This is an Open Access document downloaded from ORCA, Cardiff University’s institutional repository: https://orca.cardiff.ac.uk/id/eprint/135595/

This is the author’s version of a work that was submitted to / accepted for publication.

Citation for final published version:


Publishers page: https://doi.org/10.1016/j.jgar.2020.08.017

Please note:
Changes made as a result of publishing processes such as copy-editing, formatting and page numbers may not be reflected in this version. For the definitive version of this publication, please refer to the published source. You are advised to consult the publisher’s version if you wish to cite this paper.

This version is being made available in accordance with publisher policies. See http://orca.cf.ac.uk/policies.html for usage policies. Copyright and moral rights for publications made available in ORCA are retained by the copyright holders.
Figure 1 – Flow chart of study data

Microbiological database
Samples = 1377

Suspected sepsis database
Patients = 1141

Matched microbiological and sepsis data
Samples = 1358
Patients = 854

Zero/Single samples by patient
Samples = 387
Patients = 392

Non blood/non-rectal samples
Samples = 8
Patients = 0

Samples not on the same day
Samples = 481
Patients = 222

Multiple samples on same day
Samples = 4
Patients = 2

Samples = 971
Patients = 462

Samples = 963
Patients = 462

Samples = 482
Patients = 240

Samples = 478
Patients = 238

Pairs of blood and rectal samples = 238
Isolate results blood samples = 238
Isolate results rectal samples = 309