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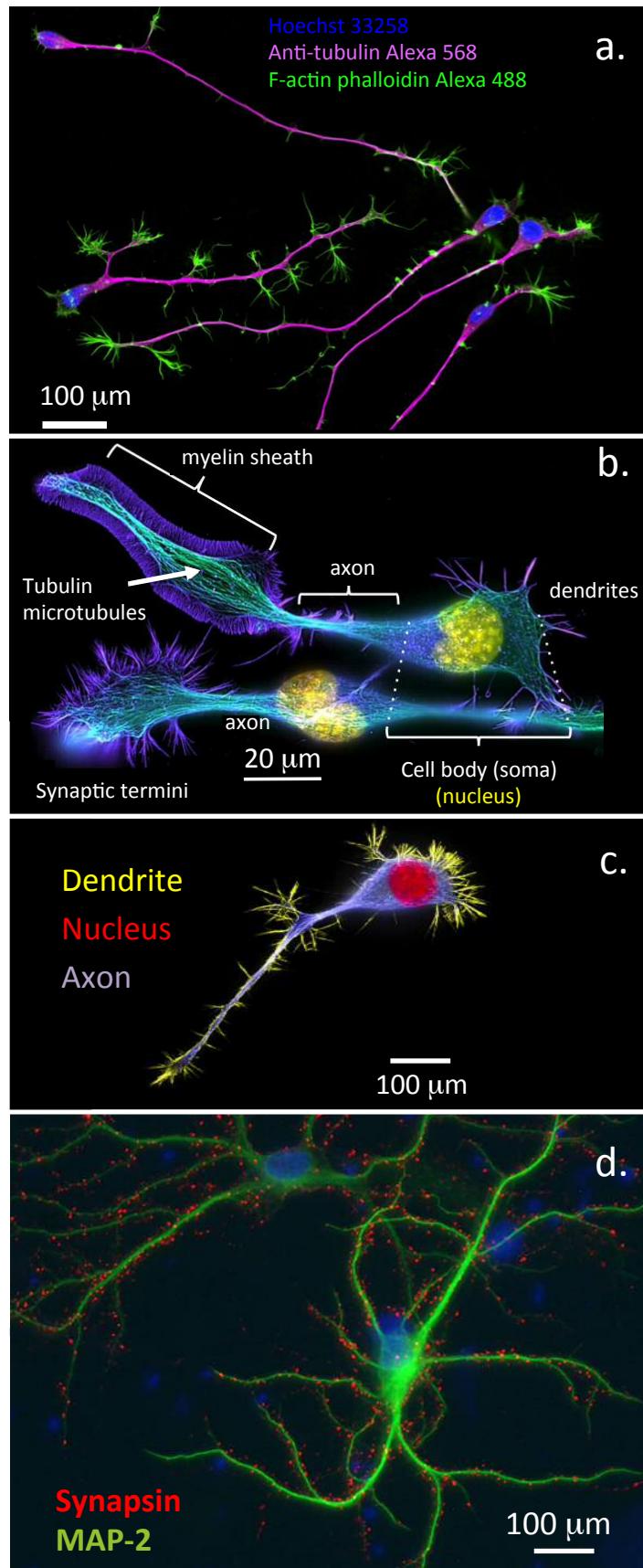
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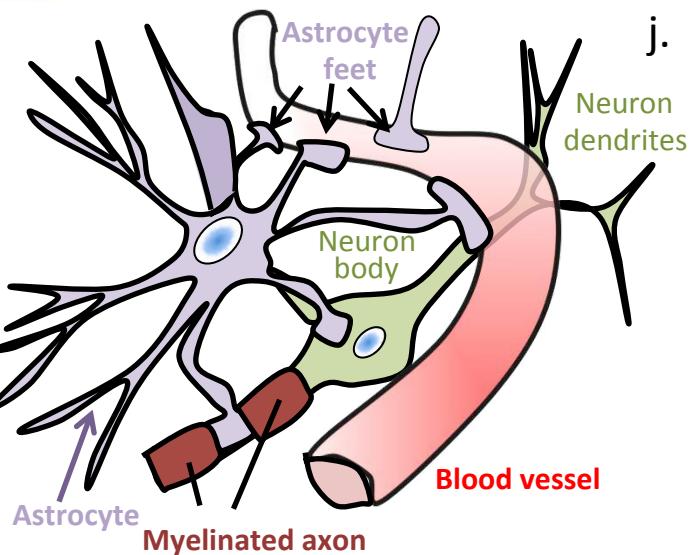
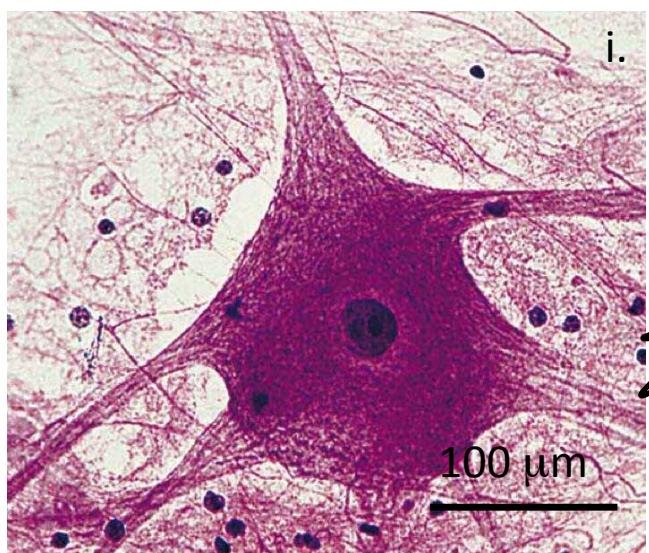
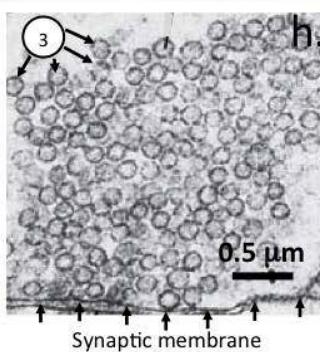
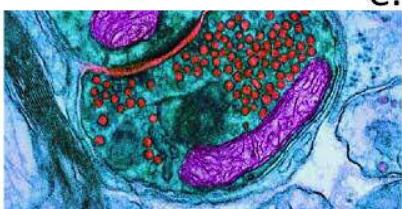
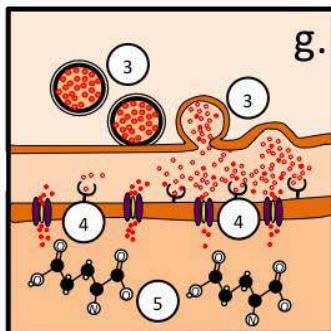
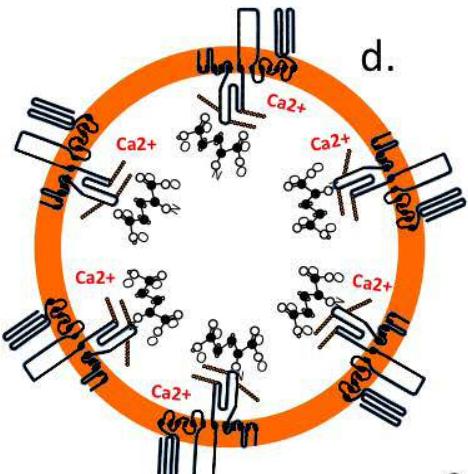
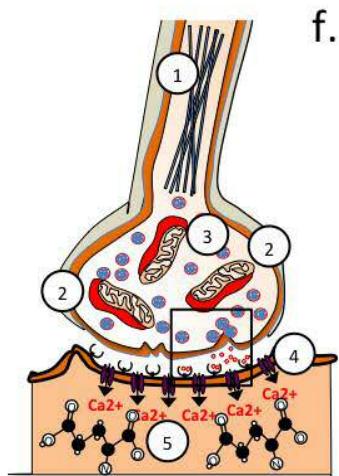
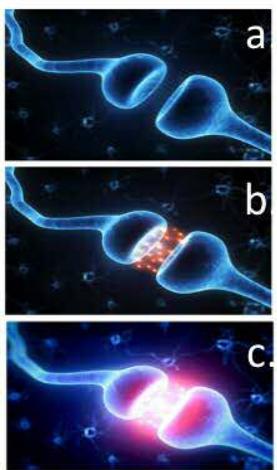
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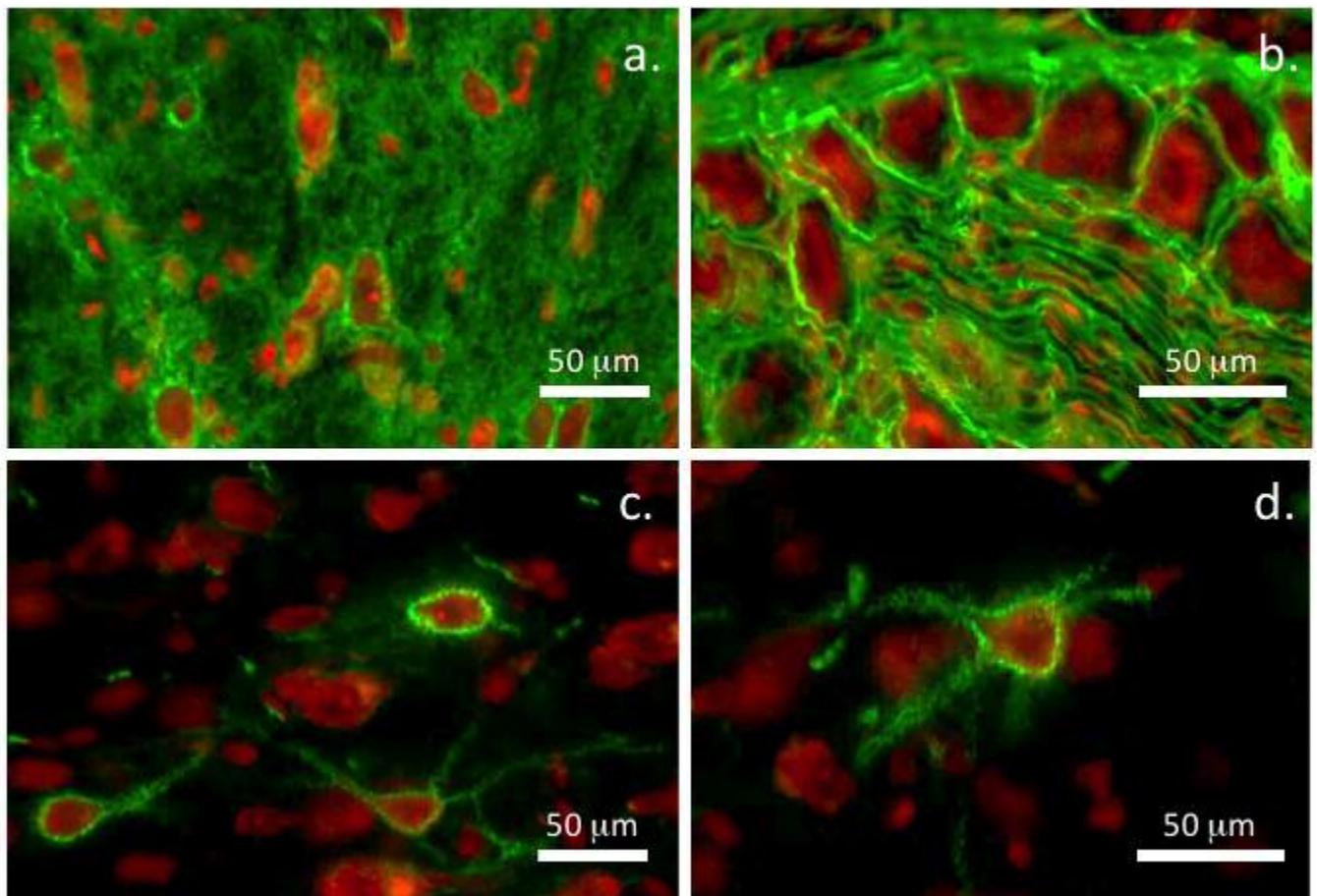
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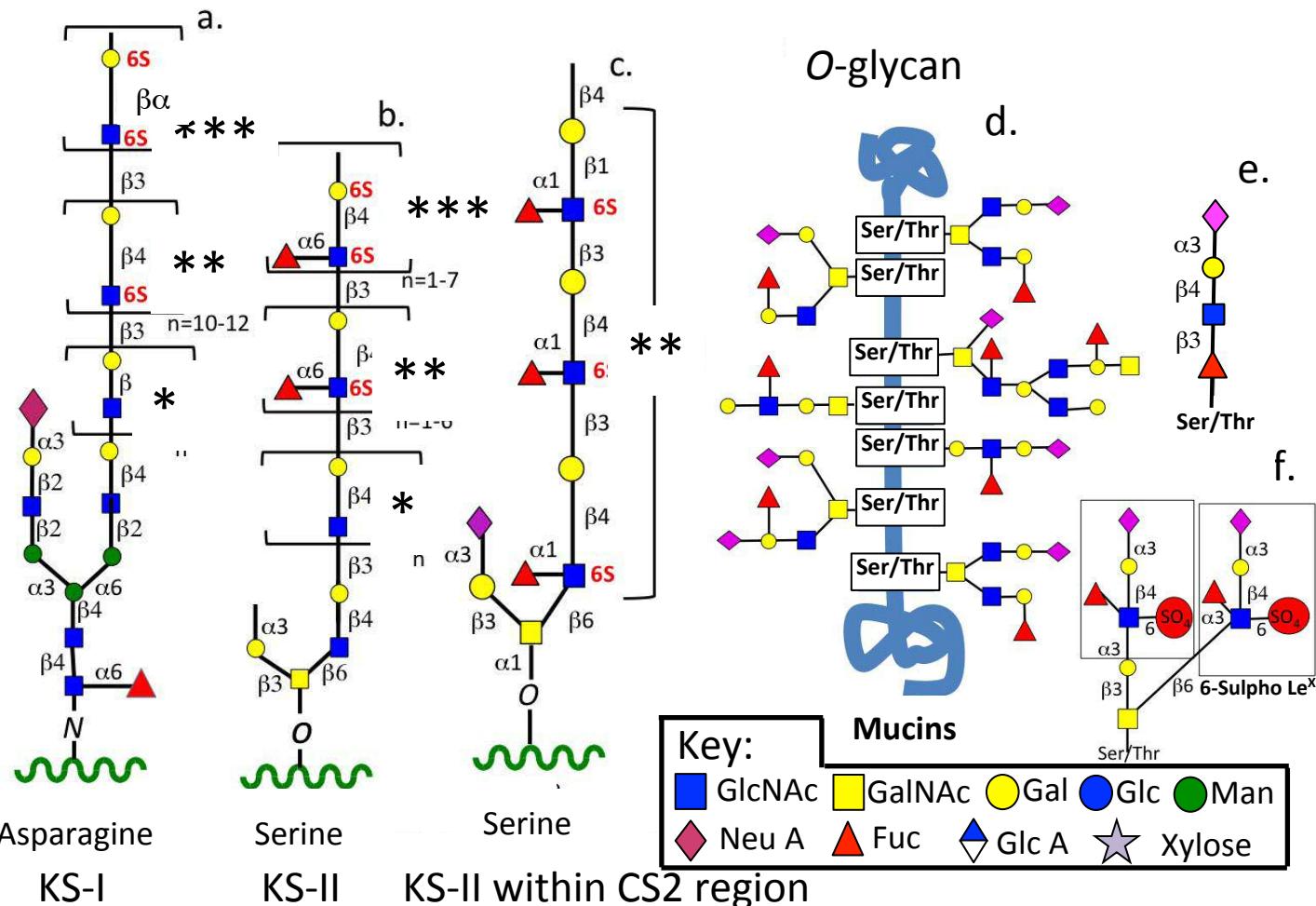


Fig 1

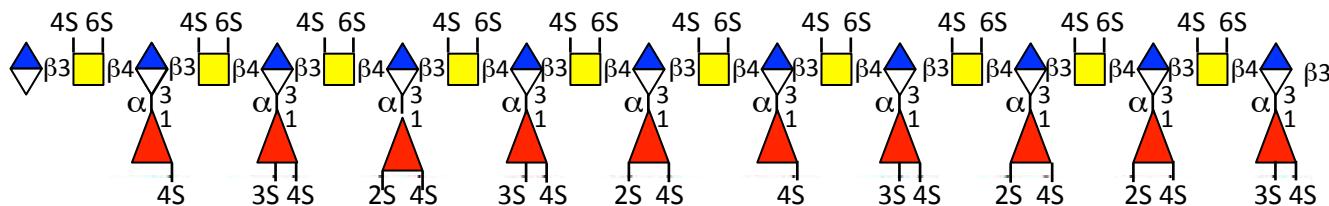




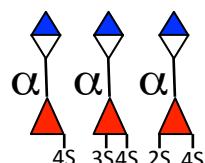




* non-sulphated ** mono-sulphated *** di-sulphated

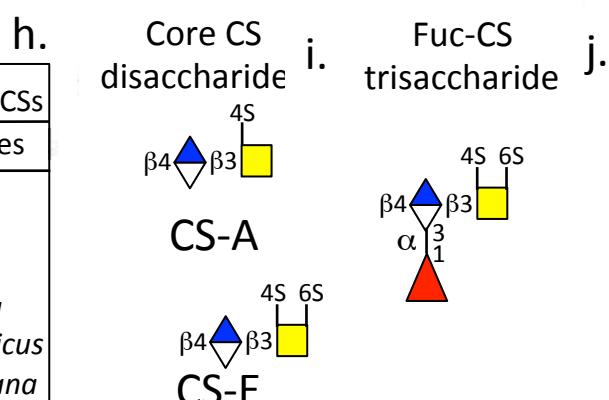


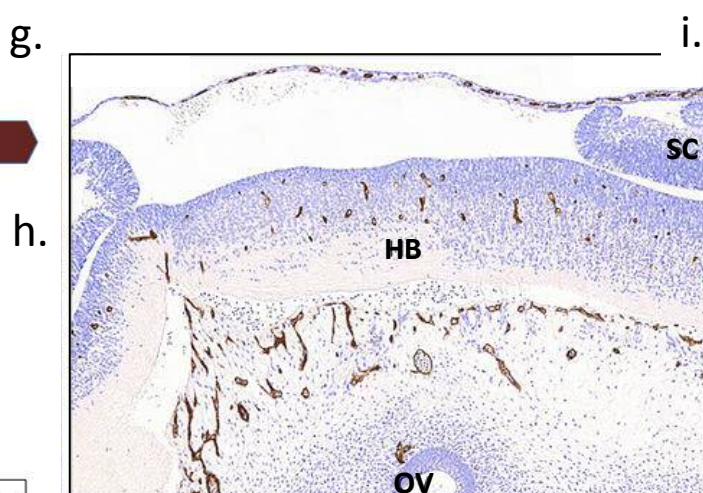
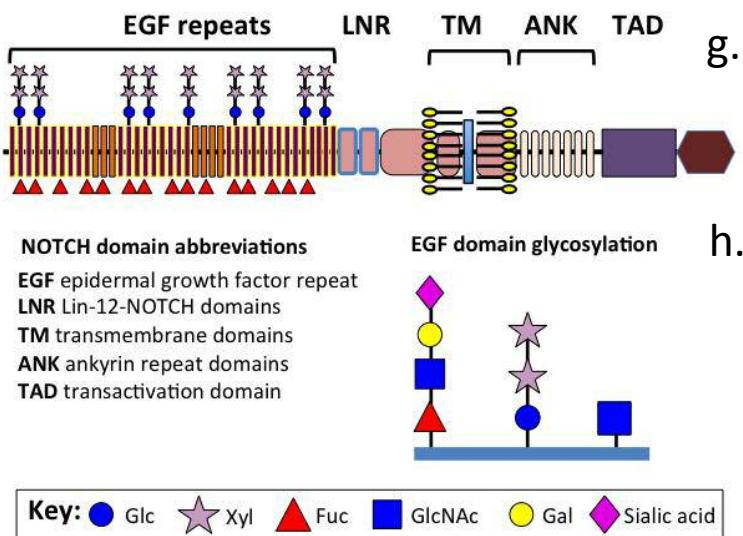
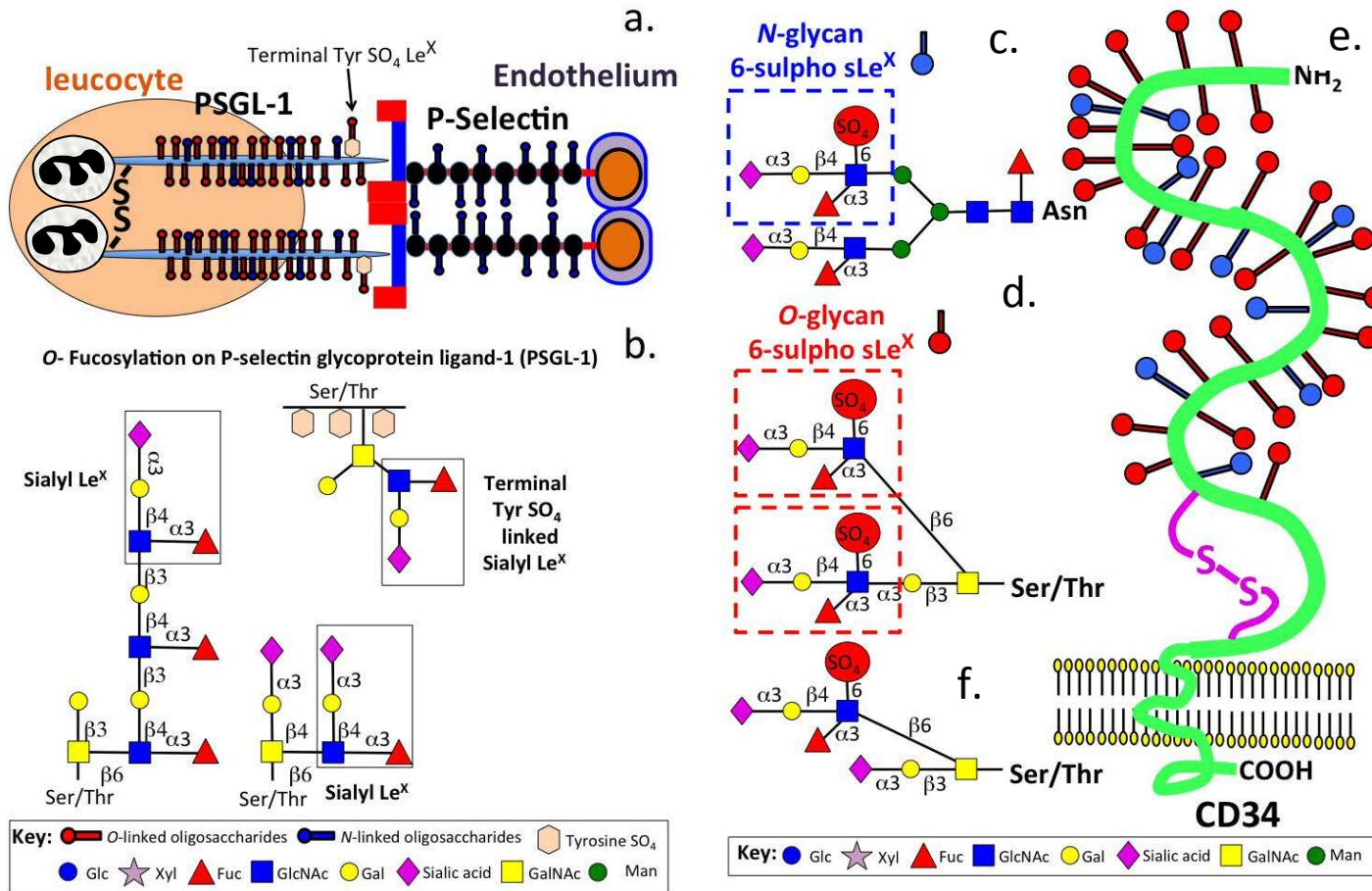
sequence of *H. forskali* Fuc-CS with a composition of 15% 4S, 46% 3,4S, 39% 2,4S

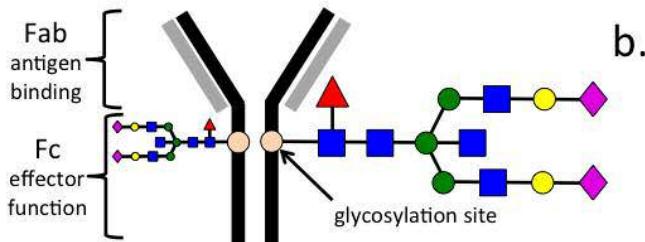
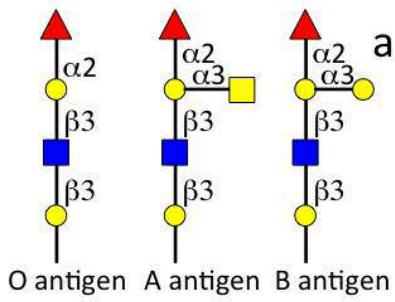


Compositions of L-Fucose side chains on Fuc-CSs				
	4S	3,4 diS	2,4 diS	Sea cucumber species
Fucose side chain	5	10	85	<i>Stichopus hermanii</i>
Sulphation Positions (% of total)	ND	80	20	<i>Cucumaria japonica</i>
	15	46	39	<i>Holothuria forskali</i>
	10	50	20	<i>Xucumaria frondosa</i>
	ND	20	60	<i>Apostichopus japonicus</i>
	ND	80	20	<i>Actinopyga mauritiana</i>

Monosulphated data not determined (ND) in some cases







C. bisecting GlcNAc

enhanced ADCC

d. core fucose

decreased ADCC

e. without core fucose

enhanced ADCC

terminal sialylation

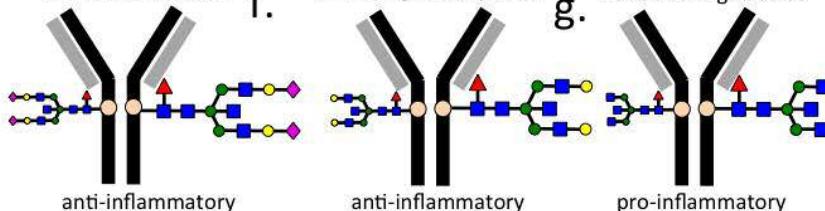
f.

terminal galactosylation

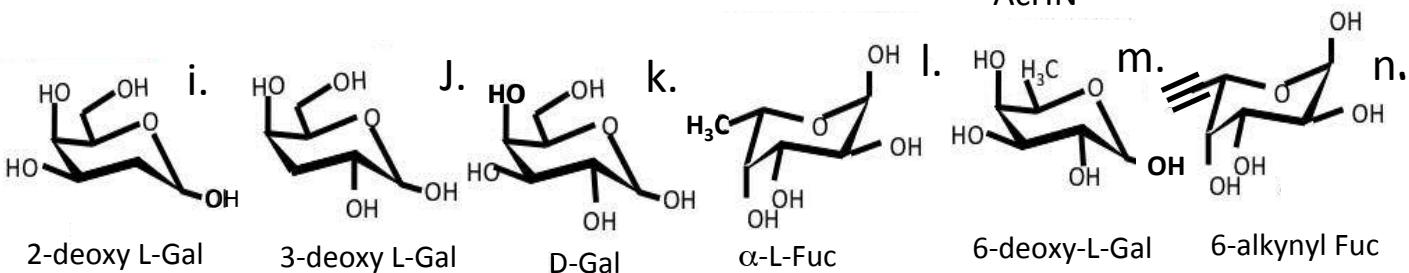
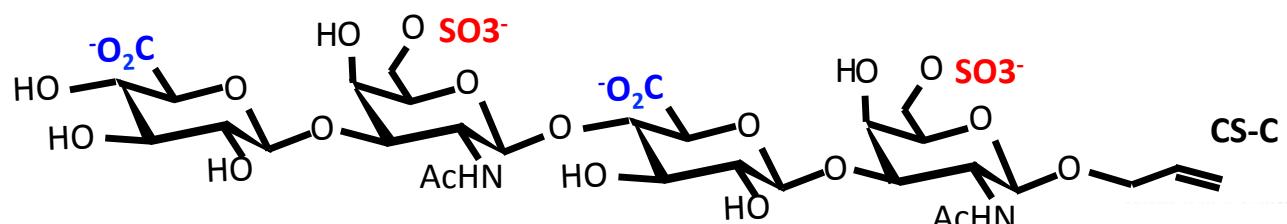
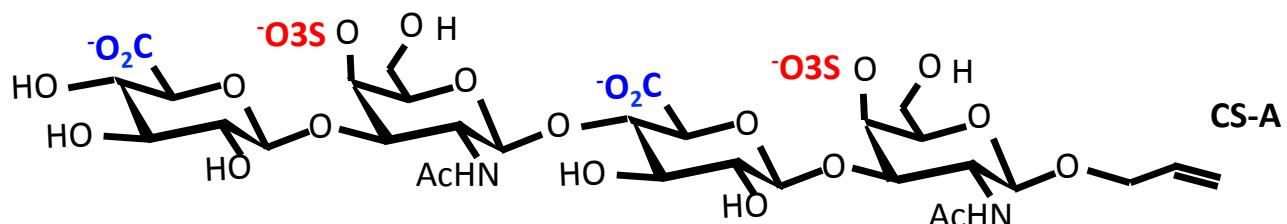
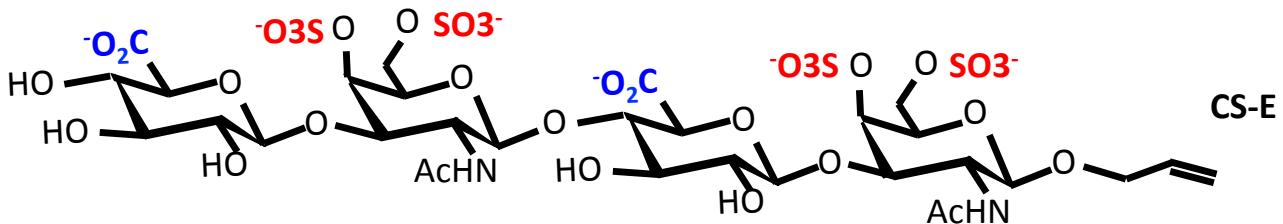
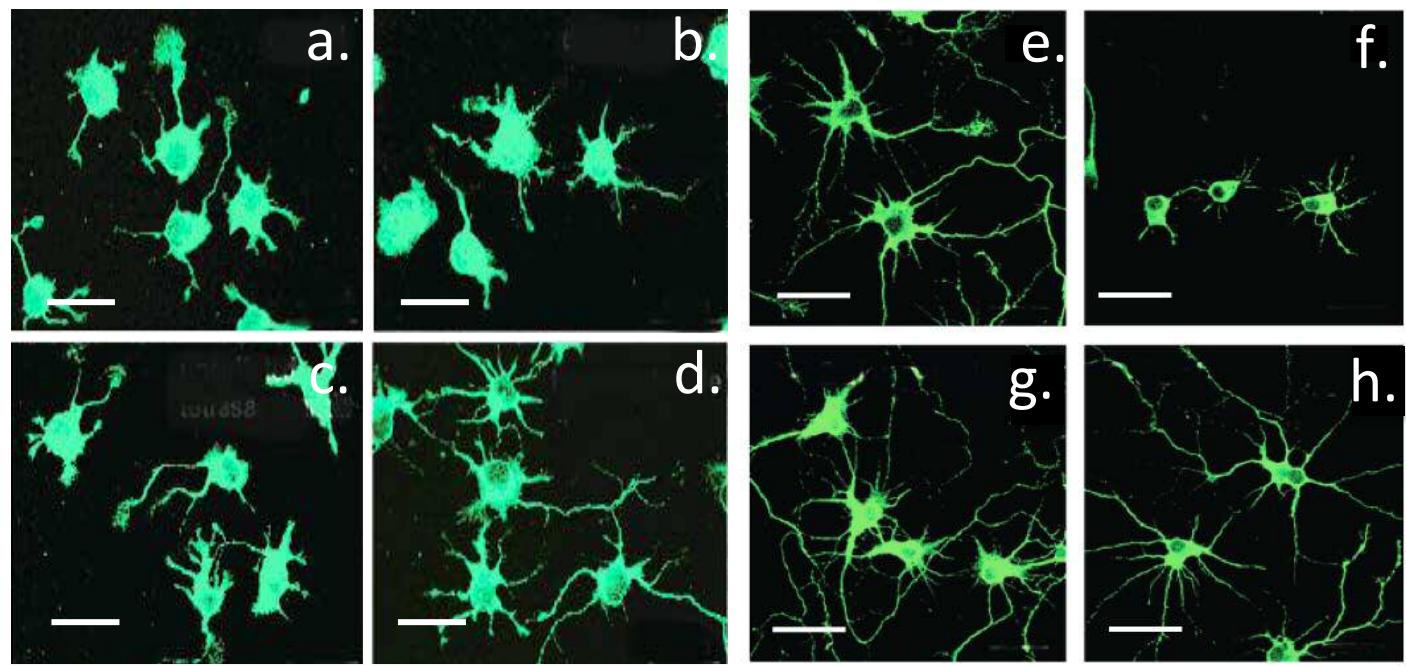
g.

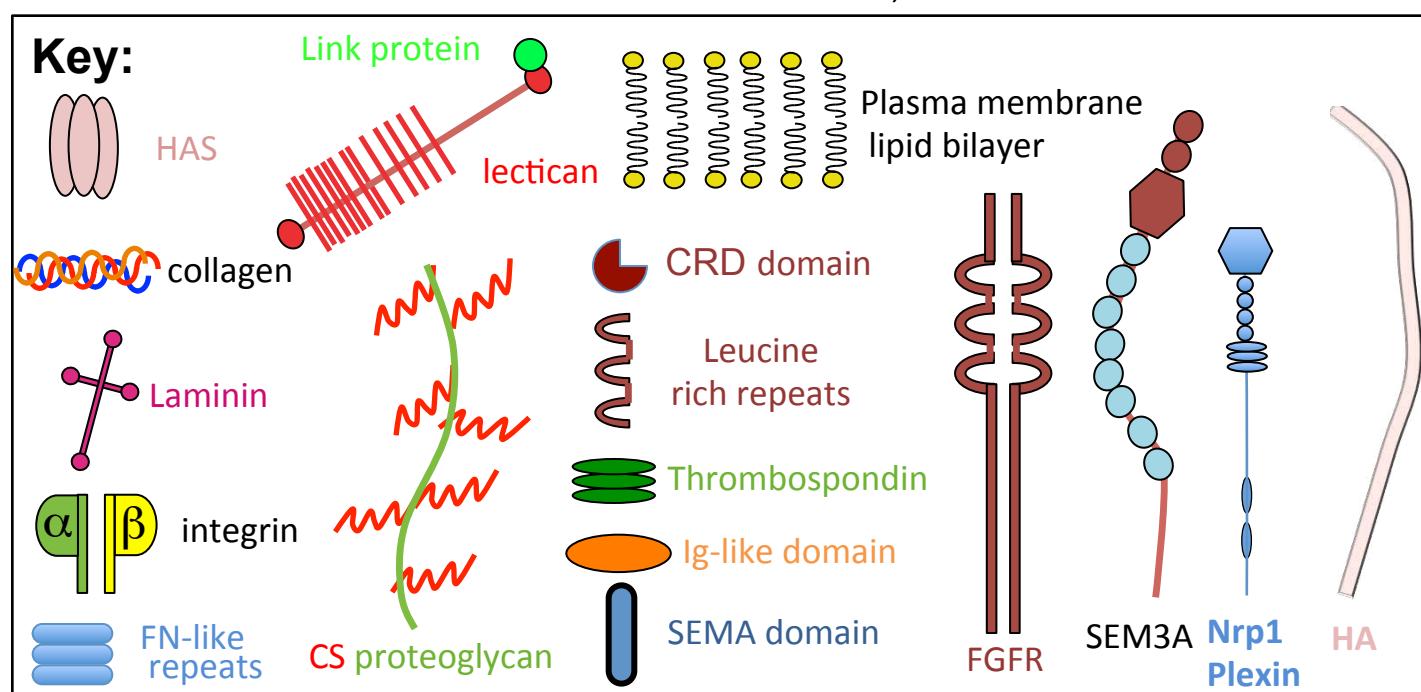
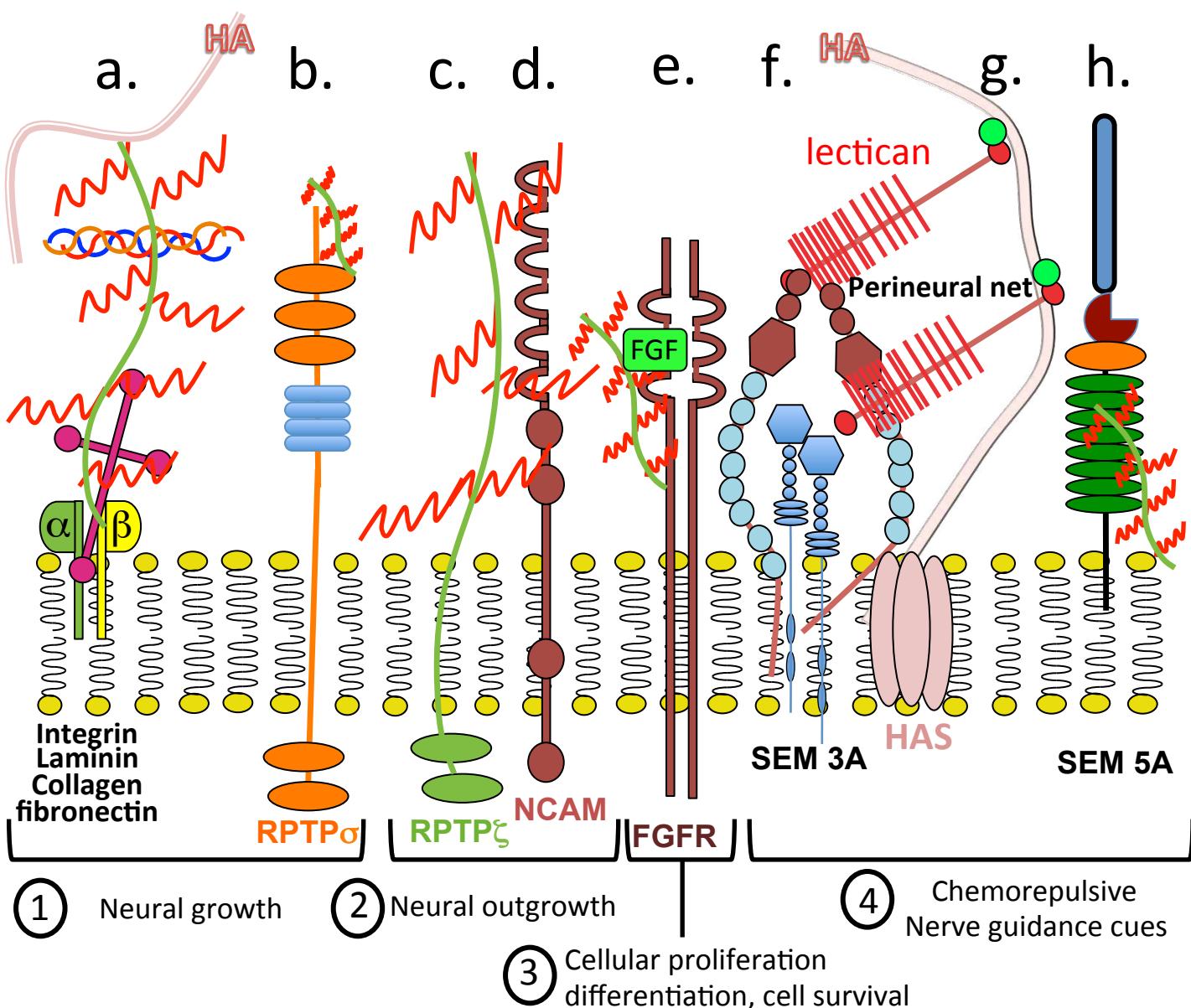
no terminal galactose

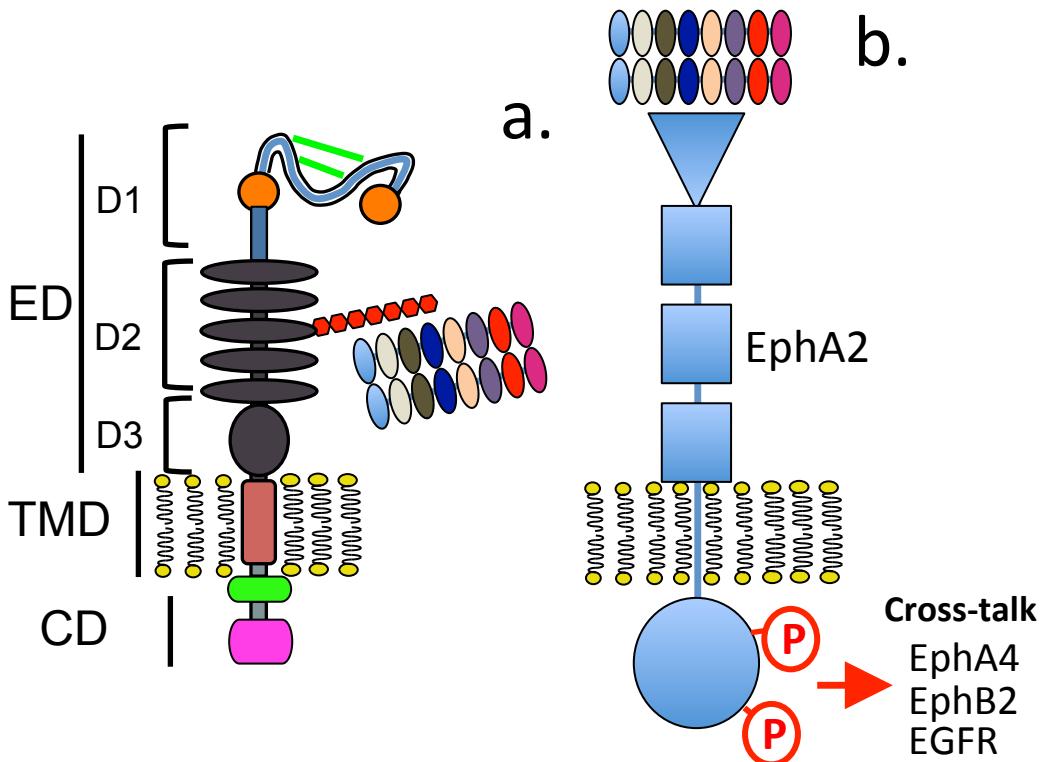
h.



Key: ● Glc ★ Xyl ▲ Fuc ■ GlcNAc ○ Gal ● Man ♦ Sialic acid







Key:

- Disulphide stabilised D1 globular domains
- NG2 D2 core repeat modules
- NG2 TM domain
- PR-PKCa domain
- PDZ-ERK-1, 2
- CS side chain
- Progranulin dimer
- Plasma membrane lipid bilayer
- Phosphorylation site (P)
- ED extracellular domain
- TMD transmembrane domain
- CD cytoplasmic domain

AGE advanced glycation end products

RAGE receptor for advanced glycation end products

