

[Log in](#)

Protein

Search

Advanced

---

GenPept ▾
Sent to: ▾

## RecName: Full=Glycerol uptake facilitator protein; AltName: Full=Aquaglyceroporin





UniProtKB/Swiss-Prot: P0AER2.1

[Identical Proteins](#)   [FASTA](#)   [Graphics](#)

[Go to:](#) ☒

LOCUS	GLPF_ECO57	281 aa	linear	BCT 03-MAY-2023
DEFINITION	RecName: Full=Glycerol uptake facilitator protein; AltName: Full=Aquaglyceroporin.			
ACCESSION	P0AER2			
VERSION	P0AER2.1			
DBSOURCE	UniProtKB; locus GLPF_ECO57, accession <a href="#">P0AER2</a> ; class: standard. extra accessions:P11244,Q46727 created: Dec 20, 2005. sequence updated: Dec 20, 2005. annotation updated: May 3, 2023. xrefs: AE005174.2, AAG59120.1, BA000007.3, BAB38275.1, D86082, D91235, NP_312879.1, WP_000084268.1 xrefs (non-sequence databases): AlphaFoldDB:P0AER2, SMR:P0AER2, STRING:155864.EDL933_5256, EnsemblBacteria:AAG59120, EnsemblBacteria:AAG59120, EnsemblBacteria:Z5472, EnsemblBacteria:BAB38275, EnsemblBacteria:BAB38275, EnsemblBacteria:ECS_4852, GeneID:66672165, GeneID:75204600, GeneID:915039, KEGG:ecce:Z5472, KEGG:ecs:ECS_4852, PATRIC:fig 386585.9.peg.5074, eggNOG:COG0580, HOGENOM:CLU_020019_9_3_6, OMA:VAYYGQF, Proteomes:UP000000558, Proteomes:UP000002519, GO:0005886, GO:0015267, CDD:cd00333, Gene3D:l.20.1080.10. InterPro:IPR023271. InterPro:IPR000425.			

### Recent activity

-  RecName: Full=Glycerol uptake facilitator protein; AltName: Full=Aquaglyceroporin Protein
-  PREDICTED: Gorilla gorilla gorilla BRCA1 DNA repair associated (BRCA1), tra Nucleotide
-  breast cancer type 1 susceptibility protein homolog isoform X27 [Gorilla gorilla... Protein
-  BRCA1 [Gorilla gorilla gorilla] Gene

[Turn Off](#)   [Clear](#)

[See more...](#)

>sp|P0AER2.1|GLPF\_ECO57 RecName: Full=Glycerol uptake facilitator protein;  
AltName: Full=Aquaglyceroporin  
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPA  
VTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPN  
PHINFVQAFVEMVITAILMGLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGP  
KVFAWLAGWGNVAFTGGRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPDIDCVVEEKETTTTPSEQKAS  
L

>sp|P0AER0|GLPF\_ECOLI Glycerol uptake facilitator protein OS=Escherichia coli (strain  
K12) OX=83333 GN=glpF PE=1 SV=1  
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLT  
GVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHH  
IVRGSVESVDLAGTFSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGPLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPDIDCVVEEKETTTTPSEQKASL

>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  
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLT  
GVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHH  
IVRGSVESVDLAGTFSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGPLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPDIDCVVEEKETTTTPSEQKASL

>tr|A0A891SJ93|A0A891SJ93\_ECOLX Aquaporin OS=Escherichia coli O157:H-  
OX=183192 GN=CSW52\_13180 PE=3 SV=1  
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLT  
GVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHH  
IVRGSVESVDLAGTFSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGPLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPDIDCVVEEKETTTTPSEQKASL

>tr|D8EEH2|D8EEH2\_ECOLX Aquaglyceroporin OS=Escherichia coli MS 119-7  
OX=679206 GN=glpF PE=3 SV=1  
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLT  
GVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHH  
IVRGSVESVDLAGTFSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGPLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPDIDCVVEEKETTTTPSEQKASL

Multiple Alignments:

Input form

Web services

Help & Documentation

Bioinformatics Tools FAQ

Feedback

Results for job clustalo-I20230606-130750-0737-32928972-p1m

Alignments

Result Summary

Guide Tree

Phylogenetic Tree

Results Viewers

Submission Details

Download Alignment File

Show Colors

>sp|P0AER2.1|GLPF\_ECO57 RecName: Full=Glycerol uptake facilitator protein; AltName: Full=Aquaglyceroporin  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL  
>sp|P0AER0|GLPF\_ECOLI Glycerol uptake facilitator protein OS=Escherichia coli (strain K12) OX=83333 GN=glpF PE=1 SV=1  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL  
>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  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL  
>tr|A0A891SJ93|A0A891SJ93\_ECOLX Aquaporin OS=Escherichia coli O157:H- OX=183192 GN=CSW52\_13180 PE=3 SV=1  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL  
>tr|D8EEH2|D8EEH2\_ECOLX Aquaglyceroporin OS=Escherichia coli MS 119-7 OX=679206 GN=glpF PE=3 SV=1  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL

Input form

Web services

Help & Documentation

Bioinformatics Tools FAQ

Feedback

Results for job clustalo-I20230606-130750-0737-32928972-p1m

Alignments

Result Summary

Guide Tree

Phylogenetic Tree

Results Viewers


Submission Details

Download Alignment File

Hide Colors

>sp|P0AER2.1|GLPF\_ECO57 RecName: Full=Glycerol uptake facilitator protein; AltName: Full=Aquaglyceroporin  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL  
>sp|P0AER0|GLPF\_ECOLI Glycerol uptake facilitator protein OS=Escherichia coli (strain K12) OX=83333 GN=glpF PE=1 SV=1  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL  
>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  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL  
>tr|A0A891SJ93|A0A891SJ93\_ECOLX Aquaporin OS=Escherichia coli O157:H- OX=183192 GN=CSW52\_13180 PE=3 SV=1  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL  
>tr|D8EEH2|D8EEH2\_ECOLX Aquaglyceroporin OS=Escherichia coli MS 119-7 OX=679206 GN=glpF PE=3 SV=1  
MSQSTLTKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTA  
GVSGAHLNPAVTIALMLFACFDKRRKVIPIVSQVAGAFCAALVYGLYYNLFDFEQTHH  
IVRGSVESVDLAGTFTSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGLAP  
LLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAMLAGWGNVFTGGRDIPYFLVPLFGP  
IVGAIVGAFAYRKLIGRHLPCDICVVEEKEETTPSEQKASL

Centre for Integrative Bioinformatics VU  
vrije Universiteit amsterdam



IBVU - www.ibv.vu.nl

Main pageResearchTeachingProgramsMembersPublicationsVacanciesRelated sites

## PRALINE sequence alignment results for job Untitled

[Back to PRALINE main page](#)

The PRALINE alignment process was completed in 283.0 seconds.

Alignment score = 15522.00  
Alignment score per aligned residue pair = 18.41  
Sequence identities = 843  
Percent sequence identity = 1.00  
Number of sequences = 3  
Alignment length = 281  
Number of residues = 843  
Number of gaps = 0

[Save all data for this job \(tar and gzipped file\)](#)

[Download the final alignment \[alignment.fasta\\_all\]](#)  
[Download PRALINE raw output file \[results.out\]](#)  
[Download PSI-BLAST output files](#)  
[Download Secondary structure prediction files](#)

### Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for **amino acid conservation**.

[Residue Type](#) [Hydrophobicity](#) [Sec.Structure](#) [Make PDF](#)

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position.  
The colour assignments are:

.....012345678910.....

The current colourscheme of the alignment is for **amino acid conservation**.

[Residue Type](#) [Hydrophobicity](#) [Sec.Structure](#) [Make PDF](#)

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position.  
The colour assignments are:

Unconserved012345678910Conserved

	.....10.....20.....30.....40.....50
sp_POAERO_GLPP	MSQSTSLKQG CIAEFLGTGL LIFFGVGCVA ALKVAGASFG QWEISVINGL
tr_AOA891S393_A	MSQSTSLKQG CIAEFLGTGL LIFFGVGCVA ALKVAGASFG QWEISVINGL
tr_AOA0H7JXJ6_A	MSQSTSLKQG CIAEFLGTGL LIFFGVGCVA ALKVAGASFG QWEISVINGL
Consistency	*****
	.....60.....70.....80.....90.....100
sp_POAERO_GLPP	GVAMAIYLTAVSGAHLNPA VTIALWLPAC FDKRRVIPFI VSQVAGAPCA
tr_AOA891S393_A	GVAMAIYLTAVSGAHLNPA VTIALWLPAC FDKRRVIPFI VSQVAGAPCA
tr_AOA0H7JXJ6_A	GVAMAIYLTAVSGAHLNPA VTIALWLPAC FDKRRVIPFI VSQVAGAPCA
Consistency	*****
	.....110.....120.....130.....140.....150
sp_POAERO_GLPP	RAALVYGLIYN LFFDFEQTHN IVRGSVESVD LAGTSTSTPN PRINPVQAPA
tr_AOA891S393_A	RAALVYGLIYN LFFDFEQTHN IVRGSVESVD LAGTSTSTPN PRINPVQAPA
tr_AOA0H7JXJ6_A	RAALVYGLIYN LFFDFEQTHN IVRGSVESVD LAGTSTSTPN PRINPVQAPA
Consistency	*****
	.....160.....170.....180.....190.....200
sp_POAERO_GLPP	VENVITAILM GLILALTDGG NGVPRGPLAP LLIGLLIAVI GASHGPLTGF
tr_AOA891S393_A	VENVITAILM GLILALTDGG NGVPRGPLAP LLIGLLIAVI GASHGPLTGF
tr_AOA0H7JXJ6_A	VENVITAILM GLILALTDGG NGVPRGPLAP LLIGLLIAVI GASHGPLTGF
Consistency	*****
	.....210.....220.....230.....240.....250
sp_POAERO_GLPP	AMNPARDPGP KVFANLAGWG NVAPTGGORDI PFPLVPLFGP IVGAIVGAPA
tr_AOA891S393_A	AMNPARDPGP KVFANLAGWG NVAPTGGORDI PFPLVPLFGP IVGAIVGAPA
tr_AOA0H7JXJ6_A	AMNPARDPGP KVFANLAGWG NVAPTGGORDI PFPLVPLFGP IVGAIVGAPA
Consistency	*****
	.....260.....270.....280.....
sp_POAERO_GLPP	YRKLIQRHLP CDICVVEEKE TTFPSEQKAS
tr_AOA891S393_A	YRKLIQRHLP CDICVVEEKE TTFPSEQKAS
tr_AOA0H7JXJ6_A	YRKLIQRHLP CDICVVEEKE TTFPSEQKAS
Consistency	*****