

Started on	Saturday, 21 October 2023, 8:31 AM
State	Finished
Completed on	Monday, 23 October 2023, 11:59 PM
Time taken	2 days 15 hours
Marks	9.50/12.00
Grade	7.92 out of 10.00 (79.17%)

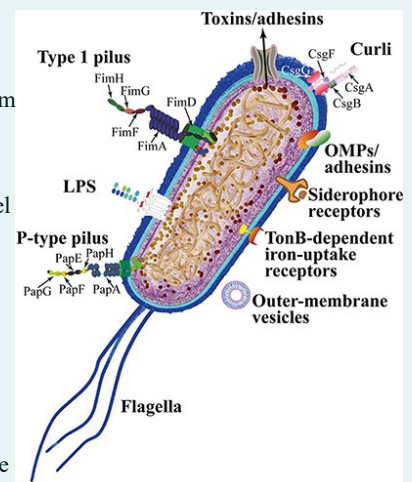
Question 1

Correct

Mark 1.00 out of 1.00

Escherichia coli is a significant cause of diarrheal illness and mortality worldwide each year, especially among children in developing countries. Pathogenic *E. coli* strains produce diverse virulence factors that allow them to overcome or subvert host defenses and to colonize, injure, and invade host cells or tissues. Today the existence of thousands of *E. coli* genomes in public databases has opened new perspectives for identification of novel virulence factors that could act as targets for treatment of infectious diseases. However, around 25% of the open reading frames (ORFs) in *E. coli* genomes remain as hypothetical genes without known function because they codify for uncharacterized proteins.

One of those ORF is the one that codifies for the uncharacterized protein YeeJ (UniProt P76347) in the *E. coli* K12 genome. Here, to better annotate function for this protein, we will combine similarity searches using protein databases with searches at pattern, domain and family databases.



Question 1. What can you say about the type of evidence that supports the existence of the protein P76347?

Select one:

- ☒ a. The existence of this protein is probable because clear orthologs exist in closely related species. ✓
- ☐ b. There are clear experimental evidences for the existence of this protein.
- ☐ c. The existence of this protein is unsure.
- ☐ d. Don't know/no answer (without penalty).
- ☐ e. Expression data indicate the existence of a transcript for this protein.

<https://www.uniprot.org/uniprotkb/P76347/entry>

https://www.uniprot.org/help/protein_existence

The value '**Protein inferred by homology**' indicates that the existence of a protein is probable because clear orthologs exist in closely related species.

The correct answer is: The existence of this protein is probable because clear orthologs exist in closely related species.

Question 2

Correct

Mark 1.00 out of 1.00

Question 2. In what biological process does this protein seem to participate?

Select one:

- ☐ a. Don't know/no answer (without penalty).
- ☐ b. Amino acid transporter
- ☐ c. Protein kinase signal transduction
- ☒ d. Cell adhesion ✓
- ☐ e. DNA replication

<https://www.uniprot.org/uniprotkb/P76347/entry#function><https://www.ebi.ac.uk/QuickGO/annotations?geneProductId=P76347>

The correct answer is: Cell adhesion

Question 3

Correct

Mark 2.00 out of 2.00

Question 3. With which nucleotide entry at the NCBI RefSeq database has this UniProt protein cross-reference? (In case of multiple possibilities, use the oldest one) ✓ (Indicate the refseq accession number)What does this refseq entry represent? ✓<https://www.uniprot.org/uniprotkb/P76347/entry#sequences>

NC_000913.3 and NZ_LN832404.1 are Refseq nucore entries linked by this Uniprot accession.

NC_000913.3 is the oldest (2006 vs 2014, you can see it in the reference paper)

NC_000913.3 is nucleotide NP_416485.4 is protein.

NC_000913.3 is complete since it only contains one contig

it is annotated: Customize view -> customize-> all features

Question 4

Correct

Mark 1.00 out of 1.00

Question 4. In other *Escherichia coli* strains different to K12, the function of this protein has been annotated as:

Select one:

- ☐ a. VacA-like protein
- ☒ b. Inverse autotransporter adhesin YeeJ / Bacterial Ig-like domain family protein ✓
- ☐ c. Agglomeration and penetration protein
- ☐ d. AIDA-1 autotransporter adhesion protein
- ☐ e. Don't know/no answer (without penalty)

We can find it in similar proteins

https://www.uniprot.org/uniprotkb/P76347/entry#similar_proteins

The correct answer is: Inverse autotransporter adhesin YeeJ / Bacterial Ig-like domain family protein

Question 5

Partially correct

Mark 0.75 out of 2.00

Question 5. Based exclusively on our protein sequence (UniProt P76347), which of these bacterial pathogens seems to be the closest to *E. coli* from an evolutionary point of view? Shigella flexneri

What function has been assigned to the homologous protein in the selected closest species? Bacterial motility

✖

In NCBI:

Blast vs nr only for those organisms.

blastnblasttblastntblastx

BLASTP programs search protein databases

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

Clear

Query subrange

From

To

Enter accession number(s), gi(s), or FASTA sequence(s)

FVQSGTNPVPIKISAIIDYSLNINGDYKATVTGGGEGIATLIPVLNGVHQAGLSTTIQFTR
AEDKIMSGTIVSVNGTDLPSTTFPSQSGFTGAYYQLNNDNFAPGKTAADYEFSSASWVDVD
ATGKVTFFKNVGSNSERITATPKSGGSPYVYEIRVKSMMWVNAEAFMIYSLAENFCSSNGY
TLPRANYLNHCSSRGIGSLYSEWGDHGYTTDAGFQSNMYWSSSPANSSEQYVVSLATGD
QSVFEKLGFAATCYKNI

Or, upload file

Browse... No file selected.

Job Title

sp|P76347|YEEJ_ECOLI Uncharacterized protein...

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database

Non-redundant protein sequences (nr)

Organism

Optional

Bacillus anthracis (taxid:1392)

Shigella flexneri (taxid:623)

Stenotrophomonas maltophilia (taxid:40324)

Vibrio cholerae (taxid:666)

exclude

exclude

exclude

exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude

Optional

☐ Models (XM/XP)

☐ Non-redundant RefSeq proteins (WP)

☐ Uncultured/environmental sample sequences

Program Selection

Algorithm

☐ Quick BLASTP (Accelerated protein-protein BLAST)

☒ blastp (protein-protein BLAST)

☐ PSI-BLAST (Position-Specific Iterated BLAST)

☐ PHI-BLAST (Pattern Hit Initiated BLAST)

☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

select all 100 sequences selected		GenPept	Graphics	Distance tree of results	Multiple alignment	MSA Viewer			
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	TPA: inverse autotransporter adhesin YeeJ [Shigella flexneri]	Shigella flexneri	4789	4789	100%	0.0	100.00%	2358	HBD6189621.1
<input checked="" type="checkbox"/>	TPA: inverse autotransporter adhesin YeeJ [Shigella flexneri]	Shigella flexneri	4785	4785	100%	0.0	99.87%	2358	HBD4498613.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2559	4989	100%	0.0	73.32%	2660	EFP8747227.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2515	4936	100%	0.0	72.07%	2660	EFW8300347.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2433	4538	100%	0.0	65.74%	2668	EFY9118459.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2410	2410	81%	0.0	68.26%	1928	EFZ4075408.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2407	2407	81%	0.0	68.16%	1937	EAA0483991.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2407	3608	81%	0.0	68.14%	1956	RIE63217.1
<input checked="" type="checkbox"/>	Ig-like domain-containing protein [Shigella flexneri]	Shigella flexneri	2406	3608	81%	0.0	68.14%	1947	WP_144038553.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2405	2405	81%	0.0	68.21%	1928	EFW4131607.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.16%	1928	EFV6700637.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1928	EFZ8507385.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	3605	81%	0.0	68.09%	1956	RIE49906.1
<input checked="" type="checkbox"/>	TPA: inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1928	HAY5349584.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1937	EGD9838738.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1928	EFV7480487.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1937	EFX2207962.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1937	EFY0858302.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1937	EAA3114360.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1937	EGD7431760.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2404	2404	81%	0.0	68.11%	1937	EGD7187710.1
<input checked="" type="checkbox"/>	Ig-like domain-containing protein [Shigella flexneri]	Shigella flexneri	2403	3603	81%	0.0	68.09%	1947	WP_133298076.1
<input checked="" type="checkbox"/>	TPA: inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2403	2403	81%	0.0	68.11%	1928	HAY5337492.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2402	2402	81%	0.0	68.11%	1928	EFZ3494640.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2402	2402	81%	0.0	68.06%	1937	EFX2216494.1
<input checked="" type="checkbox"/>	inverse autotransporter adhesin-like protein YeeJ [Shigella flexneri]	Shigella flexneri	2402	2402	81%	0.0	68.06%	1937	EAA1459946.1

In Uniprot (Slower)

BLAST

Find a protein sequence to run BLAST sequence similarity search by UniProt ID (e.g. P05067 or A4_HUMAN or UPI0000000001).

UniProt IDs

OR

Enter one or more sequences (20 max). You may also [load from a text file](#).

```
>sp|P76347|YEEJ_ECOLI OS=Escherichia coli (strain K12) OX=83333 GN=yeeJ PE=3 SV=3
MATKRRSGEE INDRQILCGM GIKLRRLTAG ICLITQLAFP MAAAAGQVNV AATQPPVPAQ
IAIAHANTVP YTLGALESQA SVAERFGISV AELRKLNQFR TFARGFDNVR QGDELDPVPAQ
VSEKKLTTPP GNSSDNLEQQ IASTSQIGS LLAEDMNSEQ AANMARGNAS SQASGAMTDW
LSRFGTARIT LGVDEDFSLK NSQDFLHPW YETPDNLFFS QHTLRHTDER TQINNGLGWR
HPTPTWMSGI NFFPDHDLR YHSRAGIGAE YWRDYLKLS NGYLRLTNWR SAPELDNDYE
AKPANGWDVR AESWLPWPH LGGKLVYEQY YGDEVALFDK DQRQSNPHAI TAGLNYTPFP
LMTFSAEQRQ GKQGENDRF AVDFTWQPS AMQKQLDPNE VAARRSLAGS RYDLVDRNNN
IVLEYRKKEL VRLTLTDPVT GKSGEVKS LV SSLQTKYALK GYNVEATALE AAGGKVVTG
KDILVTLPAY RFTSTPETDN TWPIEVTAED VKGNLSNREQ SMVVVQAPTL SQKDSVSL
TQTLNADSHS TATLTFIAHD AAGNPVVG LV LSTRHEGVQD ITLSDWKDNG DGSYQILTT
```

Your input contains 1 sequence

Target database

UniProtKB

Restrict by taxonomy

Enter taxon names or IDs to include

[Bacillus anthracis \[1392\]](#) ✕

[Shigella flexneri \[623\]](#) ✕

[Stenotrophomonas maltophilia \[40324\]](#) ✕

BLAST parameters

Identity



Score



E-Value



Taxonomy

Filter by taxonomy

Status

Reviewed (Swiss-Prot) (2)

Unreviewed (TrEMBL) (248)

Other organisms

Stenotrophomonas maltophilia (131)

BLAST 250 results found in UniProtKB

Overview Taxonomy Hit Distribution Text Output Input Parameters API Request

BLAST [Align](#) [Map IDs](#) [Download](#) [Add](#) [Resubmit](#)

Accession	Gene	Protein	Organism	Score	Identity	Accession
A0A3T2V007	DK174_19370	Inverse autotr...	Shigella flexneri	68.2%	27279.72	+5 more
A0A6N3R2...	SFCCH060_22...	Bacterial Ig-lik...	Shigella flexne...	67.5%	2503.71	+6 more
MCPK6	eahH	Attaching and ...	Shigella flexne...	59.2%	1165.46	+3 more
A0A7Z1J2G2	CEG97_00425	Adhesin	Shigella flexneri	63.1%	279.343	+5 more
A0A8H8ZBJ5	C0786_004733	Invasin (Fragm...	Shigella flexneri	65.7%	6411.720	+6 more
A0A7Z8GG...	E4T96_16630	Intimin-like ad...	Shigella flexneri	60.9%	616.439	+4 more
A0A7Z1J2...	CEG97_03485	Intimin-like ad...	Shigella flexneri	62.4%	607.446	+4 more
A0A6N3R6...	SFCCH060_22...	Bacterial Ig-lik...	Shigella flexne...	69.5%	207.882	1.4e-122
A0A6N3QL...	SGF_01677	Invasin	Shigella flexne...	68.5%	207.882	1.4e-122
A0A3T2V114	DK174_22465	Invasin	Shigella flexneri	69.5%	207.882	1.4e-122
A0A7Z1J3C0	CEG97_00420	Invasin	Shigella flexneri	61.6%	1238.079	1.7e-71
A0A6N3Q2...	SFCCH060_30...	Big-1 domain-c...	Shigella flexne...	66.5%	224.537	5.9e-63
A0A7Z1J2T8	CEG97_00435	IAT_beta doma...	Shigella flexneri	68.8%	193.356	4.4e-54
A0A7Z8M0...	ychO	Inverse autotr...	Shigella flexneri	60.9%	191.43	1.9e-51
A0A7Z1IYN6	CEG97_21315	YchO family in...	Shigella flexneri	60.9%	190.66	1.7e-51

Don't use the "reference proteomes" because if your protein is not in one of them, you will end with the wrong conclusions:

BLAST

Find a protein sequence to run BLAST sequence similarity search by UniProt ID (e.g. P05067 or A4_HUMAN or UPI0000000001).

UniProt IDs

OR

Enter one or more sequences (20 max). You may also [load from a text file](#).

```
>sp|P76347|YEEJ_ECOLI OS=Escherichia coli (strain K12) OX=83333 GN=yeeJ PE=3 SV=3
MATKRRSGEE INDRQILCGM GIKLRRLTAG ICLITQLAFP MAAAAGQVNV AATQPPVPAQ
IAIANANTVP YTLGALESQA SVAERFGISV AELRKLNQFR TFARGFDNVR QGDELDPVPAQ
VSEKKLTTPP GNSSDNLEQQ IASTSQIGS LLAEDMNSEQ AANMARGNAS SQASGAMTDW
LSRFGTARIT LGVDEDFSLK NSQDFLHPW YETPDNLFFS QHTLRHTDER TQINNGLGWR
HPTPTWMSGI NFFPDHDLR YHSRAGIGAE YWRDYLKLS NGYLRLTNWR SAPELDNDYE
AKPANGWDVR AESWLPWPH LGGKLVYEQY YGDEVALFDK DQRQSNPHAI TAGLNYTPFP
LMTFSAEQRQ GKQGENDRF AVDFTWQPS AMQKQLDPNE VAARRSLAGS RYDLVDRNNN
IVLEYRKKEL VRLTLTDPVT GKSGEVKS LV SSLQTKYALK GYNVEATALE AAGGKVVTG
KDILVTLPAY RFTSTPETDN TWPIEVTAED VKGNLSNREQ SMVVVQAPTL SQKDSVSL
TQTLNADSHS TATLTFIAHD AAGNPVVG LV LSTRHEGVQD ITLSDWKDNG DGSYQILTT
```

Your input contains 1 sequence

Target database

UniProtKB reference proteomes

Restrict by taxonomy

Enter taxon names or IDs to include

[Bacillus anthracis \[1392\]](#) ✕

[Shigella flexneri \[623\]](#) ✕

[Stenotrophomonas maltophilia \[40324\]](#) ✕

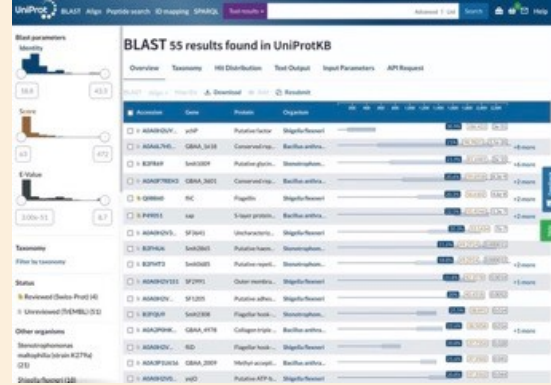
Name your BLAST job

sp|P76347|YEEJ_ECOLI

• **Advanced parameters**

Reset

Run BLAST



If you use uniprot blast vs UniprotKB we just click on the UP accession code of the first result (<https://www.uniprot.org/uniprotkb/A0A3T2V007/entry>) and we see in in Function->GO Annotations->Biological process: Cell adhesion

if you use ncbi blast

We get the best 40 NCBI IDs from the last column in the the ncbi blast results (Download -> csv, open with excel, copy the accession column) and map them to uniprot: <https://www.uniprot.org/id-mapping>

From EMBL/GeneBank/DBJ CDS to UniprotKB

and we get :

<https://www.uniprot.org/uniprotkb/A0A3T2V007/entry> mapped from EAA0483991.1 (the one previously mentioned with the uniprotKB blast search)

in the function section we see a GO code for "cell adhesion"

Question 6

Correct

Mark 1.00 out of 1.00

Question 6. What can we learn from our protein by searching at the [PROSITE](https://prosite.expasy.org/) database?

Select one:

- ☐ a. It contains one sequence fragment (domain) seems to play a role in a recombinational process of DNA repair. And several big1 domains
- ☐ b. It contains several sequence fragments (domains) seem to play a role in a recombinational process of DNA repair.
- ☒ c. It contains one sequence fragment (domain) that recognizes polysaccharides (carbohydrates) in the bacterial cell wall. And several big1 domains
- ☐ d. It contains several sequence fragments (domains) that recognize polysaccharides in the bacterial cell wall.
- ☐ e. Don't know/no answer (without penalty).

<https://prosite.expasy.org/>

and we paste P76347 sequence or this Uniprot accession and we pres scan

The correct answer is: It contains one sequence fragment (domain) that recognizes polysaccharides (carbohydrates) in the bacterial cell wall. And several big1 domains

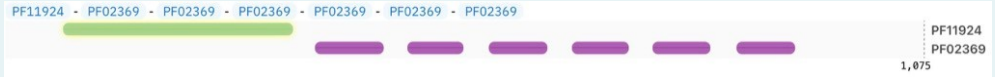

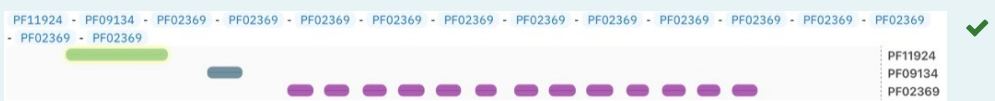
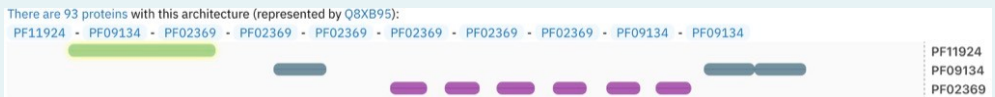
Question 7

Correct

Mark 1.00 out of 1.00

Question 7. Which of these [Pfam](#) domain architectures does our protein exhibit?

Select one:

- ☐ a. 
- ☐ b. There are 4975 proteins with this architecture (represented by P36943):

- ☒ c.  ✓
- ☐ d. Don't know/no answer (without penalty).
- ☐ e. There are 93 proteins with this architecture (represented by Q8XB95):


From Uniprot jump to pfam.

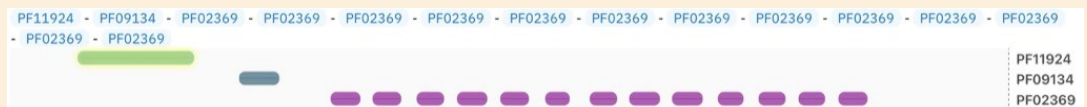
you will be redirected to interpro

<https://www.ebi.ac.uk/interpro/protein/UniProt/P76347/>

pay attention only to the pfam domains (PF...)

you will see one PF11924 followed by one PF09134 followed by thirteen PF02369

The correct answer is:

**Question 8**

Correct

Mark 1.00 out of 1.00

Question 8. Analyzing our protein at [InterPro](#) it seems that it contains much more domains or important protein signatures when compared with the result of Pfam. Why?

Select one:

- ☐ a. InterPro is a primary database and contains information for all known protein structures.
- ☐ b. InterPro consists of a collection of annotated multiple sequence alignment models available exclusively as position-specific score matrices (PSSMs).
- ☐ c. Don't know/no answer (without penalty).
- ☐ d. InterPro is a protein annotation resource for protein domain classifications based exclusively on hidden Markov models (HMMs).
- ☒ e. InterPro is an integrated database that combines protein signatures from a number of member databases. ✓

<https://www.ebi.ac.uk/interpro/about/>

The correct answer is: InterPro is an integrated database that combines protein signatures from a number of member databases.


Question 9

Correct

Mark 1.00 out of 1.00

Question 9. Based on information taken from derived protein databases (Interpro or Pfam) , what is the most likely function of the repetitive domains in our protein?

Select one:

- ☐ a. Don't know/no answer (without penalty).
- ☐ b. This repetitive unit is a phospho-relay system usually found in regulator proteins. This signal transduction system enables bacterium to sense, respond, and adapt to a wide range of environments, stressors, and growth conditions.
- ☐ c. These repetitive units have the capacity to interact with hyaluronic acid, which promotes the stability of the extra-cellular matrix.
- ☒ d. Big-1 proteins are surface-expressed proteins that mediate mammalian host cell invasion or attachment. The tandem of Ig-like domains appears to form a rod to link the bacterial outer membrane anchor to the C-terminal lectin-like domain to interact with their receptors in the host cell membrane 
- ☐ e. This multi-domain adopts a classic alpha/beta fold and contains an unusual metal ion coordination site at its surface. It has been suggested that this site represents a general metal ion-dependent adhesion site for binding protein ligands.

The repetitive domains are the "Big-1"

Big-1 domain description in interpro

<https://www.ebi.ac.uk/interpro/entry/InterPro/IPR003344/>

Take a look also at the description in the DBs that originated this interpro entry:

http://smart.embl-heidelberg.de/smart/do_annotation.pl?DOMAIN=SM00634

<https://prosite.expasy.org/PDOC51127>

Se that it is almost the same.

The correct answer is: Big-1 proteins are surface-expressed proteins that mediate mammalian host cell invasion or attachment. The tandem of Ig-like domains appears to form a rod to link the bacterial outer membrane anchor to the C-terminal lectin-like domain to interact with their receptors in the host cell membrane

Question 10

Incorrect

Mark -0.25 out of 1.00

Question 10. We finally want to know if our protein, or a protein similar to this, has a 3D structure experimentally solved.

Select one:

- ☐ a. Don't know/no answer (without penalty).
- ☒ b. Yes, protein P76347 has its 3D structure already solved. ❌
- ☐ c. There is no 3D structure for this protein. However the structures of all its known domains are known in other proteins or organisms.
- ☐ d. Yes, there is a 3D structure for this protein but only for the whole region that contains the repetitive domain Big-1.
- ☐ e. No, there is no 3D structure for this protein or for any of its domains in other proteins or close organisms.

We can see in interpro that this protein has this 3 pfam domains, and here you can see that these domains' structures have been solved in other proteins:

<https://www.ebi.ac.uk/interpro/entry/pfam/PF02369/structure/PDB/#table>

<https://www.ebi.ac.uk/interpro/entry/pfam/PF09134/structure/PDB/#table>

<https://www.ebi.ac.uk/interpro/entry/pfam/PF11924/structure/PDB/#table>

We can also see that it contains 4 CATH structural domains (Gene3D). Since CATH is a DB created from the the structure of proteins experimentally solved we can see other proteins with similar domains

<http://www.cathdb.info/version/latest/superfamily/2.60.40.10>

<http://www.cathdb.info/version/latest/superfamily/3.10.100.10>

<http://www.cathdb.info/version/latest/superfamily/2.40.160.160>

<http://www.cathdb.info/version/latest/superfamily/2.60.40.1080>

The correct answer is: There is no 3D structure for this protein. However the structures of all its known domains are known in other proteins or organisms.