Group: Isabella Brown, Karli Puri, Shahbaz Siddeeq.Mohamed Sabri Hafidi Brown_Puri_Siddeeq_Hafidi

Part 2: Alignment and quality scoring

1 Multiply Aligning:

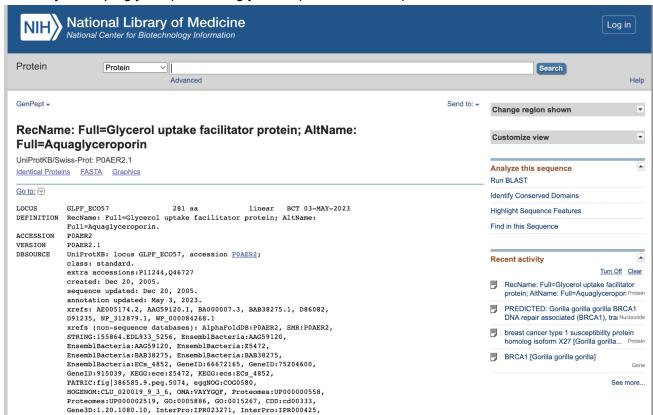
Generate four alignments of all sequences using:

Clustal Omega: www.ebi.ac.uk/Tools/msa/clustalo/

https://www.ebi.ac.uk/Tools/services/web/toolresult.ebi?jobId=clustalo-I20230606-130713-0894-13699759-p2m

When BLAST is finished, have a look at the names of the domain hits and families BLAST returns; are they all from the AQPs and GLPs sub-family? If not, what do you think is happening here?

Yes, they are aquaglyceroporin and glycerol uptake facilitator proteins.



>sp|P0AER2.1|GLPF_ECO57 RecName: Full=Glycerol uptake facilitator protein;
AltName: Full=Aquaglyceroporin

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPA
VTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPN
PHINFVQAFAVEMVITAILMGLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGP
KVFAWLAGWGNVAFTGGRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTTPSEQKAS
L

>sp|P0AER0|GLPF_ECOLI Glycerol uptake facilitator protein OS=Escherichia coli (strain K12) OX=83333 GN=glpF PE=1 SV=1

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA GVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHH IVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAILMGLILALTDDGNGVPRGPLAP LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGP IVGAIVGAFAYRKLIGRHLPCDICVVEEKETTTPSEQKASL

>sp|P0AER1|GLPF_ECOL6 Glycerol uptake facilitator protein OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) OX=199310 GN=glpF PE=3 SV=1 MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA GVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHH IVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAILMGLILALTDDGNGVPRGPLAP LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGP IVGAIVGAFAYRKLIGRHLPCDICVVEEKETTTPSEQKASL

>tr|A0A891SJ93|A0A891SJ93_ECOLX Aquaporin OS=Escherichia coli O157:H-OX=183192 GN=CSW52_13180 PE=3 SV=1

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA GVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHH IVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAILMGLILALTDDGNGVPRGPLAP LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGP IVGAIVGAFAYRKLIGRHLPCDICVVEEKETTTPSEQKASL

>tr|D8EEH2|D8EEH2_ECOLX Aquaglyceroporin OS=Escherichia coli MS 119-7 OX=679206 GN=glpF PE=3 SV=1

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA GVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHH IVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAILMGLILALTDDGNGVPRGPLAP LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGP IVGAIVGAFAYRKLIGRHLPCDICVVEEKETTTPSEQKASL

Multiple Alignments:

