b    saterius_Proteobacterios_Babeliderd_UAN2009_UBA12409</li> <li>b    saterius_Proteobacterios_Babeliderd_Brotebacterios_Ronklinesd_sporthy_Babeliderus_</li> <li>b      saterius_Proteobacterios_Babeliderd_Brotebacterios_Ronklinesd_sporthy_Babeliderus_</li> <li>b                                      </li></ul>
1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145	0 0 65 0 0 0 2 0 2 0 2	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0 0 0 0 0 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 2 0 0 2 0 0 2 2	1 0 1 2 180 0 2 0 2 0 0 0 0 0 0 0		<ul> <li>b. Jackeriagketnobacteriataketnobacteriataproviduesjoordbity.usasejood_cloke</li></ul>
1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143	0 0 65 0 2 0 2 0 2 0 2 0 0 2 0 0 2 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 5 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 1 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 9 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0	1 0 1 2 190 0 2 0 0 0 0 0 0 0 0 0 0 1 7 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. lasteriusintroductoriusintroductoriusinvaluided_Sportchitysaese_jugit_dates</li></ul>
1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145	0 0 65 0 0 2 0 0 2 0 0 2 0 0 0 0 2 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0 0 0 0 0 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0	1 1 0 1 1 1 0 0 2 0 0 0 0 0 0 1 7 7		<ul> <li>b. bacteriasintende</li></ul>
1129 1130 1131 1132 1134 1135 1136 1137 1138 1139 1140 1141 1142 1144 1145 1144 1145 1146 1147	0 0 65 0 0 0 2 0 0 2 0 0 2 0 3	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 9 0 0 2 0 2 0 2 0 2 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 1 2 0 0 0 0	1 0 1 2 180 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacteriaslectendacteriasentrobacteriasrenkibled_joordhiyaaseg_jegi_daks</li></ul>
1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1141 1141 1143 1144 1145 1144	2 0 65 0 2 0 2 0 2 0 2 0 2 0 2 0 0 2 0 0 2 0 0 2 0 0 0 2 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 2 0 0 2 0 2 0 2 0 2 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0	1 0 1 2 180 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacteriasintende</li></ul>
1129 1130 1131 1132 1134 1135 1136 1137 1138 1139 1140 1141 1142 1144 1145 1144 1145 1146 1147	2 0 65 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 0 2 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 9 0 0 2 0 2 0 2 0 2 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 1 2 0 0 0 0	1 0 1 2 180 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. bacteriaslectendacteriasentrobacteriasrenkibled_joordhiyaaseg_jegi_daks</li></ul>
1129 1130 1131 1132 1134 1135 1136 1137 1138 1139 1140 1141 1142 1144 1145 1144 1145 1146 1147	2 0 65 0 0 0 2 0 0 2 0 0 2 0 0 0 2 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		3 0 2 0 19 0 0 0 0 0 1 0 0 1 0 0 0 1 2 0 0 1 2 0 0 1 2 0 0 0 1 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 0 3 0 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 1 2 180 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lacterias_letinobacterias_rentiboler[spredbybases_letinobacterias_letin</pre>
1129 1130 1331 1133 1133 1134 1135 1136 1136 1137 1138 1140 1141 1141 1141 1141 1144 1144 114	2 0 0 65 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 9 0 2 0 2 0 2 0 0 2 0 0 2 0 0 2 0 0 0 0	1 1 1 1 1 1 0 2 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b ladorius_lotinobacterius_renubacterius_renubacterius_loginordhiyaase_jagi.daks_ b ladorius_ b ladorius_Consobacterius_Peedenabacterius_leginordhiyaase_jagi.daks_ b ladorius_renobacterius_Gammiprotobacterius_leginordhiyaase_jaginoks. b ladorius_Protobacterius_Gammiprotobacterius_Verhiyacoccaese_leginologi. b ladorius_Protobacterius_Gammiprotobacterius_Verhiyacoccaese_leginologi. b ladorius_Protobacterius_Gammiprotobacterius_Verhiyacoccaese_leginologi. b ladorius_Protobacterius_Bahagenobacterius_Verhiyacoccaese_leginologi. b ladorius_Protobacterius_Bahagenobacterius_Nethylococcaese_Interdomonatorese_Preudomonatorese eliusterius_brotobacterius_Nethylococcaese Alladorius_Protobacterius_Bahagenobacterius_Nethylococcaese Alladorius_Protobacterius_Bahagenobacterius_Nethylococcaese eliusterius_Protobacterius_Bahagenobacterius_Nethylococcaese eliusterius_Protobacterius_Bahagenobacterius_Nethylococcaese eliusterius_Protobacterius_Gammiprotobacterius_Nethylococcaese eliusterius_Protobacterius_Gammiprotobacterius_Bahabdeniated_Honducteriuse eliusterius_Protobacterius_Gammiprotobacterius_Bahabdeniated_Honducteriuse eliusterius_Protobacterius_Gammiprotobacterius_Bahabdeniated_Honducteriuse eliusterius_functoreteriuse_Gammiprotobacterius_Bahabdeniated_Honducteriuse eliusterius_functoreteriuse_Gammiprotobacterius_Bahabdeniated_Honducteriuse eliusterius_functoreteriuse_Gammiprotobacterius_Lephoneteriuse_Honducteriuse eliusterius_functoreteriuse_Gammiprotobacterius_Lephoneteriuse eliusterius_functoreteriuse_Gammiprotobacterius_Bahabdeniated_Farenobionalese_Tatoretus_ eliusterius_Gamminomodots_Bahagenobacterius_Bahabdeniated_Farenobionalese_Tatoretus_ eliusterius_Gamminomodots_Bahagenobacterius_Bahaberiuse eliusterius_Gamminomodots_Bahagenobacterius_Mahagenobacterius_Bahaberiteriuse_Tatoretuse eliusterius_Gamminomodots_Bahagenobacterius_Bahaberiteriuse_Mahagenobacterius_Bahaberiteriuse eliusterius_firmicates_Gahagenobacterius_Mahagenobacterius_Mahagenobacterius_ eliusterius_Frotobacterius_Abhagenobacterius_Mahagenobacteriu</pre>
1129 1130 1131 1133 1134 1134 1134 1134 1134	2 0 0 66 0 0 2 0 0 2 0 0 2 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 3 0 9 0 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 1 2 180 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lactorias_checholactorias_retubustorias_resubusted_Sporthhysaes_jegt_data_ b lactorias_ b lactorias_checholactorias_Checholactorias_peedatabasedes_peedatabasedeses_peedatabasedeses_CGC429 c lactorias_retubustorias_cammporteobatintas_regionedinist_repondunases_regionedas_ b lactorias_retubustorias_cammporteobatintas_Peedatabasedest_Networbsoccesses_NetWiteoccesses_ b lactorias_retubustorias_Gammporteobatintas_UNA12009_UNA12009_ b lactorias_retubustorias_babeleses_Databalentas_UNA12009_UNA12009_ b lactorias_retubustorias_babeleses_Databalentas_UNA12009_UNA12009_ b lactorias_retubustorias_babeleses_Databalentas_UNA12009_UNA12009_ b lactorias_retubustorias_Lobabaterias_UNA12009_UNA12009_ b lactorias_retubustorias_Lobabaterias_UNA12009_UNA12009_ b lactorias_retubustorias_Lobabaterias_UNA12009_UNA12009_ b lactorias_retubustorias_Lobabaterias_UNA12009_UNA12009_ b lactorias_retubustorias_Lobabaterias_UNA12009_UNA12009_ b lactorias_retubustorias_Lobabaterias_UNA12009_UNA12009_ b lactorias_retubustorias_Cammporteobaterias_Unababerias[_BorbabateriasTobabaterias_ b lactorias_retubustorias_Gammporteobaterias_Unababerias[_BorbabateriasTobabaterias_ b lactorias_retubustorias_Gammporteobaterias_UnababeriastobabateriasTobabaterias_ b lactorias_retubustorias_Cammporteobaterias_Unababeriastobabaterias_Tobabaterias_ b lactorias_retubustorias_Cammporteobaterias_Unababeriastobabaterias_Tobabaterias_Tobabaterias_Tobabaterias_ b lactorias_retubustorias_Cammporteobaterias_Unababeriastobabaterias_Tobabaterias_ b lactorias_retubustorias_Cammporteobaterias_Unababerias_ b lactorias_retubustorias_Cammporteobaterias_Unababerias_Tobabaterias_Tobabaterias_Tobabaterias_Tobabaterias_Tobabaterias_ b lactorias_retubustorias_Cammporteobaterias_Unababerias_Tobabat</pre>
1228 1230 1231 1232 1233 1234 1235 1236 1237 1238 1247 1248 1247 1248 1247 1248 1247 1248 1247 1248 1259 1251	2 0 65 0 2 0 2 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 19 0 0 0 0 0 0 0 0 1 1 0 0 0 1 2 0 0 1 2 0 0 2 2 0 2 2 2 2		0 0 9 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0	1 0 0 1 2 80 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lactoriasintroductoriasintroductoriasinvaluides'_ispontitypasesindet_is b lactoriasintroductoriasforeclacitys_percelaristypases_indet_introductoriasintervalues_INCG749. b lactoriasintroductoriasanterprotoductoriasintervalues_intervalues_INCG749. b lactoriasinterductoriasanterprotoductorias_intervalues_intervalues_Intervalues_INCG749. b lactoriasintervalues_intervalues_intervalues_intervalues_Intervalues_INCG749. b lactorias_intervalues_intervalues_Intervalues_Intervalues_Intervalues_Intervalues_INCG749. b lactorias_intervalues_intervalues_In</pre>
1129 1130 1131 1133 1134 1135 1136 1136 1137 1138 1136 1141 1141 1141 1141 1141 1141 1144 1145 1144 1145 1141 1145 1	2 0 0 66 0 0 2 0 0 2 0 0 2 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 2 0 0 1 2 2 1 2 2 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 9 0 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	1 0 1 2 180 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lactorias_lactorias_lactorias_rankinksi_joordhiyaass_jood.dks b. lactorias_lactorias_Controlsc_Controlsc_Predenabarascontest_jood.actorias_lactorias_Controlscaturias_Gonomic Controlscaturias_lactorias_lactorias_Controlscaturias_lactoriascontest_jood.actoriascontestation.ac</pre>
1129 1130 1131 1132 1134 1135 1136 1137 1137 1138 1137 1137 1140 1141 1142 1142 1144 1145 1146 1147 1146 1147 1148 1146 1147 1148	0 0 66 0 2 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 1 2 0 0 1 2 0 0 2 1 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 9 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0	1 1 2 180 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b ladorius_lotinobacterius_renuberterius_renuberels_periordihysaes_jegt_date_ b laterius_ b laterius_consolutions_Consolutions_periordinatesies_jegtordihysaes_jegt_date_ b laterius_renobacterius_generalisesies_jegtordihysaes_jegtordihysaes_jegtordihysaes_ b laterius_renobacterius_Generalisesiesies_jegtordihysaes_jegtordihysaes_jegtordihysaes_ b laterius_renobacterius_Generalisesiesiesiesiesiesiesiesiesiesiesiesies</pre>
1129 1230 1331 1332 1333 1334 1335 1336 1337 1338 1339 1339 1339 1339 1340 1341 1345 1344 1345 1344 1345 1346 1345 1346 1345 1346 1357	0 0 66 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 1 2 0 0 1 2 0 0 1 2 0 0 1 2 0 0 0 0		0 0 9 0 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0	1 1 0 1 1 1 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lasterias_intendestanti</pre>
1128 1130 1131 1133 1133 1134 1135 1136 1137 1138 1134 1134 1134 1134 1134 1134 1134	0 0 66 0 2 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 1 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	a 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 9 0 0 2 0 2 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0	1 1 1 1 1 1 1 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b lasteriasinterbasteriasinstalactingsinstalactjourdhysessejout_data</pre>
1129 1129 1131 1131 1133 1134 1135 1136 1137 1138 1136 1141 1141 1141 1141 1141 1141 1141	0 0 65 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	a 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 2 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 0 2 0	1 1 2 1 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b ladorias_lothobachrinas_lothobachrinas_rankibed_joordhiyaase_jood_data</pre>
1129 1130 1131 1132 1134 1135 1136 1137 1138 1137 1138 1140 1141 1142 1142 1144 1144 1144 1144	0 0 66 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	a 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2		<pre>b ladorius_letholadorius_letholadorius_previousing_previousin</pre>
1129 1230 1331 1333 1334 1334 1335 1339 1339 1339 1339 1340 1341 1345 1346 1344 1345 1346 1347 1348 1349 1350 1351 1359 1353 1359 1355 1355 1355 1355	0 0 65 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 2 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 0 2 0	1 1 0 1 1 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b.lstories_chronotories_chronotories_productions_forcethingsame_joid_dois_ b.lstories_chronotories_chronotories_productions_forcething_logonalizes_logonalizes b.lstories_forcething_forcething_headeralizes[_expondingsame_joid_dois b.lstories_forcething_forcething_headeralizes[_expondingsame_joid_dois b.lstories_forcething_forcething_headeralizes[_expondingsame_joid_dois b.lstories_forcething_forcething_headeralizes[_expondingsame_joid_dois b.lstories_forcething_forcething_headeralize[_expondingsame_joid_dois b.lstories_forcething_forcething_headeralizes[_expondingsame</pre>
1129 1120 1121 1121 1121 1121 1123 1124 1124 1124	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	a 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0	1 1 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b ladorisy_locksbordsty_locksbordsty_provide/space/jocksbordstypace/jocksbordstypace/jocksbordstypace/spacebordstypace/spacebordstypace/spacebordstyp</pre>
1129 1129 1131 1131 1133 1134 1135 1136 1137 1138 1136 1141 1141 1141 1141 1141 1141 1141	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	000309002020200000202431122000102	1 1 2 180 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b.lstories_chrobacteriosenvironmenteductions_resolutions_logicality_ b.lstories_chrobacterios_Camparetobacterios_equiresting_Legicality_environmenteductions_COC749. b.lstories_Protosacterios_Camparetobacterios_Protosambaceseq_Legicality_environmenteductionsProtosacterios_Protosacte</pre>
1129 1130 1131 1132 1134 1135 1136 1137 1138 1137 1138 1141 1142 1142 1144 1144 1144 1145 1151 1151	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0			3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		000200202020202024311220002026	1 1 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b ladoriay_lockobschedus_lockobschedus_produkteriay_</pre>
1229 1230 1231 1232 1234 1235 1236 1237 1238 1247 1248 1244 1244 1244 1244 1244 1244 1244	0 0 6 6 0 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 12 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	000309002020200000202431122000102	1 1 2 180 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b.lstories_chrobacteriosenvironmenteductions_resolutions_logicality_ b.lstories_chrobacterios_Chrobacterios_resolutions_logicality_logicality_logicality_ b.lstories_freeductions_commenteductions_resolutions_logicality_logicality_logicality_ b.lstories_freeductions_commenteductions_whytheococcess_logicality_logicality_ b.lstories_freeductions_devices_babelies_logicality_logica</pre>

1166	0	0	0	0	0	1	0	0	3	0	0 k_Bacteria;p_Firmicute;sc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Flavonifractor;s_
1167	2	0	1	0	0	D	0	0	0	0	0 k_Bacteria;p_Desulfobacterota;c_Desulfuromonadia;o_Desulfuromonadia;f_Geothermobacteracea;sg_Geothermobacter;s_
1168	2	0	o	0	1	1	0	D	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Gammaproteobacteria_incertae_Sedis;f_Unknown_Family;g_Unknown_Family;s_
1169	0	0	0	0	0	0	0	1	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterale;sf_Steroidobacteraceae;g_;s_
1170		0	2	0	0	0	0	0 2	1	0 0	0 k_Bacteria;p_Planttomycetota;c_Planctomyceto;vo_Gemmatale;;f_Gemmataceae; <u>p_;s_</u>
1172	0	0	o	0	o	D	0	4	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria 0 k_Bacteria;p_Chloroflexic_Gitt G5-136:6_Gitt G5-136:f_Gitt G5-136:g_Gitt G5-136:5_
1173	0	0	0	0	0	0	2	0	0	0	
1174	2	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Bdellovibrionota;c_Bdellovibrionia;o_Bdellovibrionales;f_Bdellovibrionaceae;g_OM27_clade;s_
1175	0	3	a	0	0	0	0	0	0	0	0 K_akteria 0 k_Bacteria
1176	3	0	0	0	D	4	0	0	5	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_TRA3-20;g_TRA3-20;s_
1177	0	0	0	0	0	0	0	2	0	0	0 k Bacteria;p Proteobacteria;c Alphaproteobacteria;o Elisterales;f ;g ;s_
1178	0	0	5	0	0	0	0	0	0	0	0 k Bacteria:p Firmicutes:c Negativicutes:o Veillonellales-Selenomonadales.f Veillonellaceae:g Dialister:s Dialister micraerophilus
1179	0	0	2	0	0	0	0	0	0	0	0 k_Bacteria
1180	5	0	0	0	0	2	0	0	2	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Sphingobacteriales;f_AKYH767;8_AKYH767;s_
1181	0	0	o	0	o	o	o	2	0	σ	0 k_Bacteria;p_Chloroflextc_Anaerolineae;o_SBR1031;f_AMb;g_AMb;s_
1182	1	0	σ	0	2	D	0	2	1	σ	0 k_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales:f_Bryobacteraceae;g_Bryobacter;s
1183	0	0	1	0	0	2	0	1	0	0	0 k_Bacteria
1184	0	0	0	0	0	0	0	0	2	0	$0 \ k\_Bacteria; p\_Deferrisomatota; r\_Defferrisomatia; o\_Defferrisomatales; f\_Defferrisomatacese; g\_Deferrisoma; s\_Deferrisomatacese; g\_Deferrisomatota; r\_Defferrisomatacese; g\_Deferrisomatacese; g\_Deferrisomatota; r\_Defferrisomatacese; g\_Deferrisomatacese; g\_Deferri$
1185	4	0	3	0	0	1	0	0	0	0	$0\ k\_Bacteria; p\_Proteobacteria; c\_Alphaproteobacteria; a\_Sphingomonadales; f\_Sphingomonadaceae; g\_Novosphingobium and the sphingobium and the s$
1186	3	0	0	0	1	D	0	1	1	σ	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Frankiales;f_Sporichthyaceae;g_hgcl_clade;s
1187	0	0	σ	0	z	D	0	D	0	σ	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria
1188	0	0	0	0	0	0	0	0	3	0	0 k_Bacteria;p_Firmicute;sc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Roseburia;s_
1189	1	0	2	0	2	1	0	0	1	0	0 k_Bacteria
1190	0	0	0	0	D	D	0	D	0	2	0 Unknown
1191	0	0	0	0	D	2	0	12	3	o	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria
1192	0	0	0	0	1	0	0	0	1	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Bunkholderiales;f_TRA3-20;g_TRA3-20;s_
1193	2	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Myxxcxcccta;c_Polyangia;o_Polyangiales;f_Blrii41;g_Blrii41;s_
1194	0	0	0	0	0	0	0	0	2	0	0 k_Bacteria;p_Gemmatimonadota;x_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_;s_
1195	3	1	20	8	3	4	1	10	5	0	2 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidaies;f_Rikenellaceae;g_Alistipes;s_
1196	0	0	3	0	0	1	0	0	0	0	0 k_Bacteria;p_Gemmatimonadotax_B02-11_terrestrial_group;o_B02-11_terrestrial_group;f_B02-11_terrestrial_group;g_B02-11_terrestrial_group;s_
1197	0	2	0	0	0	0	0	3	0	0	0 k_Bacteria;p_Acidobacteriota;c_Vicinamibacteria;o_Vicinamibacterale;f_Vicinamibacteraceae;g_Vicinamibacteraceae;s_
1198	٥	0	2	0	0	0	0	1	0	Q	0 k_Bacteria;p_Myxococota;c_Polyangia;o_Haliangiales;f_Haliangiaceae;g_Haliangiurn
1199	2	0	a	0	0	0	0	0	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales/_Neisseriaceae;g_Neisseria;k_Neisseria;elongata
1200	0	0	3	0	0	D	0	4	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiaks:f_Rhodocyclaceae;g_;s_
1201	0	0	0	0	2	0	0	0 7	2	0	0 k_Bacterixp_Bacteroidots;c_Bacteroida.o_Cytophagaiesf_Cytophagaeeaeg_Cytophagas0 0 k_Bacterixp_Proteobacteriacc_Gammaproteobacteriaco_Burkholderialess/_Nitrovarronadsceaeog_15.445,
1202	1	0	0	0	1	0	0	0	0	0	0 k_bacteria;p_frincular.cenac_clostridia;o_lachnospirales;f_lachnospiraceae;g_s_
1204	0	0	o	0	0	D	0	4	0	0	0 k_Bacteria;p_Chloroffex;c_IG30-KF-CM66;o_IG30-KF-CM66;f_IG30-KF-CM66;s_IG30-KF-CM66;s_
1205	0	0	0	0	0	0	0	3	0	0	0 )_Becterian_Protocolacterian_Mahaproteolacterian_Bhizobiales
1205 1206	0 2	0 0	0 0	0 0	0 3	0 D	0 0	3 D	0 0	0 0	0 k_Bacteriaxg_Protobacteriax_Mehaprotoblacteriazp_Bhipoblaks 0 k_Bacteriaxp_Protobacteriax_Cammaprotoblacteriax_CelluBronalest_Portscoccceae.g_Portscoccuss_
1206 1207 1208	2	0 0 0	0 3 23	0 0 2	3 0 11	D 2 23	0 0	0 3 42	0 6 255	0 0 0	0 k_Bisteria,p_Proteolacteria,c_Cammaproteolacteria.o_Cell+Bronales/_Portcoaccese.g_Portcoacces.g_ 0 k_Bisteria,p_Proteolacteria,c_Cammaproteolacteria.o_Bist/holdenaiss/_Comamonadaceae.g_Dimohabitanus 0 k_Bisteria,p_Proteolacteria,c_Gammaproteolacteria,o_Previotnomadaicuf_Previotnomadaceae.g_Previotnomas
1206 1207 1208 1209	2 0 154 3	0 0 0	0 3 23 0	0 0 2 0	3 0 11 0	0 2 23 0	0 0 0	0 3 42 0	0 6 255 0	0 0 0	0 k_Bisteria,p_Protokolactinia_C_Gammaprotoobacteria.p_GelinBironales(_Porticoccoses eg_Porticoccuss_ 0 k_Bisteria,p_Protokolactinia,c_Gammaprotoobacteria.p_Bistholderales/_Comanonadaceseg_Dimmohabitanis_ 0 k_Bisteria,p_Protokolactinia,c_Gammaprotoobacteria.p_Providemenadales(_Providemenadaceae_Providemenas) 0 k_Bisteria
1206 1207 1208 1209 1210	2 0 154	0 0 0 0	0 3 23 0 0	0 0 2 0 0	3 0 11 0 5	0 2 23 0 1	0 0 0 0	0 3 42 0 0	0 6 255 0 1	0 0 0 0	0 k_Bisteriap_Protechacteriac_Cammaprotechacteriao_Cellubronales/Porticoccosesez_Porticoccuss_ 0 k_Bisteriap_Protechacteriac_Cammaprotechacteriao_Buthialderales/_Comanonadacesez_Liminohabtrinss_ 0 k_Bisteriap_Protechacteriac_Cammaprotechacteriao_Presidomonadalesi/_Presidomonadacesez_Presidomonas 0 k_Bisteriap_Protechacteriac_Cammaprotechacteriao_Ingiorebias;_Lagoneliacesez_Legonelias_
1206 1207 1208 1209 1210 1211	2 0 154 3 0 2	0 0 0 0 0	0 3 23 0 0 0	0 0 2 0 0 0	3 0 11 0 5 0	D 2 23 0 1 0	0 0 0 0	0 3 42 0 0 0	0 6 255 0 1 0	0 0 0 0	0 k_Bisteriag_Protechacteriag_Cammaproteobacteriag_Cellubrooxies/_Partocacceseg_Partocaccus_ 0 k_Bisteriag_Protechacteriag_Cammaproteobacteriag_BistholderSkif_Commonaducaseg_Unmobubitrass_ 0 k_Bisteriag_Protechacteriag_Cammaproteobacteriag_Piesdomonadaksif_Piesdomonadaccesg_Piesdomonas 0 k_Bisteriag_Protechacteriag_Cammaproteobacteriag_legionelluss_Legionellaccesg_legionellus_ 0 k_Bisteriag_Notechacteriag_Cammaproteobacteriag_legionelluss_Legionellaccesg_legionellus_
1206 1207 1208 1209 1210 1211 1212	2 0 154 3 0 2 0	0 0 0 0 3	0 3 23 0 0 0 0	0 0 2 0 0 0 0	3 0 11 0 5 0	0 2 23 0 1 0 0	0 0 0 0 0 0	0 3 42 0 0 0 0	0 6 255 0 1 0	0 0 0 0 0	0 I _Bsteriag_Protebacteriag_Campapotebacteriag_Cellubrooxlesf_Partococceseg_Portococces_ 0 k_Bsteriag_Protebacteriag_Campapotebacteriag_Bubbaldersksf_Comprovaduceseg_Lumobubbtrss_ 0 k_Bsteriag_Protebacteriag_Protebacteriag_Protebacteriag_Proteomonadicsf_Proteomonadocceg_Protebacteriag_ 0 k_Bsteriag_Protebacteriag_Campapotebacteriag_legioneliasf_logioneliaceeg_legionelias_ 0 k_Bsteriag_Protebacteriag_Campapotebacteriag_Bioinformationsf_Logioneliaceeg_legionelias_ 0 k_Bsteriag_Protebacteriag_Campapotebacteriag_legioneliasf_Logioneliaceeg_legionelias_ 0 k_Bsteriag_Antisk_Protebacteriag_Campapotebacteriag_legioneliasf_Logioneliaceeg_legionelias_ 0 k_Bsteriag_Antisk_Protebacteriag_Mstick_Mstick_Mstick_Protebacteriag_Legioneliasf_Logioneliaceeg_legioneliasf_
1206 1207 1208 1209 1210 1211 1212 1213	2 0 154 3 0 2 0 0	0 0 0 0 3 0	0 3 23 0 0 0 0 0	0 2 0 0 0 0 0	3 0 11 0 5 0 0 0	0 2 23 0 1 0 0 0	0 0 0 0 0 0 0	0 3 42 0 0 0 0	0 6 255 0 1 0 0 2	0 0 0 0 0 0	0 k_Bateriag_Protebacteriag_Cammaporteobacteriag_Cellubrowskef_Portcoccose_g_Portcoccoss_ 0 k_Bateriag_Protebacteriag_Cammaporteobacteriag_Butholderskef_Commonodaceaeg_Ummohabtinss_ 0 k_Bateriag_Proteobacteriag_Cammaporteobacteriag_Proteoborneodelsef_Preudomonadesceg_Proudomonal 0 k_Bateriag_Proteobacteriag_Cammaporteobacteriag_Proteoborneodelsef_Preudomonadesceg_Proudomonal 0 k_Bateriag_Proteobacteriag_Cammaporteobacteriag_Proteoborneodelsef_Preudomonadesceg_Proteoborneodesceg_Proteobacteriag_Proteob
1206 1207 1208 1209 1210 1211 1212 1213 1214	2 0 154 3 0 2 0 0 0 0	0 0 0 0 3 0 0	0 3 23 0 0 0 0 0	0 0 2 0 0 0 0 0 0	3 0 11 0 5 0 0 0	0 2 23 0 1 0 0 0	0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 0	0 6 255 0 1 0 0 2 1	0 0 0 0 0 0	0 I_Bacteriag_Proteobacteriag_Commaproteobacteriag_CelluBronales(_Particoccuse_g_Particoccus_     1 Lacteriag_Proteobacteriag_Commaproteobacteriag_Proteo
1206 1207 1208 1209 1210 1211 1212 1213 1214 1215	2 0 154 3 0 2 0 0 0 0	0 0 0 0 3 0 0 0	0 3 23 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0	3 0 11 0 5 0 0 0 1	0 2 23 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 3	0 6 255 0 1 0 0 2 1 0	0 0 0 0 0 0 0 0	<ul> <li>b _Bateriag_Protechateriag_Cammaporteobateriag_Cellularooles(_Portcoaccese_g_Portcoacce</li></ul>
1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216	2 0 154 3 0 2 0 0 0 0 0	0 0 0 0 3 0 0 0 0	0 3 23 0 0 0 0 0 0 5	0 2 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 0 1 0 2	D 2 23 0 1 0 0 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 3 0	0 6 255 0 1 0 2 1 0 1	0 0 0 0 0 0 0 0	<ul> <li>b _Bsteries_Protechacteries_Cammaporteobacteries_Cellubrooxies/_Partococcese_2_Portococces_</li> <li>b _Bsteries_Protechacteries_Cammaporteobacteries_Previoenceses_2_ferioences</li> <li>b _Bsteries_Protechacteries_Cammaporteobacteries_legionelluss_legionellucese_legionellus_</li> <li>b _Bsteries_Protechacteries_Cammaporteobacteries_legionelluss_legionellucese_legionellus_</li> <li>b _Bsteries_Protechacteries_Cammaporteobacteries_Horemonscieles/_Incommonscieles_legionellus_</li> <li>b _Bsteries_Protechacteries_Cammaporteobacteries_legionelluss_legionellucese_legionellus_</li> <li>b _Bsteries_Astrobacteries_Cammaporteobacteries_Horemonscieles/_Incommonscieles_legionellucese_legionellus_</li> <li>c _Bsteries_Astrobacteries_Astrobacteries_Horemonscieles/_Incommonscieles/_SteriesesesSalinisores</li> <li>c _Bsteries_Astrobacteries_Astrobacteries_Jensiles/_Sortboacteries_Protechacteries</li> <li>c _Bsteries_Protechacteries_Astrobacteries_Fersiles/_SortboacteriesProtechacteries</li> <li>c _Bsteries_Protechacteries_Astrobacteries_Fersiles/_Sortboacteries_Protechacteries</li> <li>c _Bsteries_Protechacteries_Cammaporteobacteries_Sourcesed_ProtechacteriesesSolitioneres</li> <li>c _Bsteries_Protechacteries_Cammaporteobacteries_Fersiles</li> <li>c _Bsteries_Protechacteries_Cammaporteobacteries_Sourceseses_CashacteriesesNotechandere</li> <li>c _Bsteries_Protechacteries_Cammaporteobacteries_SourcesesesesesNotechandere</li> <li>c _Bsteries_Protechacteries_Cammaporteobacteries_CashacteriesesesesesesNotechander</li></ul>
1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217	2 0 154 3 0 2 0 0 0 0	0 0 0 0 0 3 0 0 0 0 0	0 3 23 0 0 0 0 0 0 5 1	0 2 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 1 0 2 0	D 2 23 0 1 0 0 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 3	0 6 255 0 1 0 2 1 0 1 0	0 0 0 0 0 0 0 0 0 0	0 i _Bsteriag_Protebacteriag_Cammaproteobacteriag_Cellubrooxiesf_Portcoccose_g_Portcoccose_ 0 k_Bsteriag_Protebacteriag_Cammaproteobacteriag_Portcoccose_g_Portcoccose_g_Portcoccose_ 0 \_Bsteria 0 \_Bsteria 0 \_Bsteria 0 \_Bsteria 0 \_Bsteria 0 \_Bsteria 0 \_Bsteriag_Protebacteriag_Cammaproteobacteriag_ingioneliass_ 0 \_Bsteriag_Protebacteriag_Cammaproteobacteriag_Ingioneliass_ 0 \_Bsteriag_Protebacteriag_Cammaproteobacteriag_Ingioneliass_ 0 \_Bsteriag_Protebacteriag_Cammaproteobacteriag_Ingioneliass_ 0 \_Bsteriag_Protebacteriag_Cammaproteobacteriag_Ingioneliass_ 0 \_Bsteriag_Protebacteriag_Astrobacteriag_Cammaproteobacteriag_Ingioneliass_ 0 \_Bsteriag_Protebacteriag_Cammaproteobacteriag_ProteingentUncomergeproteose_g_Solitioperas_ 0 \_Bsteriag_Protebacteriag_Cammaproteobacteriag_Proteing_Proteing_ProteingentUncomerg_ToriagentUncomerg_ProteingentUncomerg_ToriagentUncomerg_ProteingentUncomerg_ToriagentUn
1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216	2 0 154 3 0 2 0 0 0 0 0 1 1	0 0 0 0 3 0 0 0 0	0 3 23 0 0 0 0 0 0 5	0 2 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 0 1 0 2	D 2 23 0 1 0 0 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 3 0 0	0 6 255 0 1 0 2 1 0 1	0 0 0 0 0 0 0 0	<ul> <li>b [asteria_Protobacteria_C_Simaportobacteria_Collaboration_Coll</li></ul>
1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219	2 0 154 3 0 2 0 0 0 0 0 1 1 0	0 0 0 0 3 0 0 0 0 0 0	0 3 23 0 0 0 0 0 0 5 1 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 1 0 1 0 2 0 0	D 2 23 0 1 D 0 0 0 1 D 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 0 3 0 0 5	0 6 255 0 1 0 2 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0	<ul> <li>b _ lasteriag_frotesbacteriag_contexturiag_cellularooleg(_Portcoccuse_g_Portcoccus</li></ul>
1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218	2 0 154 3 0 2 0 0 0 0 1 1 0 1	0 0 0 0 3 0 0 0 0 0 0 0 0	0 3 23 0 0 0 0 0 5 1 0 5	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 1 0 1 0 2 0 0 2	0 2 3 0 1 0 0 1 0 1 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 3 0 0 5 0	0 6 255 0 1 0 2 1 0 1 0 1 0 0 0	0 0 0 0 0 0 0 0 0 0	<ul> <li>b _bsteries_Protechacteries_Cammaportechacteries_Cellularionalist_Particuccuss_Protechacteries_Lineachacteries_Cammaportechacteries_Butholderistsf_Commonadiceseg_Lineachacteries_</li> <li>b _bsteries_Protechacteries_Centreprotechacteries_legionelizeseg_legionelizes</li> <li>b _bsteries_Protechacteries_Centreprotechacteries_legionelizeseg_legionelizeseg_legionelizes</li> <li>b _bsteries_Protechacteries_Centreprotechacteries_Scienceseg_Networksetseg_Sterieses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Scienceseg_Networksetseg_Sterieses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Scienceseg_Networksetseg_Sterieses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Scienceseg_Networksetseg_Sterieses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Scienceses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Scienceses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Scienceses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Scienceses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Scienceses</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Centreprotechacteries</li> <li>c _bsteries_Protechacteries_Centreprotechacteries_Centreprotechacteries</li> <li>c _bsteries_Protechacteries_Lendersoteries_Centreprotechacteries</li> <li>c _bsteries_Protechacteries_Lendersoteries_Protechacteries</li> <li>c _bsteries_Protechacteries_Lendersoteries</li> <li>c _bsteries_Protechacteries_Protechacteries</li> <li>c _bsteries_Protechacteries_Protechacteries</li> <li>c _bsteries_Protechacteries_Protechacteries</li> <li>c _bsteries_Protechacteries_Protechacteries</li> <li>c _bsteries_Protechacteries_Protechacteries</li> <li>c</li></ul>
1.206 1.207 1.208 1.209 1.210 1.211 1.212 1.213 1.214 1.215 1.216 1.217 1.218 1.219 1.220	2 0 154 3 0 2 0 0 0 0 1 1 0 1	0 0 0 0 3 0 0 0 0 0 0 0 0	0 3 23 0 0 0 0 0 5 1 0 5	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 1 0 1 0 2 0 0 2	0 2 3 0 1 0 0 1 0 1 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 3 0 0 5 0	0 6 255 0 1 0 2 1 0 1 0 1 0 0 0	0 0 0 0 0 0 0 0 0	<ul> <li>b _ lasteriag_frotesbacteriag_contexturiag_cellularooleg(_Portcoccuse_g_Portcoccus</li></ul>
1.206 1.207 1.208 1.209 1.210 1.211 1.212 1.213 1.214 1.215 1.216 1.217 1.218 1.219 1.220 1.221	2 0 154 3 0 2 0 0 0 0 1 1 0 1	0 0 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0	0 3 23 0 0 0 0 0 5 1 0 5	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 1 0 1 0 2 0 0 2	0 23 0 1 0 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 3 0 0 5 0	0 6 255 0 1 0 2 1 0 1 0 1 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b _bsteries_Protechaderies_Gammaproteobaterias_Geleberoolest_Partococcese_g_Portococces_</li> <li>b _bsteries_Protechaderies_Gammaproteobaterias_Presidemonasiski_Presi</li></ul>
1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221	2 0 154 3 0 2 0 0 0 0 1 1 0 1	0 0 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0	0 3 28 0 0 0 0 0 0 0 0 5 1 0 5 1 0 5	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 0 1 0 2 0 0 2 0 0 2 0 0 0 2 0 0 0 0	0 23 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 3 0 0 5 0 1 0 2	0 6 2255 0 1 0 2 1 0 0 0 0 0 0 0 0 0 2 0 0 0 0 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jasterias, Protesbacterias, Cammaportesbacterias, University, Portocaccese g. Pertocaccese</li> <li>b. Jasterias, Protesbacterias, Cammaportesbacterias, Neudonomatikus (Presidonomatikus), Presidonomatikus, Presidonom</li></ul>
1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222	2 0 154 3 0 0 0 0 1 1 0 1 0 1 0 1 0 1 0 1	0 0 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 28 0 0 0 0 0 0 0 0 5 1 0 5 1 0 5 1 0 0 5	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 0 0 1 0 0 0 2 0 0 0 0 0 0 0 0 0	0 2 33 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 0 3 0 0 5 0 1 0 2 0	0 6 2255 0 1 0 2 1 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jasterias, Proteskacterias, Cammaporteskacterias, Bukholderiatef, Portocaccese g. Pertocaccus.</li> <li>b. Jasterias, Proteskacterias, Cammaporteskacterias, Muhholderiatef, Commonodaccesg_Lumobabtras,</li> <li>b. Jasterias, Proteskacterias, Gammaporteskacterias, Jestadomondalcus/Proteodomondalcus/Laponellas.</li> <li>b. Jasterias, Proteskacterias, Gammaporteskacterias, Jestadomondalcus/Laponellaceseg_Lumobabtras,</li> <li>b. Jasterias, Proteskacterias, Gammaporteskacterias, Jestadomondalcus/Laponellaceseg_Lumobabtras,</li> <li>b. Jasterias, Proteskacterias, Gammaporteskacterias, Jestadomondalcus/Laponellaceseg_Laponellace</li> <li>b. Jasterias, Proteskacterias, Cammaporteskacterias, Jestadomonasonaleus, Proteskacterias, Gammaporteskacterias, Proteskacterias, Jestadomonasonaleus, Micromonosonaleus, Micromonosonaleus, Jestadomonasonaleus, Jestadomonasonaleus, Jestadomonasonaleus, Jestadomonasonaleus, Proteskacterias, Activabatorea, Antenbacterias, Proteinasonaleus, Jestadomonasonaleus, Jestad</li></ul>
1206 1207 1208 1209 1210 1211 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223	2 0 154 3 0 0 0 0 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 28 0 0 0 0 0 0 0 5 1 0 5 1 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 0 0 0 1 0 0 2 0 0 0 0 0 0 0 0 0	0 2 33 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 0 3 0 0 5 0 1 0 2 0 2 0 2	0 6 255 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jasterias_Protechacterias_Cammaportechacterias_Celebranoseis/_Partocaccese_2_Pertocaccus_</li> <li>b. Jasterias_Protechacterias_Cammaportechacterias_Burbholdersiter/_CommonadaccesJureabubbtras_</li> <li>b. Jasterias_Protechacterias_Germaportechacterias_legranomadaccesIncodences</li> <li>b. Jasterias_Protechacterias_Germaportechacterias_legranomadacceslegranomadaccesIncodences</li> <li>b. Jasterias_Protechacterias_Cammaportechacterias_legranomadacceslegrano</li></ul>
1206 1207 1208 1209 1210 1211 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224	2 0 154 3 0 0 0 0 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 28 0 0 0 0 0 0 5 1 0 5 1 0 0 0 0 0 0 0 2	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 11 0 5 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0	0 2 23 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 0 3 0 0 5 0 1 0 2 0 2 0 2	0 6 255 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b _bisteriag_Protechacteriag_Cammaportechacteriag_Calibrationalsel_Participacusig_Opticipacusig_Optications_</li> <li>b _bisteriag_Protechacteriag_Cammaportechacteriag_Participacusig_OpticationsProtechacteriag_Optications_Protechacteriag_Optications_Protechacteriag_Optications_Optic</li></ul>
1206 1207 1208 1209 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1223	2 0 154 2 0 0 0 0 1 1 0 1 0 1 0 0 1 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 28 0 0 0 0 0 5 1 0 5 1 0 0 0 0 0 0 2 3	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 11 0 5 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	0 2 23 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 0 3 0 0 5 0 1 0 2 0 2 0 2	0 6 255 0 1 0 2 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jasterias_frotesbacterias_cammaportesbacterias_elluktoolesis_frotescacese_intercocus_</li> <li>b. Jasterias_frotesbacterias_cammaportesbacterias_buktoolesistif_commonodacese_intercocus_</li> <li>b. Jasterias_frotesbacterias_cammaportesbacterias_hastoonesiatesi_frotescaceses_lengumbletras_</li> <li>b. Jasterias_frotesbacterias_frotesbacterias_intercocusterias_frotescaceses_lengumbletras_</li> <li>b. Jasterias_frotesbacterias_frotesbacterias_intercocusterias_frotescaceses_intercocusterias_frotesbacterias_frotes</li></ul>
1206 1207 1208 1201 1211 1212 1213 1214 1215 1216 1217 1218 1220 1221 1222 1223 1224 1225 1226	2 54 3 0 0 0 0 0 0 1 1 0 0 1 0 0 1 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 23 0 0 0 0 5 1 0 5 1 0 5 1 0 0 0 2 0 0 2 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 11 0 5 0 0 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 23 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 0 3 0 0 5 0 1 0 2 0 2 0 2	0 6 255 0 1 0 2 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jasteria, Proteskacteria, Cammaporteskacteria, Michaelsei, Portacacuse, Portacacus,</li> <li>b. Jasteria, Proteskacteria, Cammaporteskacteria, Jeuchholeriater, Cammonodacuse, Lumohabtura,</li> <li>b. Jasteria, Proteskacteria, Gammaporteskacteria, Jeuchholeriater, Jeuchonomaticus, Lumohabtura,</li> <li>b. Jasteria, Proteskacteria, Cammaporteskacteria, Jeuchholeriater, Jeuchonomaticus, Jeuchonomaticus</li></ul>
1208 1207 1208 1209 1210 1211 1212 1213 1214 1214 1215 1216 1217 1221 1221 1221 1222 1223 1224	2 54 3 0 0 0 0 0 0 1 1 0 0 1 0 0 1 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 23 0 0 0 0 5 1 0 5 1 0 5 1 0 0 0 2 0 0 2 0 0 2 0 0 8	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 5 0 0 1 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0	0 2 3 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 6 255 0 1 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Justeriag_Protestactrisg_Cammaportestactrisg_Behaviorestact_ParticipacussProtectacuss</li></ul>
1268 1267 1268 1210 1211 1211 1213 1214 1214 1215 1214 1215 1217 1228 1227 1228 1227 1228 1227 1228	2 54 3 0 0 0 0 0 1 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 1 5 5 1 5 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 23 0 0 0 0 0 5 1 0 5 1 0 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 2 0 0 0 0 2 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 11 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 3 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 2 0 2 0 2 0 2 0 2	0 6 255 0 1 0 2 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Justerias_Protesbacterias_Gammaportesbacterias_Bubbieleriater_Commonadicase_Unmobibitats_</li> <li>b. Justerias_Protesbacterias_Gammaportesbacterias_lextbioleriater_Commonadicase_Unmobibitats_</li> <li>b. Justerias_Protesbacterias_Gammaportesbacterias_lextbioleriater_Lextbiolecieselextbioleciese_lextbioleciese_lextbioleciese_lextbiolecieselextbiolecieselextbiolecieselextbiolecieselextbioleciese_lextbioleciese_lextbioleciese_lextbiolecieselextbiolecieselextbiolecieselextbiolecieselextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese_lextbioleciese</li></ul>
1268 1267 1268 1210 1210 1211 1212 1214 1214 1215 1216 1216 1227 1228 1228 1228 1228	2 54 3 0 0 0 0 0 1 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 1 5 5 1 5 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 23 0 0 0 0 0 5 1 0 5 1 0 0 0 2 0 0 2 0 0 3 0 0 3 0 0 3 0 0 3 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 5 0 0 0 0 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	D 2 3 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 3 0 0 5 0 1 0 2 0 2 0 2 9 1 0	0 6 255 0 1 0 2 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jasterias, Proteskacterias, Cammaporteskacterias, Michaeles (Portocacces ¿Pertocacces)</li> <li>b. Jasterias, Proteskacterias, Cammaporteskacterias, Michaeles (Portocacces), Proteskacterias, Cammaporteskacterias, Proteskacterias, Cammaporteskacterias, Proteskacterias, Proteskacterias, Proteskacterias, Cammaporteskacterias, Proteskacterias, Proteskac</li></ul>
1368 1307 1308 1309 1311 1313 1314 1313 1314 1315 1314 1315 1314 1315 1314 1315 1314 1315 1314 1315 1315	2 54 3 0 0 0 0 0 1 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 1 5 5 1 5 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 23 0 0 0 0 0 5 1 0 5 1 0 0 0 2 0 0 2 0 0 3 0 0 0 3 0 0 0 0 0 0	6 6 6 7 7 8 7 8 8 7 8 7 8 7 8 7 8 7 8 7	3 11 0 5 0 0 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 38 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 3 0 0 5 0 1 0 2 0 2 0 2 9 1 0	0 6 255 0 1 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jackerias, Protesbacterias, Cammaportesbacterias, Butholderiater, Commonadaceae, Jurnobabtras,</li> <li>b. Jackerias, Protesbacterias, Cammaportesbacterias, Jeachholderiater, Commonadaceae, Jurnobabtras,</li> <li>b. Jackeria, Protesbacterias, Cammaportesbacterias, Jeachholderiater, Commonadaceae, Jurnobabtras,</li> <li>b. Jackeria, Protesbacterias, Cammaportesbacterias, Jeacomonadaceae, Jurnobabtras,</li> <li>b. Jackeria, Protesbacterias, Cammaportesbacterias, Jeacomonadaceae, Jeacomonadaceae, Jurnobabtras,</li> <li>b. Jackeria, Protesbacterias, Cammaportesbacterias, Jeacomonadaceae, Jeacomonadaceae</li></ul>
1268 1267 1268 1210 1210 1211 1212 1213 1214 1214 1215 1216 1227 1228 1227 1228 1228 1229 1228 1229 1228 1229 1228	2 0 154 0 2 0 0 0 1 1 0 1 0 1 0 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		0 28 0 0 0 0 0 5 1 0 5 1 0 0 5 1 0 0 0 2 0 0 2 0 0 3 0 0 0 0 0 0 0 0 0 0		a 5 6 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8	0 2 3 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 5 255 0 1 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerias, Proteskachniks, Cammaproteskachniks, Jackerskaker, Portocaccus, J. Pertocaccus, J. Pert</li></ul>
1268 1267 1268 1210 1211 1211 1213 1214 1214 1215 1216 1217 1228 1227 1228 1227 1228 1228 1227 1228 1229 1228	2 54 2 0 0 0 0 1 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 5 8 5 8 4 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 28 0 0 0 0 0 0 5 1 0 5 1 0 0 0 0 0 0 0 0 0	0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 5 0 0 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 23 0 1 0 0 1 0 0 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 1 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 5 0 1 0 2 0 0 2 9 1 0 0 3 4 3 0	0 6 2255 0 1 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_lstering_frotesbactering_campeteobactering_behaviorates_frotescaces_g_frotescaces_ b_lstering_frotesbactering_frotesbactering_beckenstering_beckenstering_frotescaces_g_frombactering_frotesbacteri</li></ul>
1368 1307 1308 1309 1311 1313 1314 1314 1314 1315 1314 1315 1314 1315 1316 1316 1317 1328 1329 1329 1329 1329 1329 1329 1329 1329	2 0 154 0 2 0 0 0 1 1 0 1 0 1 0 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		3 3 3 0 0 0 0 0 5 1 0 5 1 0 0 0 0 0 0 0 0 0 0	6 2 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		0 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 5 255 0 1 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_lstering_frotesbactering_campeteobactering_ehhbroolest_frotescacese_pfertescaus_</li> <li>b_lstering_frotesbactering_frotesbactering_beckbactering_headmonesia/styl_perodomonesia/stag_turnobabting_</li> <li>b_lstering_frotesbactering_frotesbactering_injertesbactering_injertesbactering_headmonesia/styl_perodomonesia/styl_pero</li></ul>
1368 1307 1308 1309 1311 1313 1314 1313 1314 1315 1326 1327 1328 1329 1329 1329 1329 1329 1329 1329 1329	2 154 3 2 0 0 0 1 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 28 0 0 0 0 5 1 0 5 1 0 5 1 0 0 0 0 0 0 0 0	6 2 6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7	3 3 3 3 3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 23 0 1 0 0 1 0 0 0 1 0 0 0 2 0 0 2 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 5 255 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_lstering_frotesbactricg_Cammportesbactricg_Behrhoderskef_Portescause_Portescause_</li> <li>b_lstering_frotesbactricg_Cammportesbactricg_heighthoderskef_Cammonadicese_Lineobelting_</li> <li>b_lstering_frotesbactricg_Gemmportesbactricg_legionelises_legioneliseselegionelises_</li> <li>b_lstering_frotesbactricg_Gemmportesbactricg_legionelisesese_legioneliseslegioneliseseseslegionelises_</li> <li>b_lstering_frotesbactricg_Gemmportesbactricg_legionelisesese_legioneliseseseslegionelises</li> <li>b_lstering_frotesbactricg_Gemmportesbactricg_frotesbactricg_frotesbactricg_frotesbactricg_legionelisesese_legioneliseseseslegioneliseseselegioneliseseselegionelisesese</li> <li>b_lstering_frotesbactricg_frot</li></ul>
1268 1267 1268 1210 1211 1212 1214 1214 1214 1215 1216 1216 1217 1218 1220 1220 1221 1224 1225 1226 1227 1228 1226 1227 1228 1226 1227 1228 1226	2 0 154 0 0 0 0 1 0 1 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		0 3 28 0 0 0 0 5 1 0 5 1 0 5 1 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0			0 2 23 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 6 255 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeria, Protokaceria, Cammprotokaceria, Johnsonski, Portocaces, Portocaces,</li></ul>
1266 1267 1268 1210 1211 1211 1213 1214 1215 1214 1215 1216 1217 1228 1227 1228 1228 1228 1229 1228 1229 1229 1229	2 154 2 0 0 0 1 1 0 0 0 0 1 0 0 0 3 5 4 0 0 0 2 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0		3 28 0 0 0 0 0 5 1 0 5 1 0 0 0 0 0 0 0 0 0 0			0 23 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 6 255 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b _ bstering_rrotesbactering_commprotesbactering_bet/solers/_fortescacese_protescace</pre>
1368 1307 1308 1310 1311 1313 1314 1314 1314 1314 1314	2 54 3 2 0 0 1 1 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		0 3 23 0 0 0 0 0 5 1 0 0 0 0 0 0 0 0 0 0 0 0 0		3 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0 2 23 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 6 255 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>bbctelsp_frotebacterisc_Cammaportebacterisc_Muthodersitef_Commonodicese_Lineobatterisc_ bbctelsp_frotebacterisc_Cammaportebacterisc_Petedomondersitef_Petrococcese_Petrococce_ bbctelsp_frotebacterisc_Cammaportebacterisc_Petedomondersitef_Petrococcese_Lineobatterisc_ bbctelsp_frotebacterisc_Cammaportebacterisc_Petedomondersitef_PetrococceseIncodomons. bbctelsp_frotebacterisc_Cammaportebacterisc_Petrodomondersitef_PetrococceseIncodomons. bbctelsp_frotebacterisc_Cammaportebacterisc_Petrology = personalitaterisc_Petrodomons. bbctelsp_frotebacterisc_Cammaportebacterisc_Petrology = personalitaterisc_Petrology = personalitaterisc_Petrodomons. bbctelsp_frotebacterisc_Cammaportebacterisc_Petrology = personalitateriscomeCambabaterisc 0bstelsp_frotebacterisc_Cammaportebacterisc_Petrology = personalitateriscomeCambabateriscomeNotebacterisc 0bstelsp_frotebacterisc_Cammaportebacterisc_Petrology = personalitateriscomeCambabateriscomeNotebacterisc 0bstelsp_frotebacterisc_Cammaportebacterisc_Petrology = personalitateriscomeCambabateriscomeNotebacterisc 0bstelsp_frotebacterisc_Pathotechalp_Bistoccalidae; Bistoccalidae; Bistocc</pre>
1266 1267 1268 1210 1211 1211 1213 1214 1215 1214 1215 1216 1217 1228 1227 1228 1228 1228 1229 1228 1229 1229 1229	2 154 2 0 0 0 1 1 0 0 0 0 1 0 0 0 3 5 4 0 0 0 2 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0		3 28 0 0 0 0 0 5 1 0 5 1 0 0 0 0 0 0 0 0 0 0			0 23 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 6 255 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b _ bstering_rrotesbactering_commprotesbactering_bet/solers/_fortescacese_protescace</pre>
1266 1207 1268 1209 1211 1213 1213 1213 1215 1215 1215 1215	2 54 3 2 0 0 1 1 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		0 3 23 0 0 0 0 5 1 0 5 1 0 0 0 0 0 0 0 0 0 0 0		3 3 3 3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 23 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 6 255 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b_lstering_frotesbactering_campertesbactering_enhancesbactering_frote</li></ul>

1244	2	0	1	0	0	1	0	0	3	0	0 k_Bacteria;p_Myxococcota;x_Myxococcia;o_Myxococcales;f_Myxococcaceae;g_P308-42;s_
1245	0	0	1	0	0	z	0	D	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Gallionellaceae;g_Candidatus_Nitrotoga;s_
1245	1	0	0	0	0	2	0	D	1	o	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Sphaerotilus
1247	0	0	0	0	0	0	0	0	2	0	0 k_Bacteria:p_Myxococcota:c_Polyangia;o_Haliangiales;f_Haliangiaceae:g_Haliangium;s
1248		0	2	0	2	2	0	0	0	0	0 k_Bacteria;p_Acidobacteriota;c_Acidobacteriac
	÷										
1249	1	0	1	0	1	1	0	1	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Gammaproteobacteria_Incertae_Sedis;f_Unknown_Famiky;g_Acidibacter;s
1250	2	0	0	0	0	0	0	0	0	0	0 Unknown
1251	0	3	0	0	0	0	0	0	0	0	0 Unknown
1252	0	0	1	0	0	35	0	2	0	0	1 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136_group
1253	0	0	0	0	0	0	0	4	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Cytophagales;f_Microscillaceae;g_Chryseolinea;s_
1254	0	0	0	0	0	D	0	2	0	0	0 k_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Saccharimonadales;g_Saccharimonadales;s_
1255	0	0	0	2	0	D	0	0	0	0	0 k Bacteria;p_ Firmicutes;c_ Clostridia;o_ Lachnospirales;f_ Lachnospiraceae
1256	0	0	2	0	0	0	0	0	0	0	0 k_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Elev-165-1166;f_Bev-165-1166;g_Elev-165-1166;s_
1257	2	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Frankiales;f_Sporichthyaceae;g_hgcl_clade
1258	0	0	2	0	0	0	0	0	0	0	0 k_Bacteria;p_Myxococcota;r_Polyangia;o_mle1-27;f_mle1-27;g_mle1-27;s_Myxococcales_bacterium
1259	1	0	0	0	1	D	0	D	1	0	0 k_Bacteria;p_Cyanobacteria;c_Cyanobacteria;o_Cyanobacteriales;f_Nostocaceae;g_Sphaerospermopsis_BCCUSP55
1260	0	0	0	0	0	D	0	5	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_;f_;g_;s_
1261	0	0	0	0	0	0	0	2	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospinilale;;f_;g_;s
1262	0	0	2	0	0	0	0	0	1	0	0 k_Bacteria;p_Actinobacteriota;c_Coriobacteria;o_Coriobacteriales;f_Atopobiaceae;g3_
1263	9	0	0	0	2	2	0	4	8	0	2 k_Bacteria;p_Cyanobacteria;c_Cyanobacteriia;o_Synechococcales;f_Cyanobiaceae;g_Cyanobium_PCC-6307;s_
1264	<u> </u>	2	1	0	0	D	0	D	0	o	
	b										3 k_Bacteria;p_Firmicutes;c_Clottridia;0_Clottridia_UCG-014;f_Clostridia_UCG-014;g_Clostridia_UCG-014;s_
1265	0	0	O	0	0	D	0	2	0	a	0 k_Bacteria;p_Myxxxxxxxxta;c_Polyangia;o_Polyangiales;f_Biril41;g_Biril41;s_
1266	0	0	0	0	0	0	0	3	0	0	0 k_Bacteria;p_Myxococcota;c_Polyangia;o_Haliangiales;f_Haliangiaceae;g_Haliangium;s
1267	0	0	2	0	0	0	0	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae
1268	1	0	0	0	1	2	0	D	1	0	0 k_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_;s_denitrifying_bacterium
1269	0	2	1	0	0	D	1	0	1	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
1270	5	0	1	0	0	0	0	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidia!es;f_Prevotellaceae;g_Prevotella;s_Prevotella_melaninogenica
1271	0	0	0	0	0	0	0	0	2	0	0 K_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Fkvicoccus
1272	0	0	0	0	0	0	0	2	1	0	0 k_Bacteria;p_Actinobacterioto;c_Actinobacteria;o_PeM15;f_PeM15;g_PeM15;s_
1273	0	6	0	0	0	D	0	0	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella
1274	0	2	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostnidia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136_group;s
1275	0	0	0	0	2	0	0	0	0	0	0 k_Bacteria
1276	2	0	0	0	0	0	0	0	0	0	1 k_Bacteria;p_Acidobacteriota;x_Acidobacteriae;o_Acidobacteriales
1277	0	0	0	0	0	0	0	4	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Cellvibrionales;f_Halieaceae;g_Halioglobus;s_
1278	0	0	o	0	0	o	0	9	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae
1279	0	0	0	0	7	D	0	0	1	0	
											0 k_Bacteria;p_Acidobacteriota;c_Subgroup_22;o_Subgroup_22;f_Subgroup_22;g_Subgroup_22;s_
1280	13	4	1	0	0	0	0	3	3	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia
1281	2	0	1	0	0	0	0	0	1	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Acetobacterales;f_Acetobacteraceae;g_Roseomonas;s_Acetobacteraceae_bacterium
1282	0	0	0	0	0	D	0	0	3	0	0 k_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae
1283	0	0	0	0	0	2	0	0	0	0	0 k_Bacteria;p_Proteobacteria;cAlphagroteobacteria
	0										0 k_Baterinag_Protobatering_Aphaprotobaterin 0 k_Baterina_Actinobateridae. Thermoloodillas Galilakif a is
1284	o	0	o	0	0	D	0	5	0	o	$0\ k\_Bacteria;p\_Actinobacteriota;c\_Thermoleophiliz;o\_Galellales;f\_;g\_;s\_$
1284 1285	0 0	0 0	0 0	0 0	0 0	D	0 0	5 2	0 0	0 0	0 k_bacteriap_Activolaceteristac_Thermoleophillace_Galekland_gs 0 k_bacteriap_Prosebacteriac_Alphaproteolacteriao_Rickttaalee
1284 1285 1286	o	0	0 0 0	0 0 0	0 0 2	D D 1	0 0 0	5 2 0	0 0 0	0 0 0	0 k_bacterisp_Activobacenotac_Thermoleophila.o_Galekleid <u>_ac_s_</u> 0 k_bacterisp_Protechacteriac_Alphaporteobactors.o_RicketSailes 0 k_bacterisp_Firmoutesc_Bacili.o_Peenbeciliedsf_PareNacciaceaeg_Peenbacilus
1284 1285	0 0	0 0	0 0	0 0	0 0	D	0 0	5 2	0 0	0 0	0 k_bacteriap_Activolaceteristac_Thermoleophillace_Galekland_gs 0 k_bacteriap_Prosebacteriac_Alphaproteolacteriao_Rickttaalee
1284 1285 1286	0 0	0 0 0	0 0 0	0 0 0	0 0 2	D D 1	0 0 0	5 2 0	0 0 0	0 0 0	0 k_bacterisp_Activobacenotac_Thermoleophila.o_Galekleid <u>_ac_s_</u> 0 k_bacterisp_Protechacteriac_Alphaporteobactors.o_RicketSailes 0 k_bacterisp_Firmoutesc_Bacili.o_Peenbeciliedsf_PareNacciaceaeg_Peenbacilus
1284 1285 1286 1287	0 0 4	0 0 0	0 0 0	0 0 0	0 0 2 0	0 D 1 0	0 0 0	5 2 0	0 0 0	0 0 0	0 i_bsterisp_Activobacenetac_Thermoleophila_Galelakes <u>f_a_s</u> _ 0 i_bsterisp_Proteobaceniac_Alphaproteobactoriao_Rickettaieks 0 k_batteriap_Firmioutesc_Bacilito_Peenbacilialest_Paenbaciliaceac_Peenbacilias 0 k_batteriap_Cyanobacteriax_Cyanobacteriap_Chioroplast_Chioroplasta_Proudochiorofla_igniensis
1284 1285 1286 1287 1288	0 0 4	0 0 0 0	0 0 0 0	0 0 0 0	0 0 2 0	D D 1 D	0 0 0 0	5 2 0 0 0	0 0 0 0	0 0 0 0	0 i _Bacteriag_Activobaceteristac_Thermoleophillaco_Galelaiesf_ac_st_ 0 i _Bacteriag_Proteobacteriac_Alphaproteobactoriaco_Riclettuaries 0 i _Bacteriag_Firmicatosc_Bacilico_Peonbaciliaiosf_Paenibaciliacosc_Peonibacilias 0 i _Bacteriag_Cyanobacteriag_Cyanobacteriaga_Chioroplast_Chioroplastg_Chioroplasts_Peoudochiorolla_signiensis 0 i _Bacteriag_Vyanobacteriag_Devyangia
1284 1285 1286 1287 1288 1289	0 0 4	0 0 0 0 0	0 0 0 0 0	0 0 0 0 0	0 0 2 0 0	D D 1 0 D D	0 0 0 0	5 2 0 0 0 0	0 0 0 0 4	0 0 0 0	0   _bacteriagActivobacteristac_Thermoleophilas_CaleNaked_gi 0  _bacteriagProteobacteriac_AphaporobelacteriaRickticules 0  _bacteriagFrencesc_Ballio_PeenbaceNatest_PeenbaceNatest_PeenbaceNates 0  _bacteriagQueenbacteriagOncorpolatef_Oncorpolatg_Coheroplants_Providentionals_ippinnes 0  _bacteriagProteobacteriag_Decorpolateriaga_Natest_Bacteriaga_Natest_Statest_PeenbaceNatest_PeenbaceNatest_ 0  _bacteriag_Proteobacteriag_Coheroplant_Oncorpolatef_Oncorpolatesf_Decorpolatesg_Statest_
1284 1285 1286 1287 1288 1289 1290 1291	0 0 4 3 0 1 0	0 0 0 0 0 0 2	0 0 0 0 0 0 0 0	0 0 0 0 0 0 0	0 2 0 0 3 0	D D 1 D D D 2 0	0 0 0 0 0 0	5 2 0 0 0 0 0 0	0 0 0 4 4 0	0 0 0 0 0 0 0	0   _Bacteriag_Activobacteristac_Thermoleophillac_Galekind_gs 0   _Bacteriag_Proteobacteristac_Alphaproteobacteriag_RicketSales 0   _Bacteriag_Proteobacteriag_Canobacteriag_Bachacollesces_Peerbacklus 0   _Bacteriag_Operotectoriag_Conobacteriag_Colorophast_Colorophats_ProvidedHoreNa_signizmo 0   _Bacteriag_Payroaccestag_Polyarqik 0   _Bacteriag_Actinobacteristac_Conobacteriaga_Conobacterialest_Experiphelacese 0   _Bacteriag_Actinobacteristac_Conobacteriaga_Conobacterialest_Experiphelacese
1284 1285 1286 1287 1288 1289 1290 1291 1291	0 0 4 3 0 1 0 4	0 0 0 0 0 0 2 0	0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0	0 2 0 0 3 0 1	D D 1 0 D 2 0 1	0 0 0 0 0 0 0	5 2 0 0 0 0 0 0	0 0 0 4 4 0	0 0 0 0 0 0 0	0  batariagActivabateristac_ThermoleophilagSakalaindgs 0  batariagProtobacetacBharporobateriagExistituies 0  batariagBrimotesc_Bacillo_Peenbacillatesf_Parabacillatesez_Peenbacillate 0  batariagMonotocitusProtopatingChirospitesfChirospitesfDevelophices_Peedochoresh_signiferins 0  batariagMonotocitusProtopatingChirospitesfChirospitesfDevelophicesez_Latropics
1284 1285 1286 1287 1288 1289 1290 1291 1291 1293	0 0 4 3 0 1 0 4 0	0 0 0 0 0 2 0 2 0	0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0	0 1 0 0 2 0 1 0	0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 3	0 0 0 4 4 0 0	0 0 0 0 0 0 0	0   _bateriagActivobacteristac_ThermoleophilasSakalaid_gs 0   _bateriagProtobacteristac_UphaporobelateriagRelativise 0   _bateriagProtobacteriagCalenderstefingDerobaciliseasg_Perebadius 0   _bateriagProtobacteriagCalenderstefingOtheropalastg_Chloroplastg_Chloroplastg_Productiverste_linginemis 0   _bateriagProtobacteriag_CalenderstefingDerobacteriag_Batholdersisesf_Batholdersisesg_Lastropiag_ 0   _bateriagActividuateriag_Contrologicativerstefing_EgentHoldersisesf_Batholdersisesg_Lastropiag_ 0   _bateriagProtobacteriag_Calenderstefing_Cammaportobacteriag_Batholdersisesf_Batholdersisesf_BAtholdersisesg_MADS 0   _bateriag_Protobacteriag_Calenderstefing_Cammaportobacteriag_Batholdersisesf_Methylogis_Licesg_MADS 0   _bateriag_Protobacteriag_Aphylogrotebacteriag_Batholdersisesf_Methylogis_Licesg_MADS 0   _bateriag_Protobacteriag_Aphylogrotebacteriag_Batholdersisesf_Methylogis_Licesg_MADS
1284 1285 1286 1287 1288 1289 1290 1291 1291 1292 1293 1294	0 0 4 3 0 1 0 4 0 14	0 0 0 0 0 2 0 2 0 0	0 0 0 0 0 0 0 0 0 0 0 2	0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0	D D 1 D D D 2 0 1 D 7	0 0 0 0 0 0 0 0 1	5 2 0 0 0 0 0 0 3 7	0 0 0 4 4 0 0 3	0 0 0 0 0 0 0 0 0	0   _bateriagActivobacteristacThermoleophilasGalekked_gi 0   _bateriagProteobacteristacAlphaproteobacteriagRickticules 0   _bateriagProteobacteriagChoropolartOkiropolartg_Choropolartg_Choropolartg_Proteobacteriag_Benerativo 0   _bateriagProteobacteriag_Corropolart_Okiropolartg_Choropolartg_Choropolartg_Choropolartg_Choropolartg_Developed 0   _bateriagProteobacteriag_Corropolarteriag_Benerativot_Egentheleriaesez_Latropics_ 0   _bateriag_Proteobacteriag_Corropolarteriag_Benerativot_Egentheleriaesez 0 Uborros 0   _bateriag_Proteobacteriag_Corropolarteriag_Benerativot_Be
1284 1285 1286 1287 1288 1289 1290 1291 1291 1293	0 0 4 3 0 1 0 4 0	0 0 0 0 0 2 0 2 0	0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0	0 1 0 0 2 0 1 0	0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 3	0 0 0 4 4 0 0	0 0 0 0 0 0 0	0   _bateriagActivobacteristac_ThermoleophilasSakalaid_gs 0   _bateriagProtobacteristac_UphaporobelateriagRelativise 0   _bateriagProtobacteriagCalenderstefingDerobaciliseasg_Perebadius 0   _bateriagProtobacteriagCalenderstefingOtheropalastg_Chloroplastg_Chloroplastg_Productiverste_linginemis 0   _bateriagProtobacteriag_CalenderstefingDerobacteriag_Batholdersisesf_Batholdersisesg_Lastropiag_ 0   _bateriagActividuateriag_Contrologicativerstefing_EgentHoldersisesf_Batholdersisesg_Lastropiag_ 0   _bateriagProtobacteriag_Calenderstefing_Cammaportobacteriag_Batholdersisesf_Batholdersisesf_BAtholdersisesg_MADS 0   _bateriag_Protobacteriag_Calenderstefing_Cammaportobacteriag_Batholdersisesf_Methylogis_Licesg_MADS 0   _bateriag_Protobacteriag_Aphylogrotebacteriag_Batholdersisesf_Methylogis_Licesg_MADS 0   _bateriag_Protobacteriag_Aphylogrotebacteriag_Batholdersisesf_Methylogis_Licesg_MADS
1284 1285 1286 1287 1288 1289 1290 1291 1291 1292 1293 1294	0 0 4 3 0 1 0 4 0 14	0 0 0 0 0 2 0 2 0 0	0 0 0 0 0 0 0 0 0 0 0 2	0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0	D D 1 D D D 2 0 1 D 7	0 0 0 0 0 0 0 0 1	5 2 0 0 0 0 0 0 3 7	0 0 0 4 4 0 0 3	0 0 0 0 0 0 0 0 0	0   _bateriagActivobacteristacThermoleophilasGalekked_gi 0   _bateriagProteobacteristacAlphaproteobacteriagRickticules 0   _bateriagProteobacteriagChoropolartOkiropolartg_Choropolartg_Choropolartg_Proteobacteriag_Benerativo 0   _bateriagProteobacteriag_Corropolart_Okiropolartg_Choropolartg_Choropolartg_Choropolartg_Choropolartg_Developed 0   _bateriagProteobacteriag_Corropolarteriag_Benerativot_Egentheleriaesez_Latropics_ 0   _bateriag_Proteobacteriag_Corropolarteriag_Benerativot_Egentheleriaesez 0 Uborros 0   _bateriag_Proteobacteriag_Corropolarteriag_Benerativot_Be
1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295	0 0 4 3 0 1 0 4 0 14 0	0 0 0 0 0 2 0 0 0 0 0	0 0 0 0 0 0 0 0 0 2 0	0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 4 0	D D 1 D D 2 0 1 D 7 0	0 0 0 0 0 0 0 0 1	5 2 0 0 0 0 0 3 7 0	0 0 0 4 4 0 0 0 3 2	0 0 0 0 0 0 0 0 0 0 0	0   _bictrisg_Activobacteristac_Thermoleophilas_Galekked_gi 0   _bictrisg_Protectuation_Aphaprotecleaturisg_Rickticules 0   _bictrisg_Protectuation_Controlsectorisg_Oncodular(_Oncodular(_Oncodular(_Oncodular())) 0   _bictrisg_Protectuation_Controlsectorisg_Development(_Oncodular()) 0   _bictrisg_Protectuation(c_Controlsectorisg_Development()) 0   _bictrisg_Protectuation()) 0   _bic
1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296	0 0 4 3 0 1 0 14 0 14 0 0	0 0 0 0 0 2 0 0 0 0 0	0 0 0 0 0 0 0 0 2 0 2 0	0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4	D 1 0 D 2 0 1 7 0 1	0 0 0 0 0 0 0 0 1 0	5 2 0 0 0 0 0 3 7 0	0 0 0 4 4 0 0 0 3 2 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0  batariagAtmohadamistacThermoleophilagSakalandgi  0  batariagAtmohadamistacAhaparotekatariagRelativist  0  batariagAtmohadamistaciacAnaparotekatariagRelativist  0  batariagAtmohadamistaciacConstructuring_Constructuring_Cohoreophilag_Cohore
1284 1285 1286 1287 1288 1289 1290 1291 1291 1293 1294 1295 1296 1297	0 0 4 3 0 1 0 14 0 14 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4 0	D 1 0 D 2 0 1 7 0 1 7 0 1 3	0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 2	5 2 0 0 0 0 0 3 7 0	0 0 0 4 4 0 0 3 2 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _bictriagActivabacteristacthemologikilae_Galekkid_gi 0   _bictriagProteobacterisdepage releasestariagRistEtaieke 0   _bictriagfreetobacteristac_depage releasestariagRistEtaieke 0   _bictriagfreetobacteristac_Careneporterobacteristaglegenbalanese 0   _bictriagfreetobacteristac_Careneporterobacteristaglegenbalanese 0   _bictriagfreetobacteristac_Careneporterobacteristaglegenbalanese 0   _bictriagfreetobacteristac_Careneporterobacteristaglegenbalanese 0   _bictriagfreetobacteristac_Careneporterobacteristaglegenbalanese 0   _bictriagfreetobacteristac_CareneporterobacteristaglegenbalaneseMMOS 0   _bictriagfreetobacteristac_CareneporterobacteristaglegenbalaneseMMOS 0   _bictriagfreetobacteristac_CareneporterobacteristaglegenbalaneseMMOS 0   _bictriagfreetobacteristac_CareneporterobacteristaglegenbalaneseMMOS 0   _bictriagfreetobacteristac_CareneporterobacteristaglegenbalaneseMMOS 0   _bictriagfreetobacteristac_CareneporterobacteristaglesebalanesesMMOS 0   _bictriagfreetobacteristac_CareneporterobacteristaglesebalanesesMMOS 0   _bictriagfreetobacteristac_CareneporterobacteristaglesebalanesesMMOS 0   _bictriagfreetobacteristaglesebalaneseslesebalanesesMMOS 0   _bictriagfreetobacteristaglesebalaneseslesebalanesesMMOS 0   _bictriagfreetobacteristaglesebalaneseslesebalanesesIMADAIA_grupe 0   _bictriagfreetobacteristaglesebalaneseseslesebalanesesIMADAIA_grupe
1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299	0 0 4 3 0 1 0 14 0 14 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 9 5 0	0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0	0 0 0 0 3 0 1 0 4 0 4 0 0 0	0 1 0 2 0 1 7 0 1 5 3 5 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 3 7 0	0 0 0 4 4 0 0 3 2 1 0 3 2 1 0 7 7 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _bictrisgAntobacteristaMenopeleolaterisgRickEtailesCheropaterisRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaRestAtailesCheropateristaCheropateristaCheropateristaCheropateristaRestAtailesCheropateristaRestAtailesEgentheliatesRestAtailes
1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1295 1295 1295 1295 1295 1295 1295	0 0 4 3 0 1 0 4 0 14 0 0 14 0 0 14 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4 0 0 4 0 0 0 0	0 1 0 2 0 1 0 1 7 0 1 1 5 5 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 0 3 2 1 0 17 0 0		0   _bitringhttps://citributoritritefiles/citributoritritefiles/citributoritritefiles/citributoritritefiles/citributoritritefiles/citributoritritefiles/citributoritrite_files/citributorites_citributorites_citributorites_citributorites_files/citributorites_citributorites_citributorites_citributorites_citributorites/
1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1295 1295 1295 1295 1299 1300 1301	0 0 4 3 0 1 0 4 0 14 0 0 14 0 0 0 0 0 0 0	0 0 0 0 2 0 0 0 0 2 0 0 2 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 2 0 1 2 0 1 1 5 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 2 5 0 2 5 5	0 0 0 4 4 0 0 3 2 1 0 17 0 0 0 0 0		<ul> <li>0   Bateriag_Activabateristac_Themologhilag_Scientificag</li></ul>
1284 1285 1286 1287 1288 1289 1290 1291 1393 1294 1295 1295 1295 1295 1295 1295 1299 1300 1301	0 0 4 3 0 1 0 4 0 14 0 0 14 0 0 14 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4 0 0 0 0 0 0 0 0	0 1 0 2 0 1 0 1 7 0 1 1 5 5 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 0 3 2 1 0 17 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _bitringfrieblactringfrieblactringfictures_ficturesfictures_ficturesfictures_ficturesfictures_ficturesfictures_ficturesfictures_ficturesfictures_fict
1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1295 1295 1295 1295 1299 1300 1301	0 0 4 3 0 1 0 4 0 14 0 0 14 0 0 0 0 0 0 0	0 0 0 0 2 0 0 0 0 2 0 0 2 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 2 0 1 2 0 1 1 5 3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 2 5 0 2 5 5	0 0 0 4 4 0 0 3 2 1 0 17 0 0 0 0 0		<ul> <li>0   Bateriag_Activabateristac_Themologhilag_Scientificag</li></ul>
1284 1285 1286 1287 1288 1289 1290 1291 1393 1294 1295 1295 1295 1295 1295 1295 1299 1300 1301	0 4 3 0 4 0 4 0 0 1 4 0 0 0 1 4 0 0 0 2	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4 0 0 0 0 0 0 0 0	0 1 0 0 2 0 1 2 0 1 1 3 1 5 0 0 0 1 1 5 0 0 1 1 5 0 0 1 1 1 0 0 1 1 0 0 1 1 0 0 0 1 1 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 2 5 0 2 5 0	0 0 0 4 4 0 0 3 2 1 0 3 2 1 0 1 7 0 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _bitringfrieblactringfrieblactringfictures_ficturesfictures_ficturesfictures_ficturesfictures_ficturesfictures_ficturesfictures_ficturesfictures_fictures_fictures_fictures_fictures_fictures_fictures_fictures_ficturesfictures_ficturesfictures_fi
1284 1285 1286 1287 1288 1289 1290 1291 1283 1294 1294 1295 1296 1295 1296 1297 1288 1299 1300 1301	0 0 4 3 0 1 0 4 0 0 0 1 4 0 0 0 2 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 1 2 0 1 5 0 0 1 5 0 0 0 1 1 5 0 0 1 1 5 0 0 1 1 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 3 2 1 0 0 3 2 1 7 0 0 0 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _bictrisgActivabacteristacfhempoleophilasGalekked_gs 0   _bictrisgfreebolactistacfhempoleophilasRicktisuke 0   _bictrisgfreebolactistacdeveloptionsRicktisuke 0   _bictrisgfreebolactistacdeveloptionsBoreland() = DeveloptionsProvideritorska_inprimes 0   _bictrisgfreebolactistac_GammaporteobacterisgBoreland() = DeveloptionsBoreland() = Developtions 0   _bictrisgfreebolactistac_GammaporteobacterisgBoreland() = Developtions 0   _bictrisgfreebolactistac_GammaporteobacterisgDeveloptions 0   _bictrisgfreebolactistac_GammaporteobacterisgDeveloptions 0   _bictrisgfreebolactistac_GammaporteobacterisgDeveloptions 0   _bictrisgfreebolactistac_GammaporteobacterisgDeveloptions 0   _bictrisgfreebolactistac_GammaporteobacterisgDeveloptions 0   _bictrisgfreebolactistac_GammaporteobacterisgDeveloptions 0   _bictrisgfreebolactistac_Gammaporteobacterisg_
1284 1285 1286 1287 1288 1290 1291 1292 1293 1294 1295 1295 1295 1295 1295 1295 1295 1295	0 0 4 3 0 1 0 4 0 0 1 4 0 0 2 1 0 0 2 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 1 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 1 2 0 1 5 5 0 0 1 1 5 0 0 1 1 5 0 0 1 1 5 0 0 1 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 0 3 2 1 0 0 3 2 1 0 0 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>a lastarias, Antoniastrias, Phenoiosphilas, Sakakind, g., j.</li> <li>b lastarias, Protokastrias, Johang toolsaturas, Richtaise</li> <li>b lastarias, Consoluctivas, Canobacterias, Chonglent, Chinoplent, Chinoplent</li></ul>
1284 1285 1286 1289 1290 1291 1293 1294 1295 1294 1295 1296 1299 1300 1301 1303 1304	0 0 4 0 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 1 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 0 3 0 1 0 4 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 2 0 1 1 5 8 5 0 0 1 1 5 0 0 1 1 2 0 0 1 1 0 0 1 0 0 1 0 1 0 0 1 0 0 0 1 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 2 5 0 2 5 0 2 5 0 2 5 0 2 5 0 2 5 0 2 5 0 2 5 0 2 0 0 0 0	0 0 0 4 4 0 0 3 2 1 0 17 0 0 1 1 1 0 3 3 3 3		<pre>0  _bitringAntobacteristaPhenologialiaGalakindg</pre>
1284 1285 1287 1287 1289 1289 1290 1291 1293 1294 1295 1295 1295 1295 1295 1295 1295 1295	0 4 1 0 4 0 4 0 1 4 0 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 1	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 3 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 2 0 1 0 7 0 1 5 8 5 0 0 1 1 5 0 0 1 1 0 0 0 1 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 3 2 10 17 0 0 1 1 0 0 1 0 0 0 0 0 0 0 0 0 0		<pre>0  </pre>
2384 2385 2386 2387 2387 2389 2399 2395 2395 2395 2395 2395 2395 239	0 0 4 0 1 4 0 0 1 4 0 0 0 1 4 0 0 0 1 0 0 0 0	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 3 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 1 0 1 1 5 3 5 0 0 1 1 5 3 5 0 0 0 1 1 0 0 0 1 1 0 0 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 3 2 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 0 1 1 1 0 0 0 1 1 1 1 1 1 0		<pre>0  _bitchip_hitchip_hitchip_lapedobitchip</pre>
1284 1285 1287 1287 1288 1289 1291 1291 1295 1295 1295 1295 1295 129	0 4 1 0 4 0 4 0 1 4 0 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 3 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 1 0 1 1 0 1 1 5 0 0 1 1 0 0 0 1 1 0 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 3 2 1 0 1 7 0 0 1 1 0 0 1 1 0 0 1 2 1 2 1 2 1 2 1 2		<pre>0  _bitringfriedbacteristfemeriesphilafakaking</pre>
2384 2385 2386 2387 2387 2389 2399 2395 2395 2395 2395 2395 2395 239	0 4 1 0 4 0 4 0 1 4 0 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 1	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 3 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 1 0 1 1 5 3 5 0 0 1 1 5 3 5 0 0 0 1 1 0 0 0 1 1 0 0 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 3 2 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 0 1 1 1 0 0 0 1 1 1 1 1 1 0		<pre>0  _bitchip_hitchip_hitchip_lapedobitchip</pre>
1284 1285 1287 1287 1288 1289 1291 1291 1295 1295 1295 1295 1295 129	0 4 1 0 4 0 4 0 1 4 0 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 2 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 3 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 1 0 1 1 0 1 1 5 0 0 1 1 0 0 0 1 1 0 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 3 2 1 0 1 7 0 0 1 1 0 0 1 1 0 0 1 2 1 2 1 2 1 2 1 2		<pre>0  _bitringfriedbacteristfemeriesphilafakaking</pre>
1284 1285 1287 1287 1288 1289 1291 1291 1291 1295 1292 1293 1293 1293 1295 1295 1295 1295 1295 1295 1295 1300 1300 1305 1305 1305 1305 1305 130	0 4 3 0 4 0 4 0 0 0 0 2 1 0 0 0 2 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 3 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 1 2 0 1 3 5 0 0 1 1 5 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 3 2 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 2 0 0 1 2 0 0 1 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>0  </pre>
1284 1285 1287 1287 1289 1290 1291 1292 1292 1293 1293 1293 1295 1295 1295 1295 1295 1295 1295 1295	0 4 3 1 0 4 0 0 1 4 0 0 2 1 0 0 2 0 0 0 2 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 1 1 1 5 0 1 1 5 0 0 1 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 4 4 0 0 3 2 1 0 0 1 1 0 0 1 1 0 0 1 2 0 0 1 2 0 0 1 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>0 l_bitring_hindebierdettherebierdeting_ficientializes_ficientializes_</pre>
1284 1285 1287 1287 1288 1289 1291 1291 1295 1295 1295 1295 1295 129	0 4 0 1 0 4 0 0 1 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 0 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 1 2 0 1 3 3 5 0 0 1 1 5 0 0 1 1 0 0 0 1 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 4 4 0 0 0 3 2 1 0 1 1 0 0 1 1 0 0 1 2 0 0 1 2 0 0 2 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>0  _bitringrimethy_activation</pre>
1284 1285 1287 1287 1288 1289 1291 1291 1292 1292 1293 1293 1293 129	0 4 1 0 1 4 0 0 1 4 0 0 1 4 0 0 1 1 0 0 0 1 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 0 3 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 1 1 1 1 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 4 4 0 0 0 3 2 1 0 0 0 1 1 0 0 0 1 2 0 0 1 2 0 0 2 1 0 0 0 1 0 0 0 0		<pre>blacktrig_https/https/https/https/blacktrig_https/blacktrig_https/h</pre>
2344 2345 2345 2345 2345 2345 2345 2345	0 4 0 1 0 4 0 0 1 4 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 0 1 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 1 0 7 0 1 153 5 0 0 1 1 0 0 0 1 1 0 0 0 0 1 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 4 4 0 0 3 2 1 0 7 0 0 1 1 0 3 0 0 1 2 0 0 2 1 4 3		<pre>0  </pre>
2384 2385 2386 2380 2380 2380 2380 2380 2380 2380 2380	0 4 1 0 1 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 1 0 1 1 1 0 0 1 1 0 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 3 7 0 0 2 5 0 2 5 0 2 0 0 1 0 3 2 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 0 0 0 4 4 0 0 0 3 2 1 0 17 0 0 0 1 1 0 3 0 0 1 2 0 0 2 1 4 3 0		<pre>blacktrisp_heinekeetekeetekeetekeetekeetekeetekeetek</pre>
2384 2385 2387 2388 2397 2398 2399 2399 2399 2399 2399 2399 2399	0 4 0 1 0 4 0 0 1 4 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 0 1 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 1 0 7 0 1 153 5 0 0 1 1 0 0 0 1 1 0 0 0 0 1 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 4 4 0 0 3 2 1 0 7 0 0 1 1 0 3 0 0 1 2 0 0 2 1 4 3		<pre>0  </pre>
2384 2385 2386 2380 2380 2380 2380 2380 2380 2380 2380	0 4 1 0 1 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 1 0 1 1 1 0 0 1 1 0 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 3 7 0 0 2 5 0 2 5 0 2 0 0 1 0 3 2 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2	0 0 0 0 4 4 0 0 0 3 2 1 0 17 0 0 0 1 1 0 3 0 0 1 2 0 0 2 1 4 3 0		<pre>blacktrisp_heinekeetekeetekeetekeetekeetekeetekeetek</pre>
1284 1285 1287 1288 1289 1299 1291 1299 1299 1299 1299	0 4 1 0 1 4 0 0 1 1 0 0 2 1 0 0 2 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 3 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 3 7 0 0 2 5 0 2 5 0 2 0 0 1 0 3 2 0 0 2 0 2 0	0 0 0 0 4 4 0 0 0 3 2 1 0 1 0 0 1 1 0 3 0 0 1 2 0 0 2 1 4 3 0 0 2 1 4 3 0 0 0 2 1 4 0 0 0 0 1 2 1 0 0 0 0 1 2 0 0 0 0 1 2 0 0 0 0		<pre>blacktrag_htenkachtekac_hennekeephlac_Gakeked_g</pre>
2344 2345 2346 2347 2348 2349 2349 2349 2349 2349 2349 2349 2349	0 4 1 0 1 4 0 0 1 4 0 0 0 1 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		022030304004000000000000000000000000000	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 3 7 0 0 2 5 0 2 5 0 2 0 0 1 0 3 2 0 0 2 0 3 0 3 7 0 3 3 0 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 0 3 3 0 3	0 0 0 0 4 4 0 0 0 3 2 1 0 17 0 0 0 1 1 0 3 0 0 1 2 0 0 2 1 4 3 0 0 8		0         Lateria, Leinekies, Teinekies/late, Teinekies/late, Leinekies/           0         Lateria, Iministra, Jahrinskies, Chierokies, Chierokies, Chierokies, Prodochieroka, Japinekie           0         Lateria, Chierokies, Chierokies, Chierokies, Chierokies, Chierokies, Prodochieroka, Japinekie           0         Lateria, Chierokies, Cammaportokaketria, Barthaderiaket, Exercise Prodochieroka, Japinekie           0         Lateria, Chierokies, Cammaportokaketria, Barthaderiaket, Exercise Prodochieroka, Japinekie           0         Lateria, Chierokateria, Conosectriaket, Egethaderia           0         Lateria, Chierokateria, Conosectriaket, Conosectriaket, Egethaderia           0         Lateria, Chierokateria, Chierokateria, Conosectriaket, Egethaderia           0         Lateria, Chierokateria, Chie
2344 2345 2345 2345 2345 2345 2345 2345	0 4 1 0 1 4 0 0 1 4 0 0 1 4 0 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 0 0 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 7 0 1 5 3 5 0 0 1 1 0 0 0 1 0 0 0 1 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 1 0 0 0 1 0 0 0 0 0 1 0	0 0 0 0 0 0 0 1 0 0 7 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0	5 2 0 0 0 0 0 3 7 0 0 2 5 0 2 5 0 2 0 0 1 0 3 2 0 0 2 0 3 0 3 7 0 3 3 0 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 3 0 3 0 3 3 0 3	0 0 0 0 4 4 0 0 0 3 2 1 0 17 0 0 0 1 1 0 3 0 0 1 2 0 0 2 1 4 3 0 0 8 0		<pre>blacktrag_Activabacterista_Phenologiala_Galakied_g</pre>

1322	0	0	0	0	0	3	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria
1323	0	2	0	0	0	D	0	3	0	0	$0\ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Xanthomonadale; f\_Rhodanobacteraceae; g\_s\_camma proteobacteria; c\_damma proteobacteria; c$
1324	2	0	0	0	0	z	0	D	0	o	0 k_Bacteria;p_Firmicute;c_Clottrida;o_Oscillospirales;f_UCG-010;g_UCG-010;s_
1325	3	0	0	0	0	0	0	0	0	0	$0 \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$
1326	1	0	0	0	0	1	0	2	1	0	$0 \ k\_Bacteria; p\_Proteobacteria; c\_Alphaproteobacteria; o\_Rhizobiales; f\_Hyphomicrobiacea; a\_Pedomicrobium; s\_robium; s\_rob$
1327	1	0	٥	0	1	D	0	D	0	3	0 k_Bacteria;p_Firmicute;c_Bacili;o_Lactobaciliales;f_Streptococcaceae;g_Lactococcus
1328	0	2	0	0	0	D	0	D	0	0	0 k_Bacteria;p_Acidobacteriota;x_Vicinamibacteria;o_Vicinamibacterales;f_Vicinamibacteraceae;g_Vicinamibacteraceae;s_
1329	3	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitutales;f_Opitutaceae;g_Lacunisphaera
1330	0	0	0	1	3	0	0	0	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Micrococcales;f_Brevibacteriaceae;g_Brevibacterium
1331	4	0	0	0	٥	0	0	0	0	0	0 k_Bacteria;p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Roseiflexaceae;g
1332	0	0	0	0	٥	D	0	0	2	0	0 k_Bacheria;p_Firmicutes;c_Clostridia;o_Clostridia;f_Hungateiclostridiaceae
1333	0	0	O	0	0	0	0	3	0	0	0 k_Bacteria;p_8dellovibrionota;c_8dellovibrionia;o_8dellovibrionale;;f_8dellovibrionaceae;g_8dellovibrio
1334	0	0	2	0	0	0	0	0	0	0	0 k_Bacteria;p_WPS-2;c_WPS-2;o_WPS-2;f_WPS-2;g_WPS-2;s_hydrothermal_vent
1335	0	0	0	0	0	0	0	2	0	0	0 k_Bacteria;p_Bacteroidota;c_SJA-28;p_SJA-28;t_SJA-28;p_SJA-28;n_
1336	1	0	0	0	0	0	0	0	1	0	0 k_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Saccharimonadales;z_Saccharimonadales;s_
1337	4	0	σ	0	D	D	0	D	0	o	0 k_Bacteria
1338	4	1	σ	105	o	D	0	1	1	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Brevundimonas
1339	0	3	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Frankiales
1340	0	0	0	0	0	0	2	0	0	0	0 k_Bacteria:p_Patescibacteria;c_Saccharimonadia;n_Saccharimonadales;f_Saccharimonadaceae;g_TM7a;s_
1341	2	0	1	0	2	5	0	1	1	0	0 k_Bacteria;p_Gemmatimonadota;x_B02-11_terrestrial_group;o_B02-11_terrestrial_group;f_B02-11_terrestrial_group;z_B02-11_terrestrial_group;z_
1342	3	0	o	0	0	D	0	D	0	o	0 k_Bacteria;p_Firmicute;c_Negativcute;o_Veilloneliales-Selenomonadales.f_Selenomonadaceae;g_Megamonass
1343	÷.	0	1	0	o	D	0	1	2	o	0 k_Bacterla;p_Protecbacterla;c_Alphaproteobacterla;a_Bhizobiale;s_Rhizobiales_Incertae_Sedis;g_Nordella;s
1344	2	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria
	2	0				0	0		0	0	0 K_Barcteria;p_Cruecular.teria;c_Cyanobacteria;o_Cyanobacteriales;f_Chroococcidiopsaceae;g_Chroococcidiopsis_SAG_2023
1345			0	0	0			0			
1345	0	0	0	0	D	1	0	0	1	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_IG36-G5-52_f_JG36-G5-52;g_JG36-G5-52;s_
1347	2	0	0	0	0	D	0	D	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria
1348	0	0	0	0	0	0	0	2	0	0	0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Pedosphaerales;f_Pedosphaeraceae
1349	2	0	0	0	0	0	0	0	1	0	0 k_Bacteria;p_Acidobacteriota;c_Vicinamibacteria;o_Vicinamibacterale;;f_;g_;s_
1350	0	0	0	0	0	D	0	2	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_;s_
1351	0	0	0	0	0	D	0	3	0	0	0 k_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_67:14;g_67:14;s_
1352	0	0	0	0	3	0	0	0	0	0	0 k_Bacteria;p_Cyanobacteria;c_Vampirivibrionia;o_Gastranaerophilales;f_Gastranaerophilales;g_Gastranaerophilales;s_
1353	2	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales;f_Bryobacteraceae;g_Bryobacter;s_
1354	0	0	0	0	0	0	0	0	2	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Cytophagales
1355	2	0	n	0	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_CoxieTales;f_CoxieTaceae;g_CoxielTacs_
1356	2	0	1	0	0	1	0	0	1	0	0 k_Bacteria;p_Bdellovibrionota;c_Oligoflexia;o_053A03-8-DI-P58;f_053A03-8-DI-P58;g_053A03-8-DI-P58;g_
1357	2	0	1	0	0	D	0	o	0	0	0 k_Bacteria;p_Nitrospirota;c_Thermodesulfovibrionia;o_;f_;g_;s_
1358	0	0	0	0	0	2	0	0	1	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_JTB23;f_JTB23;g_JTB23;s_
1359	5	0	0	0	0	0	1	0	0	0	0 k_Bacteria;p_Patescibacteria;c_Saccharimonadia;u_Saccharimonadales;f_Saccharimonadaceae;g_TM7a;s_
1360	o	3	O	0	O	D	0	D	0	o	$0\ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Enterobacteria esf\_Yersinia ceae; g\_Serratia_s\_Serratia\_lique faciens and the statement of the sta$
1361	2	0	0	0	0	0	0	0	0	0	0 Ustrour
1361 1362	2	0 0	0 0	0	0	0	0	0 B	0	0 a	0 Visinows 0 K_Bateriay_Gennatimonadotax_50134_terrestrid_groups_50134_terrestrid_groups_50134_terrestrid_groups_50134_terrestrid_groups_
1362	0	0	٥	0	o	D	o	8	o	o	0 k_Escteria;p_Gemmatimonadotax_50134_terrestrial_group;o_50134_terrestrial_group;f_50134_terrestrial_group;g_50134_terrestrial_group;s_
1362 1363	0 0	0 0	0 0	0 0	0	D D	0 0	8 0	0 3	o o	0 k_laderlap_Germatimonadotac_30134_terretrial_group.c_30134_terretrial_groupd_30134_terretrial_groupg_30134_terretrial_groups_ 0 k_laderlap_Activabacterista
1362 1363 1364	0 0 1	0 0 0	0 0 0	0 0 0	0 0 2	D D 0	0 0 0	8 0 0	0 3 3	0 0 0	0 k_bsterisp_Germatinosadots_50134_terretrisl_poupo_50134_terretrisl_poupd_50134_terretrisl_poupg_50134_terretrisl_poups_ 0 k_bsterisp_Actinobacterists 0 k_beteris
1362 1363 1364 1365	0 0 1 0	0 0 0	0 0 0	0 0 0	0 0 2 1	D D 0	0 0 0	8 D 0 1	0 3 3 1	0 0 0	0 k_Baterias_Generatinosadots_50134_terrestrial_groups_50134_terrestrial_groups_50134_terrestrial_groups_ 0 k_Baterias_Lotinobacterista 0 k_Baterias_Tototobacterias_Generatoriobacterias_Colhibrionalest_Spooglibacteratorsecs_8017_clades_
1362 1363 1364 1365 1366	0 0 1 0 2	0 0 0 0	0 0 0 0	0 0 0 0	0 0 2 1 0	0 0 0 0	0 0 0 0	8 0 1 0	0 3 3 1 0	0 0 0 0	0 k_Bateriap_Germatinosadots_50134_terretrial_groups_50134_terretrial_groups_50134_terretrial_groups_50134_terretrial_groups_ 0 k_Bateriap_Actinobacterista 0 k_Bateriap_Protochacterias_Germanprotochacteriasp_Collubricalest_Spongibacteraceses_5017.ctindess_ 0 k_Bateriap_Instanteriac_Germanprotochacteriasp_Collubricalest_Spongibacteraceses_5017.ctindess_ 0 k_Bateriap_Bateriadotsc_Bateriadaga_Bateriothissf_Parphytomonaciaceses_Parphytomonacs_Camphytomonacs_discumdentaria
1362 1363 1364 1365 1366 1367	0 1 0 2 0	0 0 0 0 0	0 0 0 0 0	0 0 0 0 0	0 2 1 0	D D 0 D D	0 0 0 0 0	8 0 1 0 3	0 3 3 1 0	0 0 0 0	0 L Sasteriap _ Germatimonadotac00134_terretrial_group.o_03134_terretrial_group.d_50134_terretrial_group.g_50134_terretrial_group.g_ 0 k_ Basteriap_Activatoriata 0 k_ Basteriap_Protobactoriac_Gammapostobactoriaa.c=Celubironates/_SpongibactoraceseB017_cloidez_ 0 k_ Basteriap_Protobactoriac_Gammapostobactoriaa.c=Celubironates/_SpongibactoraceseB017_cloidez_ 0 k_ Basteriap_Delotoriator.c=Dateredaa_Basteredatives_Porphyromenas.c=Porphyromenas.c=Porphyromenas_cloundertaria 0 k_ Basteriap_Delotoriatoricaac_Olgobieria.c=010+6030(_0110+6030e0110+6030e1010+6030e000+6030e0010+6030e0010+6030e0010+6030e0010+6030e0010+6030e000+6030e0010+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e000+6030e
1362 1363 1364 1365 1366 1367 1368	0 1 0 2 0	0 0 0 0 0 0	0 0 0 0 0	0 0 0 0 0 0	0 2 1 0 0	0 0 0 0 0 2	0 0 0 0 0	8 0 1 0 3 0	0 3 1 0 0 2	0 0 0 0 0	0 L Sasteriap_Germatimosadots_30134_terretrial_group90134_terretrial_group90134_terretrial_group90134_terretrial_groups_ 0 L Sasteria 0 L Sasteria 0 L Sasteriap_hotoobactoriac_Germanpotoobactoriag_Celubitroadeos_Socialisatoraccieg_8017_stator_ 0 L Sasteriap_hotoobactoria_Cateriadaa_Bactereobaiteria_Conjubactoraccieg_Norphycomosas_diconductaria 0 L Sasteriap_hotoobactor_Cateriadaa_01064030_01164036g_011840352_01184036g_ 0 L Sasteriap_motoosas_diconductaria
1362 1363 1364 1365 1366 1367 1368 1369	0 1 0 2 0 0	0 0 0 0 0 0	0 0 0 0 0 0	0 0 0 0 0 0 0 2	0 2 1 0 0 0	0 0 0 0 0 0 2 0	0 0 0 0 1 0	8 0 1 0 3 0	0 3 1 0 2 0	0 0 0 0 0 0 0	0 i _bsterisp_Germatimosadots_00134_terretrial_groupo_00134_terretrial_groupd_00134_terretrial_groupg_00134_terretrial_groups_ 0 i _bsterisp_Actindactorista 0 i _bsterisp_Actindactorista 0 i _bsterisp_Tetrobactorista_Germaportobactoriago_Colibionalect_Spongibacteraceseg_B017_clotdep_ 0 i _bsterisp_Tetrobactorista_Genergerobactoriago_Colibionalect_Spongibacteraceseg_B017_clotdep_ 0 i _bsterisp_Tetrobactorista_Coloreduator_DescriptionColoreducator_Porphycomonals_discundentaria 0 i _bsterisp_Tetrobactorista_Coloreduator_DescriptionColoreducator_Porphycomonals_descriptionColoreducator_De
1362 1363 1364 1365 1366 1367 1368 1369 1370	0 1 0 2 0 0 1	0 0 0 0 0 0 0	0 0 0 0 0 0 0 3	0 0 0 0 0 0 2 0	0 2 1 0 0 0 1	0 0 0 0 0 2 0 0	0 0 0 0 1 0	8 0 1 0 3 0 0	0 3 1 0 2 0 6	0 0 0 0 0 0 0	0 L Jasteria,fontolasteria,solia Lamentol poupo_3014_terretrial_groups_3014_terretrial_groups_30134_terretrial_groups_ 0 L Jasteria,solicolasteria,soniapontolasteria,soliableonales(sociablecteriaese6027_distor,) 0 L Jasteria,fontolasteriae,soliceolasteriae,fontphononaliciaegPorphytomenia;hophytomenia;distordetaria 0 L Jasteria,fontolasteriae,soliceolasteriae,fontphononaliciaegPorphytomenia;hophytomenia;distordetaria 0 L Jasteriae,fontolasteriae,doubleciae,011640260116402601164026011940206 0 L Jasteriae,fontolasteriae,soliceolasteriae,fontolateriae,fontolateriae, 0 Latoriae,Aritobateriae,Aritobateriae,MenolacteriaesegAurantimendums 0 L JasteriagAritobateriaesegAritobateriaeMenolacteriaesegAurantimendums 0 L JasteriagAritobateriaeseAritobateriaeMenolacteriaesegOsteplat
1362 1363 1364 1365 1365 1365 1367 1368 1369 1370 1371 1372	0 1 2 0 0 1 0	0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 2 0	0 0 0 0 0 2 0 0 0 0 0	0 2 1 0 0 0 1 0	0 0 0 0 0 2 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0	8 0 1 0 0 0 0 6	0 3 1 0 2 0 6 0 0	0 0 0 0 0 0 0 0 0 0	0   _bsteria,Cernatinosadota00134_terretria_[group.g00134_terretrial_group.g00134_ter
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371	0 1 2 0 0 1 0	0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 2	0 0 0 0 0 2 0 0	0 2 1 0 0 0 1 1	0 0 0 0 0 2 0 0 0 0 0	0 0 0 0 1 0 0	8 0 1 0 3 0 0	0 3 1 0 2 0 6 0	0 0 0 0 0 0 0 0	0   _bateriap_demonstreats_00131_terretrial_group03134_terretrial_group03134_terretrial_group03134_terretrial_groups_ 0   _bateriap_Activatoriats 0   _bateriap_heterologic
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373	0 1 2 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 2 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0	8 0 1 0 0 0 0 6 2	0 3 1 0 0 2 0 6 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0   _bsteria,Cernatinosadota00134_terretria_[group.g00134_terretrial_group.g00134_ter
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374	0 1 0 2 0 1 0 0 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 2 0 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0	0 2 1 0 0 1 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0	8 0 1 0 0 0 6 2 3	0 3 1 0 2 0 6 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0	U Lasteria, Cermatinosadots, 2013 Lemetria group,
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376	0 1 0 2 0 1 0 0 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 2 0 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0	0 2 1 0 0 1 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0	8 0 1 0 0 0 6 2 3	0 3 1 0 2 0 6 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0	
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377	0 1 0 2 0 1 0 0 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 2 0 0 0 0 3 2 0 0 0 3 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0 0 0 1 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 6 2 3 0 3 2	0 3 1 0 2 0 6 0 0 0 0 0 4 0 0		
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377	0 1 2 0 1 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 0 0 0 0 0 0 0 1 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 0 5 2 3 0 3 2 9	0 3 1 0 2 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		L bateriap_ferminimovadots_00134_terretrial_group_00134_terretrial_groups_00134_terretrial_groups_00134_terretrial_groups_     L bateriap_Activatoriats     L_bateriap_Activatoriats     L_bateriap_Interviduatoriats     L_bateriap_Interviduatoriats     Lotteriap_Interviduatoriats     Lotteriap_Interviduatoriats     Dateriats     Dateriap_Interviduatoriats     Dateriap_Openatoriats     Date
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1378 1377	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 7 0 0 0 3 2 0 0 0 3 2 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 5 2 3 0 3 2 9 3	0 3 1 0 2 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>L. Isakeria,fontosakeria,ontosakeria</li></ul>
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380	0 1 0 2 0 1 0 0 1 0 0 1 0 0 1 1 0 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 16	0 0 0 0 0 0 3 2 0 0 0 0 3 2 0 0 0 3 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 1 1	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 5 2 3 0 3 2 9 3 7	0 3 1 0 2 0 6 0 0 0 0 0 4 0 0 0 4 0 0 4		
1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1375 1376 1377 1378 1379 1380	0 1 0 2 0 1 0 0 1 0 0 1 0 0 1 1 0 0 1 1 1 0 0 1 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 1 1 1 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 1 0 2 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>Listeria, fermininousdots, Jossi, terretria (poop, S0314, terretria (poop, S0334, terretria (poop, S034, terretria (poop, S0344, terretria (poop, S0344, terretria (p</li></ul>
1362 1363 1364 1365 1366 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381	0 1 0 2 0 0 1 0 0 0 1 0 0 1 1 0 0 1 1 0 0 2 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 1 1 1 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 1 0 2 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>Lasteriap_Germatimosadots_00134_terretria_group_00134_terretrial_group_00134_terretrial_groups_00134_terretrial_group</li></ul>
1142 1143 1344 1344 1345 1346 1347 1348 1346 1347 1348 1347 1347 1347 1347 1347 1347 1348 1347 1348 1348 1348	0 1 0 0 0 1 0 0 1 1 00 1 1 00 1 1 0 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 2 0 0 0 3 2 0 0 0 4 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 5 2 3 0 3 2 9 3 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>L. Isaketika, Germatimovaksta, 2013 Lamethul groupo, 2013 Lamethul groups, 2013</li></ul>
1362 1363 1364 1365 1366 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381	0 1 0 2 0 0 1 0 0 0 1 0 0 1 1 0 0 1 1 0 0 2 0 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 1 0 2 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>Lasteriap_Germatimosadots_00134_terretria_group_00134_terretrial_group_00134_terretrial_groups_00134_terretrial_group</li></ul>
1142 1343 1344 1345 1346 1347 1347 1347 1373 1374 1374 1375 1376 1377 1379 1380 1381 1383 1384 1383	0 1 0 0 0 1 0 0 1 1 00 1 1 00 1 1 0 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 7 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 1 1 0 0 0 1 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 5 2 3 0 3 2 9 3 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 0 2 0 6 0 0 0 0 4 0 0 0 4 0 0 0 1		<ul> <li>Listeria, Cennationadots, Solia, Errentral group, Solia, Exercicla group, Solia, Errentral group, Solia, Solia, Solia, Solia, Solia, Solia, Solia, Solia, Solia, Errentral, Friendenteria, Errentral group, Solia, Er</li></ul>
1142 1343 1344 1345 1346 1347 1348 1347 1373 1374 1373 1374 1375 1376 1376 1376 1376 1376 1376 1370 1381 1380 1381 1383	0 1 2 0 0 1 0 0 0 1 0 0 1 1 0 1 1 0 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 0 2 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>Lasteria, Cerenationadots, Josia Lametria (prop. 3014. Lametria (prop. 3013. La</li></ul>
1142 1343 1344 1345 1346 1347 1347 1347 1373 1374 1374 1375 1376 1377 1379 1380 1381 1383 1384 1383	0 1 2 0 0 1 0 0 0 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 0 1 0 0 0 2 0 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 7 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 1 1 0 0 0 1 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 0 2 0 6 0 0 0 0 4 0 0 0 4 0 0 0 1		<ul> <li>Listeria, Cennationadots, Solia, Errentral group, Solia, Exercicla group, Solia, Errentral group, Solia, Solia, Solia, Solia, Solia, Solia, Solia, Solia, Solia, Errentral, Friendenteria, Errentral group, Solia, Er</li></ul>
1142 1343 1344 1345 1346 1347 1348 1347 1373 1374 1373 1374 1375 1376 1376 1376 1376 1376 1376 1370 1381 1380 1381 1383	0 1 0 0 1 0 0 1 0 0 1 1 0 0 1 1 1 0 0 0 1 1 0 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0 0	0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 5 2 3 0 3 2 9 3 7 0 0 2 0 7	3 3 0 2 0 6 0 0 0 0 4 0 0 0 4 0 0 0 1 0 0 1		<ul> <li>Lasteria, Cerenationadots, Josia Lametria (prop. 3014. Lametria (prop. 3013. La</li></ul>
1347 1348 1346 1346 1346 1347 1347 1347 1347 1347 1347 1347 1348 1349 1348 1348 1348 1346 1347	0 1 0 0 1 0 0 1 0 0 1 1 0 0 1 1 10 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 0 0 0 6 2 3 0 3 2 9 3 7 0 0 2 0 7 2	3 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>L. Isaketika, Germatimonaksta, 2013 Lametha Lgroup, 2013 Lemetha Lgroup, 2013 Lgroup, 2014 Lgroup,</li></ul>
1342 1343 1345 1346 1346 1347 1347 1370 1377 1376 1377 1377 1377 1377 1377 1377	0 1 0 0 1 0 0 1 0 1 0 1 0 1 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 1 0 3 0 0 0 6 2 3 0 3 2 9 3 7 0 0 0 2 0 7 2 3	3 3 1 0 2 0 6 0 0 0 4 0 0 0 4 0 0 0 0 1 0 0 0 0 0 0 0		<ul> <li>Listeria, Cennetica, Semantinovadets, Colla, Lementic propo, S014, Lementic Lapoop, S0134, Lementic Lapoop, S01344, Lementic Lapoop, S0134, Lementic Lapoop, S01344,</li></ul>
1142 1343 1345 1345 1346 1347 1348 1349 1370 1371 1374 1375 1375 1375 1375 1375 1375 1375 1380 1381 1383 1383 1384 1385 1385	0 1 0 0 0 1 0 0 0 1 0 0 1 1 0 0 0 1 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 0 1 0 3 0 0 0 6 2 3 0 3 2 9 3 7 0 0 0 2 0 7 2 3 0	3 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>Listeria, Cennetica, Sonal Lementia (prop. S014. Lementia (prop. S013. Lementia</li></ul>
1362 1363 1364 1365 1367 1368 1370 1370 1373 1375 1375 1375 1375 1375 1375 1375	0 1 0 0 0 1 0 0 0 1 0 0 1 1 0 0 0 1 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 2 0 0 0 0 0 0 0 0 0 0 0 0			0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 0 1 0 3 0 0 0 6 2 3 0 3 2 9 3 7 0 0 0 2 0 7 2 3 0 0	3 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>Lasteria, Cennatinous/stat, OSIALsimetrialgroup. SDIALsimetrialgroup. SDIALsimetrialgroup.</li> <li>Lasteria</li> <li>Lasteria, Lasteria</li> <li>Lasteria, Lasteriadosc, Batteriados, Osialsis, Prophytonosis, Charlynonesis, Charlynonesis,</li></ul>
1362 1363 1365 1365 1367 1367 1370 1370 1371 1373 1374 1375 1375 1375 1375 1375 1375 1387 1380 1383 1384 1385 1386 1385 1386 1385 1385	0 1 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 3 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0			0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 0 1 0 3 0 0 0 6 2 3 0 3 2 9 3 7 0 0 0 2 0 7 2 3 0 0 2	3 3 1 0 2 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>L. Isakelia, Germatimouskis, 2013 Lamethi Loop, 2013 Lemethi Loop, 2014 Lemethi</li></ul>
1142 1343 1344 1345 1347 1347 1347 1370 1371 1374 1375 1374 1375 1376 1377 1378 1377 1378 1379 1380 1381 1383 1384 1383 1384 1383 1384 1383 1384 1385	0 1 0 0 1 0 0 0 0 1 0 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 3 2 0 0 0 0 0 0 0 0 0 0 0 0		0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 0 0 1 0 3 0 0 0 6 2 3 0 3 2 9 3 7 0 0 0 2 0 7 2 3 0 0 2	3 3 1 0 2 0 6 0 0 4 0 0 0 4 0 0 0 4 0 0 0 1 0 0 0 1 2 0 0 1 2 0 0 1 2 0 0 0 0		<ul> <li>Lasteria, Centralationalatis, 2013 Lametria (prop. 2013 Lametria (prop. 2013) Lametria (prop. 2014) L</li></ul>
1142 1343 1343 1345 1346 1347 1348 1349 1370 1371 1374 1375 1375 1375 1375 1375 1375 1375 1375	0 1 0 0 1 0 0 0 0 1 0 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	80010300008230329370002072300211	0 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>Listeria, Cennetica, Joshi Lemetria (prop. 2014. Lemetria (prop. 2013. Lemetria</li></ul>
1342 1343 1344 1345 1347 1348 1347 1374 1375 1375 1375 1375 1375 1375 1375 1375	0 1 2 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 3 2 0 0 0 3 2 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	80010300062303293700020723002110	0 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>Lasteria, Centralinous/etic_0314_eteretria_prop0313_eteretria_prop_0313</li></ul>
1342 1343 1345 1346 1347 1347 1347 1347 1347 1347 1343 1343	0 1 2 0 0 1 0 0 1 0 0 1 1 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	800101000000010100100207230021100	0 3 3 1 0 0 2 0 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>Lasteria, Centralinous/dist, 2013/Lametria/prop.2013/Lametria/prop/2013/Lametria/Lametria/Lametria/Lametria/Lametria/L</li></ul>
1142 1343 1345 1346 1347 1347 1347 1370 1371 1372 1374 1375 1374 1375 1376 1377 1376 1377 1378 1377 1378 1379 1380 1381 1384 1385 1388 1389 1389 1389 1389 1389 1389 1389	0 1 2 0 0 1 0 0 1 0 0 1 1 0 0 1 1 10 8 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 7 7 8 7 8 7 8 8 8 8 8 8 8 8 8 8 8 8	0 2 1 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	80010100008230329370002072300211002	3 3 1 0 2 0 6 0 0 4 0 0 0 4 0 0 0 1 0 0 0 1 32 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>Lasteria, Centralizationa dela se anticipade a solutione dela solutione</li></ul>
1142 1343 1344 1345 1346 1347 1348 1349 1370 1373 1375 1375 1375 1375 1375 1375 1375	0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		8001030000523032937000207230021110022	0 3 3 1 0 0 2 0 6 0 0 4 0 0 0 4 0 0 0 1 0 0 0 1 1 2 0 0 0 0 2 2 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>Listeria, Centralization solutis, 2003 Lementia Largo p. 20</li></ul>

1400	0	0	0	0	0	1	0	0	2	0	$0 \ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Methylococcales; f\_Methylomonadaceae; g\_Methylomonas (Methylomonadaceae) \ A = 0$
1401	2	0	O	0	0	D	0	D	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria
1402	o	0	O	0	o	D	0	D	3	o	0 k_Bacteria;p_Wethylomirabilota;c_Wethylomirabilia;o_Rokubacteriales;f_WX65;g_WX65;s_
1403	0	0	0	0	2	0	0	0	0	0	0 k_Bacteria;p_Firmicutes:c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
1404	0	0	1	0	2	0	0	0	2	0	0 k_Bacteria;p_Myxococcota;c_Polyangia;o_Blfdi19;f_Blfdi19;g_Blfdi19;s_
1405	0	0	0	0	0	D	0	2	0	٥	0 k_Bacteria;p_Acidobacteriota;c_Acidobacteriae
1406	0	0	2	0	o	D	0	o	0	0	0 k_Bacteria;p_Firmicutes;c_Clostrida;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK44136_group
1407	0	0	0	0	0	0	2	0	0	0	0 k Bacteriajo Myxococcotajo: Polyangia
			0			0			0	0	
1408	0	0		0	0		2	0			0 Unknown
1409	2	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_;s_
1410	0	0	0	0	D	D	0	0	2	0	0 k_Bacteria;p_Cyanobacteria;c_Cyanobacteria;a_Chloroplast;f_Chloroplast;g_Chloroplast
1411	2	0	0	0	0	0	0	1	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Pedobacter;s_Pedobacter_sp.
1412	1	0	0	0	0	2	0	0	1	0	0 k_Bacteria;p_Bdellovibrionota;c_Oligoflexia;o_Oligoflexales;f_;g_;s
1413	0	5	0	0	0	0	0	0	0	0	0 k_Bacteria
1414	0	0	0	0	2	0	0	0	0	0	$0\ k\_Racteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Barkholderia les f\_Coma monadacea e; g\_Limnohabitans f\_Coma monadacea e; b] = 0\ and a constraints and a constrai$
1415	0	5	U	0	D	D	0	D	0	0	0 Unknown
1415	2	0	σ	0	o	D	0	o	0	0	0 Unknown
1417	0	0	0	0	0	0	0	4	0	0	0 k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Pseudonocardiaks;f_Pseudonocardiaceae;g_Pseudonocardia;s_Pseudonocardia;dioxanivorans
1418	0	0	0	0	0	0	0	3	0	0	0 k_Bacteria;p_Acidobacteriota;c_Thermoanaerobaculia;o_Thermoanaerobaculales;f_Thermoanaerobaculaceae; <u>e_</u> Subgroup_10
1419	0	0	0	0	0	0	0	2	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;z_Reyranellales;f_Reyranellaces;p_;s_
1420	2	0	o	0	0	D	0	D	0	0	
											0 k_Bacteria;p_Planctomycetota;c_Planctomycetes;o_Prellulales;f_Prellulaceae;g_Prellula;s_
1421	0	0	O	0	D	D	0	2	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;g_Legionella
1422	0	4	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Actinobacteriotacc_Acidi microbila;o_Microtrichales:f_Microtrichaceaeo;a_3_
1423	0	0	0	0	0	0	0	1	1	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Taibaiella
1424	0	0	0	0	0	2	0	D	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae
1425	0	2	0	0	D	D	0	0	0	0	0 Unknown
1426	0	0	7	0	0	0	0	2	0	0	0 kBacteria;pProteobacteria;cGammaproteobacteria;oVibrionales;fVibrionaceae;gVibrio
1427	0	0	0	0	0	2	0	0	1	0	0 k_Bacteria;p_Methylomirabilota;c_Methylomirabilia;o_Methylomirabilales;f_Methylomirabilaceae;g_Sh765B-TzT-35;s_
1428	0	0	9	0	0	0	0	0	95	0	7 k_Bacteria;p_Desulfoblacterota;c_Desulfovibrionia;a_Desulfovibrionales;f_Desulfovibrionaceae;g_;s_
1429	0	0	4	0	0	1	0	0	3	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Ramlibacter;s
1430	4	4	0	0	0	0	0	9	3	0	0 k_Bacteria;p_Actinobacteriotacc_Actinobacteria;o_Micrococcales;f_Intrasporangiaceae;g_Terrabacter;s_Terrabacter_sp.
1431	0	0	0	0	0	2	0	0	0	0	0 k Bacteriajo Firmicutes:c Clostridia o Lachnospirales;f Lachnospiraceae;g A2
1432	35	0	16	0	8	19	0	20	38	3	1 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria
1433	1	0	n	0	1	3	0	0	0	0	0 k_Bacteria;p_Protecbacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae.g_
1434	1	0	O	0	1	0	0	0	1	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Cavicella
1435	0	0	0	0	0	2	0	0	1	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderialesf_Comamonadaceae;g_Brachymonas;s_Brachymonas_denitrificans
1436	0	0	0	0	3	0	0	0	0	0	0 k_Bacteria;p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Roseiflexaceaeg_;s_
1437	0	0	1	0	0	0	0	0	0	1	0 k_Bacteria;p_Gemmatimonadota;z_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;z_
1438	0	0	O	0	2	D	0	D	0	o	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidiales;f_Munbaculaceae;g_Munbaculaceae;s_
00000	10	0	0	1940	0	0	0	3	0	0	0 k_Bacteria;p_Acidobacteriota;z_Acidobacteriae;o_Bryobacterale;sf_Bryobacteraceae;z_Bryobacter
1439	0	0	. 0	0	0	0	0	5	0		
1439	0	0	٥	0	0	D	0	3	0	0	0 k_Bacteria;p_Chloroflextc_OL814;o_OL814;f_OL814;g_OL814;s
										o o	
1440	o	0	٥	0	o	D	o	3	o		o La Laterina,NotorchikaO.18.14,O.18.44,O.18.45, D kBasterina,Notosphota,Termodeullovbronika
1440 1441 1442	o	0 0 0	0 0 0	0 0 0	0 0 0	D D 2	0 0 0	3 D 0	o z o	а 0	0 k_Bacteriag_hiteospirotas_Thermodeuslikovkironiaa_ <u>f_g_s_</u> 0 k_Bacteriag_Protoclastcrisk_Gammaprotoclasteria
1440 1441 1442 1443	0 0 3	0 0 0	0 0 0 15	0 0 0	0 0 0 11	D D 2 72	0 0 4	3 D 0 2	0 2 0 42	0 0 1	0 k_lasteria,p_lihoospirotax_Thermodexulfoxbinonia.p_t_t_s_ 0 k_lasteria,p_Protechacteria;c_Gammiprotechasteria 0 k_lasteria,p_Firmicutex_Cobstridia.p_Lachnospiratest_Lachnospiratester_Livibaterium_wylanophilum_provps_
1440 1441 1442 1443 1444	0 0 3 0	0 0 0 0	0 0 15 1	0 0 0 0	0 0 11 0	0 0 2 72 2	0 0 4 0	3 0 2 D	0 2 0 42 0	0 0 1 0	0 k_Bateriap_Nitrospirotas_Thermodesulfovbironiap_f_g_s_ 0 k_Bateriap_Frotobaterinis_Gammuprotoobatteria 0 k_Bateriap_Firmicutes_Contridap_Lachrospiratesf_Lachrospiraceaeg_Nubaterium_sylanophilum_proups_ 0 k_Bateriap_Chlordiwsiz_Anamolinaaesy_RBG:1354:94_RBG:1354:94_RBG:1354:95_
1440 1441 1442 1443 1444 1445	0 0 3 0 39	0 0 0 0 44	0 0 15 1 17	0 0 0 0 53	0 0 11 0 8	0 2 72 2 13	0 0 4 0 210	3 0 2 0 28	0 2 0 42 0 24	0 1 0 1	0  _Bacteriahtrospitotaitermodeudlovitronisoi 0  _Bacteriahtrospitotaitermodeudlovitroniso_iter
1440 1441 1442 1443 1444 1445 1446	0 0 3 0	0 0 0 44 0	0 0 15 1 17 0	0 0 0 0 53 0	0 0 11 0 8 0	0 2 72 2 13 1	0 0 4 0 210 0	3 D 2 D 2B 3	0 2 0 42 0 24 0	0 1 1 1	D k_Bateriaa_hhttpsprotax_Thermodexallowbroniaa_f_g_s_ D k_Bateriaa_Protocolarceriac_Gammaprotocolarteria D k_Bateriaa_Protocolarceriac_Gammaprotocolarteria D k_Bateriaa_Chlorothesc_Abarroineesca_RBG135449_BBG135449_BBG135449_ D k_Bateriaa_Protocolarceriac_BateriaaStaphilococciesic_Taphylococcesses D k_Bateriaa_Protocolarceriac_Abarraprotocolarteriaa_Actobateriaacee
1440 1441 1442 1443 1444 1445 1446 1447	0 0 3 0 39	0 0 0 44 0	0 0 15 1 17 0 0	0 0 0 53 0 0	0 0 11 0 8 0	D 2 72 13 1 0	0 0 4 0 210 0 0	3 0 2 0 28 3 0	0 2 0 42 0 24 0 1	0 1 0 1 0	D k_Bateriag_hitrospitotac_Thermodeuslifovbinoniag_f_g_ic_ D k_Bateriag_hitrospitotac_Thermodeuslifovbinoniag_f_g_ic_ D k_Bateriag_Chienethesi_Assumotivesag_BateCi35449(_MGCi35449(_MGCi35449(_ L_Bateriag_Chienethesi_Assumotivesag_BateCi35449(_MGCi35449(_MGCi35449(_ L_Bateriag_Thermodeus_Bateriag_Bateriag_Staphylococcessag_Staphylococcess D k_Bateriag_Thermodeus_Bateriag_Bateriag_Staphylococcessag_Staphylococcess D k_Bateriag_Thermodeus_Chienethesiag_Bateriag_Staphylococcessag_Staphylococcess D k_Bateriag_Thermodeus_Chienethesiag_Bateriag_Bateriag_Staphylococcess D k_Bateriag_Thermodeus_Chienethesiag_Bateriag_Bateriag_Staphylococcessag_Staphylococcess D k_Bateriag_Thermodeus_Chienethesiag_Bateriag
1440 1441 1442 1443 1444 1445 1446 1447 1448	0 0 3 39 2 3 4	0 0 0 44 0 0 0	0 0 15 1 7 0 0 0	0 0 0 53 0 0 0	0 0 11 0 8 0 0	D D 2 72 2 13 1 0 0	0 0 4 0 210 0 0	3 0 2 0 28 3 0 0	0 2 0 42 0 24 0 1 0	0 1 1 0 0	D k_Bateriag_Nitrospirotas_Thermodesublovbinoniag_f_g_k_ D k_Bateriag_Protocolacticiac_Gammaporotobateria D k_Bateriag_Denotinet_Colorridage_Electrospiratesig_Eschoospiraceseg_Tubateriam_vylanophilam_provas_ D k_Bateriag_Olevorinet_colorridage_Biological Statek_TBG-13-54 &g_B0-13-54 &g_B0-13-54 &g_D0-13-54 &g_D0-1
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449	0 0 3 0 39	0 0 0 44 0	0 0 15 1 17 0 0	0 0 0 53 0 0	0 0 11 0 8 0	D 2 72 13 1 0	0 0 4 0 210 0 0	3 0 2 0 28 3 0	0 2 0 42 0 24 0 1	0 1 0 1 0	D k_Bateriag_hitrospitotac_Thermodeuslifovbinoniag_f_g_ic_ D k_Bateriag_hitrospitotac_Thermodeuslifovbinoniag_f_g_ic_ D k_Bateriag_Chienethesi_Assumotivesag_BateCi35449(_MGCi35449(_MGCi35449(_ L_Bateriag_Chienethesi_Assumotivesag_BateCi35449(_MGCi35449(_MGCi35449(_ L_Bateriag_Thermodeus_Bateriag_Bateriag_Staphylococcessag_Staphylococcess D k_Bateriag_Thermodeus_Bateriag_Bateriag_Staphylococcessag_Staphylococcess D k_Bateriag_Thermodeus_Chienethesiag_Bateriag_Staphylococcessag_Staphylococcess D k_Bateriag_Thermodeus_Chienethesiag_Bateriag_Bateriag_Staphylococcess D k_Bateriag_Thermodeus_Chienethesiag_Bateriag_Bateriag_Staphylococcessag_Staphylococcess D k_Bateriag_Thermodeus_Chienethesiag_Bateriag
1440 1441 1442 1443 1444 1445 1446 1447 1448	0 0 3 39 2 3 4	0 0 0 44 0 0 0	0 0 15 1 7 0 0 0	0 0 0 53 0 0 0	0 0 11 0 8 0 0	D D 2 72 2 13 1 0 0	0 0 4 0 210 0 0	3 0 2 0 28 3 0 0	0 2 0 42 0 24 0 1 0	0 1 1 0 0	D k_Bateriag_Nitrospirotas_Thermodesublovbinoniag_f_g_k_ D k_Bateriag_Protocolacticiac_Gammaporotobateria D k_Bateriag_Denotinet_Colorridage_Electrospiratesig_Eschoospiraceseg_Tubateriam_vylanophilam_provas_ D k_Bateriag_Olevorinet_colorridage_Biological Statek_TBG-13-54 &g_B0-13-54 &g_B0-13-54 &g_D0-13-54 &g_D0-1
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449	0 0 3 0 39 2 3 4 0	0 0 0 44 0 0 0 0	0 0 15 1 17 0 0 0 0	0 0 0 53 0 0 0 0	0 0 11 0 8 0 0 0	0 2 72 13 1 0 0 0	0 0 4 0 210 0 0 0 2	3 0 2 0 28 3 0 0	0 2 0 42 0 24 0 1 0 0	0 1 0 0 0 0	0   _Bateriahreespitatathemodeudlovkronita 0   _Bateriahreespitatathemodeudlovkronita 0   _Bateriafreetosa_creating 0   _Bateria 1   _Bateria 1   _Bateria
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450	0 0 3 0 39 2 3 4 0	0 0 0 44 0 0 0 0 2	0 0 15 1 7 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0	0 2 72 13 1 0 0 0 0	0 0 4 0 210 0 0 0 2 0 2 0	3 0 2 0 28 3 0 0 0 0	0 2 0 42 0 24 0 1 0 0 0 0	0 1 0 1 0 0 0 0 0	<ul> <li>b [asteriaintroceptotaThermodeuallowbroinia</li> <li>b [asteriaintroceptotaThermodeuallowbroinia</li> <li>c [asteriaintroceptot_Contributeinterpreterobacteria</li> <li>b [asteriaintroceptot_Contributeinterpreterobacteria</li> <li>c [asteriaintroceptot_Contribute_interpreterobacteria</li> <li>c [asteriainterpreterobacteria</li> <li>c [asteria</li> <li>c [as</li></ul>
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451	0 0 3 0 39 2 3 4 0	0 0 0 44 0 0 0 0 2	0 0 15 1 7 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0	0 2 72 13 1 0 0 0 0 0	0 0 4 0 210 0 0 0 2 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 0 0	0 2 0 42 0 24 0 1 0 0 0 0 0	0 1 0 0 0 0 0	D k_Bateriaa_hthrospitotac_Thermodexilfoxbinoniaa_f_gc_ D k_Bateriaa_frincidesic_CoBurridayo_Lichhoopalaki/_Lichhoopariseeseg_Lobacteriam_vykanophilum_proups_ D k_Bateriaa_Chiorofiete_Anamoranesa_BAG135449_BBG135449_BBG135494_ D k_Bateriaa_Chiorofiete_Anamoranesa_BAG135449_BBG135494_BAG135494_ D k_Bateriaa_Chiorofiete_Anamoranesa_BAG135491_BBG135492_BBG135494_ D k_Bateriaa_frincidesic_CoBurridayo_Lichhoopalaki/_Lichhoopariseeseg_a_ D k_Bateriaa_frincidesic_CoBurridayo_Lichhoopalaki/_Lichhoopariseeseg_a_ D k_Bateriaa_frincidesic_CoBurridayo_Lichhoopalaki/_Lichhoopariseeseg_a_ D k_Bateriaa_frincidesic_CoBurridayo_Lichhoopalaki/_Lichhoopariseeseg_a_ D k_Bateriaay_Arindascorriday_And micrimbiaa_Monthholesi/_j D k_Bateriaay_Arindascorridayo_Lichhoopalaki/_Staphylooccaseseg_Staphylooccas D k_Bateriaa_Frincidesic_CoBurridayo_BitRID35f_ANbg_A455_
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1451	0 0 3 0 39 2 3 4 0 0 2 4	0 0 0 44 0 0 0 2 0	0 0 15 1 7 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0 0	D 2 72 13 1 0 0 0 0 0 0 2	0 0 4 0 210 0 0 0 7 0 0 0 0 0	3 0 2 0 28 3 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 42 0 24 0 1 0 0 0 0 0 0	0 1 0 0 0 0 0 0	0 k_Bateriag_hreedenbas_Thermodeutlovbronkag_f_g_ic_ 0 k_Bateriag_hreetoskactrike_Gammaperetoskateria 0 k_Bateriag_fordetska_Anamoreaeg_BAGC 13 544 kg_BBC 13 544 kg_BDC 10 545 kg_BDC
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1451	0 0 3 0 39 2 3 4 0 0 2 4	0 0 0 44 0 0 0 2 0	0 0 15 1 7 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0 0	D 2 72 13 1 0 0 0 0 0 0 2	0 0 4 0 210 0 0 0 7 0 0 0 0 0	3 0 2 0 28 3 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 42 0 24 0 1 0 0 0 0 0 0	0 1 0 0 0 0 0 0	0   _BoteriaIntroductiaInternoteeuflowbronise 0   _BoteriaInterdeductiaGeneratoricalitationspinesesSubstantian_vylanophilum_provas
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1453	0 0 3 0 39 2 3 4 0 0 2 4	0 0 0 44 0 0 0 2 0	0 0 15 1 0 0 0 0 0 0 0 1 0 0	0 0 0 53 0 0 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0 0 0 0 0	D 2 72 13 1 0 0 0 0 0 0 2	0 0 4 0 210 0 0 0 7 0 0 0 0 0	3 0 2 0 28 3 0 0 0 0 0 0 0 0 0 0 0 0	0 2 0 42 0 24 0 1 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b Lasteria,hrocopieta.chermodeullovkroita.g_tt</li> <li>b Lasteria,hrocopieta.chermodeullovkroita.g_tt</li> <li>b Lasteria,hrocopieta.chormodeucsharehormodeucischoopiete.ecgUstacterian_uvianophilan_proups</li> <li>b Lasteria,hrocopieta.chavenione.gBRG: 33.448BRG: 13.548RRC: 13.548RC: 13.558R</li></ul>
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454	0 0 3 0 39 2 3 4 0 0 2 4	0 0 0 44 0 0 0 0 2 0 0 2 0 0 2 0	0 0 15 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 1 0 1 0	0 0 11 0 8 0 0 0 0 0 0 0 0 0 0 0 0	D D 2 72 2 13 1 0 0 0 0 0 2 0 0 2 0 0 2 2 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 28 3 0 0 0 0 0 0 0 0 0 0 0 0	0 2 42 0 24 0 1 0 0 0 0 0 0 0 1 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   bsteriag_hrindets_Gammaportobateria_ b   bsteriag_frindets_Gammaportobateria</li> <li>c   bsteriag_frindets_Gammaportobateria_Gampaocases</li> <li>c   bsteriag_frindets_Gammaportobateria_Gammaportobateriases</li> <li>c   bsteriag_frindets_Gammaportobaterias_Gampaocases</li> <li>c   bsteriag_frindets_Gammaportobaterias_Gampaocases</li> <li>c   bsteriag_frindets_Gammaportobateriase_Gampaocases</li> <li>c   bsteriag_frindets_Gammaportobateriase_Gammaportobateriases</li> <li>c   bsteriag_frindets_Gammaportobaterias_Gampaocases</li> <li>c   bsteriag_frindets_Gammaportobaterias_Gampaocases</li> <li>c   bsteriag_frindets_Gammaportobaterias_Gampaocases</li> <li>c   bsteriag_frindets_Gammaportobaterias_Gampaocases</li> <li>c</li></ul>
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1455 1455	0 0 3 8 7 4 0 0 2 4 0 0 2 2 0 2 2 0	0 0 0 44 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0	0 0 15 1 17 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 72 2 13 1 0 0 0 0 2 0 0 2 1 0 0 2 1 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 0 0 2 0 0 2 1 1 0	0 2 42 0 24 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerisa, Introduction, Generatorocolution, Jackeria, Jakkeria, Jakkeria,</li></ul>
1440 1441 1442 1443 1444 1445 1445 1446 1447 1448 1446 1450 1451 1453 1454 1455 1456 1455 1456	0 0 3 9 2 3 4 0 0 2 4 0 0 2 2 0 0 2 2 0 0 2 0 0 2 0 0 0 0	0 0 0 44 0 0 0 0 2 0 0 0 0 2 0 0 0 2 2 2 2	0 0 15 1 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 72 2 13 1 0 0 0 0 2 0 0 2 1 0 0 2 1 0 0 2 1 0 0 0 2 1 1 0 0 0 2 0 0 0 0	0 0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 0 0 2 0 2 1 1 0 0 0 2 0 0 2 0 0 0 0	0 2 42 0 24 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   Bateria, _ Intercapatria, _ Thermodeualito/kinetika</li> <li>b   Bateria, _ Intercapatria, _ Gramaperetrobateria</li> <li>b   Bateria, _ Intercapatria, _ Endediation : _ Status :</li></ul>
1440 1441 1442 1443 1445 1446 1447 1445 1446 1447 1459 1451 1455 1455 1455 1455 1455 1455	0 0 3 0 2 4 0 2 4 0 2 2 0 2 0 2 0 2 0 2 0 2 0	0 0 0 44 0 0 0 0 2 0 0 0 0 2 0 0 0 2 2 0 0 0 2 2 0 0 0 2 2 0 0 0 2 0	0 0 15 1 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 2 72 2 13 1 0 0 0 0 2 0 0 2 1 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0	0 2 42 0 24 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 1 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	<ul> <li>b. Jasteriaa, Jahosapitota, Themodeuallovkronika,</li></ul>
1440 1441 1442 1443 1445 1446 1447 1448 1446 1447 1451 1451 1451 1453 1454 1455 1455 1455	0 0 3 9 2 3 4 0 0 2 4 0 0 2 2 0 0 2 2 0 0 2 0 0 2 0 0 0 0	0 0 0 44 0 0 0 0 2 0 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 0 2 0	0 0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D 2 72 2 13 1 0 0 0 0 2 0 0 2 1 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 42 0 24 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jasteriaa, Jarospitota, Thermodeusliokinosia, j.g., j.</li> <li>b. Jasteriaa, Jarospitota, Jarospitota, Jarospitota, Jastonspitote, Jastonspitote, Jastonspitote, Jasteriaa, Jarospitote, Jastonspitote, Jas</li></ul>
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1455 1455 1455 1455 1455	0 0 3 0 2 4 0 2 4 0 2 2 0 2 0 2 0 2 0 2 0 2 0	0 0 0 44 0 0 0 0 2 0 0 0 2 0 0 0 2 2 0 0 0 2 0	0 0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 2 72 2 13 1 0 0 0 0 2 1 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 2 0 2 1 1 0 0 0 2 1 1 0 0 0 2 1 1 0 0 2 3 0 0 0 2 3 0 0 0 2 8 3 0 0 0 2 8 3 0 0 0 2 8 8 3 0 0 0 0 2 8 8 3 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 0	0 2 42 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jackeria, _intercolucta, _internoluctaria.j</li></ul>
1440 1441 1442 1443 1445 1446 1447 1448 1446 1447 1451 1451 1451 1453 1454 1455 1455 1455	0 0 3 0 2 4 0 2 4 0 2 2 0 2 0 2 0 2 0 2 0 2 0	0 0 0 44 0 0 0 0 2 0 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 0 2 0	0 0 15 1 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 2 72 2 13 1 0 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 42 0 24 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jakteria,hotospitata,termodeullovkroita.g.,</li></ul>
1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1455 1455 1455 1455 1455	0 0 3 0 2 4 0 2 4 0 2 2 0 2 0 2 0 2 0 2 0 2 0	0 0 0 44 0 0 0 0 2 0 0 0 2 0 0 0 2 2 0 0 0 2 0	0 0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 2 72 2 13 1 0 0 0 0 2 1 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 2 0 2 1 1 0 0 0 2 1 1 0 0 0 2 1 1 0 0 2 3 0 0 0 2 3 0 0 0 2 8 3 0 0 0 2 8 3 0 0 0 2 8 8 3 0 0 0 0 2 8 8 3 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 0	0 2 42 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jackeria, _intercolucta, _internoluctaria.j</li></ul>
1441 1441 1442 1443 1444 1445 1446 1447 1446 1451 1451 1451 1455 1455 1455 1455	0 0 3 0 3 8 2 4 0 2 2 0 2 2 0 0 2 2 0 0 2 2 0 0 2 2 0 0	0 0 0 44 0 0 0 0 2 0 0 0 0 2 2 0 0 0 0 2 2 0 0 0 0 2 0 0 0 0 2 0	0 0 15 1 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D 2 72 2 13 1 0 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 2 0 2 1 1 0 0 0 2 1 1 0 0 0 2 1 1 0 0 0 2 0 2	0 2 42 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jakteria,hotospitata,termodeullovkroita.g.,</li></ul>
1440 1441 1442 1443 1444 1445 1445 1445 1446 1446 1446 1446	0 0 3 0 2 4 0 2 2 0 0 2 0 0 2 0 0 0 0 0 0 0 0	0 0 0 44 0 0 2 0 0 2 0 0 0 2 2 0 0 0 2 2 0 0 0 2 2 0 0 0 2 0 0 0 2 0 0 0 2 0	0 0 15 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		D 2 72 2 13 1 0 0 0 2 1 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 3 0 0 0 0 2 2 0 2 1 1 0 0 0 2 1 1 0 0 0 2 1 1 0 0 0 2 0 0 0 0	0 2 42 0 24 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jasteria, _ heteopieta, _ heteopieta, _ isonopieteo isoteria,</li></ul>
1440 1441 1442 1444 1445 1446 1445 1447 1448 1449 1449 1451 1451 1455 1455 1455 1455	00302400220022002	0 0 0 44 0 0 2 0 0 2 0 0 0 2 2 0 0 0 2 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 0 2 0	0 0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		D D 2 72 2 1 0 0 0 2 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 28 3 0 0 0 0 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0	0 2 42 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jasteriaa, Introspitota, Thermodeutlovbronika, J., j., L.</li> <li>b. Jasteriaa, Introspitota, Gammotorcobatteria</li> <li>c. Jasteriaa, Introspitota, Cobridae, Laboreobatteria</li> <li>c. Jasteriaa, Introspitota, Jasteriaa, Jaste</li></ul>
1440 1441 1442 1443 1444 1445 1444 1445 1445 1445 1445	003022400220022002	0 0 0 44 0 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 0 0 2 0	0 0 15 1 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		D 2 72 2 13 1 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 7 8 3 0 0 0 0 2 0 2 2 1 0 0 0 2 2 1 0 0 0 0 2 0 2	0 2 42 0 24 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jackeria, Jerecekateria, Germangerecekateria</li> <li>c. Jackeria, Jerecekateria, Jerecekateria, Jerecekateria</li> <li>c. Jackeria, Jerecekateria, Jerecekateria</li> <li>c. Jackeria, Jerecekateria, Jerecekateria</li> <li>c. Jackeria, Jerecekateria</li> <li>c. Jackeria</li> <li>j. Jackeria</li> <li></li></ul>
1440 1441 1442 1443 1444 1445 1444 1445 1445 1446 1445 1446 1445 1446 1451 1464 1465 1466 1466	003022400220022002	0 0 44 0 0 0 2 0 0 2 0 0 0 2 0 0 0 0 2 0	0 0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		D 2 72 2 13 1 0 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 2 8 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0	0 2 42 0 24 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jaktriag. Jantospitata. [hermodeullovkroita.g. []</li> <li>b. Jaktriag. Jantospitata. [hermodeullovkroita.g. []</li> <li>b. Jaktriag. Jantospitata. [hermodeullovkroita.g. []</li> <li>b. Jaktriag. Jantospitata.g. []</li> <li>b. Jaktriag. []</li> <li>b. Jaktriag.</li></ul>
1440 1441 1442 1443 1444 1445 1445 1446 1446 1446 1446 1455 1456 1456	003032400220022002	0 0 44 0 0 0 2 0 0 2 0 0 0 2 0 0 0 0 2 0	0 0 15 1 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		D 2 72 2 13 1 0 0 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 0 0 0 0 0 2 0 0 0 0 2 0 0 0 0 0 2 1 0 0 0 0	0 2 42 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>bbsteriabrougetotatermodeut/outronisf</pre>
1440 1441 1442 1443 1444 1445 1444 1445 1445 1445 1455 145	0 0 3 0 3 2 3 4 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 0 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 72 2 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		3 0 2 0 0 0 0 0 2 0 2 1 1 0 0 0 2 5 2 0 0 0 2 5 2 0 0 0 0 2 5 0 0 0 0	0 2 42 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b. Jaktria, Januaria, Janua</li></ul>
1440 1441 1442 1443 1444 1445 1444 1445 1445 1446 1445 1446 1445 1446 1453 1464 1462 1464 1464 1464 1466 1466 1466	000303234002200220022000	0 0 0 44 0 0 2 0 0 2 0 0 0 2 0 0 0 0 2 0 0 0 0	0 0 15 1 17 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 11 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 72 3 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 210 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 7 7 8 3 0 0 0 2 0 2 0 2 0 2 0 2 0 2 0 0 0 0 0	0 2 42 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ b.terisptreicebacteris</pre>
1440 1441 1442 1443 1444 1445 1445 1446 1446 1446 1455 1456 1456	0 0 0 1 0 1 1 1 0 0 1 4 0 0 1 2 0 0 1 2 0 0 1 0 1 0 1 0 1 0 0 0 1 0 0 0 1 0	0 0 0 44 0 0 2 0 0 0 2 0 0 0 2 0 0 0 0 0	0 15 1 17 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 11 8 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 72 2 1 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		2 0 2 0 2 0 0 0 2 0 2 0 2 0 2 0 2 0	0 2 0 42 0 24 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ bateriabrougetatefermodetate_bateriatef</pre>
1440 1441 1442 1444 1445 1444 1445 1447 1448 1449 1449 1440 1445 1455 1455 1455 1455 1455 1455	001010111110011001100010000000000000000	0 0 0 44 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0 11 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 72 3 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 2 2 2 3 0 0 0 0 2 2 1 0 0 0 0 2 2 1 0 0 0 0 0 2 5 0 0 0 0 2 0 0 0 0 0 0 0 0	0 2 42 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ bsteria_ brougetota_ fermodeut/outronia</pre>
1440 1441 1442 1443 1444 1445 1444 1445 1449 1449 1449 1449	0 0 3 0 28 2 3 4 0 0 2 2 0 0 2 2 0 0 2 2 0 0 2 0 0 0 0	0 0 0 44 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 72 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 2 3 0 0 0 0 2 0 2 0 0 0 0 0 0 0 0	0 2 0 2 2 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ b.teriag_hrendestrisgfermidest_b.terinspirate_j</pre>
1440 1441 1442 1443 1444 1445 1445 1445 1445 1455 1455	0001001	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 1 17 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 72 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 210 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 2 7 8 8 0 0 0 0 2 0 2 0 2 0 2 0 0 0 0 0 0 0	0 2 42 0 24 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ b.teriagtericebateriagierecobater</pre>
1440 1441 1442 1443 1444 1445 1444 1445 1446 1446 1446 1453 1456 1456 1456 1466 1466 1466 1466 1466	0 0 3 0 28 2 3 4 0 0 2 2 0 0 2 2 0 0 2 2 0 0 2 0 0 0 0	0 0 0 44 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 15 1 7 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 72 3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 2 3 0 0 0 0 2 0 2 0 0 0 0 0 0 0 0	0 2 0 2 2 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ b.teriag_hrendestrisgfermidest_b.terinspirate_j</pre>
1440 1441 1442 1443 1444 1445 1445 1445 1445 1455 1455	0001001	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 1 17 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 53 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 2 72 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 210 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 2 7 8 8 0 0 0 0 2 0 2 0 2 0 2 0 0 0 0 0 0 0	0 2 42 0 24 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ b.teriagtericebateriagierecobater</pre>
1440 1441 1442 1443 1444 1445 1444 1445 1446 1446 1446 1453 1456 1456 1456 1466 1466 1466 1466 1466	0 0 0 1 1 1 1 0 0 1 1 0 0 1 2 0 0 1 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 15 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 11 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 72 1 1 0 0 0 0 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 4 0 210 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 0 2 8 3 0 0 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0	0 2 4 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _ b.teriagtericebate_is</pre>

1478	3	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Acidobacteriota;c_Subgroup_11;o_Subgroup_11;f_Subgroup_11;g_Subgroup_11;x_
1479	3	0	2	0	0	1	0	D	0	o	0 k_Bacteria;p_Firmicutes;c_Bacili;o_Paenibaciliales;f_Paenibaciliaceae;g_Paenibacilius
1480	o	5	o	0	o	D	0	D	0	0	0 k_Bacteria;p_Firmicute;;c_Clostrida;o_Lachnospirales;f_Lachnospiraceae
1481	2	0	0	0	0	0	0	0	0	0	0 k_Bacteria
1482	0	0	4	0	1	5	0	1	4	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Aquabacterium;s_
1483	1	0	1	0	2	D	0	1	0	0	0 k_Bacteria;p_Chloroflex;c_OL814;o_OL814;f_OL814;g_OL814;s
1484	0	0	0	0	0	2	0	o	0	0	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagale;:f_Saprospiraceae;g_:s_
1485	0	3	0	0	0	0	0	0	0	0	0 k_Bacteria;p_doidbacteriotaxsubgroup_5;o_subgroup_5;f_subgroup_5;g_subgroup_5;s
1486	5	0	1	0	0	0	0	0	1	0	0 k_Bacteria;p_Actinobacteriotacc_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Arthrobacter;s_Arthrobacter_agiis
1487	0	0	2	0	0	1	0	2	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales/_&calgenaceaeg_GKS98_freshwater_group
1488	1	8	0	0	0	D	0	0	0	0	0 k_Bacteria;p_Fusobacteriota;c_Fusobacteria;o_Fusobacteriales;f_Fusobacteriaceae.g_Fusobacterium
1489	0	0	0	0	0	2	0	0	0	0	0 k_Bacteria;p_Bdellovibrionota;c_Bdellovibrionia;o_Bdellovibrionales;f_Bdellovibrionaceae;g_OM27_clade;s_
1490	0	0	2	0	0	0	0	0	0	0	0 k_Bacteria;p_Armatimonadota;c_Fimbri inonadia;o_Fimbri imonadales;f_Fimbri imonadaceae;g_Fimbri imonadaceae;s_
1491	0	0	0	0	0	1	0	3	0	0	$0\ k\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Burkholderiales;f\_Hydrogenophilaceae;g\_Thiobacillus;s\_i=1,2,3,3,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4$
1492	0	0	2	0	0	0	0	0	0	0	$0\ k\_Bacteria; p\_Proteobacteria; c\_Gamma proteobacteria; o\_Methylococcales; f\_Methylococcaceae and the state of the stat$
1493	o	0	σ	0	o	1	0	D	z	σ	0 k_Bacteria;p_Hrmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_UBA1819;s_
1494	2	0	σ	0	0	0	0	0	0	σ	0 k_Bacteria;p_Firmicutes;c_Bacili
1495	0	0	2	0	2	0	0	0	0	0	0 k_Bacteria;p_Myxococcota;c_Polyangia;o_Polyangiales;f_Sandaracinaceae;g_
1496	0	0	0	0	0	0	0	0	0	3	0 Unknown
1497	0	0	0	2	0	0	0	0	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG-014;f_Clostridia_UCG-014;g_Clostridia_UCG-014;s_
1498	č	0	0	0	0	D	0	D	0	0	
	3										0 k_Bacteria;p_Firmicute;c_Clostrida;o_Lachnospirales;f_Lachnospiraceae;g_Moryella;s_Moryella;sp.
1499	1	0	1	0	0	D	0	D	1	0	0 k_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_GaleBales;f_;8_;1
1500	0	0	0	0	0	0	0	3	0	0	0 k_Bacteria;p_Chloroflexi;c_Chloroflexia;o_Chloroflexales;f_Chloroflexaceae;g_0scillochloris;s_
1501	0	0	0	0	0	0	0	0	2	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136_group
1502	2	0	0	0	1	D	0	D	1	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;g_Legionella;s_
1503	0	1	1	0	1	D	0	o	0	0	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae
1504	0	0	0	0	0	0	0	4	0	0	0 k_Bacteria;p_Myxococcota;c_Polyangia;o_Polyangiales;f_Polyangiaceae;g_Polyangium;s_
1505	0	0	1	0	0	2	0	0	0	0	0 k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiac;o_Pedosphaerales;f_Pedosphaeraceae;g_DEV114;s_
1506	0	0	0	0	0	0	2	0	0	.0	0 k_Bacteria;p_Firmicutes;c_Clostridia
1507	0	2	0	0	0	D	0	0	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales/_Burkholderiaceae;g_Raistonia;s_Raistonia;insidiosa
1508	0	0	1	0	2	2	0	0	0	0	0 k_Bacteria;p_MBNT15;c_MBNT15;o_MBNT15;f_MBNT15;m_MBNT15
1509	1	0	0	0	0	0	0	0	3	0	0 k_Bacteria;p_Firmicutes;c_Bacilla.o_Bacillales;f_Sporolactobacillaceae;g_Tuberibacillus;r_Tuberibacillus;r_alidus
1510	,	0	3	0	0	0	0	0	0	0	0 k_Bacteria;p_Verrucamicrobiota;c_Chlamydiae;o_Chlamydiales
1511		0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Firmicute;c_Bacili;p_Lactobaciliale;;f_Carnobacteriaceae
		2			0	0		0	0		
1512	0		o	0			0			0	0 Unknown
1513	0	0	O	0	0	0	0	2	0	0	0 k_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales
1514	0	0	0	0	0	0	0	2	0	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;1_Marinomonadaceae;z_Marinomonas;s_
1515	0	0	0	0	0	0	0	0	2	0	0 k_Bacteria;p_Firmicutes;c_Bacilico_RF39;f_RF39;g_RF39;s_
1515	0	0	O	0	0	D	0	D	3	0	0 k_Bacteria;p_NB1+;c_NB1+;o_NB1+jf_NB1+jg_NB1+js_
1517	2	0	0	0	0	0	0	0	0	0	0 k_Bacteria;p_Bdellovibrionota;c_Oligoflexia;o_0319-6620;f_0319-6620;g_0319-6620;a_
1517 1518	2 0	0 0	0 0	0 0	0 0	0 D	0 0	0 2	0	0 0	0 k_Berterian_Betelevibrionetac_Okgathenian_0319.66200f_0319.66200g_0319.66200g_ 0 k_Barterian_Chicordienic_Anaerolineeae.g5881031
1518	o	0	O	o	0	D	0	2	o	o	0 k_laderias_Chlordind;_Anarolineaso_S181131 0 k_laderias_Protecladerias_Cannuprotecladerias_Xanthomonadalesf_Xanthomonadaeseeg_lysobatter
1518 1519 1520	0 0 0	0 0	0 0 1	0 0 0	0	D D 0	0 0 0	2 5	0 0 1	0 0 0	0 k_bacterisy_chlordfied;_Anaerolnesey_SIRIIIII 0 k_bacterisy_Proteobacteriac_Cammaproteobacteriay_Kanthomonadalersf_Xanthomonadaceaeg_ispobacter 0 k_bacteriag_Plantomycetotax_Planctomycetoso_Generatalesf_Generataceaeg_is_
1518 1519 1520 1521	0 0 1	0 0 0	0 0 1 0	0 0 0	0 0 3	D D 0 0	0 0 0	2 5 0	0 0 1 2	0 0 0	0 k_bateriay_chlordfeet
1518 1519 1520 1521 1522	0 0 0	0 0 0 0	0 0 1 0	0 0 0 0	0 0 3 0	D D 0 D	0 0 0 2	2 5 0 0 0	0 0 1 2 0	0 0 0 0	0 k_baterias_chlordfekt_Anaeroinese_SIRII31 0 k_baterias_Proteobaterias_Gammaproteobaterias_Kamthemonadalesf_Xanthomonadaesesg_Lysobater 0 k_baterias_Plentomycetotas_Plentomycetotas_Genmatalesf_Genmatacese_ss_ 0 k_baterias_Baternidotas_Baterroidas_Chlinophagatesf_Chlinophagatesesg_Drighubaterss_ 0 k_baterias_Baternidotas_Baterroidas_Cytophagalesf_Chlinophagatesesg_Sproxytophagas_
1518 1519 1520 1521 1522 1523	0 0 1 0 1	0 0 0 0	0 0 1 0 0 2	0 0 0 0 0	0 0 3 0 3	0 0 0 0 2	0 0 0 2 0	2 5 0 0 0 2	0 1 2 0	0 0 0 0	0 k_bisterias_Chordfeet_Asamolneses_SHA1131 0 k_bisterias_Protosiasterias_Cannaportesbatterias_Kanthomonadaleid_Kanthomonadaseese_Lysobacter 0 k_bisterias_Printomycettasa_Fanctomycettasa_Genmatalest_Genmatacere_sis_ 0 k_bisterias_Bisterindistas_Batterindista_Childrophagetere_Dhildrophageteres_Dhildrophageteres_ 0 k_bisterias_Bisterindistas_Batterindistas_Childrophageteres_Childrophageteres_ 0 k_bisterias_bisterindistas_Batterindistas_Childrophageteres_Domonytophagets_ 0 k_bisterias_bisterindistas_Batterindistas_Childrophageteres_Domonytophagets_
1518 1519 1520 1521 1522 1523 1524	0 0 1	0 0 0 0 0 0	0 0 1 0 2 0	0 0 0 0 0 0	0 0 3 0 3 0	0 0 0 0 3 0	0 0 0 2 0	2 5 0 0 0 2 1	0 0 1 2 0 1 3	0 0 0 0 0	0 k_baterias_Chlordred;_Anarolineaso_SH41331 0 k_baterias_Proteolaceriac_Carmaiproteolacteriaso_Karthamionadalesf_Xarthamionadaeseg_systelacter 0 k_bateriaso_Bhatteriotetas_Planetoriata_Centralitatist_Communatorecar 0 k_bateriaso_Bateriotetasc_Bateriotetasc_Chlinophagetesc_Chlinophagetesc_Chlinophagetesc_ 0 k_bateriaso_Bateriotetasc_Bateriotetaso_Contendagetesc_Chlinophagetesc_01812sc 0 k_bateriaso_Bateriotetasc_Bateriotetaso_Contendagetesc_Otablegaesed_00812sc 0 k_bateriaso_Bateriotetasc_Bateriotetaso_Contendagetesc_Otablegaesed_00812sc 0 k_bateriaso_Bateriotetasc_Bateriotetaso_Bateriaso_Bathbateriaks
1518 1519 1520 1521 1522 1523 1524 1525	0 0 1 0 1	0 0 0 0 0 0 0	0 1 0 2 0 0	0 0 0 0 0 0 0	0 0 3 0 3 0 0	D D 0 0 3 0 0	0 0 0 2 0 0	2 5 0 0 0 2	0 1 2 0 1 3 0	0 0 0 0 0 0	0 k_baterias_ChlordinetAnarolineaso_SMIIDI 0 k_baterias_Proteolacterias_Garmuiporteolacterias_Karthomonadalesf_Karthomonadasese_Lisobatter 0 k_baterias_Baterinidetas_Plantemyettes_Germatalesf_Germatacete_s 0 k_baterias_Baterinidetas_Baterinidetas_Chlordingtasist_Chlordingtaseseg_Domphabeters_ 0 k_baterias_Baterinidetas_Baterinidetas_Chlordingtasist_Groupplageasg_Domphabeters_ 0 k_baterias_Baterinidetas_Baterinidetas_Chlordingtasist_Groupplageasg_Domphabeters_ 0 k_baterias_Paterinidetas_Baterinidetas_Chlordingtasist_Groupplageasg_Domphabeters_ 0 k_bateriasg_Interinidetas_Baterinidetas_Chlordingtasist_MorealDaseasg_Domphabeters_ 0 k_bateriasg_Proteolacterias_Garmuiporteolacteriasg_Batholdorialesi 0 k_bateriasg_Northylownabitetas_Wethylownabitetas_MorealDaseasg_Rolubaterialesg_Rolubaterialess_
1518 1519 1520 1521 1522 1523 1524 1525 1525	0 0 1 0 1 0 4 1	0 0 0 0 0 0 0 0	0 1 0 2 0 0 0	0 0 0 0 0 0 0	0 0 3 0 3 0 0 0	D 0 0 0 3 0 0 0	0 0 0 2 0 0 0	2 5 0 0 7 2 1 1 1	0 1 2 0 1 3 0 0	0 0 0 0 0 0 0	<ul> <li>b. bacteriag_Chlordfect_chareolneses_5401331</li> <li>b. bacteriag_Protostacteriag_Cammaporteolacteriag_Cammadales(_Xanthomonadaeses_Lipsobarter</li> <li>b. bacteriag_Protostacteriotarc_Bacteriadaes_Chlorophagescaes_Dorphabacterag_</li> <li>b. bacteriag_bacteriadaes_Bacteriadaes_Chlorophageses_Chlorophagescaes_Dorphabacterag_</li> <li>b. bacteriag_bacteriadaes_Bacteriadaes_Chlorophageses_Chlorophagescaes_Dorphabacterag_</li> <li>b. bacteriag_bacteriadaes_Bacteriadaes_Chlorophageses_Chlorophageses_Chlorophages_Chl</li></ul>
1518 1519 1520 1521 1522 1523 1524 1525 1526 1527	0 0 1 0 1 0 4	0 0 0 0 0 0 0 0 0	0 0 1 0 2 0 0 0 0	0 0 0 0 0 0 0 0	0 0 3 0 3 0 0 0	D D O D 3 0 0 0 0 0 0 0	0 0 2 0 0 0 0	2 5 0 0 2 1 1 1 3	0 1 2 0 1 3 0 0 0	0 0 0 0 0 0 0	<ul> <li>b. Jackerias_Chordrekt_Anarolneses_SHID31</li> <li>b. Jackerias_Protosizating_Cammiproteolatintas_Kambinonadakinf_Xambinonadakese_Liysobacter</li> <li>b. Jackerias_Protosizating_Backeriadosa_Chipologiases_Chipologiases_Dehubactors</li> <li>b. Jackerias_Backeriadosa_Chipologiasist_Chipologiases_Chipologiases_</li> <li>b. Jackerias_Internotors_Cammiproteolatintas_Linternotopiases_Chipologiases_</li> <li>b. Jackerias_Protosizating_Chipologiases_Chipologiases_Chipologiases_Chipologiases_</li> <li>b. Jackerias_Protosizating_Cammiproteolatintas_Linternotopiases</li> <li>c. Jackerias_Protosizating_Chipologiasess_Chipologiasess_Chipologiasess_Chipologiasess_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologias</li></ul>
1518 1519 1520 1521 1522 1523 1524 1525 1525	0 0 1 0 1 0 4 1	0 0 0 0 0 0 0 0	0 1 0 2 0 0 0	0 0 0 0 0 0 0	0 0 3 0 3 0 0 0	D 0 0 0 3 0 0 0	0 0 0 2 0 0 0	2 5 0 0 7 2 1 1 1	0 1 2 0 1 3 0 0	0 0 0 0 0 0 0	<ul> <li>b. bacteriag_Chlordfect_chareolneses_5401331</li> <li>b. bacteriag_Protostacteriag_Cammaporteolacteriag_Cammadales(_Xanthomonadaeses_Lipsobarter</li> <li>b. bacteriag_Protostacteriotarc_Bacteriadaes_Chlorophagescaes_Dorphabacterag_</li> <li>b. bacteriag_bacteriadaes_Bacteriadaes_Chlorophageses_Chlorophagescaes_Dorphabacterag_</li> <li>b. bacteriag_bacteriadaes_Bacteriadaes_Chlorophageses_Chlorophagescaes_Dorphabacterag_</li> <li>b. bacteriag_bacteriadaes_Bacteriadaes_Chlorophageses_Chlorophageses_Chlorophages_Chl</li></ul>
1518 1519 1520 1521 1522 1523 1524 1525 1526 1527	0 0 1 0 1 0 4 1	0 0 0 0 0 0 0 0 0	0 0 1 0 2 0 0 0 0	0 0 0 0 0 0 0 0	0 0 3 0 3 0 0 0	D D O D 3 0 0 0 0 0 0 0	0 0 2 0 0 0 0	2 5 0 0 2 1 1 1 3	0 1 2 0 1 3 0 0 0	0 0 0 0 0 0 0	<ul> <li>b. Jackerias_Chordrekt_Anarolneses_SHID31</li> <li>b. Jackerias_Protosizating_Cammiproteolatintas_Kambinonadakinf_Xambinonadakese_Liysobacter</li> <li>b. Jackerias_Protosizating_Backeriadosa_Chipologiases_Chipologiases_Dehubactors</li> <li>b. Jackerias_Backeriadosa_Chipologiasist_Chipologiases_Chipologiases_</li> <li>b. Jackerias_Internotors_Cammiproteolatintas_Linternotopiases_Chipologiases_</li> <li>b. Jackerias_Protosizating_Chipologiases_Chipologiases_Chipologiases_Chipologiases_</li> <li>b. Jackerias_Protosizating_Cammiproteolatintas_Linternotopiases</li> <li>c. Jackerias_Protosizating_Chipologiasess_Chipologiasess_Chipologiasess_Chipologiasess_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologiasessa_Chipologias</li></ul>
1518 1519 1520 1521 1523 1524 1525 1526 1526 1527	0 0 1 0 4 1 0	0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 0 1	0 0 0 0 0 0 0 0 0	0 0 3 0 3 0 0 0 0	D D D D 3 0 0 0 0 0 3 3	0 0 2 0 0 0 0 0 0	2 5 0 0 2 1 1 3 2	0 1 2 0 1 3 0 0 0 0 2	0 0 0 0 0 0 0 0 0	<ul> <li>b   bateriay_Chordhetic_Asarohnese_SHA1031</li> <li>b   bateriay_Chordhetic_Asarohnese_SHA1031</li> <li>c   bateriay_Proteioateria_Casenaporesbateriay_Centrabalesi_Xanthomonadalesi_Xanthomonadaeseg_Lysobacter</li> <li>b   bateriay_bateriay_bateriay_Contentionagescom_Chinophagacese_Chipubateriay_</li> <li>b   bateriay_bateriadaes_Bateriadaes_Chipubagaist_Chipubagaist_SpontyTobagas_</li> <li>b   bateriay_bateriadaes_Bateriadaes_Chipubagist_Chipubaga</li></ul>
1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529	0 0 1 0 4 1 0	0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0	0 0 3 0 3 0 0 0 0 0	D D 0 D 3 0 0 0 0 3 0	0 0 2 0 0 0 0 0 0 0	2 5 0 0 2 1 1 3 2	0 1 2 0 1 3 0 0 0 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b   lacteriay_Chordhetic_Anarolinasay_SHII31</li> <li>c   lacteriay_Protoclacteriay_Communications_Communications_Communications_Linearity_Protoclacteriay_Protoclact</li></ul>
1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530	0 0 1 0 4 1 0 1 0 6	0 0 0 0 0 0 0 0 0 0 0 0 0 1	0 0 1 0 2 0 0 0 0 1 0 20	0 0 0 0 0 0 0 0 0 1	0 0 3 0 0 0 0 0 0 0 19	0 0 0 0 3 0 0 0 3 0 5	0 0 2 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 1 3 8	0 1 2 0 1 3 0 0 0 2 0 54	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 5	<ul> <li>b. Jackeriag_ChordnetAnaeolneses_5801331</li> <li>b. Jackeriag_Proteinateriag_Commission</li></ul>
1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530	0 0 1 0 4 1 0 1 0 6	0 0 0 0 0 0 0 0 0 0 0 0 0 1	0 0 1 0 2 0 0 0 0 1 0 20	0 0 0 0 0 0 0 0 0 1	0 0 3 0 0 0 0 0 0 0 19	0 0 0 0 3 0 0 0 3 0 5	0 0 2 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 1 3 8	0 1 2 0 1 3 0 0 0 2 0 54	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bacterias_ChordnetAnarolnas.eSHID31</li> <li>b. bacterias_Derectedacterias_Cammaprotecidations_Lambanonadateris_Cambonomadateses_Lysobacter</li> <li>b. bacterias_Denetorecettas_Cambonomadateses_CombabateriasDerechatorias_anarolicas_Derectedaca_Cambonomadateses_Longhabaterias_</li> <li>b. bacterias_beteriodaca_Casteriadaa_Cytophagiesef_Ohitophagecearg_Derechatorias_Relativeses_Cambonomadateses_Control (Relativeses)</li> <li>b. bacterias_beteriodaca_Casteriadaa_Cytophagiesef_Ohitophagecearg_Ohitophagieseg_</li> <li>b. bacterias_beteriodaca_Casteriadaa_Cytophagiesef_Ohitophagecearg_Ohitophagieseg_</li> <li>b. bacterias_beteriodaca_Casteriadaa_Cytophagiesef_Ohitophagecearg_Ohitophagieseg_</li> <li>b. bacterias_beteriodaca_Casteriadaa_Contendenterias_Beteriodaca_Casteriadaa_Relativeses_</li> <li>b. bacterias_beteriodacaca_Casteriadaa_Contendenterias_Relativatives_Beteriadaa_Relativatives_</li> <li>b. bacterias_Protectaacterias_Networkenterias_Relativatives_Candidates_Linguitativatives_Beteriodates_Casteriadaa_</li> <li>b. bacterias_Protectaacterias_Networkenterias_Relativatives_Pareliadaacteriag_Relativativativativativativativativativativ</li></ul>
1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532	0 0 1 0 4 1 0 1 0 6	0 0 0 0 0 0 0 0 0 0 0 0 0 1	0 0 1 0 2 0 0 0 0 1 0 20	0 0 0 0 0 0 0 0 0 1	0 0 3 0 0 0 0 0 0 0 19	0 0 0 0 3 0 0 0 3 0 5	0 0 2 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 1 3 8	0 1 2 0 1 3 0 0 0 2 0 54	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackerias_ Chordnekc_Asaeoinases_SAB1031</li> <li>c. Jackerias_ Interiorecturas_Casemaporeobacterias_Kanthomonadalesis_Kanthomonadaeose_Lysobacteri</li> <li>d. Jackerias_Interiorecturas_Chordnetteras_Centralists_Commarcece</li></ul>
1518 1519 1520 1521 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532	0 0 1 0 4 1 0 6 0 9 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 28 0	0 0 1 0 2 0 0 0 0 1 0 20 0 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 1 3 8	0 1 2 0 1 3 0 0 0 2 0 64 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackeriag, — Proteinatoria, _ Camarolinase, _ Santasi.</li> <li>b. Jackeriag, — Proteinatoria, _ Camarolinase, _ Fandaminonadales/_ Xanthomonadacese _ Lysobacter</li> <li>b. Jackeriag, _ Proteinatorice, _ Camarolinase, _ Genmatoles/_ Genmatoles/_ Cambrobacterag Analysobacterag_</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Chrisphages.exg Lysobacterag_</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Chrisphages.exg Lysobacterag_</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Chrisphages.g.</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Morsolalaosaeg D.B12.c.,</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Morsolalaosaeg D.B12.c.,</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Morsolalaosaeg D.B12.c.,</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Morsolalaosaeg D.B12.c.,</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Morsolalaosaeg D.B12.c.,</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Chrisphagies/_ Morsolalaosaeg D.B12.c.,</li> <li>b. Jackeriag, _ Proteinatorice, _ Bacteriadag, _ Paribadidariada, _ Jacgeriacolag Condutata, Jacgeriadag, _ Conductata, _ Jackeriadag, _ Conductata, _ Jackeriadag, _ Jackeriadag, _ Jackeriadag, _ Conductata, _ Jackeriadag, _ Conductata, _ Jackeriadag, _ Conductatag, _ Jackeriadag, _ Jacke</li></ul>
1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1530 1531 1532 1533	0 0 1 0 4 1 0 6 0 9 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 28 0 0 0 28 0 0 0	0 0 1 0 0 0 0 0 0 0 1 0 20 0 1 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 1 3 2 3 8 0 0 0 0 3	0 1 2 0 1 3 0 0 0 2 0 64 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. backning_Chordhekt_Anarolnases_SHID31</li> <li>b. backning_Chordhekt_Anarolnases_SHID31</li> <li>b. backning_Chordhekt_Anarolnases_SHID31</li> <li>b. backning_Chordhekt_S_Shindprotebackning_Chernhaldskirf_Xardhemonadasese_Lysobackning</li> <li>b. backning_Backnindskar_Shindprotebackning_Chernhaldskirf_Yardhemonadasese_Lysobackning</li> <li>b. backning_Backnindskar_Shindprotebackning_Chernhaldskirf_Yardhemonadasese_Dubbackning_Chernhaldskirf</li> <li>b. backning_Backnindskar_Shindprotebackning_Maket_Moreachaeaaeg_OB12A_</li> <li>b. backning_Protebackning_Chernhaldskirf</li> <li>b. backning_Protebackning_Chernhaldskirf</li> <li>b. backning_Protebackning_Chernhaldskirf</li> <li>b. backning_Protebackning_MaketMoreachaeag_Dubbackning_Robuskarinises_</li> <li>b. backning_Protebackning_MaketMoreachaeag_Parabachaeag_Notepring</li> <li>b. backning_Protebackning_MaketMoreachaeag_Notepring</li> <li>b. backning_Frotebackning_MaketMoreachaeag_Notepring</li> <li>b. backning_Frotebackning_MaketMoreachaeag_Notepring</li> <li>b. backning_Frotebackning_Docklopping</li> <li>b. backning_Frotebackning_Docklopping</li> <li>b. backning_Frotebackning_Parabachaeaders</li> <li>b. backning_Frotebackning_Docklopping</li> <li>b. backning_Frotebackning_Docklopping</li> <li>b. backning_Frotebackning_Parabachaeaders</li> <li>b. backning_Frotebackning_Docklopping</li> <li>b. backning_Frotebackning_Docklopping</li> <li>b. backning_Frotebackning_Parabachaeaders</li> <li>b. backning_Frotebackning_Docklopping</li> <li>b. backning_Frotebackning_Docklopping</li> <li>b. backning_Frotebackning_Bakklowknings_Backning</li> <li>b. backning_Frotebackning_Bakklowknings_Backning</li> <li>b. backning_Frotebackning_Bakklowknings_Backlowknings</li> <li>b. backning_Frotebackning_Bakklowknings_Backlowknings</li> <li>b. backning_Frotebackning_Bakklowknings_Backlowknings</li> <li>b. backning_Frotebackning_Bakklowknings</li> <li>b. backning_Frotebackning_Bakklowknings</li> <li>b. backning_Frotebackning_Bakklowknings</li> <li>b. backning_Frotebackning_Ba</li></ul>
1518 1519 1520 1521 1522 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535	0 0 1 0 4 1 0 4 0 9 2 0 9 2 0 19 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 28 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 1 0 0 1 1 0 0 1 1 0 1 1	0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 3 0 0 3 0	0 0 3 0 0 0 0 0 0 0 19 3 0 0 0 4 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 1 3 2 3 8 0 0 0 3 0	0 1 2 0 1 3 0 0 0 2 0 64 0 1 0 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. lacteria, _ Mordiekt_Asarolnase,_SAB1031</li> <li>c. Lacteria, _ Mordiekt_Asarolnase,_SAB1031</li> <li>c. Lacteria, _ MordiektAsarolnase,_Sciennaldski_Cardononsdaseseiysobatter</li> <li>d Lacteria, _ Mordiekta,_ Batterioda,_Chinophysics,_Chinophysics,_Chinophysics,_</li> <li>d Lacteria, _ Mordiekta,_ Batterioda,_Chinophysics,'_ Moroaclaceaeg_, Oki25,_</li> <li>d Lacteria, _ Mordiekta,_ Batterioda,_Chinophysics,'' Moroaclaceaeg_, Oki25,_</li> <li>d Lacteria, _ Moroaclater, _ Moroaclater, _ Zenthalist, _ Lentholder, _ Lentholder, _ Lentholder, _ Lacteriae, _ Moroaclater, _ Dechtaiaeg, _ Moroaclater, _ Dechtaiaeg, _ Moroaclater, _ Dechtaiaeg, _ Dechtaiaeg, _ Dechtaiaeg, _ Nonopiciae, _ Moroaclater, _ Dechtaiaeg, _ Dechtai</li></ul>
1518 1519 1520 1521 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535	0 0 1 0 4 1 0 4 1 0 6 0 9 2 0 9	0 0 0 0 0 0 0 0 0 0 1 0 28 0 0 1 0 1 0 1 0	0 1 0 2 0 0 0 0 0 1 20 0 1 1 0 0 1 1 0 0 1 1 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 19 3 0 0 0 19 3 0 0 0 19 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 3 2 3 8 0 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 2 0 1 3 0 0 0 2 0 54 0 1 0 1 0 54 0 1 0 1 0 0 1 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jackrisz, _ Mordiekz, _ Asarolnasz, _ Skittöl</li> <li>c. Jackrisz, _ Mordiekz, _ Dackrowicz, _ Germatorsz, _ Scientalisz, _ Germatorsz,</li></ul>
1518 1519 1520 1521 1523 1524 1525 1526 1527 1528 1529 1530 1531 1531 1533 1533 1535 1536 1537	0 0 1 0 4 1 0 6 9 2 0 19 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 0 1 20 0 1 1 0 0 1 1 0 0 1 0 0 1 0 0 1 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 19 3 0 0 0 19 3 0 0 0 19 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 3 2 3 8 0 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 2 0 1 3 0 0 0 2 0 64 0 1 0 64 0 1 0 1 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 3 0 0 0 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. backets,forefact,Anarolness,SANDAL</li> <li>b. backets,forefact,forefact,formations,</li></ul>
1518 1519 1520 1521 1522 1524 1525 1526 1526 1527 1528 1530 1531 1532 1532 1534 1535 1536 1536 1537	0 0 1 0 1 0 4 1 0 6 0 9 2 0 19 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 2 0 0 0 1 0 1 0 1 1 0 0 1 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 4 1 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 2 1 1 1 3 2 3 8 0 0 0 5 2 4	0 1 2 0 1 3 0 0 2 0 64 0 1 0 3 0 1 0 1 0 1 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. backnis, _ Mordinki, _ Anarolnasia, _ SANDAI</li> <li>b. backnis, _ Mordinki, _ Cammiproteobacknis, _ Kanhamonadakis/_ Xanhamonadakeseisobacknis.</li> <li>b. backnis, _ Montonycettaka, _ Fankamynetaka, _ Kanhamonadakese, _ Lankama, _ Lanka</li></ul>
1518 1519 1520 1521 1522 1524 1524 1525 1526 1527 1528 1529 1530 1531 1543 1544 1535 1544 1535 1549 1540	0 0 1 0 4 1 0 4 1 0 5 0 9 2 0 9 0 0 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0	0 1 0 2 0 0 0 1 0 1 0 1 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 19 3 0 0 4 1 0 0 0 4 1 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 1 3 8 0 0 3 0 5 2 4 0	0 1 2 0 1 3 0 0 2 0 64 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jacksing_Chordhet_Charaolnases_SHID31</li> <li>c. Jacksing_Chordhet_Charaolnases_SHID31</li> <li>c. Jacksing_Chordhet_Charaolnases_Scientalist_Combinedustics_Carbonoussesse_Lysobacter</li> <li>d. Jacksing_Deterministry_Carbonoussesse_Combinations_Combinations_Carbonoussesse_Lysobacter</li> <li>d. Jacksing_Deterministry_Carbonoussesse_Combinations_Carbonoussesse_Combinations_</li> <li>d. Jacksing_Deterministry_Carbonoussesse</li> <li>d. Jacksing_Deterministry_Deterministry_Deterministry_Deterministry_Carbonoussesses_Carbonoussessesses_Carbonoussessesses_Larbonoussesses_Larbonoussesses_Larbonoussessesses_Larbonousses</li></ul>
1518 1519 1520 1521 1522 1524 1525 1526 1526 1527 1528 1530 1531 1532 1532 1534 1535 1536 1536 1537	0 0 1 0 1 0 4 1 0 6 0 9 2 0 19 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 2 0 0 0 1 0 1 0 1 1 0 0 1 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 4 1 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 2 1 1 1 3 2 3 8 0 0 0 5 2 4	0 1 2 0 1 3 0 0 2 0 64 0 1 0 3 0 1 0 1 0 1 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. backnis, _ Mordinki, _ Anarolnasia, _ SANDAI</li> <li>b. backnis, _ Mordinki, _ Cammiproteobacknis, _ Kanhamonadakis/_ Xanhamonadakeseisobacknis.</li> <li>b. backnis, _ Montonycettaka, _ Fankamynetaka, _ Kanhamonadakese, _ Lankama, _ Lanka</li></ul>
1518 1519 1520 1521 1522 1524 1524 1525 1526 1527 1528 1529 1530 1531 1543 1544 1535 1544 1535 1549 1540	0 0 1 0 4 1 0 4 1 0 5 0 9 2 0 9 0 0 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0	0 1 0 2 0 0 0 1 0 1 0 1 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 19 3 0 0 4 1 0 0 0 4 1 0 0 0 0 0 0 0 0 0 0 0	D D D D D D D D D D D D D D D D D D D	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 1 3 8 0 0 3 0 0 5 2 4 0	0 1 2 0 1 3 0 0 2 0 64 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. backsigChordhetAssesSuperSuperSuperSuperSuperSuperSuperSuper</li></ul>
1518 1519 1520 1522 1523 1523 1524 1525 1526 1527 1528 1529 1530 1534 1535 1534 1535 1534 1535 1534 1537 1539 1540	001010101010100100000000000000000000000	0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 1 0	0 1 0 2 0 0 0 0 1 1 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 2 1 1 1 3 8 0 0 3 0 5 2 4 0 2	0 1 2 0 1 3 0 0 2 0 64 0 1 0 3 0 1 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. Jacksing_Chordhekt_Anarobiases_SABUSI</li> <li>c. Jacksing_Proteinstanting_Commerces_Commatisess_Commatisess_Commatisess_Commatisess_Commatisess_Commatisess_Commatisessca_Comm</li></ul>
<ul> <li>1518</li> <li>1519</li> <li>1521</li> <li>1522</li> <li>1523</li> <li>1524</li> <li>1525</li> <li>1506</li> <li>1537</li> <li>1536</li> <li>1537</li> <li>1536</li> <li>1537</li> <li>1536</li> <li>1537</li> <li>1540</li> <li>1541</li> <li>1541</li> </ul>	001010101010100100000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 0 0 0 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 3 2 3 8 0 0 5 2 4 0 2 2 2 2	0 1 2 0 1 3 0 0 2 0 64 0 1 0 3 0 1 0 3 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. backsigChordhetAssesSuperSuperSuperSuperSuperSuperSuperSuper</li></ul>
1518 1519 1520 1522 1523 1523 1524 1525 1526 1527 1528 1529 1530 1534 1535 1534 1535 1534 1535 1534 1537 1539 1540	0 0 1 0 4 1 0 6 9 2 0 9 0 0 0 1 0 0 0 1 0 0 0 0 1 0 0 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 0 1 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 19 3 0 0 0 19 3 0 0 0 0 19 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 3 2 3 8 0 0 5 2 4 0 2 2 2 2	0 1 2 0 1 3 0 0 2 0 64 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b. bateria, _ forefact, _ handbingenetisstatiss, _ Kardbingenadekie / Jardbenenadasese _ Lysobater</li> <li>b. bateria, _ handbingenetissta, _ Bateriadekie, _ Cardbingenadekie / Jardbenenadasese _ Lysobater</li> <li>b. bateria, _ handbingenetissta, _ Bateriadekie, _ Chiphigasese, _ Dephibeteria, _</li> <li>b. bateria, _ handbingenetissta, _ Bateriadekie, _ Chiphigasese, _ Dephibeteria, _</li> <li>b. bateria, _ handbingenetissta, _ Bateriadekie, _ Chiphigasese, _ Dephibeteria, _</li> <li>b. bateria, _ handbingenetissta, _ Bateriadekie, _ Chiphigasese, _ Obliphieteriadekie, _ Materiadekie, _ Bateriadekie, _ Gateriadekie, _ Chiphigasese, _ Dephibeteriadekie, _ Materiadekie, _ Materiadeki</li></ul>
1518 1519 1520 1522 1522 1522 1522 1522 1523 1525 1526 1537 1538 1539 1534 1534 1534 1534 1534 1534 1534 1544	0 0 1 0 1 0 4 1 0 1 0 6 0 9 2 0 19 0 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 1 2 0 1 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 1 0 0 0 0 1 9 3 0 0 0 4 1 0 0 0 4 1 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 2 1 1 3 2 3 8 0 0 5 2 4 0 2 2 2 2	0 1 2 0 1 3 0 0 2 0 64 0 1 0 0 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<ul> <li>b_batelay_chordhet_Anarohasay_SHIDH</li> <li>b_batelay_chordhet_Anarohasay_SHIDH</li> <li>b_batelay_chordhet_C_Anarohasay_chordhetay_chordhetay_chordhetayse_jupabelaters</li></ul>
<ul> <li>1518</li> <li>1519</li> <li>1521</li> <li>1522</li> <li>1523</li> <li>1524</li> <li>1525</li> <li>1526</li> <li>1527</li> <li>1528</li> <li>1528</li> <li>1529</li> <li>1531</li> <li>1532</li> <li>1534</li> <li>1535</li> <li>1536</li> <li>1537</li> <li>1538</li> <li>1536</li> <li>1537</li> <li>1538</li> <li>1536</li> <li>1540</li> <li>1541</li> <li>1542</li> <li>1544</li> <li>1544</li> </ul>	0 0 0 1 0 1 0 1 0 1 0 6 0 9 2 0 19 0 0 0 1 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 7 2 1 1 1 3 2 3 8 0 0 3 0 0 5 2 4 0 2 2 0 4 3	0 1 2 0 1 3 0 0 7 0 64 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<ul> <li>b_batelay_chordhot_Assess_SABUSI</li> <li>b_batelay_chordhot_Assess_SABUSI</li> <li>b_batelay_chordhot_Assess_SABUSI</li> <li>b_batelay_chordhot_Assess_SABUSI</li> <li>b_batelay_chordhot_Assess_SABUSI</li> <li>b_batelay_batelay_batelay_chordhotysest_Chordhotysest_Chordhotysest_Doublabers</li></ul>
1518 1500 1502 1502 1502 1502 1503 1504 1505 1506 1506 1506 1506 1507 1508 1506 1507 1508 1506 1507 1508 1509 1504 1504 1504 1504	0 0 1 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 1 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 2 1 1 1 3 2 3 8 0 0 0 3 0 0 5 2 4 0 2 2 0 4 3 4	0 1 2 0 1 3 0 0 2 0 64 0 1 0 0 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	<pre>b _bsteing_flordietAnaroinaseSHIDH b _bsteinisNanotanyoutietsGammaproteckettingKambanonakistafanaronanakseseiysokattin b _bsteinisNanotanyoutietsBatanyoutietsGammaproteckettingKambanonakistafanaronanakseseiysokattin b _bsteinisNanotanyoutietsBatanyoutietsGammaproteckettingMainpopagesesDopubsteinism b _bsteinisNanotanyoutietsGammaproteckettingMainpopagesesOphysheters b _bsteinisNanotanyoutietsGammaproteckettingMainpopagesesOphysheters b _bsteinisInteractionsBatanyoutietsGammaprotecketting_MainpopagesesOphysheters b _bsteinisInteractionsBatanyoutietsGammaprotecketting_MainpopagesesDopubsteinism b _bsteinisInteractionsMainportecketting_MainpopagesesNanotanyo_Batanyoutiets b _bsteinisInteractionsMainportecketting_MainpopagesesNanotanyo_Batanyoutiets b _bsteinisInteractionsMainportecketting_MainpopagesesNanotanyo_Batanyoutiets b _bsteinisInteractionsMainportecketting_MainpopagesesNanotanyo_Batanyoutiets b _bsteinisInteractionsMainportecketting_MainpopagesesNanotanyo_Batanyoutiets b _bsteinisInteractionsMainportecketting_Mainpole b _bsteinisInteractionsMainportecketting_Mainpole b _bsteinisInteractionsMainpole b _bsteinisInteractionsMainpoletationsInteractions_</pre>
1518 1500 1502 1502 1502 1502 1502 1503 1505 1506 1507 1508 1509 1504 1505 1506 1507 1504 1502 1504 1504 1504 1504 1505	0 0 1 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 0 1 1 0 0 1 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 2 1 1 1 3 2 3 8 0 0 0 3 0 0 5 2 4 0 2 2 0 4 3 4	0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0	。 。 。 。 。 。 。 。 。 。 。 。 。 。 。 。 。 。 。	<pre>b _ bateria_ / brochet</pre>
1518           1509           1502           1502           1502           1502           1502           1502           1502           1502           1502           1502           1502           1503           1504           1505           1506           1507           1508           1509           1504           1504           1504           1504           1504           1504           1504           1504           1504           1504           1504           1504           1504	0 0 1 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 0 0 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 0 0 0 19 3 0 0 0 4 1 0 0 0 0 0 0 0 2 3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 2 1 1 1 3 2 3 8 0 0 0 3 0 0 5 2 4 0 2 2 0 4 3 4	0 1 2 0 1 3 0 0 2 0 64 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	。 。 。 。 。 。 。 。 。 。 。 。 。 。 。 。 。 。 。	<pre>b laderia_lorderide_lorderide_generatives_controllederide_lorderides_lorderides_lorderides_lorderides_betweet_controllederides_lorderides_betweet_controllederides_bet</pre>
<ul> <li>1518</li> <li>1500</li> <li>1501</li> <li>1502</li> <li>1502</li> <li>1502</li> <li>1503</li> <li>1504</li> <li>1505</li> </ul>	0 0 1 0 1 0 1 0 1 0 6 0 9 2 0 19 0 0 0 1 0 0 0 0 0 2 6 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 2 1 1 1 3 2 3 8 0 0 0 3 0 0 5 2 4 0 2 2 0 4 3 4 0 1 0 0	0 0 1 2 0 1 3 0 0 2 0 64 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _bately_CloreletAnarolese_SABLESE b _bately_CloreletCloreletSamaprotestationsAnarohematakiesCardenomatakeseissetations b _bately_EntensionsEntensionsEntensionsObiophysicsObiophysicsObiophysicsObiophysics b _bately_bately_bateletistsEntensionsObiophysics_ObiophysicsObiophysicsObiophysics b _bately_bateletistsEntensionsEntensionsObiophysicsObiophysicsObiophysicsObiophysics b _bateletisbateletistsEntensionsObiophysicsObiophysicsParlateletistsEntensions b _bateletisbateletistsBateletistsObiophysicsBateletistsEntensionsObiophysicsBateletists b _bateletisbateletistsBateletistsConductorsBateletistsConductorsBateletistsEntensionsObiophysicsAdvectistsBateletistsConductorsBateletistsBateletistsConductorsBateletistsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsBateletistsConductorsBateletistsBateletistsConductorsBateletistsConductorsBateletistsBateletistsConductorsBateletistsBateletistsConductorsBateletistsBateletistsConductorsBateletistsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsConductorsBateletistsBatelet</pre>
1518 1500 1502 1502 1502 1502 1503 1504 1505 1506 1507 1508 1509 1504 1507 1508 1509 1504 1502 1504 1504 1505 1506 1506	0 0 0 1 0 1 0 1 0 1 0 6 0 9 2 0 19 0 0 0 1 0 0 0 0 0 0 2 6 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	000000000000000000000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 2 1 1 1 1 2 3 8 0 0 0 3 0 0 5 2 4 0 2 2 0 4 3 4 0 1 0 0 0	0 0 1 2 0 1 3 0 0 2 0 66 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b _bstoring_frontext</pre>
1518 1518 1510 1522 1522 1523 1523 1523 1525 1526 1527 1528 1534 1535 1534 1535 1534 1535 1534 1534	001010101010000000000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 1 0 1 0 1 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 2 1 1 1 3 2 3 8 0 0 0 3 0 0 5 2 4 0 2 2 0 4 3 4 0 1 0 0 0 0 0	0 0 1 2 0 1 3 0 0 0 2 0 66 0 1 0 0 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b_bbctsis_ChordwetAusoinausSHIDMI b_bctsisProtecturintCommonretesturintsKendmonradskistContensionauxeesLysobacter b_bctsissInitiany_initiany_initiany_initiany_initiany_initiany_approxesDephabeters</pre>
<ul> <li>1518</li> <li>1518</li> <li>1521</li> <li>1522</li> <li>1523</li> <li>1524</li> <li>1525</li> <li>1526</li> <li>1527</li> <li>1528</li> <li>1526</li> <li>1521</li> <li>1526</li> <li>1531</li> <li>1546</li> <li>1546</li> <li>1546</li> <li>1544</li> <li>1548</li> <li>1546</li> <li>1544</li> <li>1546</li> <li>1547</li> <li>1548</li> <li>1546</li> <li>1546</li> <li>1546</li> <li>1547</li> <li>1548</li> <li>1548</li> <li>1548</li> <li>1549</li> <li>1542</li> <li>1552</li> <li>1553</li> </ul>		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 3 0 3 0 0 0 0 9 3 0 0 0 4 1 0 0 0 0 0 0 0 0 0 2 3 0 0 2 1 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 2 1 1 1 3 2 3 8 0 0 0 3 0 0 5 2 4 0 2 2 0 4 3 4 0 1 0 0 0 0 0	0 0 1 2 0 1 3 0 0 0 2 0 66 0 1 0 0 3 0 1 0 0 0 0 0 0 0 0 0 1 0 0 4 2		<pre>b laderia_lorderide_Anaroinase_SABUSI b laderia_brindery_tetraks_fendermeterse_Genmakerse_anaroitets_Genmakerse_anaroitets_ b laderia_brindery_tetraks_fendermeterse_Genmakerse_anaroitets_ b laderia_brindery_tetraks_fendermeterse_Genmakerse_anaroitets_ b laderia_brindery_tetraks_fendermeterse_Genmakerse_anaroitets_ b laderia_brindery_tetraks_fendermeterse_Genmakerse_anaroitets_ b laderia_brindery_tetraks_fendermeterse_Genmakerse_anaroitets_ b laderia_brindery_tetraks_fendermeterse_Brindery b laderia_brindery_tetraks_fendermeterse_Brinderia b laderia_brindery_tetraks_fendermeterse_Brinderia b laderia_brindery_tetraks_fendermeterse_Brinderia b laderia_brindery_tetraks_fendermeterse_Brinderia b laderia_brindery_tetraks_fendermeterse_Brinderia b laderia_brindery_tetraks_fendermeterse_Brinderia b laderia_brindery_tetraks_fendermeterse_brinder b laderia_brindery_tetraks_fendermeterse_brinder b laderia_brindery_tetraks_fendermeterse_brinder b laderia_brindery_tetraks_fendermeterse_br</pre>
1518 1518 1510 1522 1522 1523 1523 1523 1525 1526 1527 1528 1534 1535 1534 1535 1534 1535 1534 1534	001010101010000000000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 1 0 2 0 0 0 0 1 0 1 0 1 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 5 0 0 0 2 1 1 1 3 2 3 8 0 0 0 3 0 0 5 2 4 0 2 2 0 4 3 4 0 1 0 0 0 0 0	0 0 1 2 0 1 3 0 0 0 2 0 66 0 1 0 0 3 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0		<pre>b_bbctsis_ChordwetAusoinausSHIDMI b_bctsisProtecturintCommonretesturintsKendmonradskistContensionauxeesLysobacter b_bctsissInitiany_initiany_initiany_initiany_initiany_initiany_approxesDephabeters</pre>

1556	1	0	1	0	0	0	0	0	2	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria
1557	0	0	2	0	0	D	0	1	1	0	0 k_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Uneage_IV:f_Uneage_IV:g_Uneage_IV:s_
1558	3	0	0	0	0	1	0	D	0	o	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriales;f_Weekseliaceae;g_Chryseobacterium
1559	1	0	1	0	1	0	0	0	0	0	0 k_Bacteria;p_Bdellovibrionota;c_Bdellovibrionia;o_Bdellovibrionales;f_Bdellovibrionaceae;g_Bdellovibrio;s
1560	0	0	0	0	0	0	0	0	37	0	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Alcaligenaceac;g_Paenalcaligenes;s_Paenalcaligenes_hominis
1561	0	3	0	0	0	D	0	D	0	٥	0 k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_;g_;s
1562	0	0	0	0	0	0	0	2	0	0	0 k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_;f_;g_;s_
1563	1	0	0	0	0	0	0	4	0	1	0 k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Woeseiaceae;g_JTB255_marine_benthic_group;s_