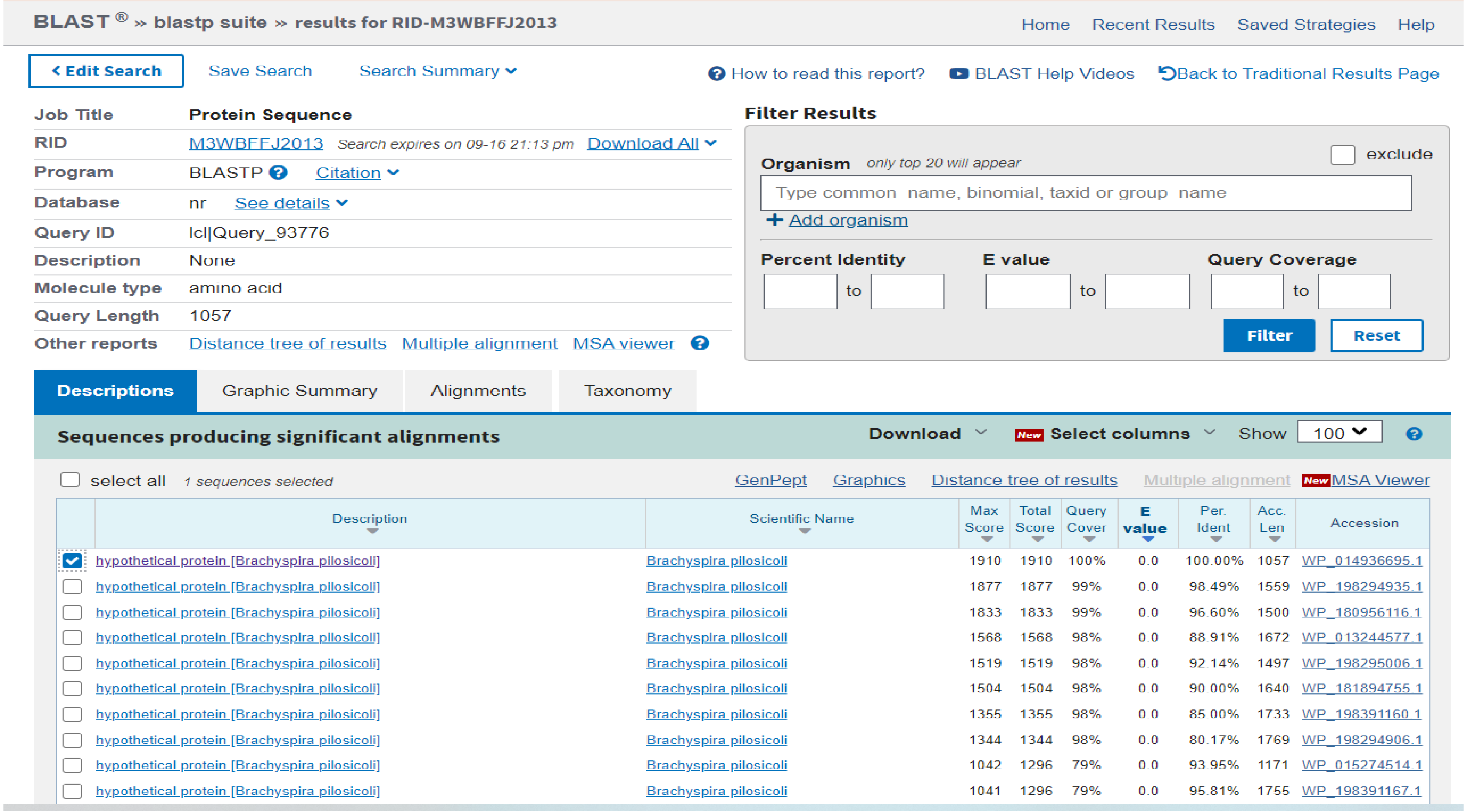
PROTEINA 1

```
>fig|6666666.171271.peg.2319
MKLNNSNIFDDNNDISLDEYDIDSLVDKNIEINENNFPTVSIGTESPSIHSSIIDDSITSASDENIAIENNNQEASVEA
YTEEENKIYNEIES NIGISEDDLNIISDVDDFNLENHFQNVNNDETVEAYTEEENRIYNEIENNVGISEDDLNAISDV
DDFNLESFFANSAPSIEDTAENDSNNNEDTISIDEISEDNTNDVNNETVEAYTEEENRAYNEIESNVGISEDDLNAISD
VDDFNLESFFANSTPIIEDSSNNATSINNEEAANEISETNDNLENNNDIAENIEENNDIAIDDNITEENDTTFETTVND
EINNALD NYLEAENSNSNDNNDIAENIEENNDIAIDDNITEENDTTFETTVNDKINNALNNYLESESFENNNDNLENT
EIRENIDTDIINNETNNDEVIDELEKLDDLVENLDNTEYIEDNNNNNIADIVSQGLAEIENIEYAENSSLQNDDSVVEI
IDEESYINENNANINKENDTTFETTINDEINNALDNYLEAESFENNNDNLENTEIKENIDTDIINNETNNDEVIDELEK
LDDLVENLDNTEYDNNNIADIVSQGLAEIENIEYAENNSLKSDDNIIKIVDDNNDDVAAMVSEGLDEIENIEHSLDNDD
KNITTENIHNIDVPDIDDVDYIDESNYINENNNQDDIIELSGNELDLITKDENIEYKYIQNNNKEYMDMNKIKKDIEEL
EIDELSNEENSIYNNQISDADNNEVYELTDAEVNMYKEYIENNELDENELSNEEIDMYKSYIEGKEYTNIKEEESINNL
EGIDKKEDINDLTDEEVNMYKEYIDRDDSEDKTDELTDEEELMYKAYIENSSSDTSIENESNKTSDDLLSTEYKEEINN
NSESVQNSQEENKIIEEEKKDTIEEQAEDNNDFLTKLKQMNEEYKKEKEDKKEEENKEEDSNNFLAKLKQMNEEYKREK
EEKRKEEIKESNDFLLKQVNEEYKEENKIEENKIEENKIYEEKKEEQNKEEDNNDFLAKLKQMNEEYKEEEKERKEEES
KKEEKESNDFLAKLKQMNEEYIKEEEEKKTKN
```



Job Title	**Protein Sequence**
RID	M3WBFFJ2013 *Search expires on 09-16 21:13 pm* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_93776
Description	None
Molecule type	amino acid
Query Length	1057
Other reports	Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism *only top 20 will appear* ☐ exclude

Type common name, binomial, taxid or group name

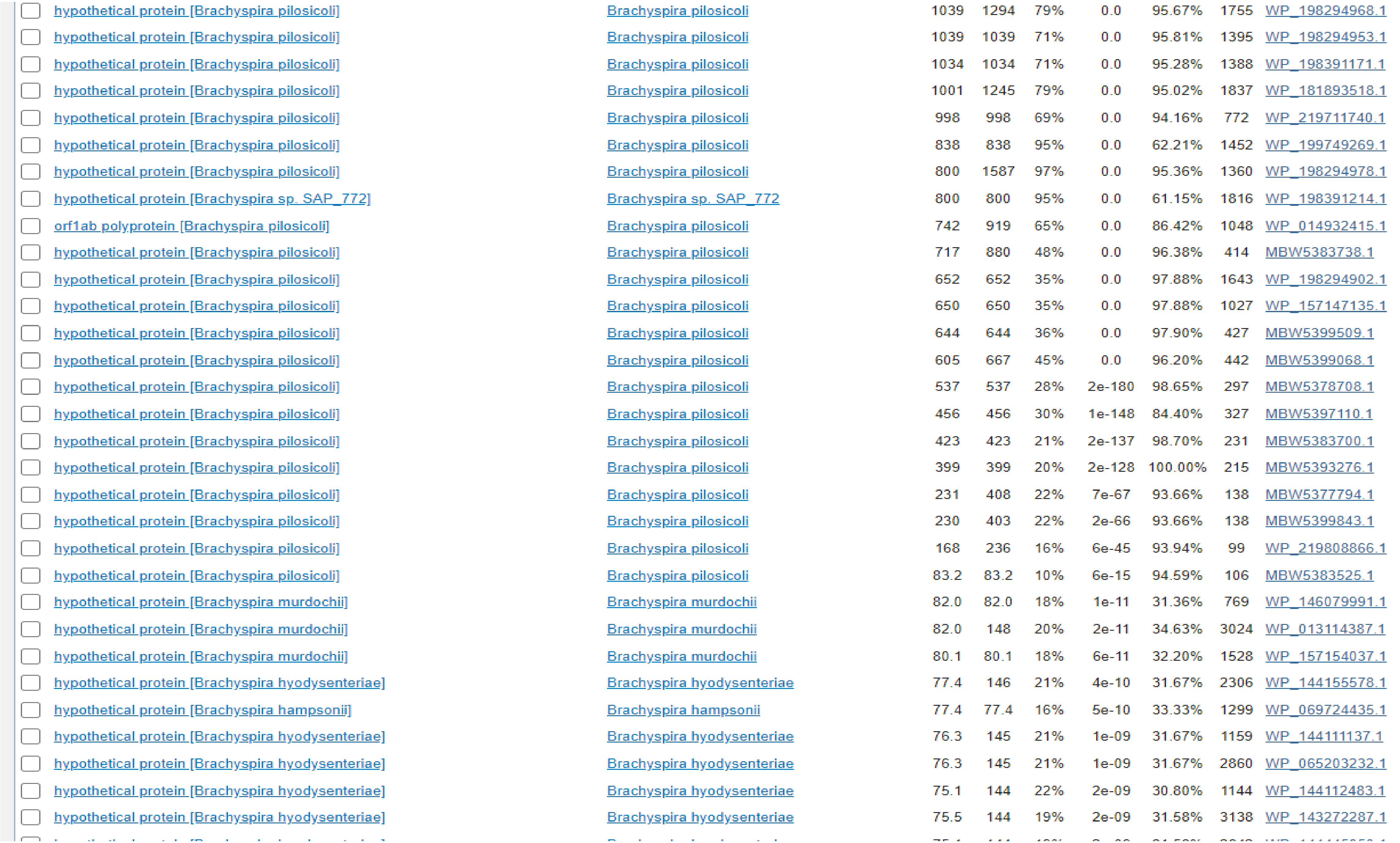
+ Add organism

Percent Identity ☐ to ☐ **E value** ☐ to ☐ **Query Coverage** ☐ to ☐

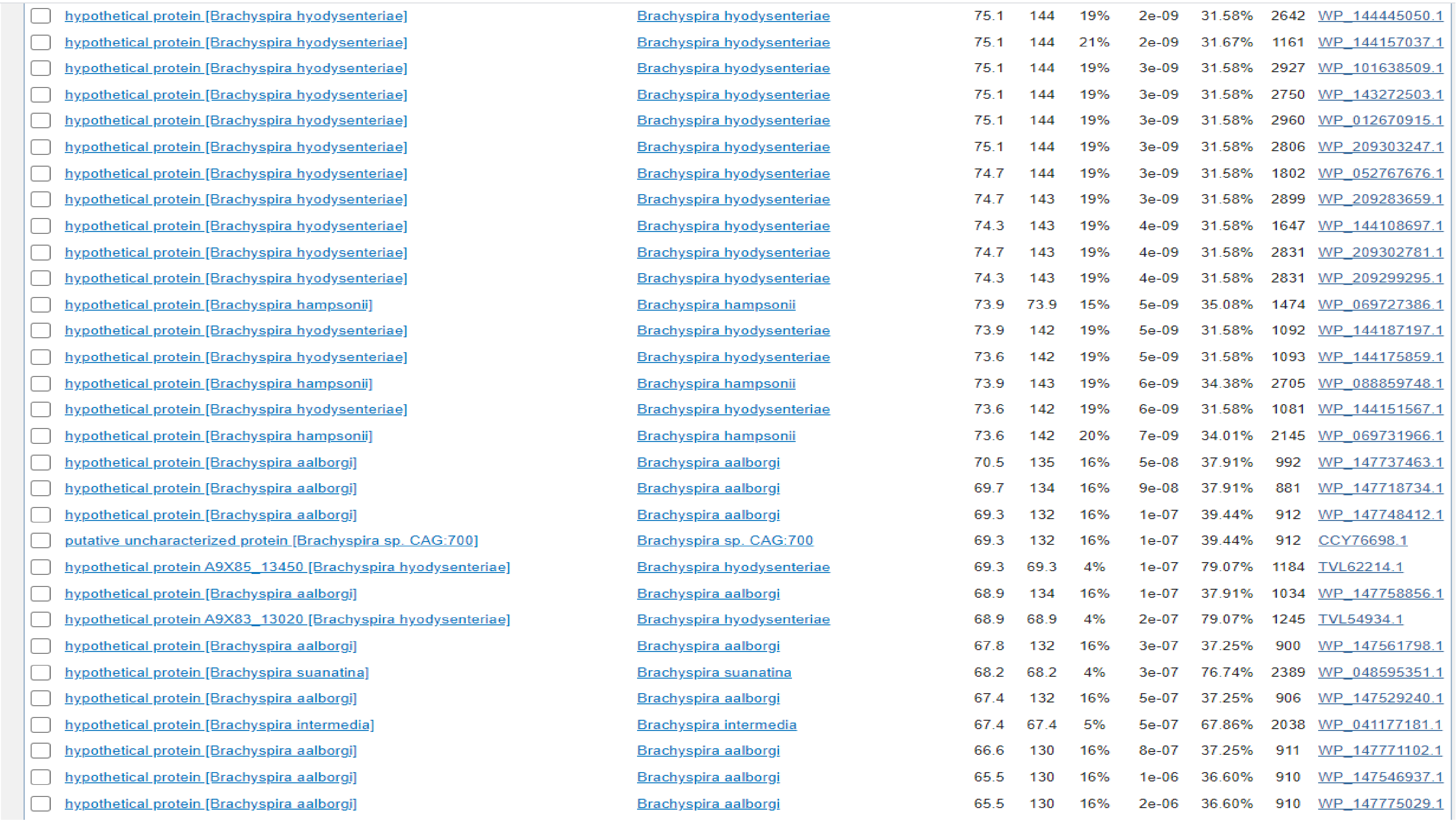
Sequences producing significant alignments

☐ select all *1 sequences selected*

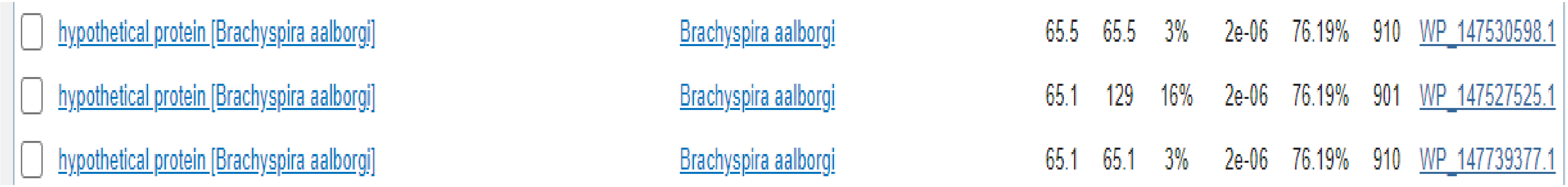
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1910	1910	100%	0.0	100.00%	1057	WP_014936695.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1877	1877	99%	0.0	98.49%	1559	WP_198294935.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1833	1833	99%	0.0	96.60%	1500	WP_180956116.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1568	1568	98%	0.0	88.91%	1672	WP_013244577.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1519	1519	98%	0.0	92.14%	1497	WP_198295006.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1504	1504	98%	0.0	90.00%	1640	WP_181894755.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1355	1355	98%	0.0	85.00%	1733	WP_198391160.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1344	1344	98%	0.0	80.17%	1769	WP_198294906.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1042	1296	79%	0.0	93.95%	1171	WP_015274514.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1041	1296	79%	0.0	95.81%	1755	WP_198391167.1



☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1039	1294	79%	0.0	95.67%	1755	WP_198294968.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1039	1039	71%	0.0	95.81%	1395	WP_198294953.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1034	1034	71%	0.0	95.28%	1388	WP_198391171.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1001	1245	79%	0.0	95.02%	1837	WP_181893518.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	998	998	69%	0.0	94.16%	772	WP_219711740.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	838	838	95%	0.0	62.21%	1452	WP_199749269.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	800	1587	97%	0.0	95.36%	1360	WP_198294978.1
☐	hypothetical protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	800	800	95%	0.0	61.15%	1816	WP_198391214.1
☐	orf1ab polyprotein [Brachyspira pilosicoli]	Brachyspira pilosicoli	742	919	65%	0.0	86.42%	1048	WP_014932415.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	717	880	48%	0.0	96.38%	414	MBW5383738.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	652	652	35%	0.0	97.88%	1643	WP_198294902.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	650	650	35%	0.0	97.88%	1027	WP_157147135.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	644	644	36%	0.0	97.90%	427	MBW5399509.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	605	667	45%	0.0	96.20%	442	MBW5399068.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	537	537	28%	2e-180	98.65%	297	MBW5378708.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	456	456	30%	1e-148	84.40%	327	MBW5397110.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	423	423	21%	2e-137	98.70%	231	MBW5383700.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	399	399	20%	2e-128	100.00%	215	MBW5393276.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	231	408	22%	7e-67	93.66%	138	MBW5377794.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	230	403	22%	2e-66	93.66%	138	MBW5399843.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	168	236	16%	6e-45	93.94%	99	WP_219808866.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	83.2	83.2	10%	6e-15	94.59%	106	MBW5383525.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	82.0	82.0	18%	1e-11	31.36%	769	WP_146079991.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	82.0	148	20%	2e-11	34.63%	3024	WP_013114387.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	80.1	80.1	18%	6e-11	32.20%	1528	WP_157154037.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	77.4	146	21%	4e-10	31.67%	2306	WP_144155578.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	77.4	77.4	16%	5e-10	33.33%	1299	WP_069724435.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	76.3	145	21%	1e-09	31.67%	1159	WP_144111137.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	76.3	145	21%	1e-09	31.67%	2860	WP_065203232.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	75.1	144	22%	2e-09	30.80%	1144	WP_144112483.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	75.5	144	19%	2e-09	31.58%	3138	WP_143272287.1

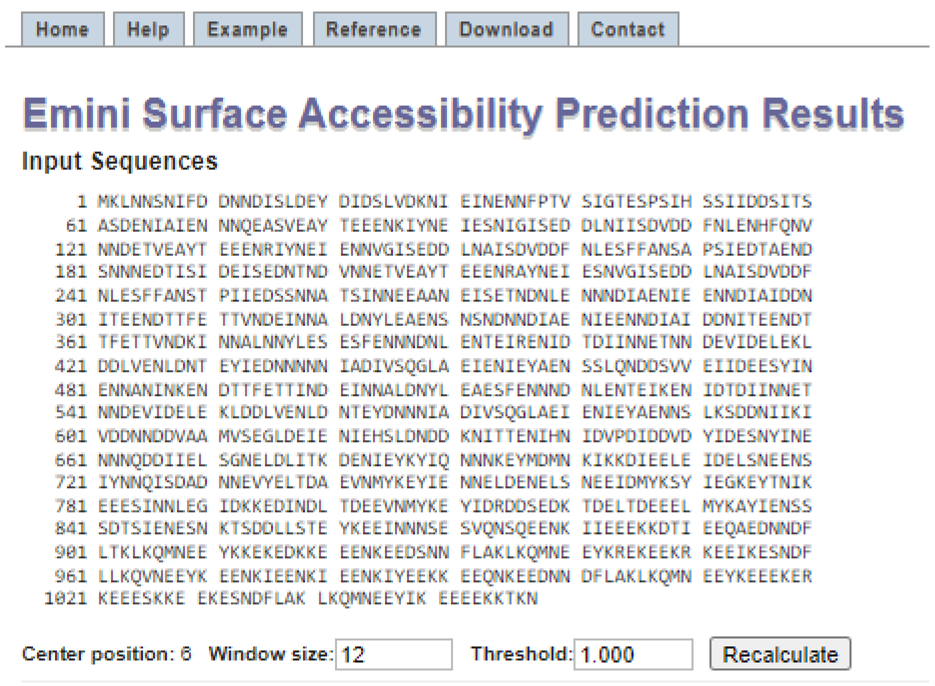


☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	75.1	144	19%	2e-09	31.58%	2642	WP_144445050.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	75.1	144	21%	2e-09	31.67%	1161	WP_144157037.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	75.1	144	19%	3e-09	31.58%	2927	WP_101638509.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	75.1	144	19%	3e-09	31.58%	2750	WP_143272503.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	75.1	144	19%	3e-09	31.58%	2960	WP_012670915.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	75.1	144	19%	3e-09	31.58%	2806	WP_209303247.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	74.7	144	19%	3e-09	31.58%	1802	WP_052767676.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	74.7	143	19%	3e-09	31.58%	2899	WP_209283659.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	74.3	143	19%	4e-09	31.58%	1647	WP_144108697.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	74.7	143	19%	4e-09	31.58%	2831	WP_209302781.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	74.3	143	19%	4e-09	31.58%	2831	WP_209299295.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	73.9	73.9	15%	5e-09	35.08%	1474	WP_069727386.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	73.9	142	19%	5e-09	31.58%	1092	WP_144187197.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	73.6	142	19%	5e-09	31.58%	1093	WP_144175859.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	73.9	143	19%	6e-09	34.38%	2705	WP_088859748.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	73.6	142	19%	6e-09	31.58%	1081	WP_144151567.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	73.6	142	20%	7e-09	34.01%	2145	WP_069731966.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	70.5	135	16%	5e-08	37.91%	992	WP_147737463.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	69.7	134	16%	9e-08	37.91%	881	WP_147718734.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	69.3	132	16%	1e-07	39.44%	912	WP_147748412.1
☐	putative uncharacterized protein [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	69.3	132	16%	1e-07	39.44%	912	CCY76698.1
☐	hypothetical protein A9X85_13450 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	69.3	69.3	4%	1e-07	79.07%	1184	TVL62214.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	68.9	134	16%	1e-07	37.91%	1034	WP_147758856.1
☐	hypothetical protein A9X83_13020 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	68.9	68.9	4%	2e-07	79.07%	1245	TVL54934.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	67.8	132	16%	3e-07	37.25%	900	WP_147561798.1
☐	hypothetical protein [Brachyspira suanatina]	Brachyspira suanatina	68.2	68.2	4%	3e-07	76.74%	2389	WP_048595351.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	67.4	132	16%	5e-07	37.25%	906	WP_147529240.1
☐	hypothetical protein [Brachyspira intermedia]	Brachyspira intermedia	67.4	67.4	5%	5e-07	67.86%	2038	WP_041177181.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	66.6	130	16%	8e-07	37.25%	911	WP_147771102.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	65.5	130	16%	1e-06	36.60%	910	WP_147546937.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	65.5	130	16%	2e-06	36.60%	910	WP_147775029.1



☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	65.5	65.5	3%	2e-06	76.19%	910	WP_147530598.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	65.1	129	16%	2e-06	76.19%	901	WP_147527525.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	65.1	65.1	3%	2e-06	76.19%	910	WP_147739377.1

Threshold: 1.000 Window: 12

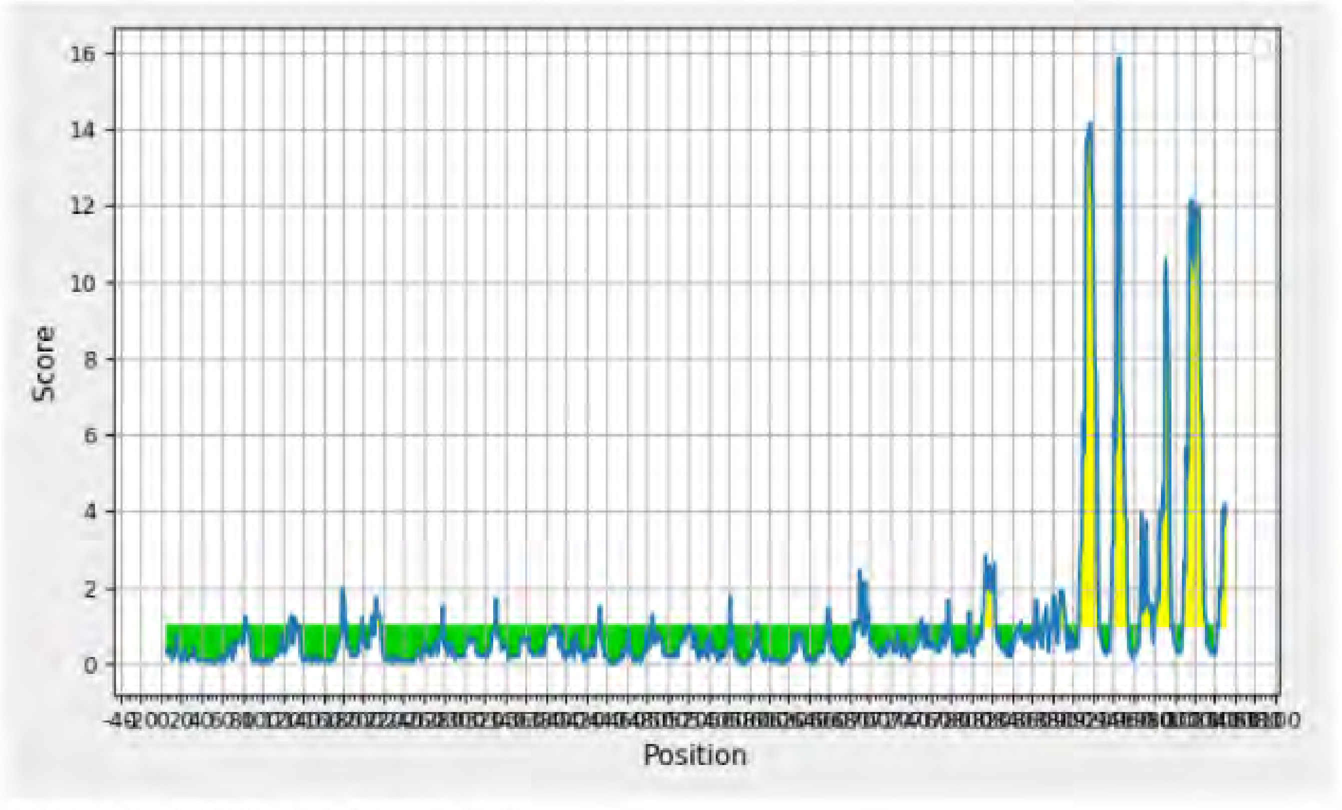


Emini Surface Accessibility Prediction Results

Input Sequences

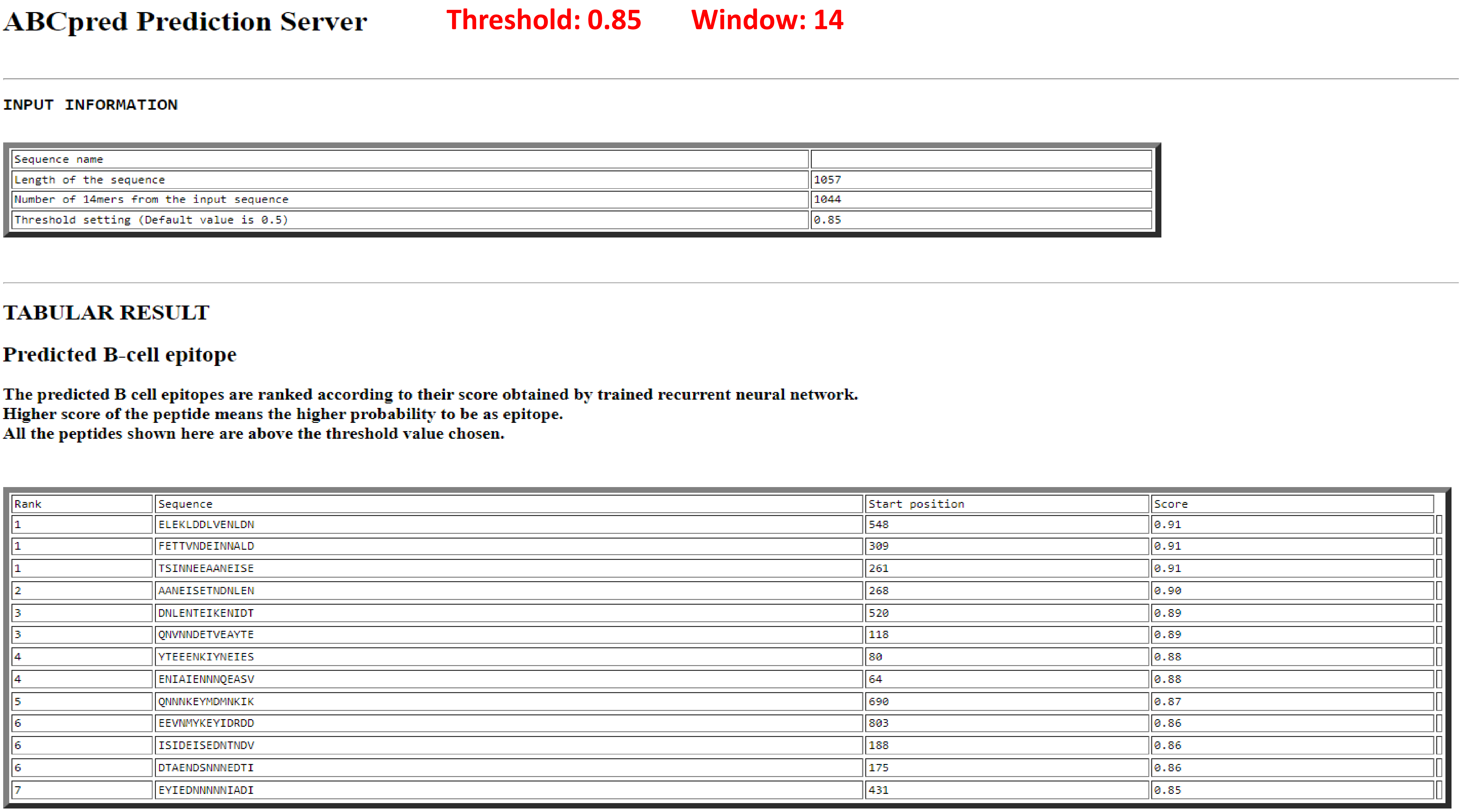
```
   1 MKLNNSNIFD DNNDISLDEY DIDSLVDKNI EINENNFPTV SIGTESPSIH SSIIDDSITS
  61 ASDENIAIEN NNQEASVEAY TEEENKIYNE IESNIGISED DLNIISDVDD FNLENHFQNV
 121 NNDETVEAYT EEENRIYNEI ENNVGISEDD LNAISDVDDF NLESFFANSA PSIEDTAEND
 181 SNNNEDTISI DEISEDNTND VNNETVEAYT EEENRAYNEI ESNVGISEDD LNAISDVDDF
 241 NLESFFANST PIIEDSSNNA TSINNEEAAN EISETNDNLE NNNDIAENIE ENNDIAIDDN
 301 ITEENDTTFE TTVNDEINNA LDNYLEAENS NSNDNNDIAE NIEENNDIAI DDNITEENDT
 361 TFETTVNDKI NNALNNYLES ESFENNNDNL ENTEIRENID TDIINNETNN DEVIDELEKL
 421 DDLVENLDNT EYIEDNNNNN IADIVSQGLA EIENIEYAEN SSLQNDDSVV EIIDEESYIN
 481 ENNANINKEN DTTFETTIND EINNALDNYL EAESFENNND NLENTEIKEN IDTDIINNET
 541 NNDEVIDELE KLDDLVENLD NTEYDNNNIA DIVSQGLAEI ENIEYAENNS LKSDDNIIKI
 601 VDDNNDDVAA MVSEGLDEIE NIEHSLDNDD KNITTENIHN IDVPDIDDVD YIDESNYINE
 661 NNNQDDIIEL SGNELDLITK DENIEYKYIQ NNNKEYMDMN KIKKDIEELE IDELSNEENS
 721 IYNNQISDAD NNEVYELTDA EVNMYKEYIE NNELDENELS NEEIDMYKSY IEGKEYTNIK
 781 EEESINNLEG IDKKEDINDL TDEEVNMYKE YIDRDDSEDK TDELTDEEEL MYKAYIENSS
 841 SDTSIENESN KTSDDLLSTE YKEEINNNSE SVQNSQEENK IIEEEKKDTI EEQAEDNNDF
 901 LTKLKQMNEE YKKEKEDKKE EENKEEDSNN FLAKLKQMNE EYKREKEEKR KEEIKESNDF
 961 LLKQVNEEYK EENKIEENKI EENKIYEEKK EEQNKEEDNN DFLAKLKQMN EEYKEEEKER
1021 KEEESKKE EKESNDFLAK LKQMNEEYIK EEEEKKTKN
```

Center position: 6 Window size: 12 Threshold: 1.000 Recalculate



Average: 1.000 Minimum: 0.015 Maximum: 15.848

MKLNNSNIFDDNNDISLDEYDIDSLVDKNIEINENNFPTVSIGTESPSIHSSIIDDSITSASDENIAIENNNQEASV EAYTEEENKIYNEIES NIGISEDDLNIISDVDDFNLENHFQNVNNDETVEAYTEEENRIYNEIENNVGI
SEDDLNAISDVDDFNLESFFANSAPSIEDTAENDSNNNEDTISIDEISEDNTNDV NNETVEAYTEEENRAYNEIESNVGISEDDLNAISDVDDFNLESFFANSTPIIEDSSNNATSINNEEAANEISE TNDNLENNNDIAENIEEN
NDIAIDDNITEENDTTFETTVNDEINNALD NYLEAENSNSNDNNDIAENIEENNDIAIDDNITEENDTTFETTVNDKINNALNNYLESESFENNNDNLENTEIRENIDTDIINNETNNDEVIDELEKL DDLVENLDNT EYIEDNNN
NNIADI VSQGLAEIENIEYAENSSLQNDDSVVEIIDEESYINENNANINKENDTTFETTINDEINNALDNYLEAESFENNNDNLENTEIKENIDT DIINNETNNDEVIDELEKLDDLVENLDNTEYDNNNIADIVSQGLAEIENIE
YAENNSLKSDDNIIKIVDDNNDDVAAMVSEGLDEIENIEHSLDNDDKNITTENIHNIDVPDIDDVDYIDESNYINENNNQDDIIELSGNELDLITKDENIEYKYIQNNNKEYMDMNKIK KDIEELEIDELSNEENSIYNNQISDAD
NNEVYELTDAEVNMYKEYIENNELDENELSNEEIDMYKSYIEGKEYTNIKEEESINNLEGIDKKEDINDLTDEEVNMYKEYIDRDD SEDKTDELTDEEELMYKAYIENSSSDTSIENESNKTSDDLLSTEYKEEINNNSESVQNSQ
EENKIIEEEKKDTIEEQAEDNNDFLTKLKQMNEEYKKEKEDKKEEENKEEDSNNFLAKLKQMNEEYKREKEEKRKEEIKESNDFLLKQVNEEYKEENKIEENKIEENKIYEEKKEEQNKEEDNNDFLAKLKQMNEEYKEEEKERKE
EESKKEEKESNDFLAKLKQMNEEYIKEEEEKKTKN



ABCpred Prediction Server

Threshold: 0.85 **Window: 14**

INPUT INFORMATION

Sequence name	
Length of the sequence	1057
Number of 14mers from the input sequence	1044
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

**The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.**

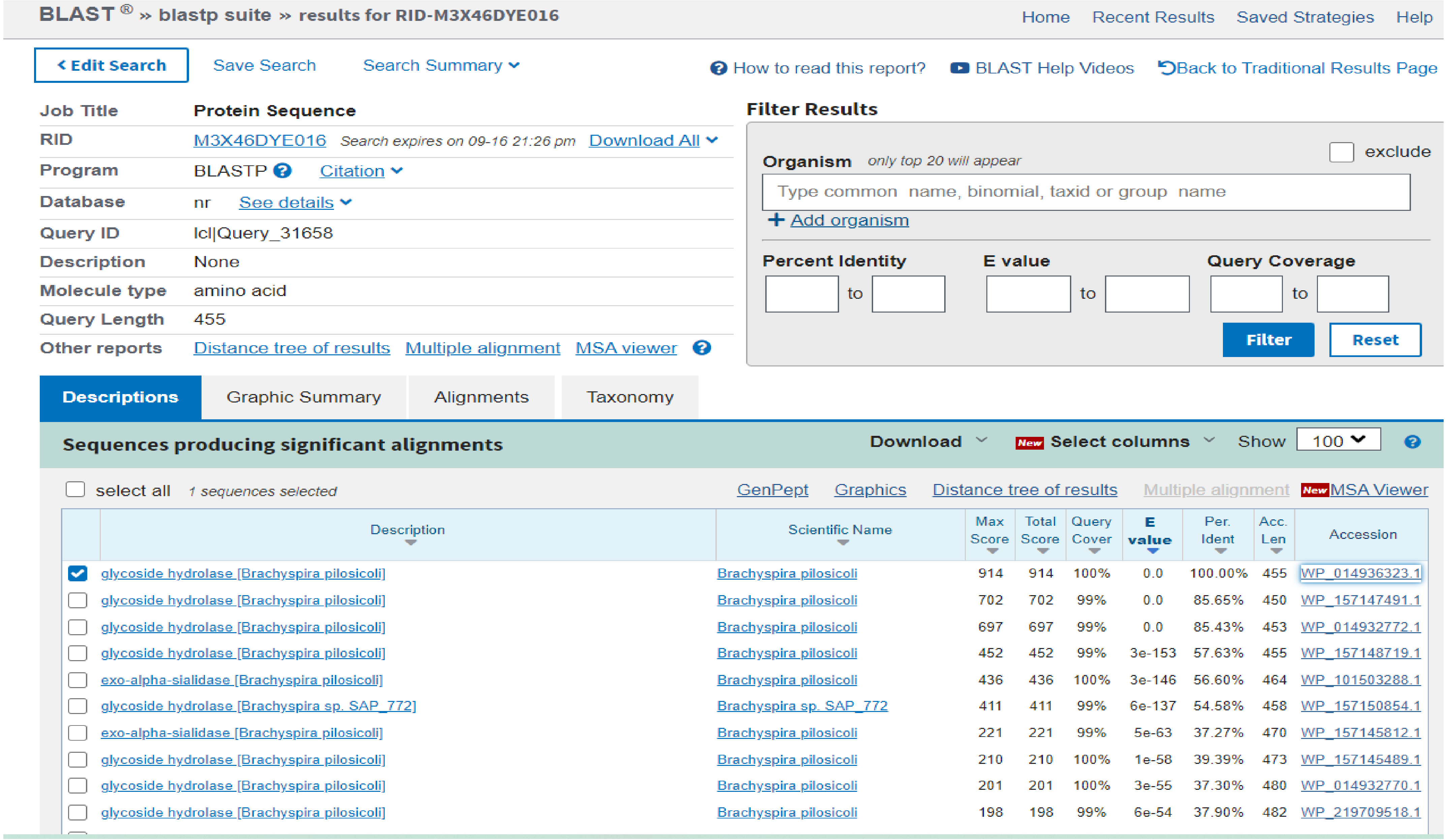
Rank	Sequence	Start position	Score
1	ELEKLDDLVENLDN	548	0.91
1	FETTVNDEINNALD	309	0.91
1	TSINNEEAANEISE	261	0.91
2	AANEISETNDNLEN	268	0.90
3	DNLENTEIKENIDT	520	0.89
3	QNVNNDETVEAYTE	118	0.89
4	YTEEENKIYNEIES	80	0.88
4	ENIAIENNNQEASV	64	0.88
5	QNNNKEYMDMNKIK	690	0.87
6	EEVNMYKEYIDRDD	803	0.86
6	ISIDEISEDNTNDV	188	0.86
6	DTAENDSNNNEDTI	175	0.86
7	EYIEDNNNNNIADI	431	0.85

PROTEINA 1

```
>fig|6666666.171271.peg.2319
MKLNNSNIFDDNNDISLDEYDIDSLVDKNIEINENNFPTVSIGTESPSIHSSIIDDSITSASDENIAIENNNQEASV EAY
TEEENKIYNEIES NIGISEDDLNIISDVDDFNLENHFQNVNNDETVEAYTEEENRIYNEIENNVGISEDDLNAISDVDDF
NLESFFANSAPSIEDTAENDSNNNEDTISIDEISEDNTNDV NNETVEAYTEEENRAYNEIESNVGISEDDLNAISDVDDF
NLESFFANSTPIIEDSSNNATSINNEEAANEISE TNDNLENNNDIAENIEENNDIAIDDNITEENDTTFETTVNDEINNA
LD NYLEAENSNSNDNNDIAENIEENNDIAIDDNITEENDTTFETTVNDKINNALNNYLESESFENNNDNLENTEIRENID
TDIINNETNNDEVIDELEKLDDLVENLDNTEYIEDNNNNNIADI VSQGLAEIENIEYAENSSLQNDDSVVEIIDEESYIN
ENNANINKENDTTFETTINDEINNALDNYLEAESFENNNDNLENTEIKENIDT DIINNETNNDEVIDELEKLDDLVENLD
NTEYDNNNIADIVSQGLAEIENIEYAENNSLKSDDNIIKIVDDNNDDVAAMVSEGLDEIENIEHSLDNDDKNITTENIHN
IDVPDIDDVDYIDESNYINENNNQDDIIELSGNELDLITKDENIEYKYIQNNNKEYMDMNKIK KDIEELEIDELSNEENS
IYNNQISDADNNEVYELTDAEVNMYKEYIENNELDENELSNEEIDMYKSYIEGKEYTNIKEEESINNLEGIDKKEDINDL
TDEEVNMYKEYIDRDDSEDKTDELTDEEELMYKAYIENSSSDTSIENESNKTSDDLLSTEYKEEINNNSESVQNSQEENK
IIEEEKKDTIEEQAEDNNDFLTKLKQMNEEYKKEKEDKKEEENKEEDSNNFLAKLKQMNEEYKREKEEKRKEEIKESNDF
LLKQVNEEYKEENKIEENKIEENKIYEEKKEEQNKEEDNNDFLAKLKQMNEEYKEEEKERKEEESKKEEKESNDFLAKLK
QMNEEYIKEEEEKKTKN
```

PROTEINA 2

```
>fig|6666666.171271.peg.1802
MSKKIIYLLSLLMALSLVFAGCKKASTAPGGEGPTKEDEVKPPTNLGGTGLFTDSGELDKYKGDPIQKSTEVAKYENGNYMRNP
VITVVGGSTVVVFYEIRYQTAGAGNDVALTGENAVSIAYVQSKDSGISFSTTGMGEIKYVGGAASSGAADAHGAPIVFNTGDKI
IVVASAGIGLSSGVYNGNDKVSKLQYSVATITGNTVGEFGAWKDIVPEDKGTITTAGYTQFGTHSARGTVADDGTLLLPVTLAN
YQQSPSKFGYVLYTGTVNGDKVTWTQKGNKVDMPNSSGVVKETRIPKGTSESDYVYLAVSSDTVRISQGKGANSISSANIQGSD
GSVGTLVVPNWQGAASYDPSNYATNSGTKQAILSHVLGTEQNLAIRLVDENFASQTSGNFALGGAYEANAKSSSMDVLKDGTIV
MIAEGGKVTDAATRPFYIYFSRFSQAYIASKTSGK
```



Job Title	**Protein Sequence**
RID	M3X46DYE016 *Search expires on 09-16 21:26 pm* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_31658
Description	None
Molecule type	amino acid
Query Length	455
Other reports	Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism *only top 20 will appear* ☐ exclude

Type common name, binomial, taxid or group name

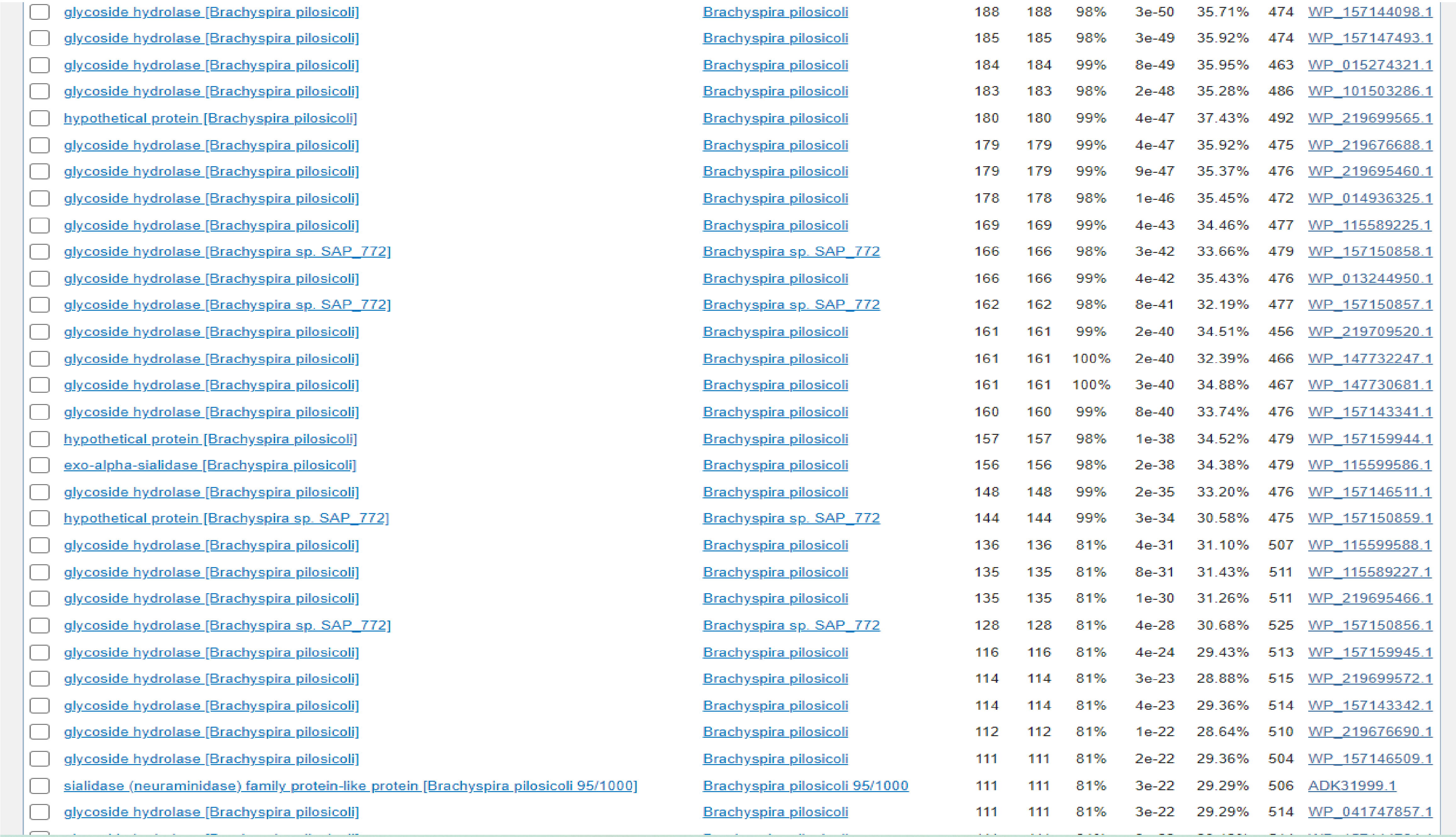
+ Add organism

Percent Identity ☐ to ☐ **E value** ☐ to ☐ **Query Coverage** ☐ to ☐

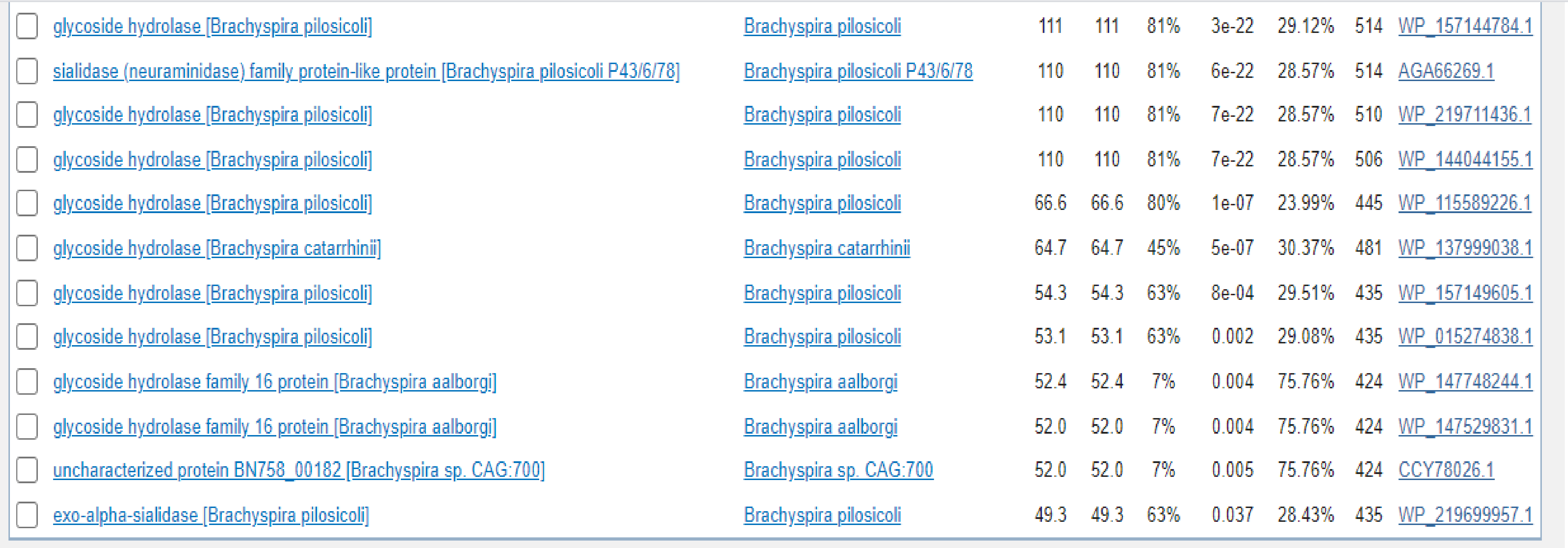
Sequences producing significant alignments

☐ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	914	914	100%	0.0	100.00%	455	WP_014936323.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	702	702	99%	0.0	85.65%	450	WP_157147491.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	697	697	99%	0.0	85.43%	453	WP_014932772.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	452	452	99%	3e-153	57.63%	455	WP_157148719.1
☐	exo-alpha-sialidase [Brachyspira pilosicoli]	Brachyspira pilosicoli	436	436	100%	3e-146	56.60%	464	WP_101503288.1
☐	glycoside hydrolase [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	411	411	99%	6e-137	54.58%	458	WP_157150854.1
☐	exo-alpha-sialidase [Brachyspira pilosicoli]	Brachyspira pilosicoli	221	221	99%	5e-63	37.27%	470	WP_157145812.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	210	210	100%	1e-58	39.39%	473	WP_157145489.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	201	201	100%	3e-55	37.30%	480	WP_014932770.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	198	198	99%	6e-54	37.90%	482	WP_219709518.1

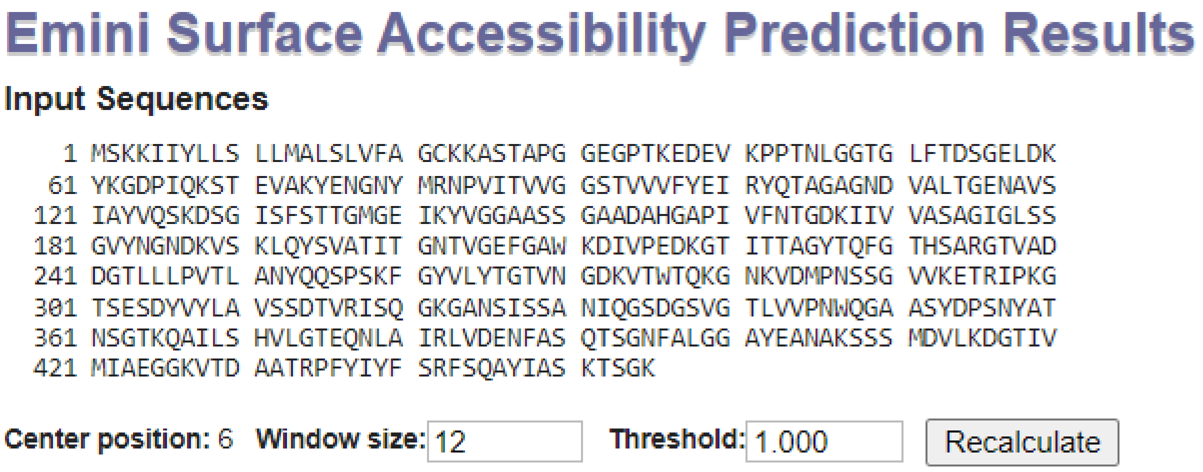


☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	188	188	98%	3e-50	35.71%	474	WP_157144098.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	185	185	98%	3e-49	35.92%	474	WP_157147493.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	184	184	99%	8e-49	35.95%	463	WP_015274321.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	183	183	98%	2e-48	35.28%	486	WP_101503286.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	180	180	99%	4e-47	37.43%	492	WP_219699565.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	179	179	99%	4e-47	35.92%	475	WP_219676688.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	179	179	99%	9e-47	35.37%	476	WP_219695460.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	178	178	98%	1e-46	35.45%	472	WP_014936325.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	169	169	99%	4e-43	34.46%	477	WP_115589225.1
☐	glycoside hydrolase [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	166	166	98%	3e-42	33.66%	479	WP_157150858.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	166	166	99%	4e-42	35.43%	476	WP_013244950.1
☐	glycoside hydrolase [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	162	162	98%	8e-41	32.19%	477	WP_157150857.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	161	161	99%	2e-40	34.51%	456	WP_219709520.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	161	161	100%	2e-40	32.39%	466	WP_147732247.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	161	161	100%	3e-40	34.88%	467	WP_147730681.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	160	160	99%	8e-40	33.74%	476	WP_157143341.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	157	157	98%	1e-38	34.52%	479	WP_157159944.1
☐	exo-alpha-sialidase [Brachyspira pilosicoli]	Brachyspira pilosicoli	156	156	98%	2e-38	34.38%	479	WP_115599586.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	148	148	99%	2e-35	33.20%	476	WP_157146511.1
☐	hypothetical protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	144	144	99%	3e-34	30.58%	475	WP_157150859.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	136	136	81%	4e-31	31.10%	507	WP_115599588.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	135	135	81%	8e-31	31.43%	511	WP_115589227.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	135	135	81%	1e-30	31.26%	511	WP_219695466.1
☐	glycoside hydrolase [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	128	128	81%	4e-28	30.68%	525	WP_157150856.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	116	116	81%	4e-24	29.43%	513	WP_157159945.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	114	114	81%	3e-23	28.88%	515	WP_219699572.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	114	114	81%	4e-23	29.36%	514	WP_157143342.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	112	112	81%	1e-22	28.64%	510	WP_219676690.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	111	111	81%	2e-22	29.36%	504	WP_157146509.1
☐	sialidase (neuraminidase) family protein-like protein [Brachyspira pilosicoli 95/1000]	Brachyspira pilosicoli 95/1000	111	111	81%	3e-22	29.29%	506	ADK31999.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	111	111	81%	3e-22	29.29%	514	WP_041747857.1



☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	111	111	81%	3e-22	29.12%	514	WP_157144784.1
☐	sialidase (neuraminidase) family protein-like protein [Brachyspira pilosicoli P43/6/78]	Brachyspira pilosicoli P43/6/78	110	110	81%	6e-22	28.57%	514	AGA66269.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	110	110	81%	7e-22	28.57%	510	WP_219711436.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	110	110	81%	7e-22	28.57%	506	WP_144044155.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	66.6	66.6	80%	1e-07	23.99%	445	WP_115589226.1
☐	glycoside hydrolase [Brachyspira catarrhinii]	Brachyspira catarrhinii	64.7	64.7	45%	5e-07	30.37%	481	WP_137999038.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	54.3	54.3	63%	8e-04	29.51%	435	WP_157149605.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	53.1	53.1	63%	0.002	29.08%	435	WP_015274838.1
☐	glycoside hydrolase family 16 protein [Brachyspira aalborgi]	Brachyspira aalborgi	52.4	52.4	7%	0.004	75.76%	424	WP_147748244.1
☐	glycoside hydrolase family 16 protein [Brachyspira aalborgi]	Brachyspira aalborgi	52.0	52.0	7%	0.004	75.76%	424	WP_147529831.1
☐	uncharacterized protein BN758_00182 [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	52.0	52.0	7%	0.005	75.76%	424	CCY78026.1
☐	exo-alpha-sialidase [Brachyspira pilosicoli]	Brachyspira pilosicoli	49.3	49.3	63%	0.037	28.43%	435	WP_219699957.1

Threshold: 1.000 **Window: 12**

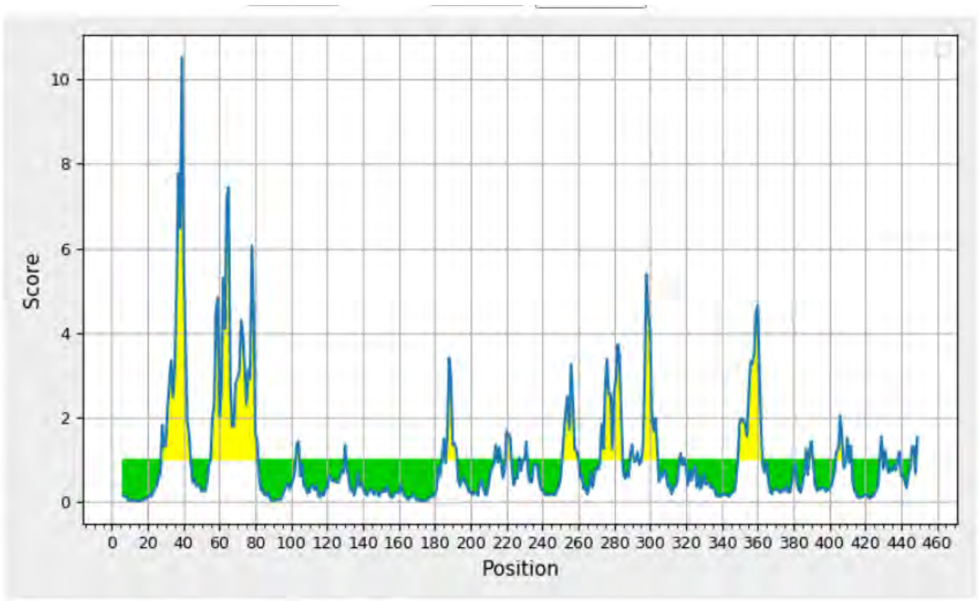


Emini Surface Accessibility Prediction Results

Input Sequences

```
  1 MSKKIIYLLS LLMALSLVFA GCKKASTAPG GEGPTKEDEV KPPTNLGGTG LFTDSGELDK
 61 YKGDPIQKST EVAKYENGNY MRNPVITVVG GSTVVVFYEI RYQTAGAGND VALTGENAVS
121 IAYVQSKDSG ISFSTTGMGE IKYVGGAASS GAADAHGAPI VFNTGDKIIV VASAGIGLSS
181 GVYNGNDKVS KLQYSVATIT GNTVGEFGAW KDIVPEDKGT ITTAGYTQFG THSARGTVAD
241 DGTLLLPVTL ANYQQSPSKF GYVLYTGTVN GDKVTWTQKG NKVDMPNSSG VVKETRIPKG
301 TSESDYVYLA VSSDTVRISQ GKGANSISSA NIQGSDGSVG TLVVPNWQGA ASYDPSNYAT
361 NSGTKQAILS HVLGTEQNLA IRLVDENFAS QTSGNFALGG AYEANAKSSS MDVLKDGTIV
421 MIAEGGKVTD AATRPFYIYF SRFSQAYIAS KTSGK
```

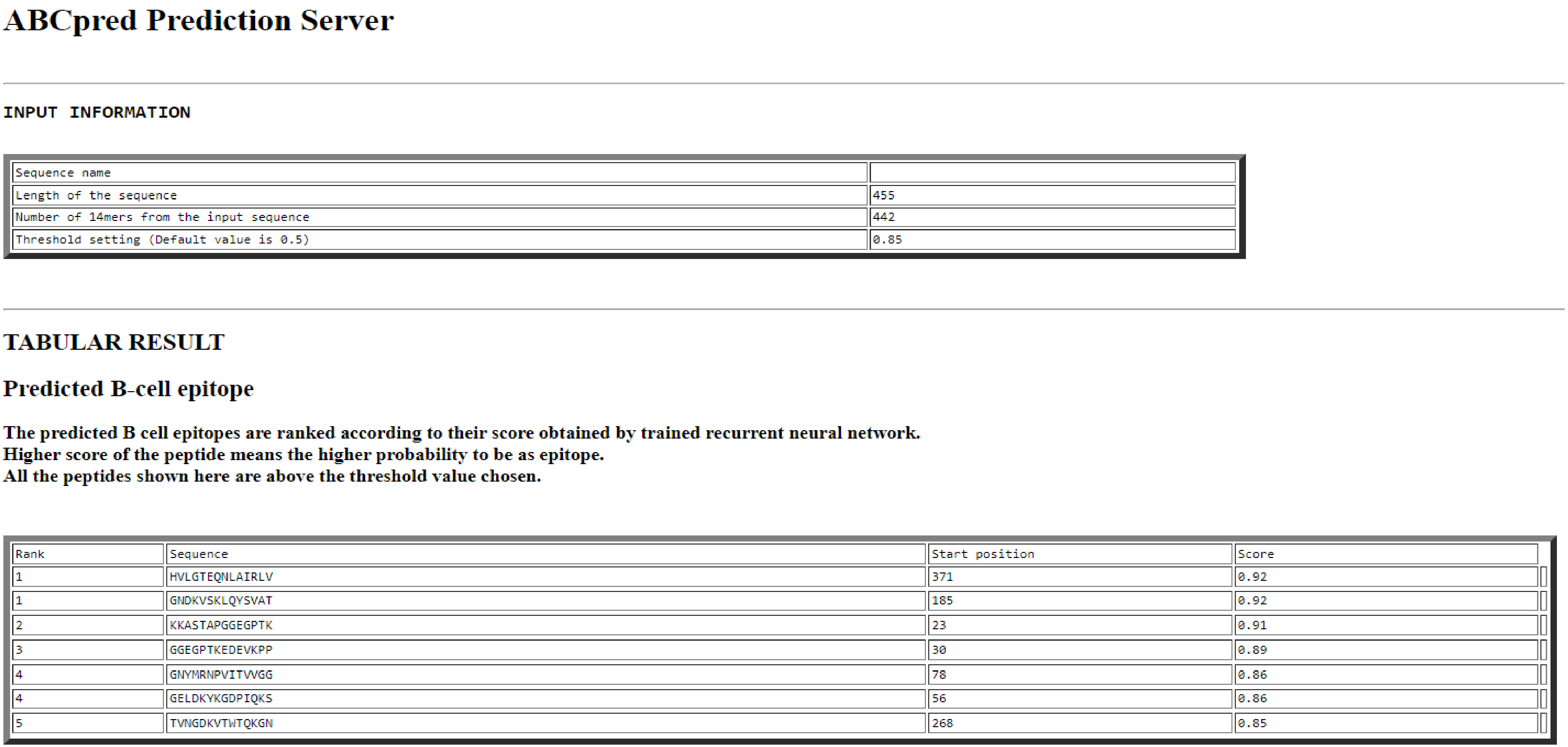
Center position: 6 **Window size:** 12 **Threshold:** 1.000



Average: 1.000 **Minimum:** 0.012 **Maximum:** 10.528

MSKKIIYLLSLLMALSLVFAGCKKASTAPGGEGPTKEDEVKPPTNLGGTGLFTDSGELDKYKGDPIQKSTEVAKYENGNYMRNP
VITVVGGSTVVVFYEIRYQTAGAGNDVALTGENAVSIAYVQSKDSGISFSTTGMGEIKYVGGAASSGAADAHGAPIVFNTGDKI
IVVASAGIGLSSGVYNGNDKVSKLQYSVATITGNTVGEFGAWKDIVPEDKGTITTAGYTQFGTHSARGTVADDGTLLLPVTLAN
YQQSPSKFGYVLYTGTVNGDKVTWTQKGNKVDMPNSSGVVKETRIPKGTSESDYVYLAVSSDTVRISQGKGANSISSANIQGSD
GSVGTLVVPNWQGAASYDPSNYATNSGTKQAILSHVLGTEQNLAIRLVDENFASQTSGNFALGGAYEANAKSSSMDVLKDGTIV
MIAEGGKVTDAATRPFYIYFSRFSQAYIASKTSGK

Threshold: 0.85 Window: 14



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	455
Number of 14mers from the input sequence	442
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

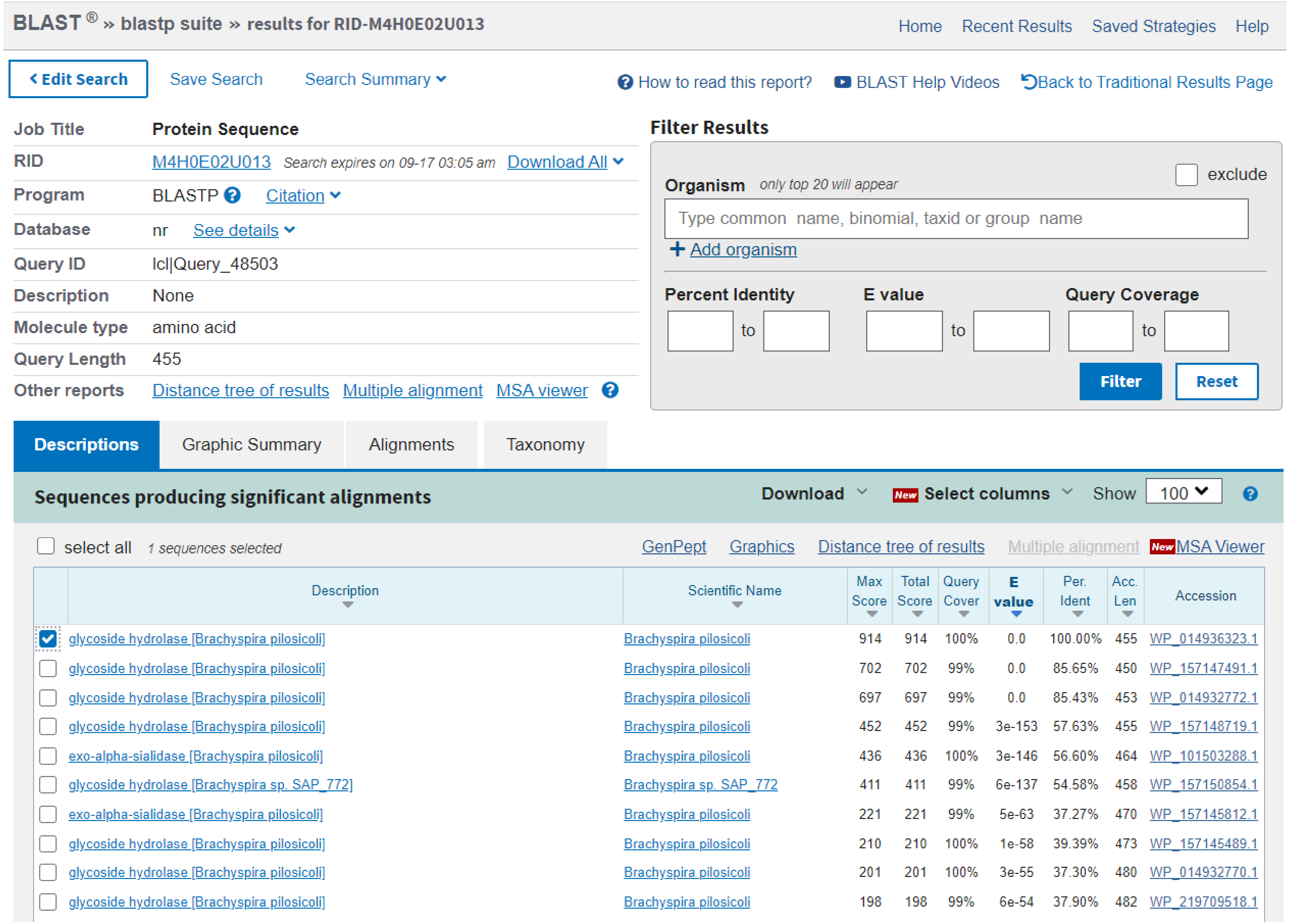
Rank	Sequence	Start position	Score
1	HVLGTEQNLAIRLV	371	0.92
1	GNDKVSKLQYSVAT	185	0.92
2	KKASTAPGGEGPTK	23	0.91
3	GGEGPTKEDEVKPP	30	0.89
4	GNYMRNPVITVVGG	78	0.86
4	GELDKYKGDPIQKS	56	0.86
5	TVNGDKVTWTQKGN	268	0.85

PROTEINA 2

```
>fig|6666666.171271.peg.1802
MSKKIIYLLSLLMALSLVFAGCKKASTAPGGEGPTKEDEVKPPTNLGGTGLFTDSGELDKYKGDPIQKSTEVAKYENGNYMRNP
VITVVGGSTVVVFYEIRYQTAGAGNDVALTGENAVSIAYVQSKDSGISFSTTGMGEIKYVGGAASSGAADAHGAPIVFNTGDKI
IVVASAGIGLSSGVYNGNDKVSKLQYSVATITGNTVGEFGAWKDIVPEDKGTITTAGYTQFGTHSARGTVADDGTLLLPVTLAN
YQQSPSKFGYVLYTGTVNGDKVTWTQKGNKVDMPNSSGVVKETRIPKGTSESDYVYLAVSSDTVRISQGKGANSISSANIQGSD
GSVGTLVVPNWQGAASYDPSNYATNSGTKQAILSHVLGTEQNLAIRLVDENFASQTSGNFALGGAYEANAKSSSMDVLKDGTIV
MIAEGGKVTDAATRPFYIYFSRFSQAYIASKTSGK
```

PROTEINA 3

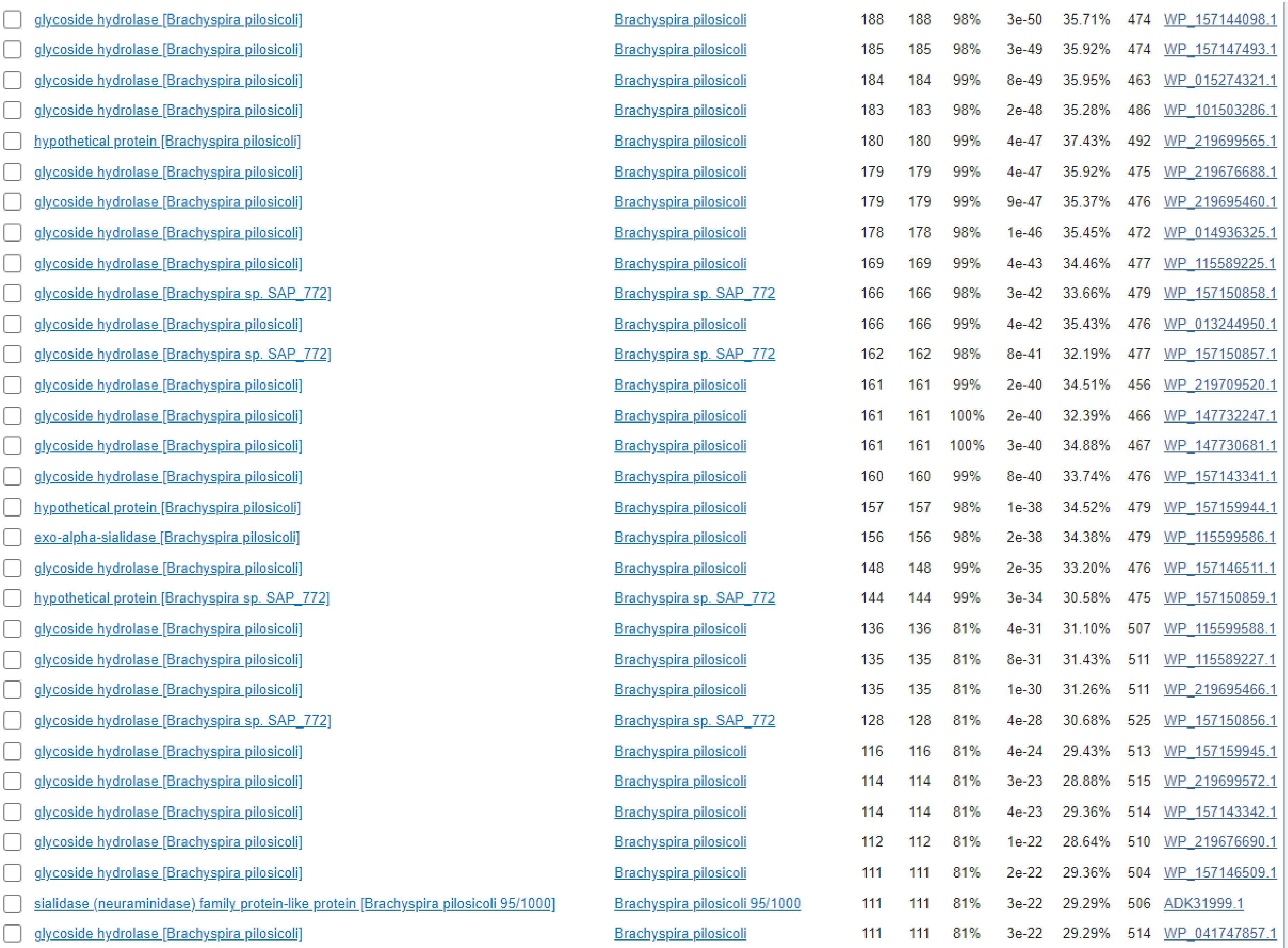
```
>fig|6666666.171271.peg.1804
MSKKIIYLLSLLMALSLVFASCKKNNGLDPNNGGLEPPKEEDNTAGKIDAETGLVTDDQVSSLPADKPLKKVTIFKGDANNY
LRNPVVVVMGTDRSTPVVFAEKRYNGPGAANDVGIDGKATVDVVYKVGAQSGQNFGAETIVSRGATGPNDSHGAPVVFKVGD
NQVVVVASAGAGIARTEEAASAKAASKIEYAVGTLSGTTFTWDTPWTELKVNNQSLLDTIKTIKTGNNSDNFEQMGTQAARG
YVGIDNKTLILPVVMAQQGTTSSVKELMGVYFVKGTVSGNTVNWQNLGTDARVVFTAKTDSNFSTHKESQVIAGTSDSDVKY
VAVPSPWGSPVTDNYGLGTGKTDQPKATQIKGHDGAPGYLAFKWFGATSYQASTYKDQAADAGLFLGPKNNAANITLYLVNK
DTLNKEGKADGFELNAIGKSGSIDVLGDGTVVTAAEEGNNGDRNYYTSFTRYSQSYLASILQ
```



Job Title	**Protein Sequence**
RID	M4H0E02U013 *Search expires on 09-17 03:05 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_48503
Description	None
Molecule type	amino acid
Query Length	455
Other reports	Distance tree of results Multiple alignment MSA viewer

Sequences producing significant alignments

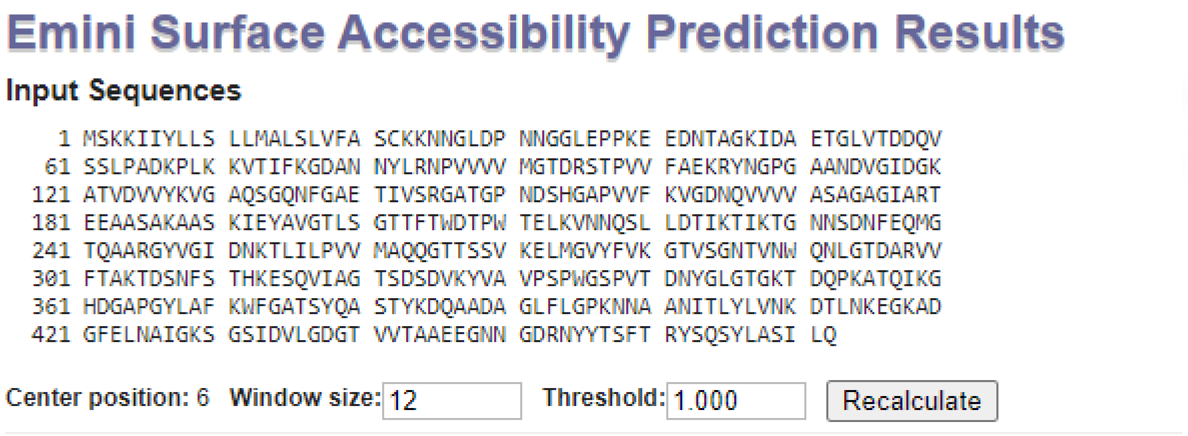
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	914	914	100%	0.0	100.00%	455	WP_014936323.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	702	702	99%	0.0	85.65%	450	WP_157147491.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	697	697	99%	0.0	85.43%	453	WP_014932772.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	452	452	99%	3e-153	57.63%	455	WP_157148719.1
☐	exo-alpha-sialidase [Brachyspira pilosicoli]	Brachyspira pilosicoli	436	436	100%	3e-146	56.60%	464	WP_101503288.1
☐	glycoside hydrolase [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	411	411	99%	6e-137	54.58%	458	WP_157150854.1
☐	exo-alpha-sialidase [Brachyspira pilosicoli]	Brachyspira pilosicoli	221	221	99%	5e-63	37.27%	470	WP_157145812.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	210	210	100%	1e-58	39.39%	473	WP_157145489.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	201	201	100%	3e-55	37.30%	480	WP_014932770.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	198	198	99%	6e-54	37.90%	482	WP_219709518.1



☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	188	188	98%	3e-50	35.71%	474	WP_157144098.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	185	185	98%	3e-49	35.92%	474	WP_157147493.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	184	184	99%	8e-49	35.95%	463	WP_015274321.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	183	183	98%	2e-48	35.28%	486	WP_101503286.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	180	180	99%	4e-47	37.43%	492	WP_219699565.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	179	179	99%	4e-47	35.92%	475	WP_219676688.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	179	179	99%	9e-47	35.37%	476	WP_219695460.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	178	178	98%	1e-46	35.45%	472	WP_014936325.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	169	169	99%	4e-43	34.46%	477	WP_115589225.1
☐	glycoside hydrolase [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	166	166	98%	3e-42	33.66%	479	WP_157150858.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	166	166	99%	4e-42	35.43%	476	WP_013244950.1
☐	glycoside hydrolase [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	162	162	98%	8e-41	32.19%	477	WP_157150857.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	161	161	99%	2e-40	34.51%	456	WP_219709520.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	161	161	100%	2e-40	32.39%	466	WP_147732247.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	161	161	100%	3e-40	34.88%	467	WP_147730681.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	160	160	99%	8e-40	33.74%	476	WP_157143341.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	157	157	98%	1e-38	34.52%	479	WP_157159944.1
☐	exo-alpha-sialidase [Brachyspira pilosicoli]	Brachyspira pilosicoli	156	156	98%	2e-38	34.38%	479	WP_115599586.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	148	148	99%	2e-35	33.20%	476	WP_157146511.1
☐	hypothetical protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	144	144	99%	3e-34	30.58%	475	WP_157150859.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	136	136	81%	4e-31	31.10%	507	WP_115599588.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	135	135	81%	8e-31	31.43%	511	WP_115589227.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	135	135	81%	1e-30	31.26%	511	WP_219695466.1
☐	glycoside hydrolase [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	128	128	81%	4e-28	30.68%	525	WP_157150856.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	116	116	81%	4e-24	29.43%	513	WP_157159945.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	114	114	81%	3e-23	28.88%	515	WP_219699572.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	114	114	81%	4e-23	29.36%	514	WP_157143342.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	112	112	81%	1e-22	28.64%	510	WP_219676690.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	111	111	81%	2e-22	29.36%	504	WP_157146509.1
☐	sialidase (neuraminidase) family protein-like protein [Brachyspira pilosicoli 95/1000]	Brachyspira pilosicoli 95/1000	111	111	81%	3e-22	29.29%	506	ADK31999.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	111	111	81%	3e-22	29.29%	514	WP_041747857.1

☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	111	111	81%	3e-22	29.12%	514	WP_157144784.1
☐	sialidase (neuraminidase) family protein-like protein [Brachyspira pilosicoli P43/6/78]	Brachyspira pilosicoli P43/6/78	110	110	81%	6e-22	28.57%	514	AGA66269.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	110	110	81%	7e-22	28.57%	510	WP_219711436.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	110	110	81%	7e-22	28.57%	506	WP_144044155.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	66.6	66.6	80%	1e-07	23.99%	445	WP_115589226.1
☐	glycoside hydrolase [Brachyspira catarrhinii]	Brachyspira catarrhinii	64.7	64.7	45%	5e-07	30.37%	481	WP_137999038.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	54.3	54.3	63%	8e-04	29.51%	435	WP_157149605.1
☐	glycoside hydrolase [Brachyspira pilosicoli]	Brachyspira pilosicoli	53.1	53.1	63%	0.002	29.08%	435	WP_015274838.1
☐	glycoside hydrolase family 16 protein [Brachyspira aalborgi]	Brachyspira aalborgi	52.4	52.4	7%	0.004	75.76%	424	WP_147748244.1
☐	glycoside hydrolase family 16 protein [Brachyspira aalborgi]	Brachyspira aalborgi	52.0	52.0	7%	0.004	75.76%	424	WP_147529831.1
☐	uncharacterized protein BN758_00182 [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	52.0	52.0	7%	0.005	75.76%	424	CCY78026.1
☐	exo-alpha-sialidase [Brachyspira pilosicoli]	Brachyspira pilosicoli	49.3	49.3	63%	0.037	28.43%	435	WP_219699957.1

Threshold: 1.000 Window: 12

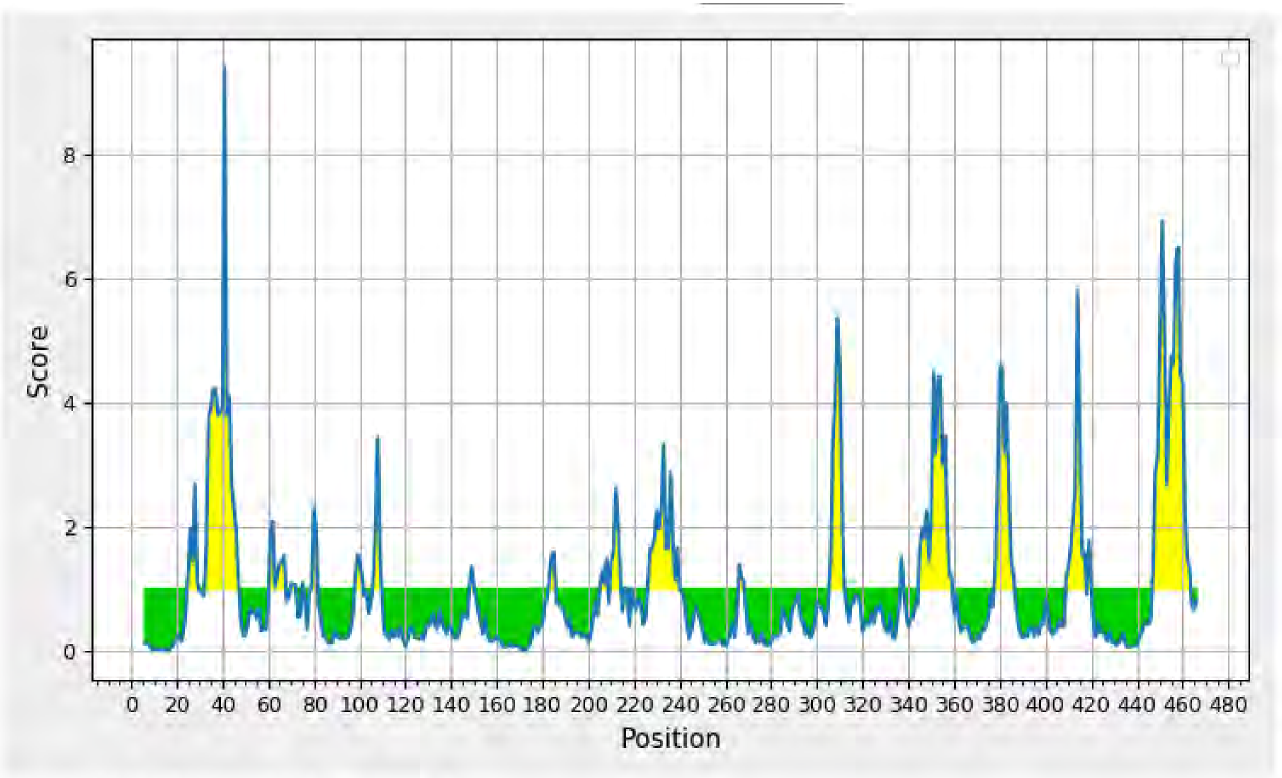


Emini Surface Accessibility Prediction Results

Input Sequences

```
  1 MSKKIIYLLS LLMALSLVFA SCKKNNGLDP NNGGLEPPKE EDNTAGKIDA ETGLVTDDQV
 61 SSLPADKPLK KVTIFKGDAN NYLRNPVVVV MGTDRSTPVV FAEKRYNGPG AANDVGIDGK
121 ATVDVVYKVG AQSGQNFGAE TIVSRGATGP NDSHGAPVVF KVGDNQVVVV ASAGAGIART
181 EEAASAKAAS KIEYAVGTLS GTTFTWDTPW TELKVNNQSL LDTIKTIKTG NNSDNFEQMG
241 TQAARGYVGI DNKTLILPVV MAQQGTTSSV KELMGVYFVK GTVSGNTVNW QNLGTDARVV
301 FTAKTDSNFS THKESQVIAG TSDSDVKYVA VPSPWGSPVT DNYGLGTGKT DQPKATQIKG
361 HDGAPGYLAF KWFGATSYQA STYKDQAADA GLFLGPKNNA ANITLYLVNK DTLNKEGKAD
421 GFELNAIGKS GSIDVLGDGT VVTAAEEGNN GDRNYYTSFT RYSQSYLASI LQ
```

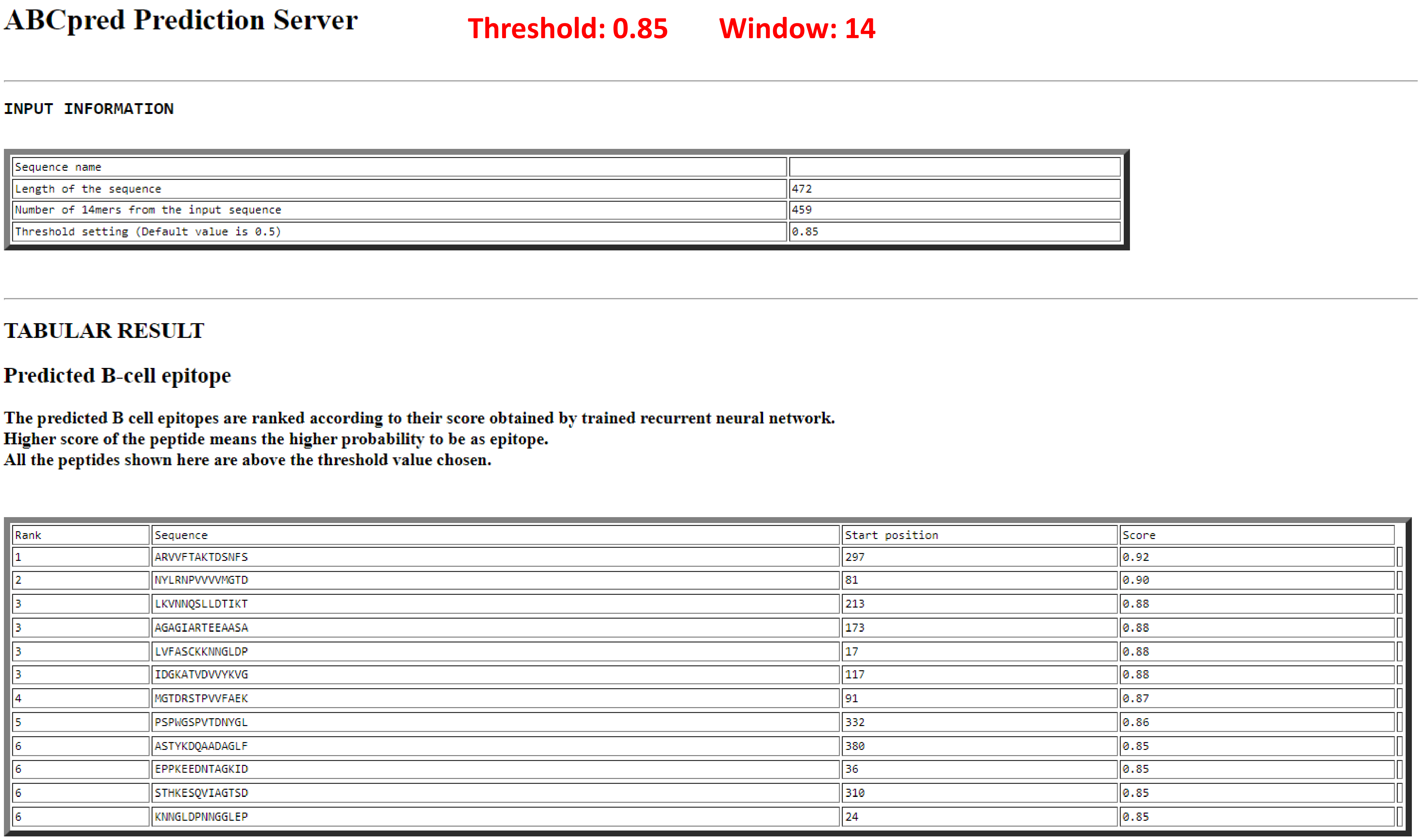
Center position: 6 Window size: 12 Threshold: 1.000



Average: 1.000 Minimum: 0.014 Maximum: 9.386

MSKKIIYLLSLLMALSLVFASCKKNNGLDPNNGGLEPPKEEDNTAGKIDAETGLVTDDQVSSLPADKPLKKVTIFKGDANNYLRNPV
VVVMGTDRSTPVVFAEKRYNGPGAANDVGIDGKATVDVVYKVGAQSGQNFGAETIVSRGATGPNDSHGAPVVFKVGDNQVVVVASAG
AGIARTEEAASAKAASKIEYAVGTLSGTTFTWDTPWTELKVNNQSLLDTIKTIKTGNNSDNFEQMGTQAARGYVGIDNKTLILPVVM
AQQGTTSSVKELMGVYFVKGTVSGNTVNWQNLGTDARVVFTAKTDSNFSTHKESQVIAGTSDSDVKYVAVPSPWGSPVTDNYGLGTG
KTDQPKATQIKGHDGAPGYLAFKWFGATSYQASTYKDQAADAGLFLGPKNNAANITLYLVNKDTLNKEGKADGFELNAIGKSGSIDV
LGDGTVVTAAEEGNNGDRNYYTSFTRYSQSYLASILQ

Threshold: 0.85   Window: 14



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	472
Number of 14mers from the input sequence	459
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

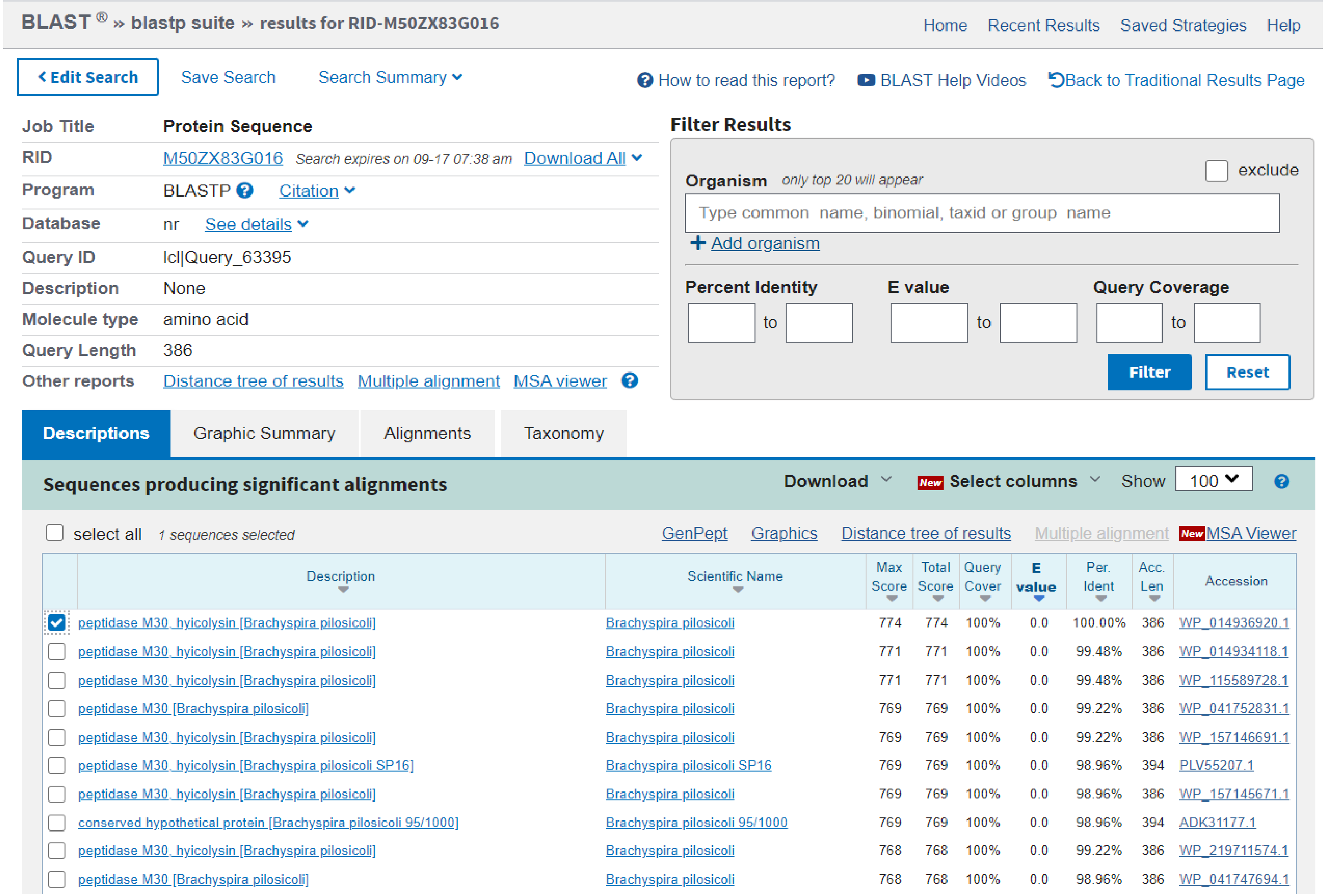
Rank	Sequence	Start position	Score
1	ARVVFTAKTDSNFS	297	0.92
2	NYLRNPVVVVMGTD	81	0.90
3	LKVNNQSLLDTIKT	213	0.88
3	AGAGIARTEEAASA	173	0.88
3	LVFASCKKNNGLDP	17	0.88
3	IDGKATVDVVYKVG	117	0.88
4	MGTDRSTPVVFAEK	91	0.87
5	PSPWGSPVTDNYGL	332	0.86
6	ASTYKDQAADAGLF	380	0.85
6	EPPKEEDNTAGKID	36	0.85
6	STHKESQVIAGTSD	310	0.85
6	KNNGLDPNNGGLEP	24	0.85

PROTEINA 3

```
>fig|6666666.171271.peg.1804
MSKKIIYLLSLLMALSLVFASCKKNNGLDPNNGGLEPPKEEDNTAGKIDAETGLVTDDQVSSLPADKPLKKVTIFKGDANNYLRNP
VVVVMGTDRSTPVVFAEKRYNGPGAANDVGIDGKATVDVVYKVGAQSGQNFGAETIVSRGATGPNDSHGAPVVFKVGDNQVVVVAS
AGAGIARTEEAASAKAASKIEYAVGTLSGTTFTWDTPWTELKVNNQSLLDTIKTIKTGNNSDNFEQMGTQAARGYVGIDNKTLILP
VVMAQQGTTSSVKELMGVYFVKGTVSGNTVNWQNLGTDARVVFTAKTDSNFSTHKESQVIAGTSDSDVKYVAVPSPWGSPVTDNYG
LGTGKTDQPKATQIKGHDGAPGYLAFKWFGATSYQASTYKDQAADAGLFLGPKNNAANITLYLVNKDTLNKEGKADGFELNAIGK
SGSIDVLGDGTVVTAAEEGNNGDRNYYTSFTRYSQSYLASILQ
```

PROTEINA 4

```
>fig|6666666.171271.peg.2646
MMKKIFVLILMSLNTLILNANINSILNQNKTYEIYKADYKEKTFNAVRYINNNYSKDKIKAKNIYSTSSIDVYLENGLTVDE
KILKEILSQTMKAYELEKYLYGDIKTKLILLIMDINGGHTGAKPYMQGYSIFEGNYNEIENENKNIIFLDYINGWDNVDSVL
NTIIHELQHIIHYSNLRESKKTDFDVWVDEALSEAAVIAYRGYLPENRLQYYNSDSMYLITKGDYFVNWSSGYTVHKYATVS
LFMYWLAIHSKNGFEIYKDIANAPEEYKHTYKAILYAANKNIKQFKDWSELYATWLEANYKNEASGLYGYKGIINTKPKVIT
ASANFPMSPGAAIYVQGDFFSDDKLLRYVELGNNVYVVYNPDVNAKGKDRYLILNSYY
```

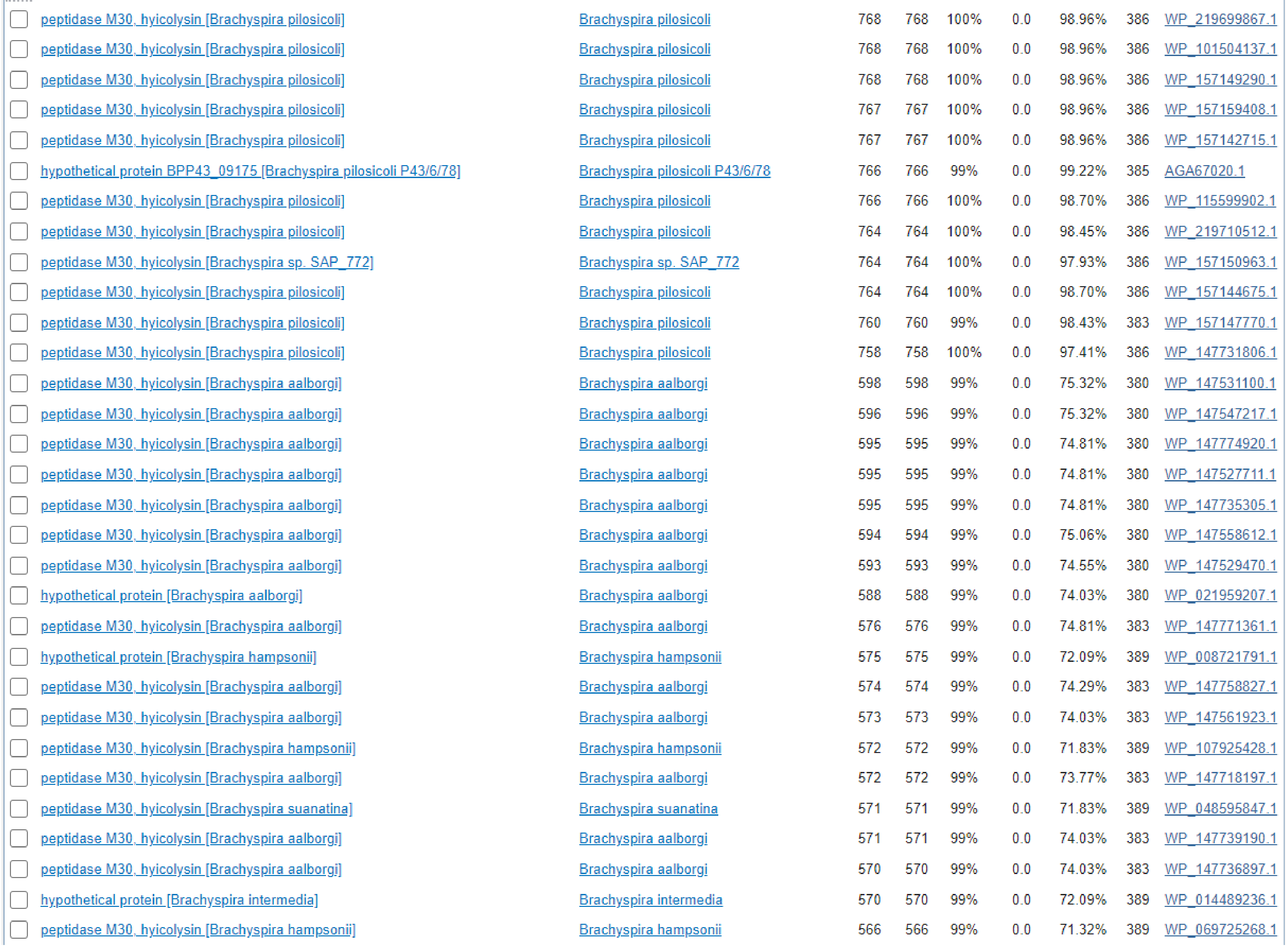


Job Title	**Protein Sequence**
RID	M50ZX83G016 *Search expires on 09-17 07:38 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_63395
Description	None
Molecule type	amino acid
Query Length	386
Other reports	Distance tree of results Multiple alignment MSA viewer

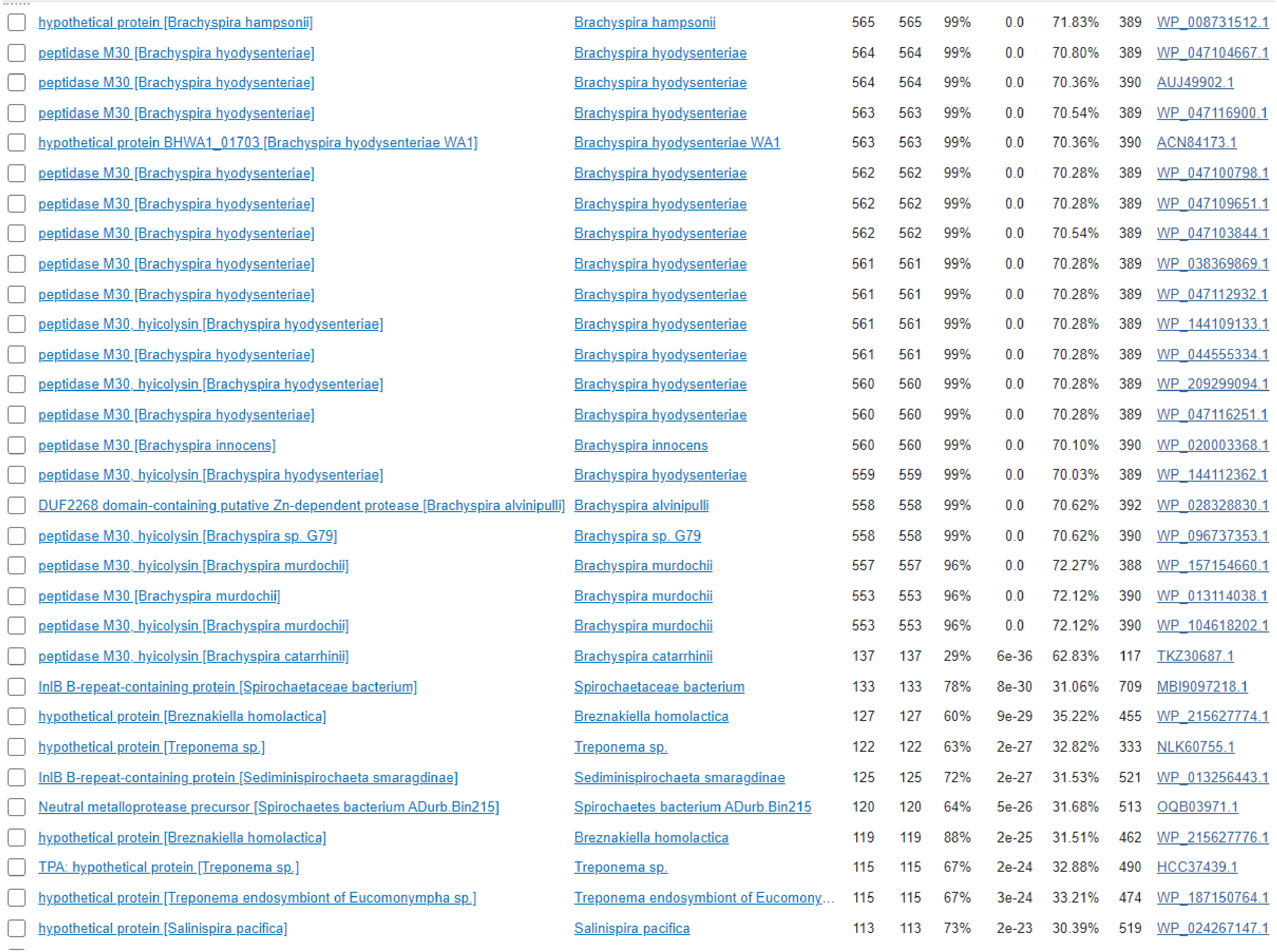
Sequences producing significant alignments

1 sequences selected

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	774	774	100%	0.0	100.00%	386	WP_014936920.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	771	771	100%	0.0	99.48%	386	WP_014934118.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	771	771	100%	0.0	99.48%	386	WP_115589728.1
☐	peptidase M30 [Brachyspira pilosicoli]	Brachyspira pilosicoli	769	769	100%	0.0	99.22%	386	WP_041752831.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	769	769	100%	0.0	99.22%	386	WP_157146691.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli SP16]	Brachyspira pilosicoli SP16	769	769	100%	0.0	98.96%	394	PLV55207.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	769	769	100%	0.0	98.96%	386	WP_157145671.1
☐	conserved hypothetical protein [Brachyspira pilosicoli 95/1000]	Brachyspira pilosicoli 95/1000	769	769	100%	0.0	98.96%	394	ADK31177.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	768	768	100%	0.0	99.22%	386	WP_219711574.1
☐	peptidase M30 [Brachyspira pilosicoli]	Brachyspira pilosicoli	768	768	100%	0.0	98.96%	386	WP_041747694.1



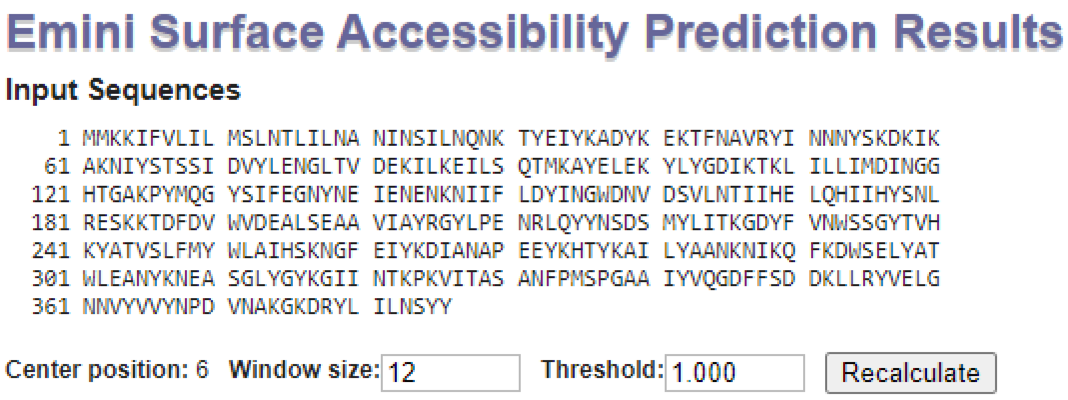
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	768	768	100%	0.0	98.96%	386	WP_219699867.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	768	768	100%	0.0	98.96%	386	WP_101504137.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	768	768	100%	0.0	98.96%	386	WP_157149290.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	767	767	100%	0.0	98.96%	386	WP_157159408.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	767	767	100%	0.0	98.96%	386	WP_157142715.1
☐	hypothetical protein BPP43_09175 [Brachyspira pilosicoli P43/6/78]	Brachyspira pilosicoli P43/6/78	766	766	99%	0.0	99.22%	385	AGA67020.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	766	766	100%	0.0	98.70%	386	WP_115599902.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	764	764	100%	0.0	98.45%	386	WP_219710512.1
☐	peptidase M30, hyicolysin [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	764	764	100%	0.0	97.93%	386	WP_157150963.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	764	764	100%	0.0	98.70%	386	WP_157144675.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	760	760	99%	0.0	98.43%	383	WP_157147770.1
☐	peptidase M30, hyicolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	758	758	100%	0.0	97.41%	386	WP_147731806.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	598	598	99%	0.0	75.32%	380	WP_147531100.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	596	596	99%	0.0	75.32%	380	WP_147547217.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	595	595	99%	0.0	74.81%	380	WP_147774920.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	595	595	99%	0.0	74.81%	380	WP_147527711.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	595	595	99%	0.0	74.81%	380	WP_147735305.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	594	594	99%	0.0	75.06%	380	WP_147558612.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	593	593	99%	0.0	74.55%	380	WP_147529470.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	588	588	99%	0.0	74.03%	380	WP_021959207.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	576	576	99%	0.0	74.81%	383	WP_147771361.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	575	575	99%	0.0	72.09%	389	WP_008721791.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	574	574	99%	0.0	74.29%	383	WP_147758827.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	573	573	99%	0.0	74.03%	383	WP_147561923.1
☐	peptidase M30, hyicolysin [Brachyspira hampsonii]	Brachyspira hampsonii	572	572	99%	0.0	71.83%	389	WP_107925428.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	572	572	99%	0.0	73.77%	383	WP_147718197.1
☐	peptidase M30, hyicolysin [Brachyspira suanatina]	Brachyspira suanatina	571	571	99%	0.0	71.83%	389	WP_048595847.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	571	571	99%	0.0	74.03%	383	WP_147739190.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	570	570	99%	0.0	74.03%	383	WP_147736897.1
☐	hypothetical protein [Brachyspira intermedia]	Brachyspira intermedia	570	570	99%	0.0	72.09%	389	WP_014489236.1
☐	peptidase M30, hyicolysin [Brachyspira hampsonii]	Brachyspira hampsonii	566	566	99%	0.0	71.32%	389	WP_069725268.1



☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	565	565	99%	0.0	71.83%	389	WP_008731512.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	564	564	99%	0.0	70.80%	389	WP_047104667.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	564	564	99%	0.0	70.36%	390	AUJ49902.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	563	563	99%	0.0	70.54%	389	WP_047116900.1
☐	hypothetical protein BHWA1_01703 [Brachyspira hyodysenteriae WA1]	Brachyspira hyodysenteriae WA1	563	563	99%	0.0	70.36%	390	ACN84173.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	562	562	99%	0.0	70.28%	389	WP_047100798.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	562	562	99%	0.0	70.28%	389	WP_047109651.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	562	562	99%	0.0	70.54%	389	WP_047103844.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	561	561	99%	0.0	70.28%	389	WP_038369869.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	561	561	99%	0.0	70.28%	389	WP_047112932.1
☐	peptidase M30, hyicolysin [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	561	561	99%	0.0	70.28%	389	WP_144109133.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	561	561	99%	0.0	70.28%	389	WP_044555334.1
☐	peptidase M30, hyicolysin [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	560	560	99%	0.0	70.28%	389	WP_209299094.1
☐	peptidase M30 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	560	560	99%	0.0	70.28%	389	WP_047116251.1
☐	peptidase M30 [Brachyspira innocens]	Brachyspira innocens	560	560	99%	0.0	70.10%	390	WP_020003368.1
☐	peptidase M30, hyicolysin [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	559	559	99%	0.0	70.03%	389	WP_144112362.1
☐	DUF2268 domain-containing putative Zn-dependent protease [Brachyspira alvinipulli]	Brachyspira alvinipulli	558	558	99%	0.0	70.62%	392	WP_028328830.1
☐	peptidase M30, hyicolysin [Brachyspira sp. G79]	Brachyspira sp. G79	558	558	99%	0.0	70.62%	390	WP_096737353.1
☐	peptidase M30, hyicolysin [Brachyspira murdochii]	Brachyspira murdochii	557	557	96%	0.0	72.27%	388	WP_157154660.1
☐	peptidase M30 [Brachyspira murdochii]	Brachyspira murdochii	553	553	96%	0.0	72.12%	390	WP_013114038.1
☐	peptidase M30, hyicolysin [Brachyspira murdochii]	Brachyspira murdochii	553	553	96%	0.0	72.12%	390	WP_104618202.1
☐	peptidase M30, hyicolysin [Brachyspira catarrhinii]	Brachyspira catarrhinii	137	137	29%	6e-36	62.83%	117	TKZ30687.1
☐	InlB B-repeat-containing protein [Spirochaetaceae bacterium]	Spirochaetaceae bacterium	133	133	78%	8e-30	31.06%	709	MBI9097218.1
☐	hypothetical protein [Breznakiella homolactica]	Breznakiella homolactica	127	127	60%	9e-29	35.22%	455	WP_215627774.1
☐	hypothetical protein [Treponema sp.]	Treponema sp.	122	122	63%	2e-27	32.82%	333	NLK60755.1
☐	InlB B-repeat-containing protein [Sediminispirochaeta smaragdinae]	Sediminispirochaeta smaragdinae	125	125	72%	2e-27	31.53%	521	WP_013256443.1
☐	Neutral metalloprotease precursor [Spirochaetes bacterium ADurb.Bin215]	Spirochaetes bacterium ADurb.Bin215	120	120	64%	5e-26	31.68%	513	OQB03971.1
☐	hypothetical protein [Breznakiella homolactica]	Breznakiella homolactica	119	119	88%	2e-25	31.51%	462	WP_215627776.1
☐	TPA: hypothetical protein [Treponema sp.]	Treponema sp.	115	115	67%	2e-24	32.88%	490	HCC37439.1
☐	hypothetical protein [Treponema endosymbiont of Eucomonympha sp.]	Treponema endosymbiont of Eucomony...	115	115	67%	3e-24	33.21%	474	WP_187150764.1
☐	hypothetical protein [Salinispira pacifica]	Salinispira pacifica	113	113	73%	2e-23	30.39%	519	WP_024267147.1

☐	hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	110	110	67%	2e-22	31.56%	456	MBP9023691.1
☐	fibronectin type III domain-containing protein [Treponema azotonutricium]	Treponema azotonutricium	110	110	68%	2e-22	32.42%	570	WP_015710250.1
☐	hypothetical protein [Treponema primitia]	Treponema primitia	105	105	68%	6e-21	32.63%	487	WP_026043726.1
☐	InlB B-repeat-containing protein [Treponema endosymbiont of Eucomonympha sp.]	Treponema endosymbiont of Eucomony…	102	102	62%	3e-19	30.50%	671	WP_187152012.1
☐	hypothetical protein [Spirochaetales bacterium]	Spirochaetales bacterium	97.8	97.8	45%	6e-19	33.83%	295	MBN2625595.1
☐	hypothetical protein [Brachyspira innocens]	Brachyspira innocens	93.6	93.6	86%	7e-17	26.30%	413	WP_020005714.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	93.2	93.2	70%	1e-16	30.58%	417	WP_147775031.1
☐	TPA: hypothetical protein [Spirochaetales bacterium]	Spirochaetales bacterium	92.4	92.4	72%	3e-16	27.44%	526	HFK08524.1
☐	Ig-like domain-containing protein [Bacillus glennii]	Bacillus glennii	92.8	92.8	62%	3e-16	30.71%	702	WP_117324178.1
☐	Ig-like domain-containing protein [Mesobacillus zeae]	Mesobacillus zeae	92.4	92.4	69%	4e-16	28.97%	709	WP_119114810.1
☐	Neutral metalloprotease precursor [Mycobacteroides abscessus subsp. abscessus]	Mycobacteroides abscessus subsp. abs…	91.7	91.7	54%	8e-16	29.78%	847	SHP74721.1
☐	peptidase M30, hyicolysin [Brachyspira sp.]	Brachyspira sp.	90.5	90.5	70%	8e-16	30.60%	422	MBS4763408.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	90.5	90.5	70%	9e-16	30.11%	421	WP_147748414.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	90.1	90.1	70%	1e-15	30.60%	422	WP_147559086.1
☐	peptidase M30 [Brachyspira murdochii]	Brachyspira murdochii	89.7	89.7	83%	1e-15	26.35%	413	WP_013112805.1
☐	neutral metalloprotease [Treponema primitia]	Treponema primitia	89.7	89.7	50%	2e-15	32.55%	464	WP_015706389.1
☐	Ig-like domain-containing protein [Caldibacillus debilis]	Caldibacillus debilis	89.7	89.7	73%	4e-15	26.71%	719	WP_154652884.1
☐	peptidase M30, hyicolysin [Brachyspira aalborgi]	Brachyspira aalborgi	88.6	88.6	70%	4e-15	30.25%	422	WP_147778427.1
☐	peptidase M30, hyicolysin [Brachyspira sp. G79]	Brachyspira sp. G79	88.6	88.6	95%	4e-15	25.06%	413	WP_096736129.1
☐	peptidase M30 [Brachyspira aalborgi]	Brachyspira aalborgi	88.6	88.6	70%	4e-15	30.96%	422	WP_147530603.1
☐	Ig-like domain-containing protein [Bacillus sp. FJAT-49736]	Bacillus sp. FJAT-49736	89.0	89.0	74%	5e-15	28.94%	735	WP_213094614.1
☐	hypothetical protein BAA00_21750 [Parageobacillus thermoglucosidasius]	Parageobacillus thermoglucosidasius	89.0	89.0	73%	6e-15	27.78%	942	OUM85007.1
☐	hypothetical protein [Bacillaceae bacterium]	Bacillaceae bacterium	88.2	88.2	73%	8e-15	27.45%	510	MBY6274109.1
☐	Peptidase M30 [Caldibacillus debilis GB1]	Caldibacillus debilis GB1	88.2	88.2	73%	8e-15	27.72%	549	RKO62845.1
☐	Ig-like domain-containing protein [Weizmannia coagulans]	Weizmannia coagulans	88.6	88.6	67%	1e-14	31.16%	947	WP_153013449.1
☐	peptidase M30 [Brachyspira aalborgi]	Brachyspira aalborgi	87.4	87.4	70%	1e-14	28.62%	417	WP_147738022.1
☐	Ig-like domain-containing protein [Bacillus rubiinfantis]	Bacillus rubiinfantis	88.2	88.2	67%	1e-14	29.86%	1027	WP_148347763.1
☐	hypothetical protein B4100_0899 [Weizmannia coagulans]	Weizmannia coagulans	88.2	88.2	67%	1e-14	31.16%	928	KYC62688.1

Threshold: 1.000 Window: 12

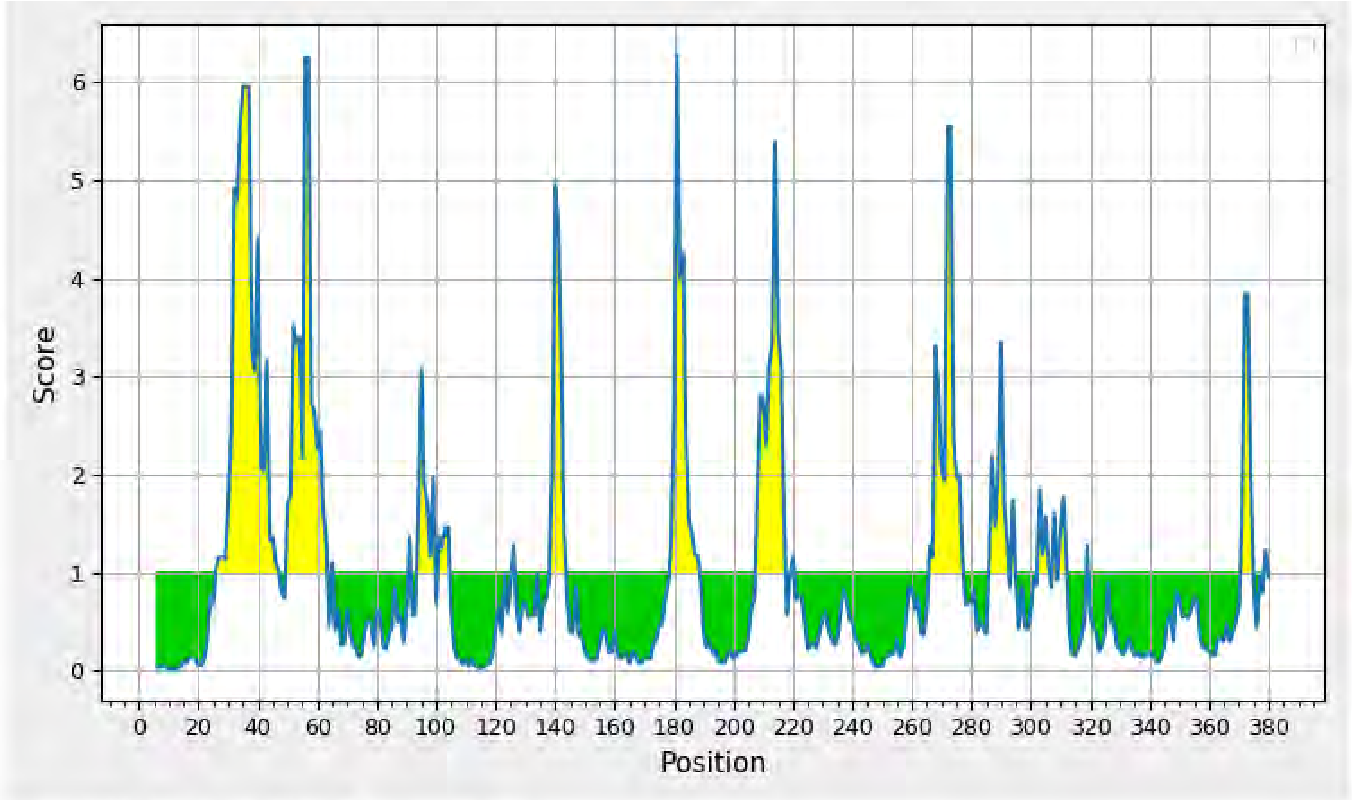


Emini Surface Accessibility Prediction Results

Input Sequences

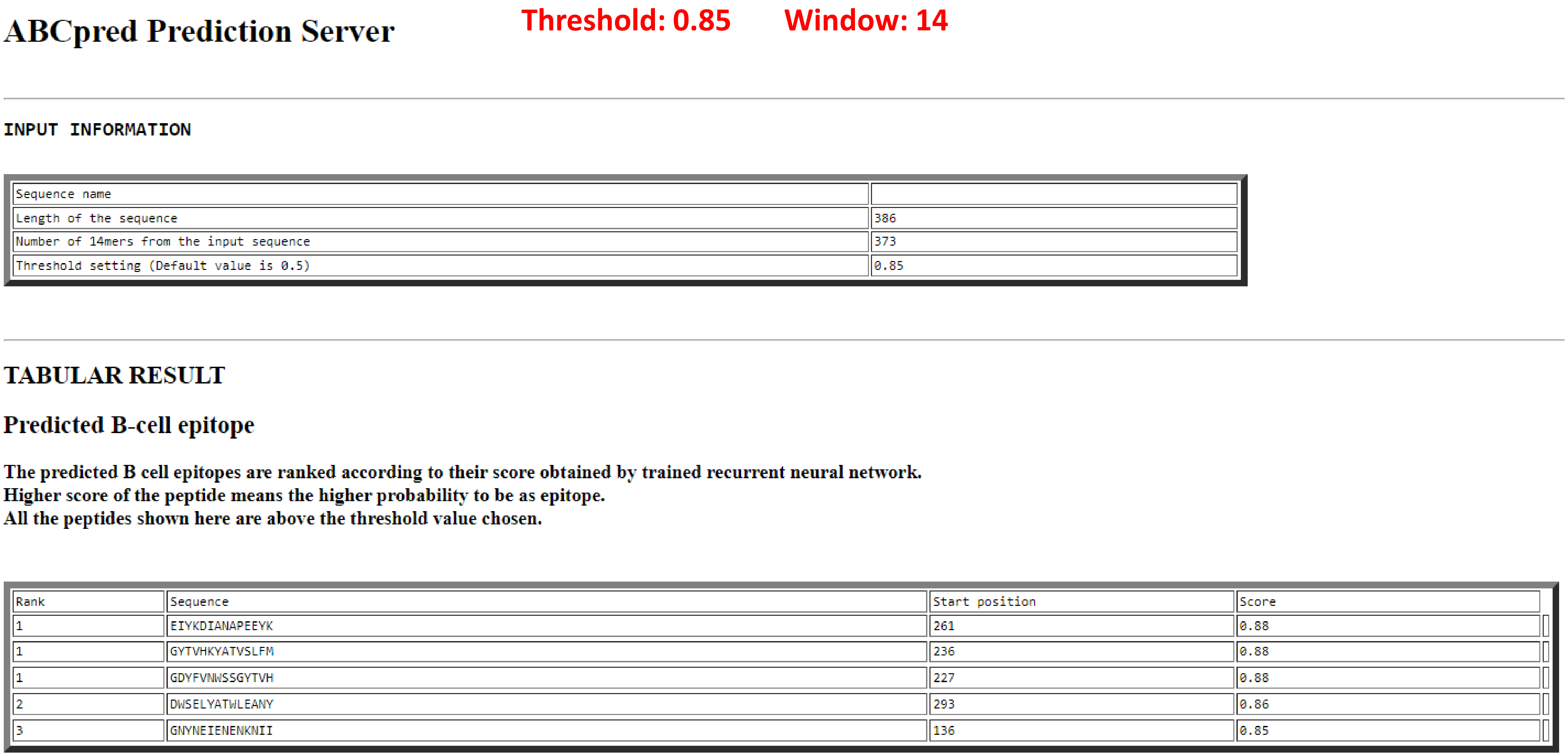
```
  1 MMKKIFVLIL MSLNTLILNA NINSILNQNK TYEIYKADYK EKTFNAVRYI NNNYSKDKIK
 61 AKNIYSTSSI DVYLENGLTV DEKILKEILS QTMKAYELEK YLYGDIKTKL ILLIMDINGG
121 HTGAKPYMQG YSIFEGNYNE IENENKNIIF LDYINGWDNV DSVLNTIIHE LQHIIHYSNL
181 RESKKTDFDV WVDEALSEAA VIAYRGYLPE NRLQYYNSDS MYLITKGDYF VNWSSGYTVH
241 KYATVSLFMY WLAIHSKNGF EIYKDIANAP EEYKHTYKAI LYAANKNIKQ FKDWSELYAT
301 WLEANYKNEA SGLYGYKGII NTKPKVITAS ANFPMSPGAA IYVQGDFFSD DKLLRYVELG
361 NNVYVVYNPD VNAKGKDRYL ILNSYY
```

Center position: 6 Window size: 12 Threshold: 1.000



Average: 1.000 Minimum: 0.016 Maximum: 6.276

MMKKIFVLILMSLNTLILNANINSILNQNKTYEIYKADYKEKTFNAVRYINNNYSKDKIKAKNIYSTSSIDVYLENGLTVDEKI
LKEILSQTMKAYELEKYLYGDIKTKLILLIMDINGGHTGAKPYMQGYSIFEGNYNEIENENKNIIFLDYINGWDNVDSVLNTII
HELQHIIHYSNLRESKKTDFDVWVDEALSEAAVIAYRGYLPENRLQYYNSDSMYLITKGDYFVNWSSGYTVHKYATVSLFMYWL
AIHSKNGFEIYKDIANAPEEYKHTYKAILYAANKNIKQFKDWSELYATWLEANYKNEASGLYGYKGIINTKPKVITASANFPMS
PGAAIYVQGDFFSDDKLLRYVELGNNVYVVYNPDVNAKGKDRYLILNSYY



Threshold: 0.85 **Window: 14**

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	386
Number of 14mers from the input sequence	373
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

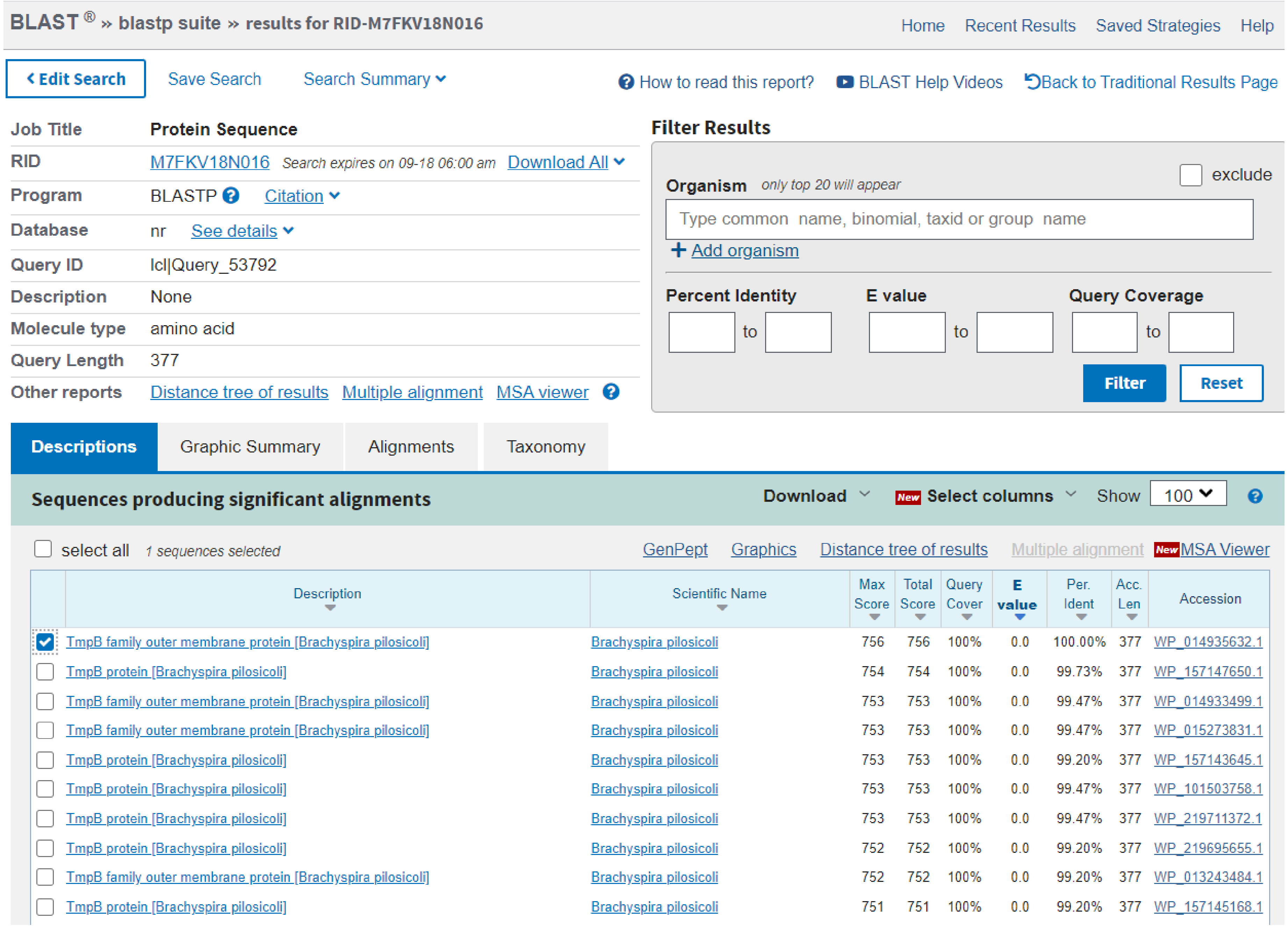
Rank	Sequence	Start position	Score
1	EIYKDIANAPEEYK	261	0.88
1	GYTVHKYATVSLFM	236	0.88
1	GDYFVNWSSGYTVH	227	0.88
2	DWSELYATWLEANY	293	0.86
3	GNYNEIENENKNII	136	0.85

PROTEINA 4

```
>fig|6666666.171271.peg.2646
MMKKIFVLILMSLNTLILNANINSILNQNKTYEIYKADYKEKTFNAVRYINNNYSKDKIKAKNIYSTSSIDVYLENGLTVDEKIL
KEILSQTMKAYELEKYLYGDIKTKLILLIMDINGGHTGAKPYMQGYSIFEGNYNEIENENKNIIFLDYINGWDNVDSVLNTIIHE
LQHIIHYSNLRESKKTDFDVWVDEALSEAAVIAYRGYLPENRLQYYNSDSMYLITKGDYFVNWSSGYTVHKYATVSLFMYWLAIH
SKNGFEIYKDIANAPEEYKHTYKAILYAANKNIKQFKDWSELYATWLEANYKNEASGLYGYKGIINTKPKVITASANFPMSPGAA
IYVQGDFFSDDKLLRYVELGNNVYVVYNPDVNAKGKDRYLILNSYY
```

PROTEINA 5

```
>fig|6666666.171271.peg.840
MKKVLLILFAACYLIYGQDTNITNENIKDSEDYQLAQRYRELAIEAHNAGDYTQSVEFSKQSKEYSDKVIAKFGVYGLVLNAQRY
AERNLALLKGVGGDTNESSISLYEDSVMDYESGNTIFNAATNDTDYSNSITKYTDSSLKSKLGYDLVSIGLRRDYLINEGAITNA
DSNDNKILNLRYNAVMFSKAKDYNNSISNANEAINILDMLEAPIAYAKAQEALNKAKEDGYNETKMTNYNQASTTLIFAKQALDG
EDFSNSLFNSKLVIEMVNAMYNGADYNQETTIVETTGVLFPKYYKVQYRKVGTDSLWKIASYDFIYGDGNLWKKIYEANKDKIKD
PNIIINGQILLIPSLKGETRDGTYDSNNEYGNIKDIK
```

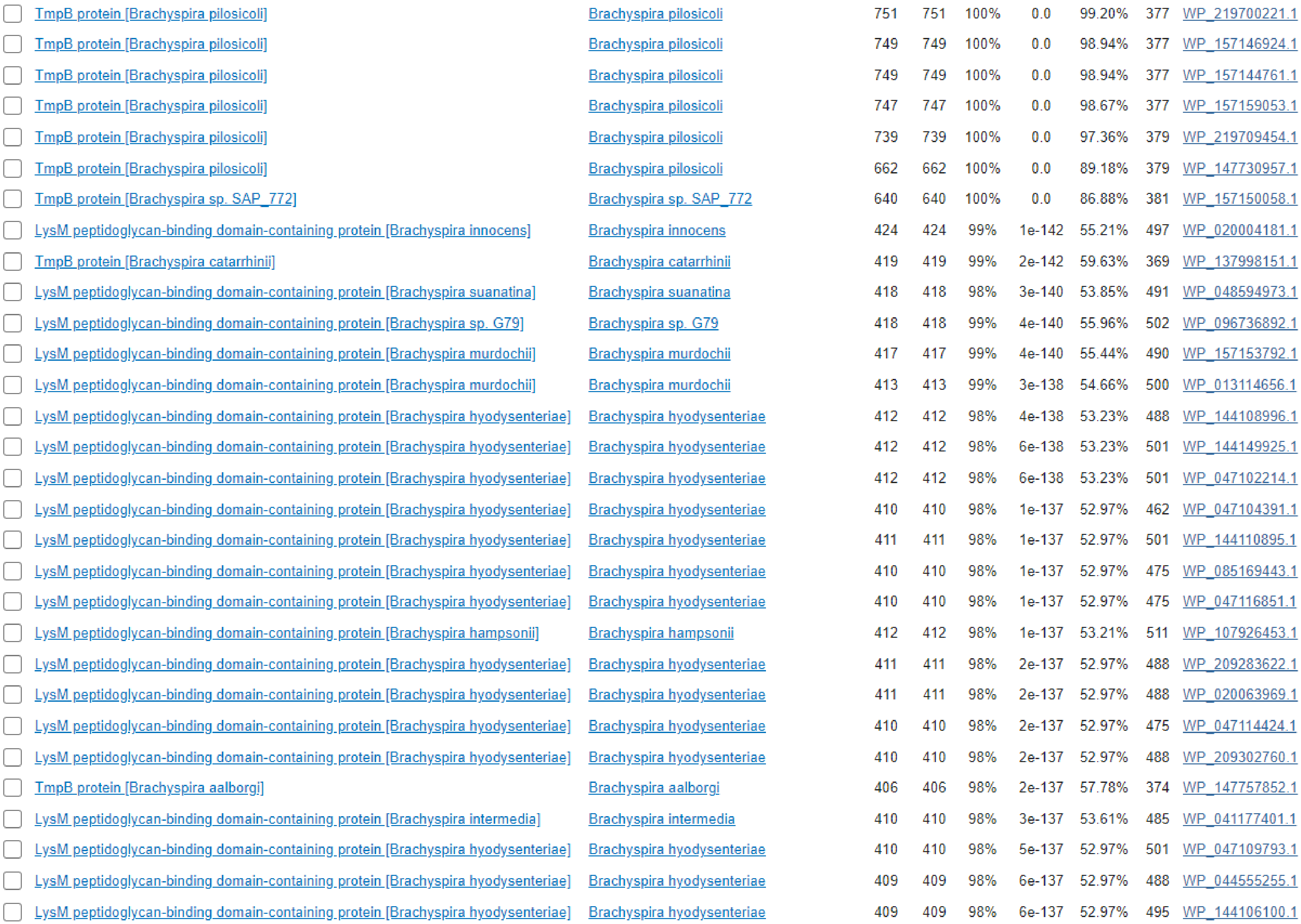


Job Title	**Protein Sequence**
RID	M7FKV18N016 *Search expires on 09-18 06:00 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_53792
Description	None
Molecule type	amino acid
Query Length	377
Other reports	Distance tree of results Multiple alignment MSA viewer

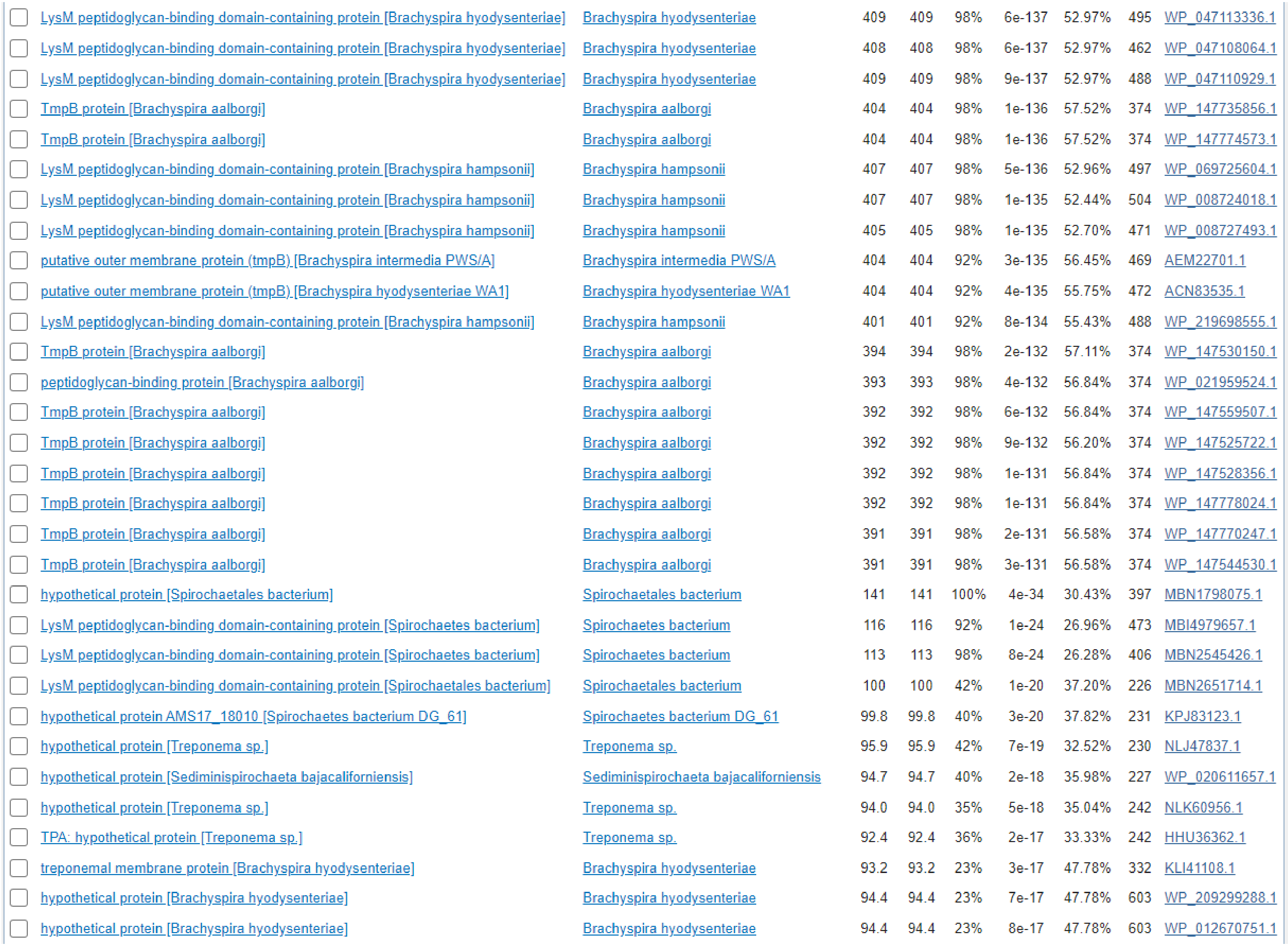
Sequences producing significant alignments

☐ select all *1 sequences selected*

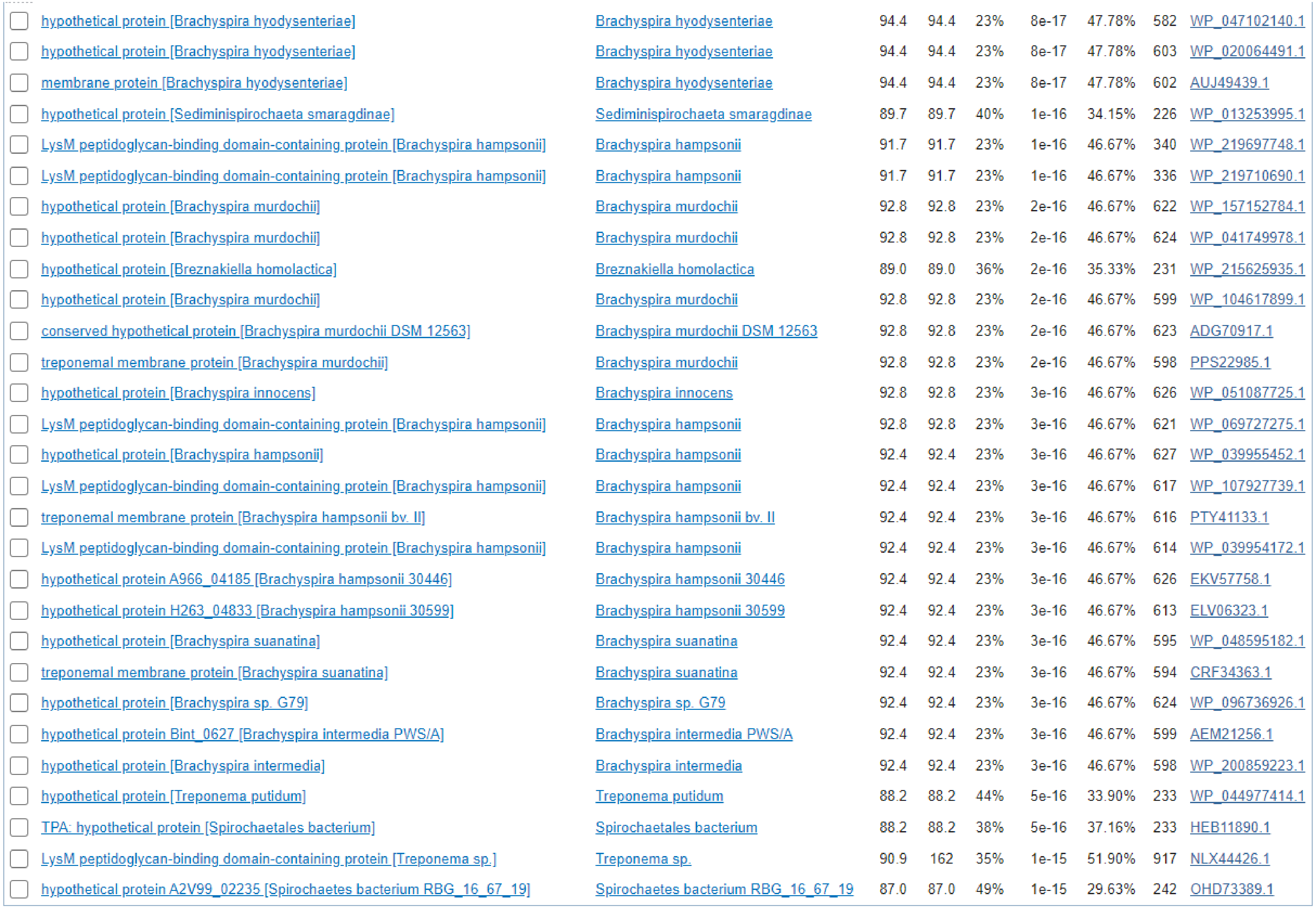
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	TmpB family outer membrane protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	756	756	100%	0.0	100.00%	377	WP_014935632.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	754	754	100%	0.0	99.73%	377	WP_157147650.1
☐	TmpB family outer membrane protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	753	753	100%	0.0	99.47%	377	WP_014933499.1
☐	TmpB family outer membrane protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	753	753	100%	0.0	99.47%	377	WP_015273831.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	753	753	100%	0.0	99.20%	377	WP_157143645.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	753	753	100%	0.0	99.47%	377	WP_101503758.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	753	753	100%	0.0	99.47%	377	WP_219711372.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	752	752	100%	0.0	99.20%	377	WP_219695655.1
☐	TmpB family outer membrane protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	752	752	100%	0.0	99.20%	377	WP_013243484.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	751	751	100%	0.0	99.20%	377	WP_157145168.1



☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	751	751	100%	0.0	99.20%	377	WP_219700221.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	749	749	100%	0.0	98.94%	377	WP_157146924.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	749	749	100%	0.0	98.94%	377	WP_157144761.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	747	747	100%	0.0	98.67%	377	WP_157159053.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	739	739	100%	0.0	97.36%	379	WP_219709454.1
☐	TmpB protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	662	662	100%	0.0	89.18%	379	WP_147730957.1
☐	TmpB protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	640	640	100%	0.0	86.88%	381	WP_157150058.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira innocens]	Brachyspira innocens	424	424	99%	1e-142	55.21%	497	WP_020004181.1
☐	TmpB protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	419	419	99%	2e-142	59.63%	369	WP_137998151.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira suanatina]	Brachyspira suanatina	418	418	98%	3e-140	53.85%	491	WP_048594973.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira sp. G79]	Brachyspira sp. G79	418	418	99%	4e-140	55.96%	502	WP_096736892.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira murdochii]	Brachyspira murdochii	417	417	99%	4e-140	55.44%	490	WP_157153792.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira murdochii]	Brachyspira murdochii	413	413	99%	3e-138	54.66%	500	WP_013114656.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	412	412	98%	4e-138	53.23%	488	WP_144108996.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	412	412	98%	6e-138	53.23%	501	WP_144149925.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	412	412	98%	6e-138	53.23%	501	WP_047102214.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	410	410	98%	1e-137	52.97%	462	WP_047104391.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	411	411	98%	1e-137	52.97%	501	WP_144110895.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	410	410	98%	1e-137	52.97%	475	WP_085169443.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	410	410	98%	1e-137	52.97%	475	WP_047116851.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	412	412	98%	1e-137	53.21%	511	WP_107926453.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	411	411	98%	2e-137	52.97%	488	WP_209283622.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	411	411	98%	2e-137	52.97%	488	WP_020063969.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	410	410	98%	2e-137	52.97%	475	WP_047114424.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	410	410	98%	2e-137	52.97%	488	WP_209302760.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	406	406	98%	2e-137	57.78%	374	WP_147757852.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira intermedia]	Brachyspira intermedia	410	410	98%	3e-137	53.61%	485	WP_041177401.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	410	410	98%	5e-137	52.97%	501	WP_047109793.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	409	409	98%	6e-137	52.97%	488	WP_044555255.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	409	409	98%	6e-137	52.97%	495	WP_144106100.1

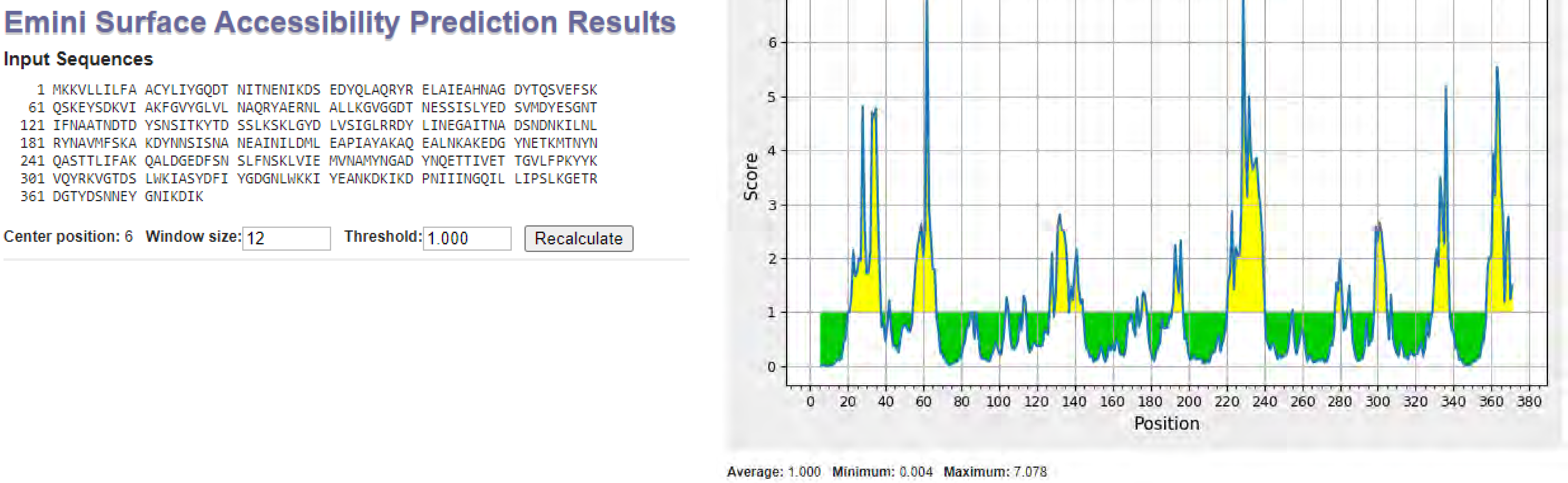


☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	409	409	98%	6e-137	52.97%	495	WP_047113336.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	408	408	98%	6e-137	52.97%	462	WP_047108064.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	409	409	98%	9e-137	52.97%	488	WP_047110929.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	404	404	98%	1e-136	57.52%	374	WP_147735856.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	404	404	98%	1e-136	57.52%	374	WP_147774573.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	407	407	98%	5e-136	52.96%	497	WP_069725604.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	407	407	98%	1e-135	52.44%	504	WP_008724018.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	405	405	98%	1e-135	52.70%	471	WP_008727493.1
☐	putative outer membrane protein (tmpB) [Brachyspira intermedia PWS/A]	Brachyspira intermedia PWS/A	404	404	92%	3e-135	56.45%	469	AEM22701.1
☐	putative outer membrane protein (tmpB) [Brachyspira hyodysenteriae WA1]	Brachyspira hyodysenteriae WA1	404	404	92%	4e-135	55.75%	472	ACN83535.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	401	401	92%	8e-134	55.43%	488	WP_219698555.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	394	394	98%	2e-132	57.11%	374	WP_147530150.1
☐	peptidoglycan-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	393	393	98%	4e-132	56.84%	374	WP_021959524.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	392	392	98%	6e-132	56.84%	374	WP_147559507.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	392	392	98%	9e-132	56.20%	374	WP_147525722.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	392	392	98%	1e-131	56.84%	374	WP_147528356.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	392	392	98%	1e-131	56.84%	374	WP_147778024.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	391	391	98%	2e-131	56.58%	374	WP_147770247.1
☐	TmpB protein [Brachyspira aalborgi]	Brachyspira aalborgi	391	391	98%	3e-131	56.58%	374	WP_147544530.1
☐	hypothetical protein [Spirochaetales bacterium]	Spirochaetales bacterium	141	141	100%	4e-34	30.43%	397	MBN1798075.1
☐	LysM peptidoglycan-binding domain-containing protein [Spirochaetes bacterium]	Spirochaetes bacterium	116	116	92%	1e-24	26.96%	473	MBI4979657.1
☐	LysM peptidoglycan-binding domain-containing protein [Spirochaetes bacterium]	Spirochaetes bacterium	113	113	98%	8e-24	26.28%	406	MBN2545426.1
☐	LysM peptidoglycan-binding domain-containing protein [Spirochaetales bacterium]	Spirochaetales bacterium	100	100	42%	1e-20	37.20%	226	MBN2651714.1
☐	hypothetical protein AMS17_18010 [Spirochaetes bacterium DG_61]	Spirochaetes bacterium DG_61	99.8	99.8	40%	3e-20	37.82%	231	KPJ83123.1
☐	hypothetical protein [Treponema sp.]	Treponema sp.	95.9	95.9	42%	7e-19	32.52%	230	NLJ47837.1
☐	hypothetical protein [Sediminispirochaeta bajacaliforniensis]	Sediminispirochaeta bajacaliforniensis	94.7	94.7	40%	2e-18	35.98%	227	WP_020611657.1
☐	hypothetical protein [Treponema sp.]	Treponema sp.	94.0	94.0	35%	5e-18	35.04%	242	NLK60956.1
☐	TPA: hypothetical protein [Treponema sp.]	Treponema sp.	92.4	92.4	36%	2e-17	33.33%	242	HHU36362.1
☐	treponemal membrane protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	93.2	93.2	23%	3e-17	47.78%	332	KLI41108.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	94.4	94.4	23%	7e-17	47.78%	603	WP_209299288.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	94.4	94.4	23%	8e-17	47.78%	603	WP_012670751.1



☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	94.4	94.4	23%	8e-17	47.78%	582	WP_047102140.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	94.4	94.4	23%	8e-17	47.78%	603	WP_020064491.1
☐	membrane protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	94.4	94.4	23%	8e-17	47.78%	602	AUJ49439.1
☐	hypothetical protein [Sediminispirochaeta smaragdinae]	Sediminispirochaeta smaragdinae	89.7	89.7	40%	1e-16	34.15%	226	WP_013253995.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	91.7	91.7	23%	1e-16	46.67%	340	WP_219697748.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	91.7	91.7	23%	1e-16	46.67%	336	WP_219710690.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	92.8	92.8	23%	2e-16	46.67%	622	WP_157152784.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	92.8	92.8	23%	2e-16	46.67%	624	WP_041749978.1
☐	hypothetical protein [Breznakiella homolactica]	Breznakiella homolactica	89.0	89.0	36%	2e-16	35.33%	231	WP_215625935.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	92.8	92.8	23%	2e-16	46.67%	599	WP_104617899.1
☐	conserved hypothetical protein [Brachyspira murdochii DSM 12563]	Brachyspira murdochii DSM 12563	92.8	92.8	23%	2e-16	46.67%	623	ADG70917.1
☐	treponemal membrane protein [Brachyspira murdochii]	Brachyspira murdochii	92.8	92.8	23%	2e-16	46.67%	598	PPS22985.1
☐	hypothetical protein [Brachyspira innocens]	Brachyspira innocens	92.8	92.8	23%	3e-16	46.67%	626	WP_051087725.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	92.8	92.8	23%	3e-16	46.67%	621	WP_069727275.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	92.4	92.4	23%	3e-16	46.67%	627	WP_039955452.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	92.4	92.4	23%	3e-16	46.67%	617	WP_107927739.1
☐	treponemal membrane protein [Brachyspira hampsonii bv. II]	Brachyspira hampsonii bv. II	92.4	92.4	23%	3e-16	46.67%	616	PTY41133.1
☐	LysM peptidoglycan-binding domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	92.4	92.4	23%	3e-16	46.67%	614	WP_039954172.1
☐	hypothetical protein A966_04185 [Brachyspira hampsonii 30446]	Brachyspira hampsonii 30446	92.4	92.4	23%	3e-16	46.67%	626	EKV57758.1
☐	hypothetical protein H263_04833 [Brachyspira hampsonii 30599]	Brachyspira hampsonii 30599	92.4	92.4	23%	3e-16	46.67%	613	ELV06323.1
☐	hypothetical protein [Brachyspira suanatina]	Brachyspira suanatina	92.4	92.4	23%	3e-16	46.67%	595	WP_048595182.1
☐	treponemal membrane protein [Brachyspira suanatina]	Brachyspira suanatina	92.4	92.4	23%	3e-16	46.67%	594	CRF34363.1
☐	hypothetical protein [Brachyspira sp. G79]	Brachyspira sp. G79	92.4	92.4	23%	3e-16	46.67%	624	WP_096736926.1
☐	hypothetical protein Bint_0627 [Brachyspira intermedia PWS/A]	Brachyspira intermedia PWS/A	92.4	92.4	23%	3e-16	46.67%	599	AEM21256.1
☐	hypothetical protein [Brachyspira intermedia]	Brachyspira intermedia	92.4	92.4	23%	3e-16	46.67%	598	WP_200859223.1
☐	hypothetical protein [Treponema putidum]	Treponema putidum	88.2	88.2	44%	5e-16	33.90%	233	WP_044977414.1
☐	TPA: hypothetical protein [Spirochaetales bacterium]	Spirochaetales bacterium	88.2	88.2	38%	5e-16	37.16%	233	HEB11890.1
☐	LysM peptidoglycan-binding domain-containing protein [Treponema sp.]	Treponema sp.	90.9	162	35%	1e-15	51.90%	917	NLX44426.1
☐	hypothetical protein A2V99_02235 [Spirochaetes bacterium RBG_16_67_19]	Spirochaetes bacterium RBG_16_67_19	87.0	87.0	49%	1e-15	29.63%	242	OHD73389.1

Threshold: 1.000   Window: 12



Emini Surface Accessibility Prediction Results

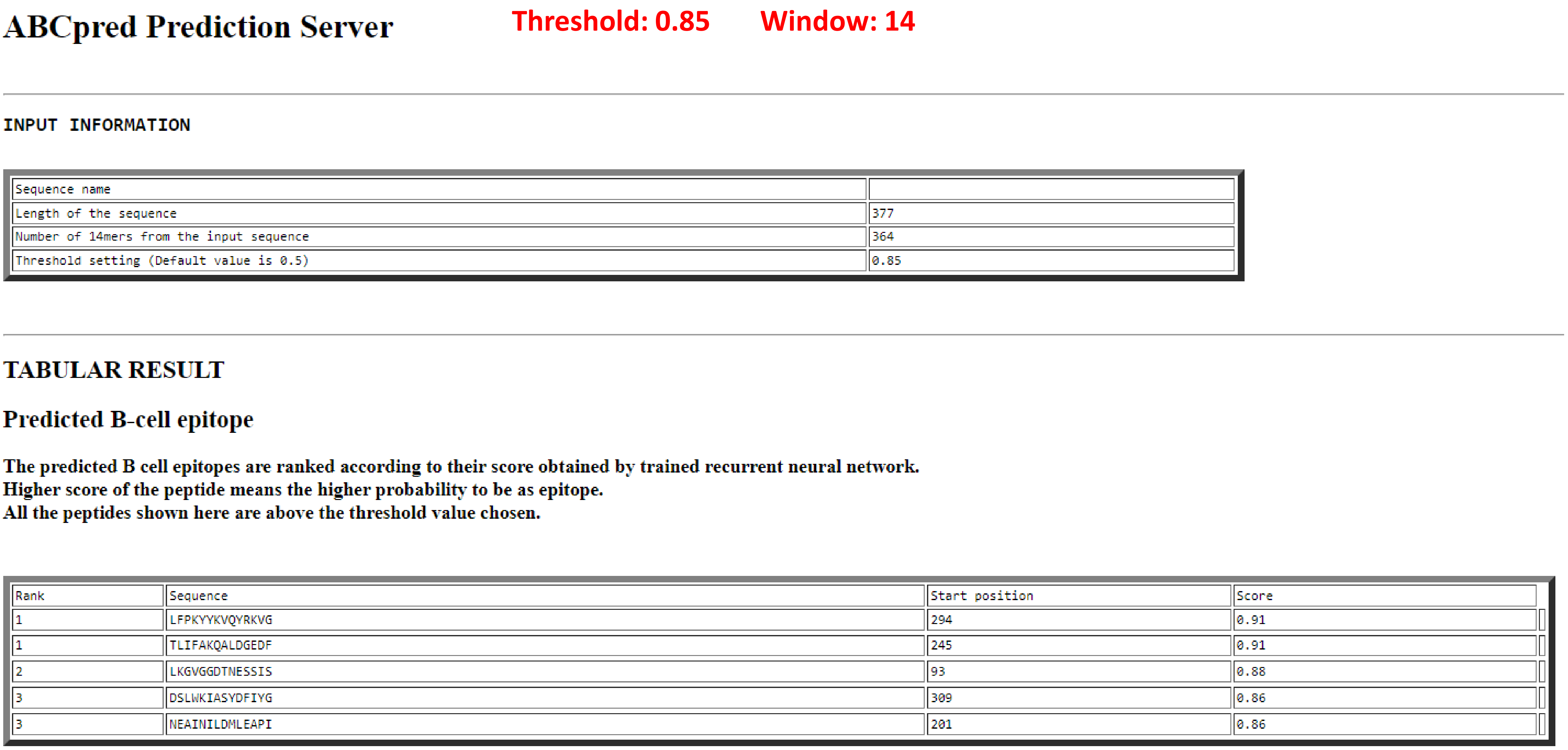
Input Sequences

```
  1 MKKVLLILFA ACYLIYGQDT NITNENIKDS EDYQLAQRYR ELAIEAHNAG DYTQSVEFSK
 61 QSKEYSDKVI AKFGVYGLVL NAQRYAERNL ALLKGVGGDT NESSISLYED SVMDYESGNT
121 IFNAATNDTD YSNSITKYTD SSLKSKLGYD LVSIGLRRDY LINEGAITNA DSNDNKILNL
181 RYNAVMFSKA KDYNNSISNA NEAINILDML EAPIAYAKAQ EALNKAKEDG YNETKMTNYN
241 QASTTLIFAK QALDGEDFSN SLFNSKLVIE MVNAMYNGAD YNQETTIVET TGVLFPKYYK
301 VQYRKVGTDS LWKIASYDFI YGDGNLWKKI YEANKDKIKD PNIIINGQIL LIPSLKGETR
361 DGTYDSNNEY GNIKDIK
```

Center position: 6   Window size: 12   Threshold: 1.000

Average: 1.000   Minimum: 0.004   Maximum: 7.078

MKKVLLILFAACYLIYGQDTNITNENIKDSEDYQLAQRYRELAIEAHNAGDYTQSVEFSKQSKEYSDKVIAKFGVYGLVLNAQR
YAERNLALLKGVGGDTNESSISLYEDSVMDYESGNTIFNAATNDTDYSNSITKYTDSSLKSKLGYDLVSIGLRRDYLINEGAIT
NADSNDNKILNLRYNAVMFSKAKDYNNSISNANEAINILDMLEAPIAYAKAQEALNKAKEDGYNETKMTNYNQASTTLIFAKQA
LDGEDFSNSLFNSKLVIEMVNAMYNGADYNQETTIVETTGVLFPKYYKVQYRKVGTDSLWKIASYDFIYGDGNLWKKIYEANKD
KIKDPNIIINGQILLIPSLKGETRDGTYDSNNEYGNIKDIK



ABCpred Prediction Server

Threshold: 0.85 **Window: 14**

INPUT INFORMATION

Sequence name	
Length of the sequence	377
Number of 14mers from the input sequence	364
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

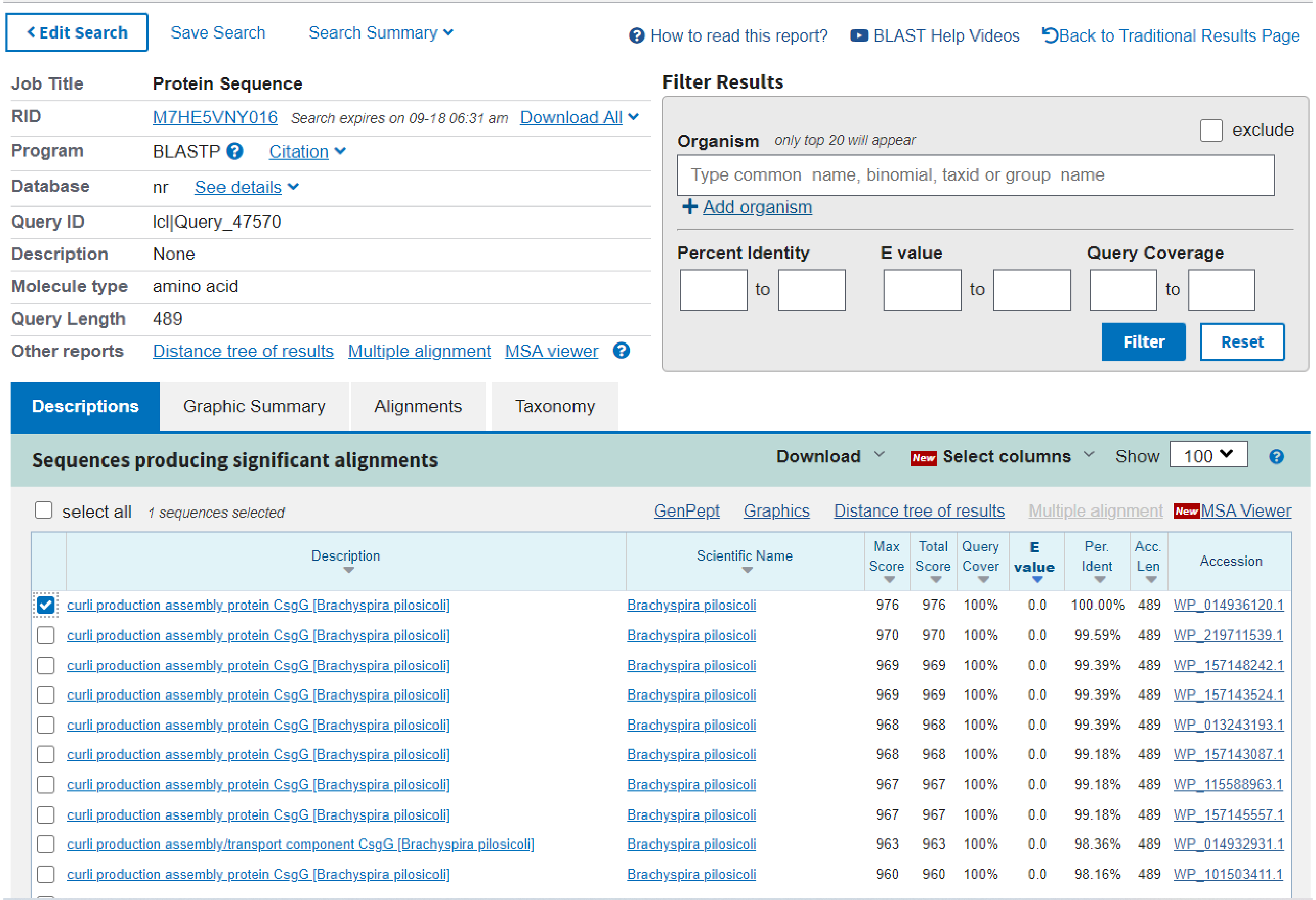
Rank	Sequence	Start position	Score
1	LFPKYYKVQYRKVG	294	0.91
1	TLIFAKQALDGEDF	245	0.91
2	LKGVGGDTNESSIS	93	0.88
3	DSLWKIASYDFIYG	309	0.86
3	NEAINILDMLEAPI	201	0.86

PROTEINA 5

```
>fig|6666666.171271.peg.840
MKKVLLILFAACYLIYGQDTNITNENIKDSEDYQLAQRYRELAIEAHNAGDYTQSVEFSKQSKEYSDKVIAKFGVYGLVLNAQR
YAERNLALLKGVGGDTNESSISLYEDSVMDYESGNTIFNAATNDTDYSNSITKYTDSSLKSKLGYDLVSIGLRRDYLINEGAIT
NADSNDNKILNLRYNAVMFSKAKDYNNSISNANEAINILDMLEAPIAYAKAQEALNKAKEDGYNETKMTNYNQASTTLIFAKQA
LDGEDFSNSLFNSKLVIEMVNAMYNGADYNQETTIVETTGVLFPKYYKVQYRKVGTDSLWKIASYDFIYGDGNLWKKIYEANKD
KIKDPNIIINGQILLIPSLKGETRDGTYDSNNEYGNIKDIK
```

PROTEINA 6

```
>fig|6666666.171271.peg.1529
MIRKLFYIIFIILFCSNLFSQIVKNEISEKYIKENIAVFEIQDVSTGYSKDLGKKVTTLIENSLTRMKRFNIVDRENLYKY
LKEMELQLTGITDEQVIEMGKIYGYSKAITGKITHSSTRYDYDSDDGTGTIYANVDLVLQIVDVSTTKILYSSKVSGSSYY
SIDRYPSQAFRDAAIDEACNDLVYKVSAKMRNIFKITLKISDITDGNIILLAGYDHGLTKNTRFKVYSKSEDIVLPSGNVI
EGQYKQKGTLRIKDMGSEYSIATISRGRNIQVGDIVRETYIGNFIFGLNINYASYKINPLVKEFQGTNSAGGKIKVNLNKN
DYALGMHLKFGYDFQLFSPNLSMGLLFGDFFKTSYGIDTRFNFDINIKIYQEIVRFVLTPYVGLGVTFTDIGEVYGGDYRN
GNLLIPNGTKIKSTDVMLGIGLLANIQYNITDTLGINAGVGYRFYTKPINAGTYYEDNSFNMPEEIKTVNLTGLEFMVGVY
GLF
```

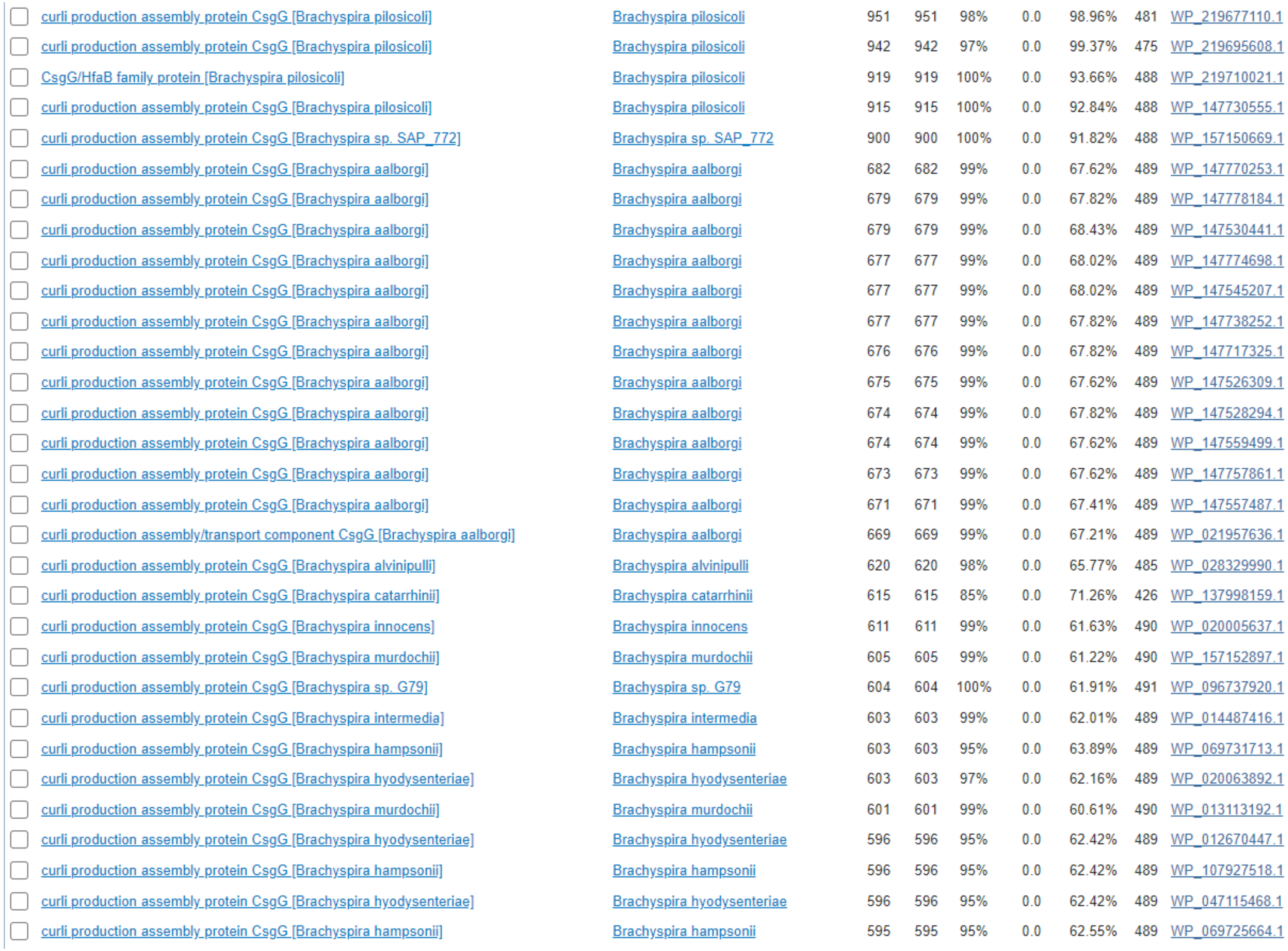


Job Title	Protein Sequence
RID	M7HE5VNY016 *Search expires on 09-18 06:31 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_47570
Description	None
Molecule type	amino acid
Query Length	489
Other reports	Distance tree of results Multiple alignment MSA viewer

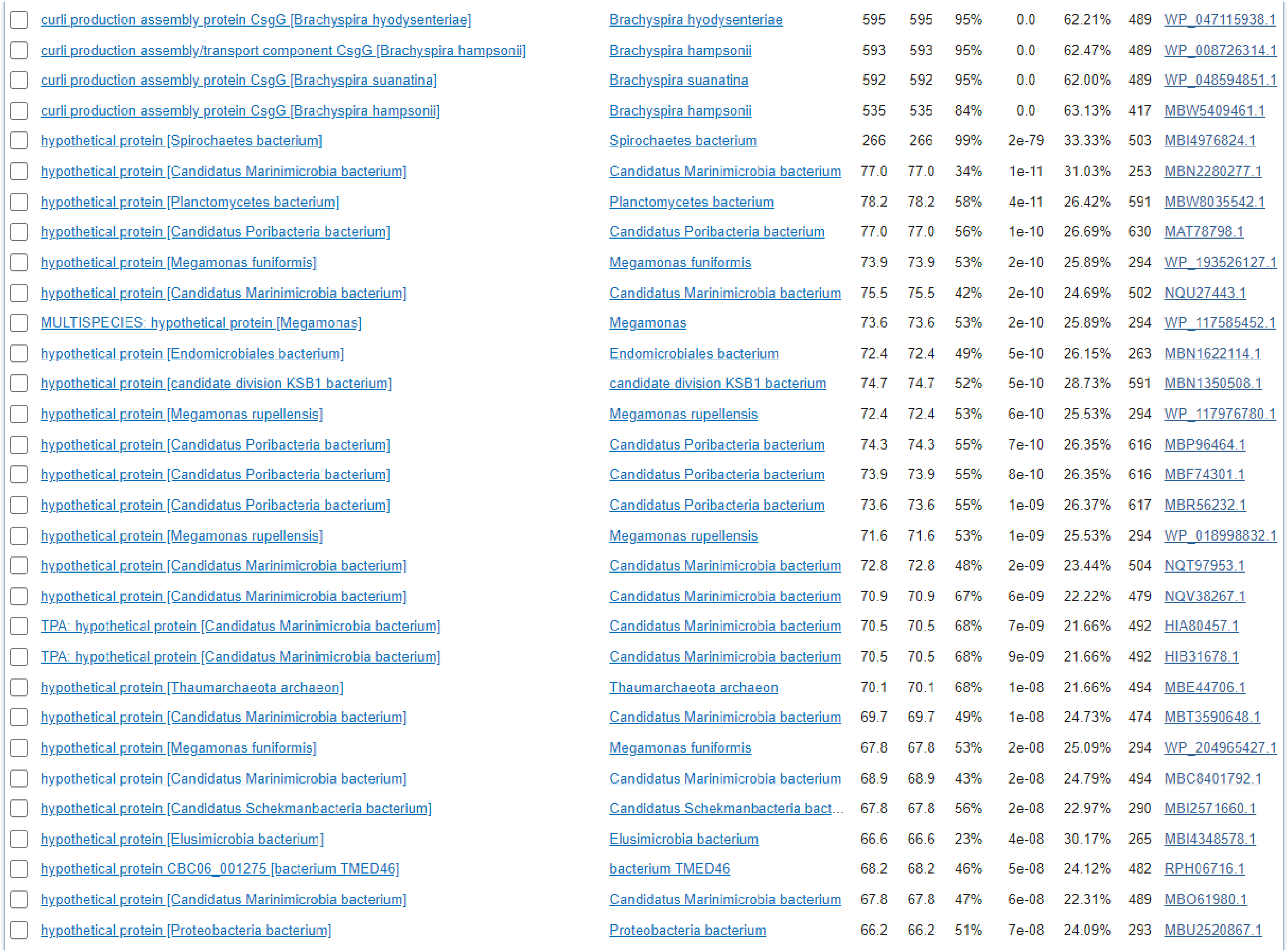
Sequences producing significant alignments

☐ select all *1 sequences selected*

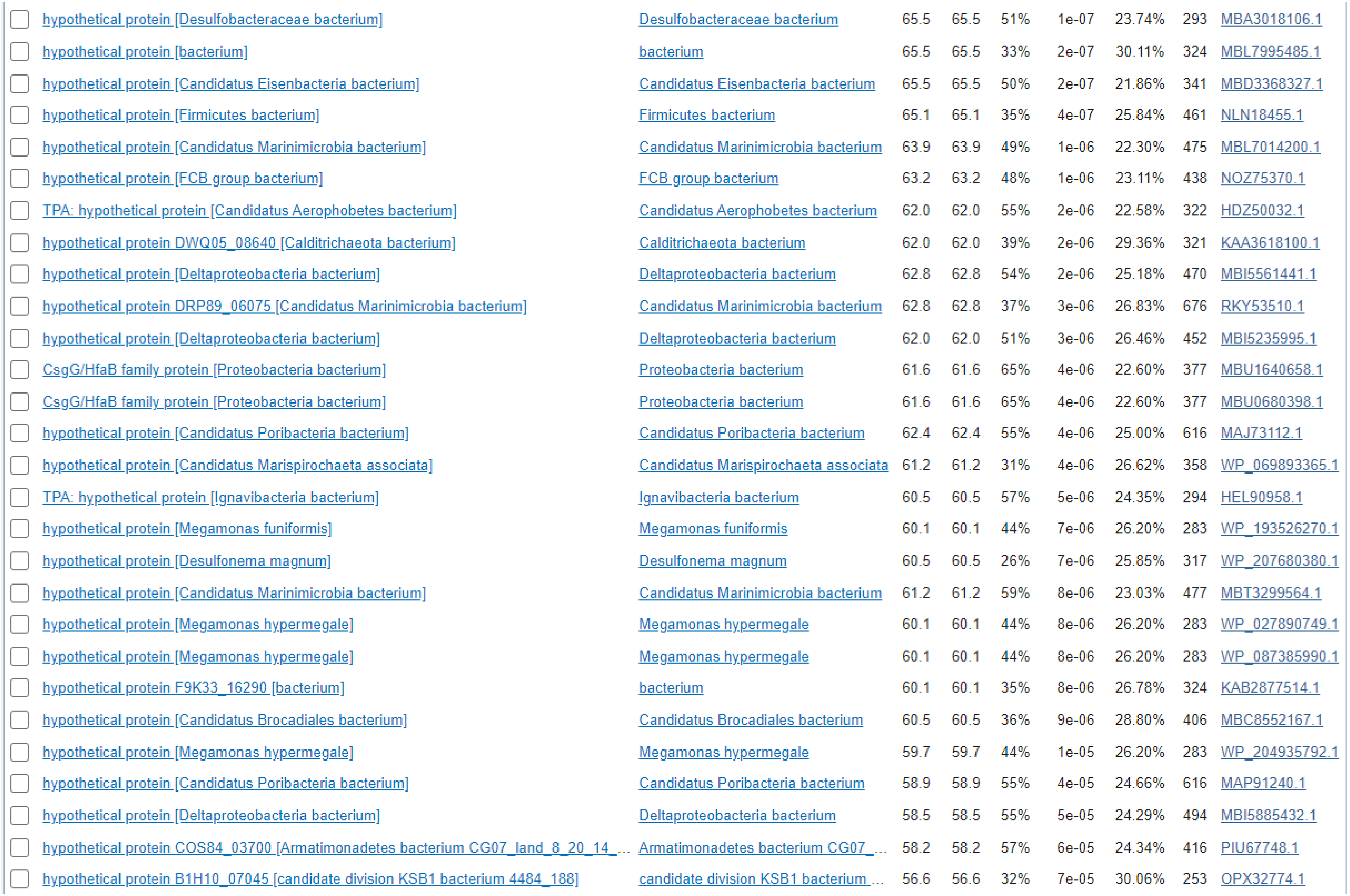
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	976	976	100%	0.0	100.00%	489	WP_014936120.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	970	970	100%	0.0	99.59%	489	WP_219711539.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	969	969	100%	0.0	99.39%	489	WP_157148242.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	969	969	100%	0.0	99.39%	489	WP_157143524.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	968	968	100%	0.0	99.39%	489	WP_013243193.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	968	968	100%	0.0	99.18%	489	WP_157143087.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	967	967	100%	0.0	99.18%	489	WP_115588963.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	967	967	100%	0.0	99.18%	489	WP_157145557.1
☐	curli production assembly/transport component CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	963	963	100%	0.0	98.36%	489	WP_014932931.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	960	960	100%	0.0	98.16%	489	WP_101503411.1



☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	951	951	98%	0.0	98.96%	481	WP_219677110.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	942	942	97%	0.0	99.37%	475	WP_219695608.1
☐	CsgG/HfaB family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	919	919	100%	0.0	93.66%	488	WP_219710021.1
☐	curli production assembly protein CsgG [Brachyspira pilosicoli]	Brachyspira pilosicoli	915	915	100%	0.0	92.84%	488	WP_147730555.1
☐	curli production assembly protein CsgG [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	900	900	100%	0.0	91.82%	488	WP_157150669.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	682	682	99%	0.0	67.62%	489	WP_147770253.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	679	679	99%	0.0	67.82%	489	WP_147778184.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	679	679	99%	0.0	68.43%	489	WP_147530441.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	677	677	99%	0.0	68.02%	489	WP_147774698.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	677	677	99%	0.0	68.02%	489	WP_147545207.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	677	677	99%	0.0	67.82%	489	WP_147738252.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	676	676	99%	0.0	67.82%	489	WP_147717325.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	675	675	99%	0.0	67.62%	489	WP_147526309.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	674	674	99%	0.0	67.82%	489	WP_147528294.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	674	674	99%	0.0	67.62%	489	WP_147559499.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	673	673	99%	0.0	67.62%	489	WP_147757861.1
☐	curli production assembly protein CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	671	671	99%	0.0	67.41%	489	WP_147557487.1
☐	curli production assembly/transport component CsgG [Brachyspira aalborgi]	Brachyspira aalborgi	669	669	99%	0.0	67.21%	489	WP_021957636.1
☐	curli production assembly protein CsgG [Brachyspira alvinipulli]	Brachyspira alvinipulli	620	620	98%	0.0	65.77%	485	WP_028329990.1
☐	curli production assembly protein CsgG [Brachyspira catarrhinii]	Brachyspira catarrhinii	615	615	85%	0.0	71.26%	426	WP_137998159.1
☐	curli production assembly protein CsgG [Brachyspira innocens]	Brachyspira innocens	611	611	99%	0.0	61.63%	490	WP_020005637.1
☐	curli production assembly protein CsgG [Brachyspira murdochii]	Brachyspira murdochii	605	605	99%	0.0	61.22%	490	WP_157152897.1
☐	curli production assembly protein CsgG [Brachyspira sp. G79]	Brachyspira sp. G79	604	604	100%	0.0	61.91%	491	WP_096737920.1
☐	curli production assembly protein CsgG [Brachyspira intermedia]	Brachyspira intermedia	603	603	99%	0.0	62.01%	489	WP_014487416.1
☐	curli production assembly protein CsgG [Brachyspira hampsonii]	Brachyspira hampsonii	603	603	95%	0.0	63.89%	489	WP_069731713.1
☐	curli production assembly protein CsgG [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	603	603	97%	0.0	62.16%	489	WP_020063892.1
☐	curli production assembly protein CsgG [Brachyspira murdochii]	Brachyspira murdochii	601	601	99%	0.0	60.61%	490	WP_013113192.1
☐	curli production assembly protein CsgG [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	596	596	95%	0.0	62.42%	489	WP_012670447.1
☐	curli production assembly protein CsgG [Brachyspira hampsonii]	Brachyspira hampsonii	596	596	95%	0.0	62.42%	489	WP_107927518.1
☐	curli production assembly protein CsgG [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	596	596	95%	0.0	62.42%	489	WP_047115468.1
☐	curli production assembly protein CsgG [Brachyspira hampsonii]	Brachyspira hampsonii	595	595	95%	0.0	62.55%	489	WP_069725664.1

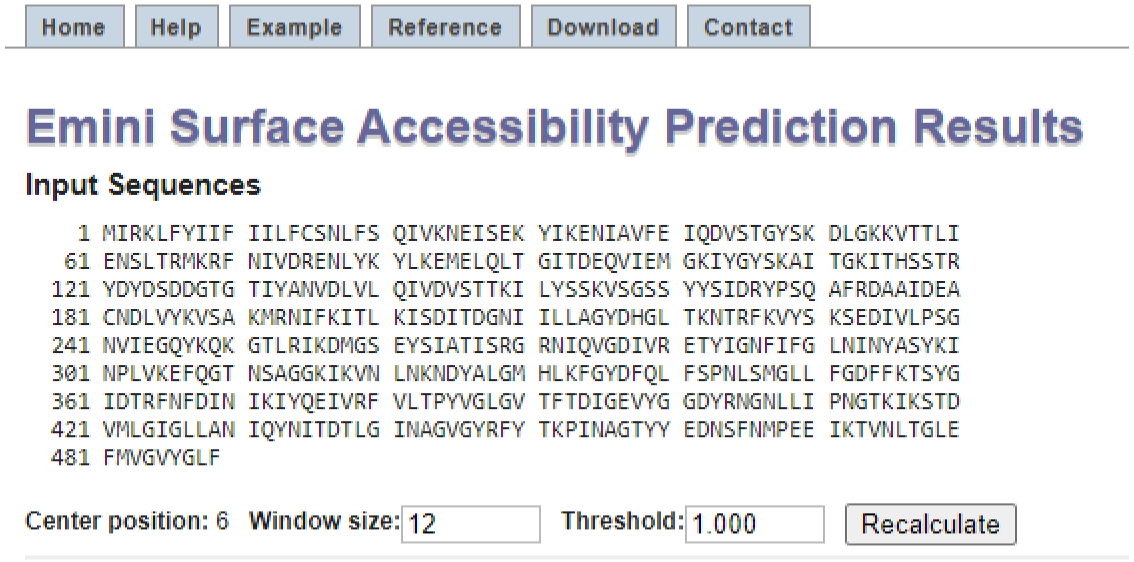


☐	curli production assembly protein CsgG [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	595	595	95%	0.0	62.21%	489	WP_047115938.1
☐	curli production assembly/transport component CsgG [Brachyspira hampsonii]	Brachyspira hampsonii	593	593	95%	0.0	62.47%	489	WP_008726314.1
☐	curli production assembly protein CsgG [Brachyspira suanatina]	Brachyspira suanatina	592	592	95%	0.0	62.00%	489	WP_048594851.1
☐	curli production assembly protein CsgG [Brachyspira hampsonii]	Brachyspira hampsonii	535	535	84%	0.0	63.13%	417	MBW5409461.1
☐	hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	266	266	99%	2e-79	33.33%	503	MBI4976824.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	77.0	77.0	34%	1e-11	31.03%	253	MBN2280277.1
☐	hypothetical protein [Planctomycetes bacterium]	Planctomycetes bacterium	78.2	78.2	58%	4e-11	26.42%	591	MBW8035542.1
☐	hypothetical protein [Candidatus Poribacteria bacterium]	Candidatus Poribacteria bacterium	77.0	77.0	56%	1e-10	26.69%	630	MAT78798.1
☐	hypothetical protein [Megamonas funiformis]	Megamonas funiformis	73.9	73.9	53%	2e-10	25.89%	294	WP_193526127.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	75.5	75.5	42%	2e-10	24.69%	502	NQU27443.1
☐	MULTISPECIES: hypothetical protein [Megamonas]	Megamonas	73.6	73.6	53%	2e-10	25.89%	294	WP_117585452.1
☐	hypothetical protein [Endomicrobiales bacterium]	Endomicrobiales bacterium	72.4	72.4	49%	5e-10	26.15%	263	MBN1622114.1
☐	hypothetical protein [candidate division KSB1 bacterium]	candidate division KSB1 bacterium	74.7	74.7	52%	5e-10	28.73%	591	MBN1350508.1
☐	hypothetical protein [Megamonas rupellensis]	Megamonas rupellensis	72.4	72.4	53%	6e-10	25.53%	294	WP_117976780.1
☐	hypothetical protein [Candidatus Poribacteria bacterium]	Candidatus Poribacteria bacterium	74.3	74.3	55%	7e-10	26.35%	616	MBP96464.1
☐	hypothetical protein [Candidatus Poribacteria bacterium]	Candidatus Poribacteria bacterium	73.9	73.9	55%	8e-10	26.35%	616	MBF74301.1
☐	hypothetical protein [Candidatus Poribacteria bacterium]	Candidatus Poribacteria bacterium	73.6	73.6	55%	1e-09	26.37%	617	MBR56232.1
☐	hypothetical protein [Megamonas rupellensis]	Megamonas rupellensis	71.6	71.6	53%	1e-09	25.53%	294	WP_018998832.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	72.8	72.8	48%	2e-09	23.44%	504	NQT97953.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	70.9	70.9	67%	6e-09	22.22%	479	NQV38267.1
☐	TPA: hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	70.5	70.5	68%	7e-09	21.66%	492	HIA80457.1
☐	TPA: hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	70.5	70.5	68%	9e-09	21.66%	492	HIB31678.1
☐	hypothetical protein [Thaumarchaeota archaeon]	Thaumarchaeota archaeon	70.1	70.1	68%	1e-08	21.66%	494	MBE44706.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	69.7	69.7	49%	1e-08	24.73%	474	MBT3590648.1
☐	hypothetical protein [Megamonas funiformis]	Megamonas funiformis	67.8	67.8	53%	2e-08	25.09%	294	WP_204965427.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	68.9	68.9	43%	2e-08	24.79%	494	MBC8401792.1
☐	hypothetical protein [Candidatus Schekmanbacteria bacterium]	Candidatus Schekmanbacteria bact...	67.8	67.8	56%	2e-08	22.97%	290	MBI2571660.1
☐	hypothetical protein [Elusimicrobia bacterium]	Elusimicrobia bacterium	66.6	66.6	23%	4e-08	30.17%	265	MBI4348578.1
☐	hypothetical protein CBC06_001275 [bacterium TMED46]	bacterium TMED46	68.2	68.2	46%	5e-08	24.12%	482	RPH06716.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	67.8	67.8	47%	6e-08	22.31%	489	MBO61980.1
☐	hypothetical protein [Proteobacteria bacterium]	Proteobacteria bacterium	66.2	66.2	51%	7e-08	24.09%	293	MBU2520867.1



☐	hypothetical protein [Desulfobacteraceae bacterium]	Desulfobacteraceae bacterium	65.5	65.5	51%	1e-07	23.74%	293	MBA3018106.1
☐	hypothetical protein [bacterium]	bacterium	65.5	65.5	33%	2e-07	30.11%	324	MBL7995485.1
☐	hypothetical protein [Candidatus Eisenbacteria bacterium]	Candidatus Eisenbacteria bacterium	65.5	65.5	50%	2e-07	21.86%	341	MBD3368327.1
☐	hypothetical protein [Firmicutes bacterium]	Firmicutes bacterium	65.1	65.1	35%	4e-07	25.84%	461	NLN18455.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	63.9	63.9	49%	1e-06	22.30%	475	MBL7014200.1
☐	hypothetical protein [FCB group bacterium]	FCB group bacterium	63.2	63.2	48%	1e-06	23.11%	438	NOZ75370.1
☐	TPA: hypothetical protein [Candidatus Aerophobetes bacterium]	Candidatus Aerophobetes bacterium	62.0	62.0	55%	2e-06	22.58%	322	HDZ50032.1
☐	hypothetical protein DWQ05_08640 [Calditrichaeota bacterium]	Calditrichaeota bacterium	62.0	62.0	39%	2e-06	29.36%	321	KAA3618100.1
☐	hypothetical protein [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	62.8	62.8	54%	2e-06	25.18%	470	MBI5561441.1
☐	hypothetical protein DRP89_06075 [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	62.8	62.8	37%	3e-06	26.83%	676	RKY53510.1
☐	hypothetical protein [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	62.0	62.0	51%	3e-06	26.46%	452	MBI5235995.1
☐	CsgG/HfaB family protein [Proteobacteria bacterium]	Proteobacteria bacterium	61.6	61.6	65%	4e-06	22.60%	377	MBU1640658.1
☐	CsgG/HfaB family protein [Proteobacteria bacterium]	Proteobacteria bacterium	61.6	61.6	65%	4e-06	22.60%	377	MBU0680398.1
☐	hypothetical protein [Candidatus Poribacteria bacterium]	Candidatus Poribacteria bacterium	62.4	62.4	55%	4e-06	25.00%	616	MAJ73112.1
☐	hypothetical protein [Candidatus Marispirochaeta associata]	Candidatus Marispirochaeta associata	61.2	61.2	31%	4e-06	26.62%	358	WP_069893365.1
☐	TPA: hypothetical protein [Ignavibacteria bacterium]	Ignavibacteria bacterium	60.5	60.5	57%	5e-06	24.35%	294	HEL90958.1
☐	hypothetical protein [Megamonas funiformis]	Megamonas funiformis	60.1	60.1	44%	7e-06	26.20%	283	WP_193526270.1
☐	hypothetical protein [Desulfonema magnum]	Desulfonema magnum	60.5	60.5	26%	7e-06	25.85%	317	WP_207680380.1
☐	hypothetical protein [Candidatus Marinimicrobia bacterium]	Candidatus Marinimicrobia bacterium	61.2	61.2	59%	8e-06	23.03%	477	MBT3299564.1
☐	hypothetical protein [Megamonas hypermegale]	Megamonas hypermegale	60.1	60.1	44%	8e-06	26.20%	283	WP_027890749.1
☐	hypothetical protein [Megamonas hypermegale]	Megamonas hypermegale	60.1	60.1	44%	8e-06	26.20%	283	WP_087385990.1
☐	hypothetical protein F9K33_16290 [bacterium]	bacterium	60.1	60.1	35%	8e-06	26.78%	324	KAB2877514.1
☐	hypothetical protein [Candidatus Brocadiales bacterium]	Candidatus Brocadiales bacterium	60.5	60.5	36%	9e-06	28.80%	406	MBC8552167.1
☐	hypothetical protein [Megamonas hypermegale]	Megamonas hypermegale	59.7	59.7	44%	1e-05	26.20%	283	WP_204935792.1
☐	hypothetical protein [Candidatus Poribacteria bacterium]	Candidatus Poribacteria bacterium	58.9	58.9	55%	4e-05	24.66%	616	MAP91240.1
☐	hypothetical protein [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	58.5	58.5	55%	5e-05	24.29%	494	MBI5885432.1
☐	hypothetical protein COS84_03700 [Armatimonadetes bacterium CG07_land_8_20_14_...	Armatimonadetes bacterium CG07_...	58.2	58.2	57%	6e-05	24.34%	416	PIU67748.1
☐	hypothetical protein B1H10_07045 [candidate division KSB1 bacterium 4484_188]	candidate division KSB1 bacterium ...	56.6	56.6	32%	7e-05	30.06%	253	OPX32774.1

Threshold: 1.000 Window: 12

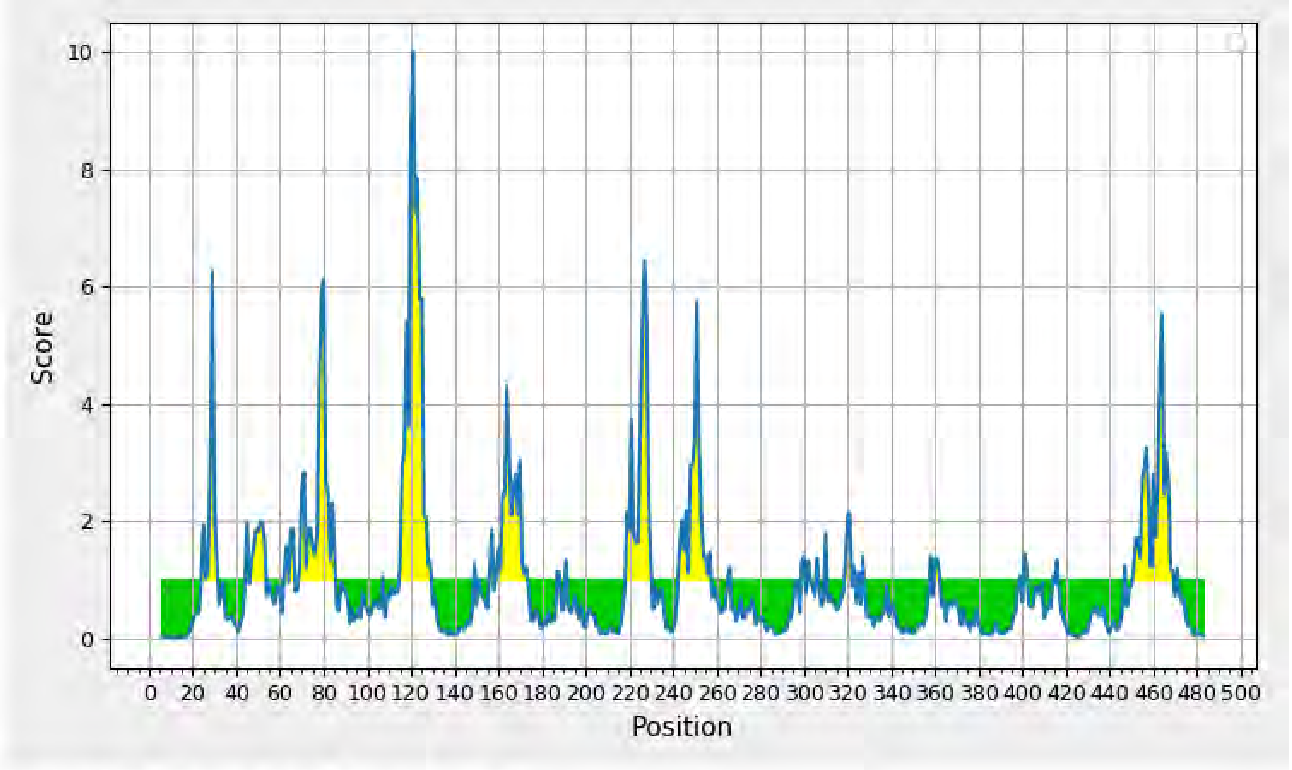


Emini Surface Accessibility Prediction Results

Input Sequences

```
  1 MIRKLFYIIF IILFCSNLFS QIVKNEISEK YIKENIAVFE IQDVSTGYSK DLGKKVTTLI
 61 ENSLTRMKRF NIVDRENLYK YLKEMELQLT GITDEQVIEM GKIYGYSKAI TGKITHSSTR
121 YDYDSDDGTG TIYANVDLVL QIVDVSTTKI LYSSKVSGSS YYSIDRYPSQ AFRDAAIDEA
181 CNDLVYKVSA KMRNIFKITL KISDITDGNI ILLAGYDHGL TKNTRFKVYS KSEDIVLPSG
241 NVIEGQYKQK GTLRIKDMGS EYSIATISRG RNIQVGDIVR ETYIGNFIFG LNINYASYKI
301 NPLVKEFQGT NSAGGKIKVN LNKNDYALGM HLKFGYDFQL FSPNLSMGLL FGDFFKTSYG
361 IDTRFNFDIN IKIYQEIVRF VLTPYVGLGV TFTDIGEVYG GDYRNGNLLI PNGTKIKSTD
421 VMLGIGLLAN IQYNITDTLG INAGVGYRFY TKPINAGTYY EDNSFNMPEE IKTVNLTGLE
481 FMVGVYGLF
```

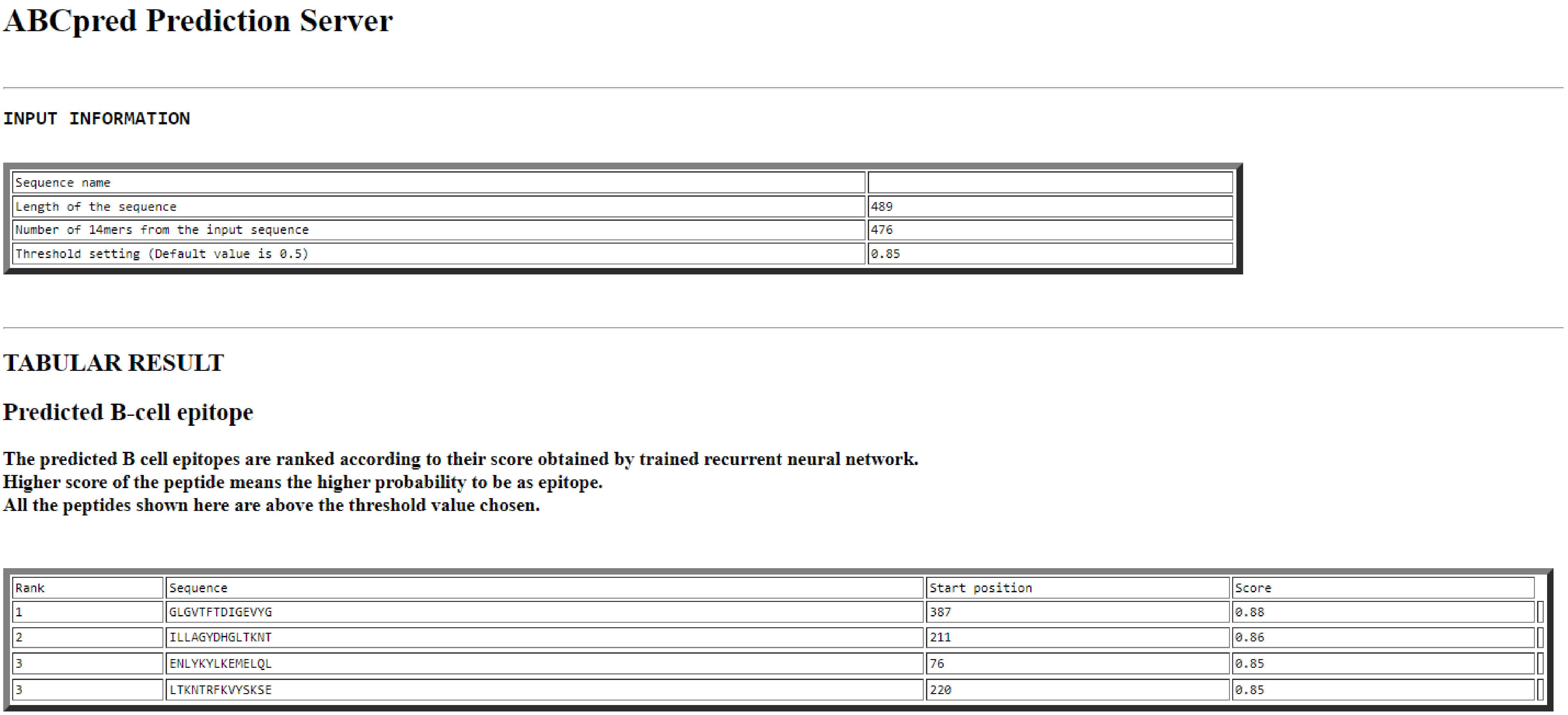
Center position: 6 Window size: 12 Threshold: 1.000



Average: 1.000 Minimum: 0.007 Maximum: 10.009

MIRKLFYIIFIILFCSNLFSQIVKNEISEKYIKENIAVFEIQDVSTGYSKDLGKKVTTLIENSLTRMKRFNIVDRENLYKYLK
EMELQLTGITDEQVIEMGKIYGYSKAITGKITHSSTRYDYDSDDGTGTIYANVDLVLQIVDVSTTKILYSSKVSGSSYYSIDR
YPSQAFRDAAIDEACNDLVYKVSAKMRNIFKITLKISDITDGNIILLAGYDHGLTKNTRFKVYSKSEDIVLPSGNVIEGQYKQ
KGTLRIKDMGSEYSIATISRGRNIQVGDIVRETYIGNFIFGLNINYASYKINPLVKEFQGTNSAGGKIKVNLNKNDYALGMHL
KFGYDFQLFSPNLSMGLLFGDFFKTSYGIDTRFNFDINIKIYQEIVRFVLTPYVGLGVTFTDIGEVYGGDYRNGNLLIPNGTK
IKSTDVMLGIGLLANIQYNITDTLGINAGVGYRFYTKPINAGTYYEDNSFNMPEEIKTVNLTGLEFMVGVYGLF

Threshold: 0.85 Window: 14



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	489
Number of 14mers from the input sequence	476
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

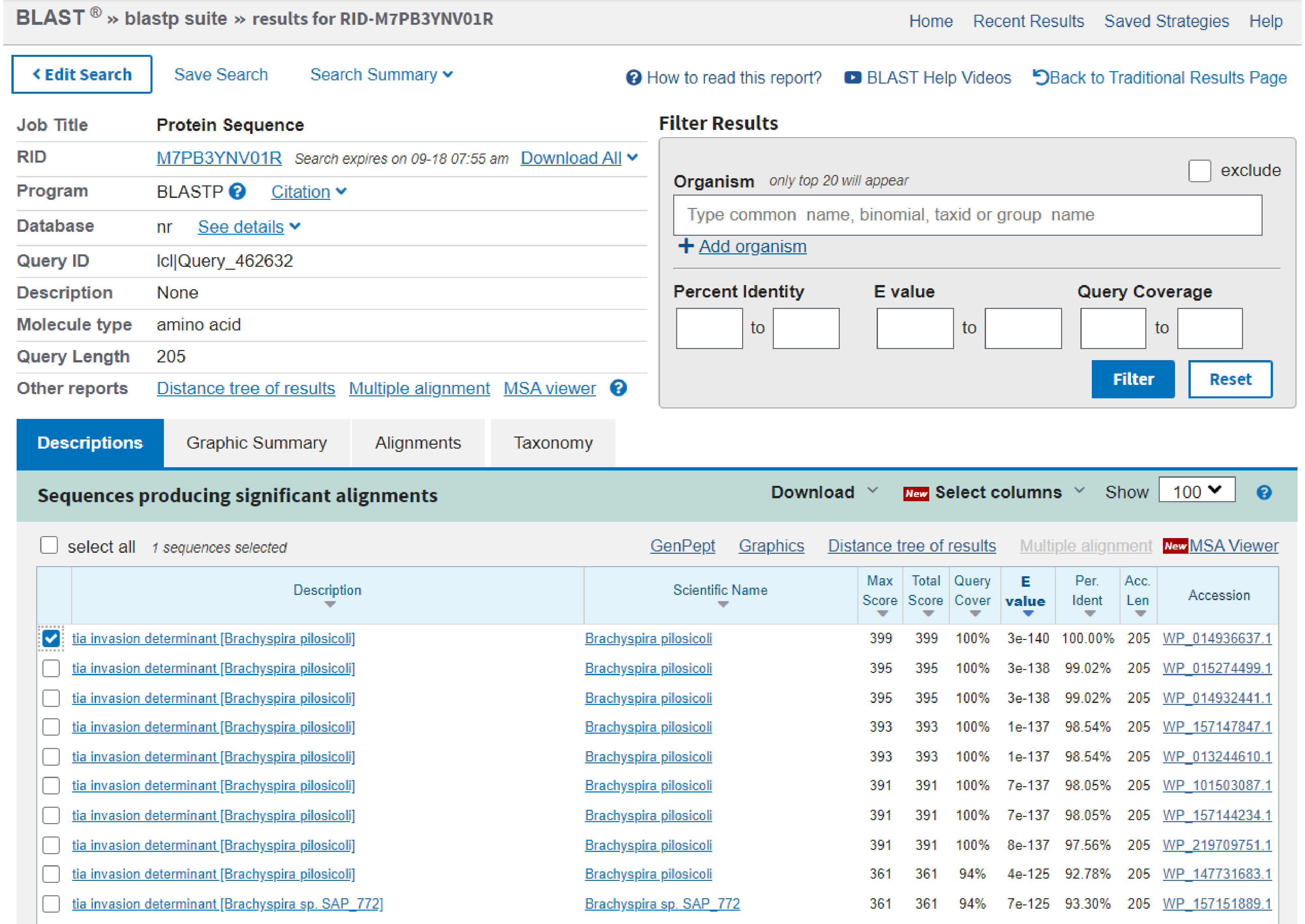
Rank	Sequence	Start position	Score
1	GLGVTFTDIGEVYG	387	0.88
2	ILLAGYDHGLTKNT	211	0.86
3	ENLYKYLKEMELQL	76	0.85
3	LTKNTRFKVYSKSE	220	0.85

PROTEINA 6

```
>fig|6666666.171271.peg.1529
MIRKLFYIIFIILFCSNLFSQIVKNEISEKYIKENIAVFEIQDVSTGYSKDLGKKVTTLIENSLTRMKRFNIVDRENLYKYLK
EMELQLTGITDEQVIEMGKIYGYSKAITGKITHSSTRYDYDSDDGTGTIYANVDLVLQIVDVSTTKILYSSKVSGSSYYSIDR
YPSQAFRDAAIDEACNDLVYKVSAKMRNIFKITLKISDITDGNIILLAGYDHGLTKNTRFKVYSKSEDIVLPSGNVIEGQYKQ
KGTLRIKDMGSEYSIATISRGRNIQVGDIVRETYIGNFIFGLNINYASYKINPLVKEFQGTNSAGGKIKVNLNKNDYALGMHL
KFGYDFQLFSPNLSMGLLFGDFFKTSYGIDTRFNFDINIKIYQEIVRFVLTPYVGLGVTFTDIGEVYGGDYRNGNLLIPNGTK
IKSTDVMLGIGLLANIQYNITDTLGINAGVGYRFYTKPINAGTYYEDNSFNMPEEIKTVNLTGLEFMVGVYGLF
```

PROTEINA 7

```
>fig|6666666.171271.peg.2232
MIKKILIIVVICLSFANISYSFQNGVYISPKFIYSIKGNNNMFVGAGAS
IGYNFNILSKYSPIRVEFEYLYKNGLEVNNYPNNIDNINIHSMLFNAYY
DINLIYINYDGEENNIYRNGKRHIMTISLGFSLGGNIDYSLSSSFNEKF
GLVKNYSYSDNFAFMYGPNISFGFHLNPTITLELGYRLLLDTAINLNHD
VLLFMRLNF
```



Job Title	Protein Sequence
RID	M7PB3YNV01R *Search expires on 09-18 07:55 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_462632
Description	None
Molecule type	amino acid
Query Length	205
Other reports	Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism *only top 20 will appear* ☐ exclude

Type common name, binomial, taxid or group name

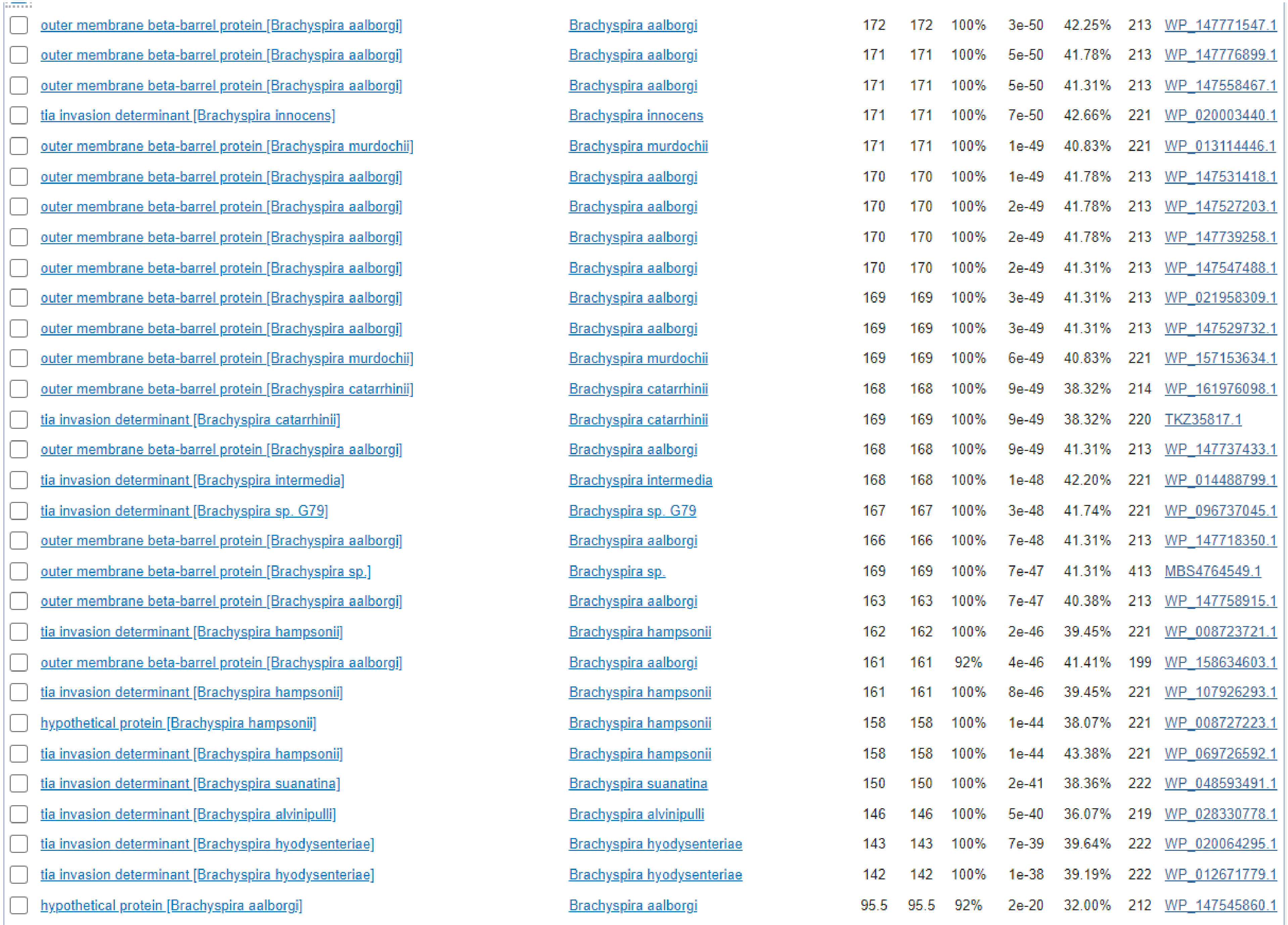
+ Add organism

Percent Identity ☐ to ☐ **E value** ☐ to ☐ **Query Coverage** ☐ to ☐

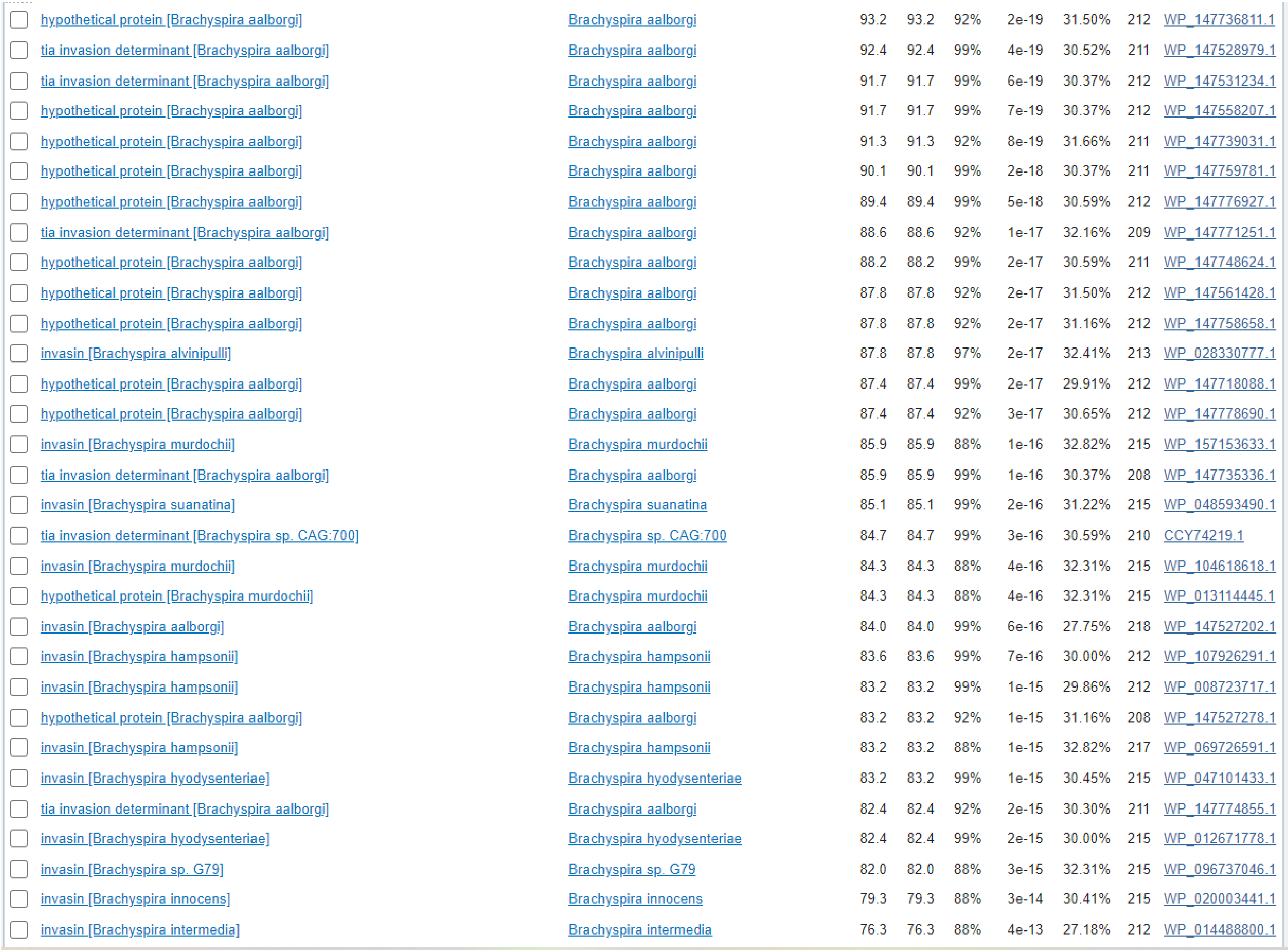
Sequences producing significant alignments

☐ select all *1 sequences selected*

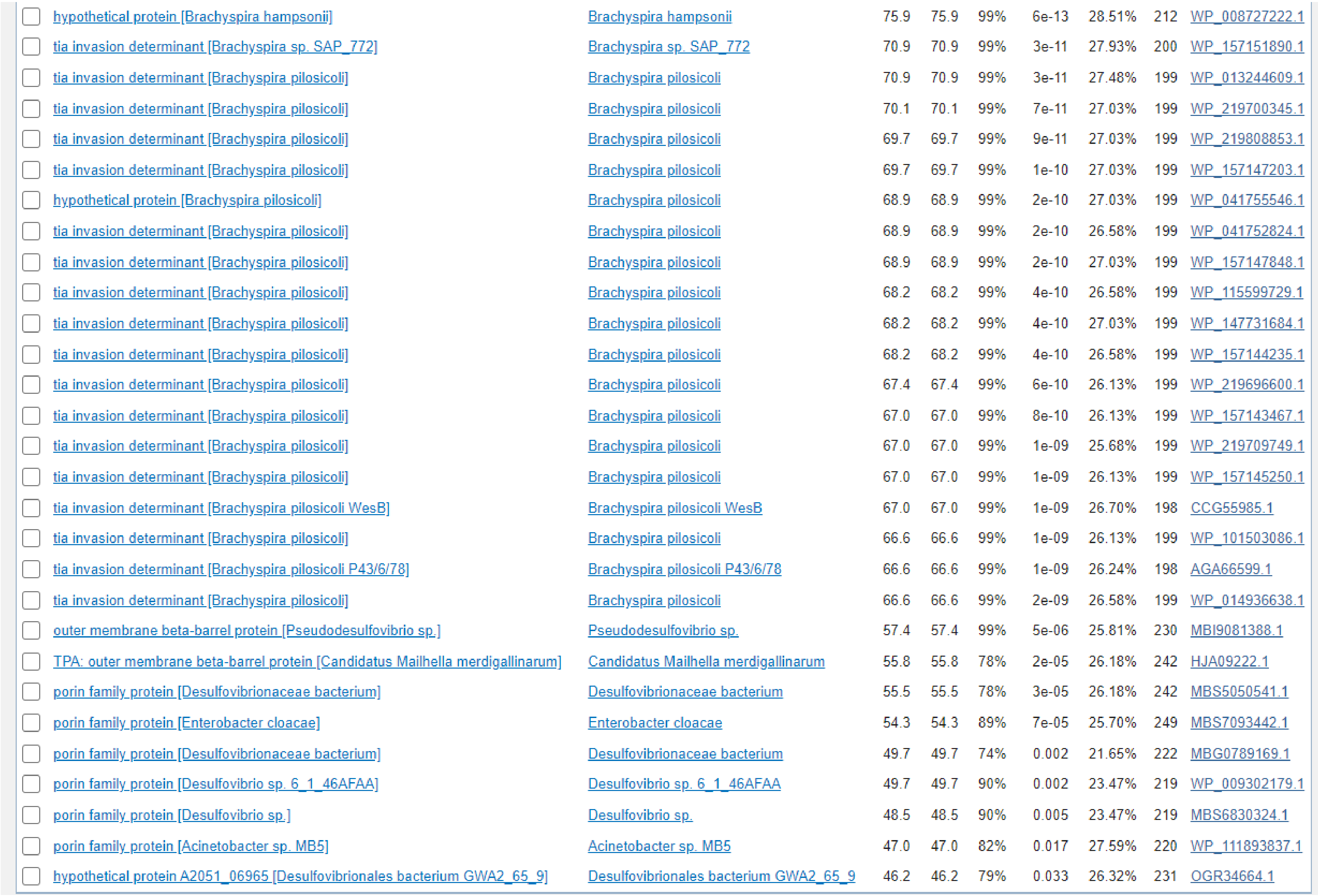
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	399	399	100%	3e-140	100.00%	205	WP_014936637.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	395	395	100%	3e-138	99.02%	205	WP_015274499.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	395	395	100%	3e-138	99.02%	205	WP_014932441.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	393	393	100%	1e-137	98.54%	205	WP_157147847.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	393	393	100%	1e-137	98.54%	205	WP_013244610.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	391	391	100%	7e-137	98.05%	205	WP_101503087.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	391	391	100%	7e-137	98.05%	205	WP_157144234.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	391	391	100%	8e-137	97.56%	205	WP_219709751.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	361	361	94%	4e-125	92.78%	205	WP_147731683.1
☐	tia invasion determinant [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	361	361	94%	7e-125	93.30%	205	WP_157151889.1



☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	172	172	100%	3e-50	42.25%	213	WP_147771547.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	171	171	100%	5e-50	41.78%	213	WP_147776899.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	171	171	100%	5e-50	41.31%	213	WP_147558467.1
☐	tia invasion determinant [Brachyspira innocens]	Brachyspira innocens	171	171	100%	7e-50	42.66%	221	WP_020003440.1
☐	outer membrane beta-barrel protein [Brachyspira murdochii]	Brachyspira murdochii	171	171	100%	1e-49	40.83%	221	WP_013114446.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	170	170	100%	1e-49	41.78%	213	WP_147531418.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	170	170	100%	2e-49	41.78%	213	WP_147527203.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	170	170	100%	2e-49	41.78%	213	WP_147739258.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	170	170	100%	2e-49	41.31%	213	WP_147547488.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	169	169	100%	3e-49	41.31%	213	WP_021958309.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	169	169	100%	3e-49	41.31%	213	WP_147529732.1
☐	outer membrane beta-barrel protein [Brachyspira murdochii]	Brachyspira murdochii	169	169	100%	6e-49	40.83%	221	WP_157153634.1
☐	outer membrane beta-barrel protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	168	168	100%	9e-49	38.32%	214	WP_161976098.1
☐	tia invasion determinant [Brachyspira catarrhinii]	Brachyspira catarrhinii	169	169	100%	9e-49	38.32%	220	TKZ35817.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	168	168	100%	9e-49	41.31%	213	WP_147737433.1
☐	tia invasion determinant [Brachyspira intermedia]	Brachyspira intermedia	168	168	100%	1e-48	42.20%	221	WP_014488799.1
☐	tia invasion determinant [Brachyspira sp. G79]	Brachyspira sp. G79	167	167	100%	3e-48	41.74%	221	WP_096737045.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	166	166	100%	7e-48	41.31%	213	WP_147718350.1
☐	outer membrane beta-barrel protein [Brachyspira sp.]	Brachyspira sp.	169	169	100%	7e-47	41.31%	413	MBS4764549.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	163	163	100%	7e-47	40.38%	213	WP_147758915.1
☐	tia invasion determinant [Brachyspira hampsonii]	Brachyspira hampsonii	162	162	100%	2e-46	39.45%	221	WP_008723721.1
☐	outer membrane beta-barrel protein [Brachyspira aalborgi]	Brachyspira aalborgi	161	161	92%	4e-46	41.41%	199	WP_158634603.1
☐	tia invasion determinant [Brachyspira hampsonii]	Brachyspira hampsonii	161	161	100%	8e-46	39.45%	221	WP_107926293.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	158	158	100%	1e-44	38.07%	221	WP_008727223.1
☐	tia invasion determinant [Brachyspira hampsonii]	Brachyspira hampsonii	158	158	100%	1e-44	43.38%	221	WP_069726592.1
☐	tia invasion determinant [Brachyspira suanatina]	Brachyspira suanatina	150	150	100%	2e-41	38.36%	222	WP_048593491.1
☐	tia invasion determinant [Brachyspira alvinipulli]	Brachyspira alvinipulli	146	146	100%	5e-40	36.07%	219	WP_028330778.1
☐	tia invasion determinant [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	143	143	100%	7e-39	39.64%	222	WP_020064295.1
☐	tia invasion determinant [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	142	142	100%	1e-38	39.19%	222	WP_012671779.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	95.5	95.5	92%	2e-20	32.00%	212	WP_147545860.1

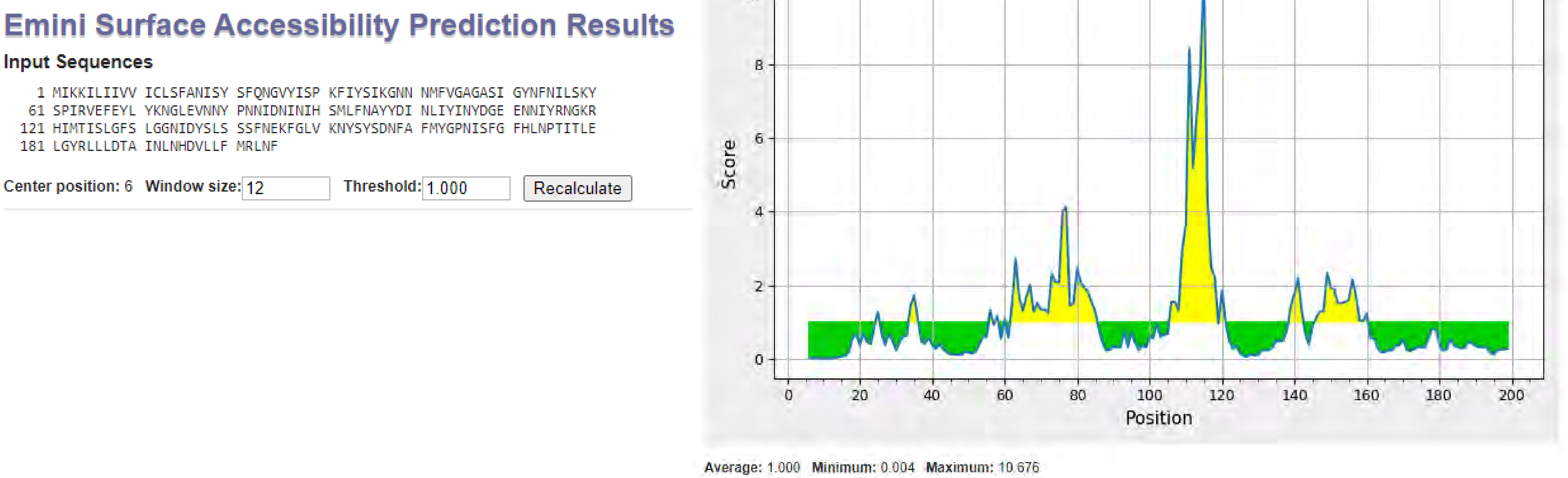


☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	93.2	93.2	92%	2e-19	31.50%	212	WP_147736811.1
☐	tia invasion determinant [Brachyspira aalborgi]	Brachyspira aalborgi	92.4	92.4	99%	4e-19	30.52%	211	WP_147528979.1
☐	tia invasion determinant [Brachyspira aalborgi]	Brachyspira aalborgi	91.7	91.7	99%	6e-19	30.37%	212	WP_147531234.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	91.7	91.7	99%	7e-19	30.37%	212	WP_147558207.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	91.3	91.3	92%	8e-19	31.66%	211	WP_147739031.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	90.1	90.1	99%	2e-18	30.37%	211	WP_147759781.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	89.4	89.4	99%	5e-18	30.59%	212	WP_147776927.1
☐	tia invasion determinant [Brachyspira aalborgi]	Brachyspira aalborgi	88.6	88.6	92%	1e-17	32.16%	209	WP_147771251.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	88.2	88.2	99%	2e-17	30.59%	211	WP_147748624.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	87.8	87.8	92%	2e-17	31.50%	212	WP_147561428.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	87.8	87.8	92%	2e-17	31.16%	212	WP_147758658.1
☐	invasin [Brachyspira alvinipulli]	Brachyspira alvinipulli	87.8	87.8	97%	2e-17	32.41%	213	WP_028330777.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	87.4	87.4	99%	2e-17	29.91%	212	WP_147718088.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	87.4	87.4	92%	3e-17	30.65%	212	WP_147778690.1
☐	invasin [Brachyspira murdochii]	Brachyspira murdochii	85.9	85.9	88%	1e-16	32.82%	215	WP_157153633.1
☐	tia invasion determinant [Brachyspira aalborgi]	Brachyspira aalborgi	85.9	85.9	99%	1e-16	30.37%	208	WP_147735336.1
☐	invasin [Brachyspira suanatina]	Brachyspira suanatina	85.1	85.1	99%	2e-16	31.22%	215	WP_048593490.1
☐	tia invasion determinant [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	84.7	84.7	99%	3e-16	30.59%	210	CCY74219.1
☐	invasin [Brachyspira murdochii]	Brachyspira murdochii	84.3	84.3	88%	4e-16	32.31%	215	WP_104618618.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	84.3	84.3	88%	4e-16	32.31%	215	WP_013114445.1
☐	invasin [Brachyspira aalborgi]	Brachyspira aalborgi	84.0	84.0	99%	6e-16	27.75%	218	WP_147527202.1
☐	invasin [Brachyspira hampsonii]	Brachyspira hampsonii	83.6	83.6	99%	7e-16	30.00%	212	WP_107926291.1
☐	invasin [Brachyspira hampsonii]	Brachyspira hampsonii	83.2	83.2	99%	1e-15	29.86%	212	WP_008723717.1
☐	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	83.2	83.2	92%	1e-15	31.16%	208	WP_147527278.1
☐	invasin [Brachyspira hampsonii]	Brachyspira hampsonii	83.2	83.2	88%	1e-15	32.82%	217	WP_069726591.1
☐	invasin [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	83.2	83.2	99%	1e-15	30.45%	215	WP_047101433.1
☐	tia invasion determinant [Brachyspira aalborgi]	Brachyspira aalborgi	82.4	82.4	92%	2e-15	30.30%	211	WP_147774855.1
☐	invasin [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	82.4	82.4	99%	2e-15	30.00%	215	WP_012671778.1
☐	invasin [Brachyspira sp. G79]	Brachyspira sp. G79	82.0	82.0	88%	3e-15	32.31%	215	WP_096737046.1
☐	invasin [Brachyspira innocens]	Brachyspira innocens	79.3	79.3	88%	3e-14	30.41%	215	WP_020003441.1
☐	invasin [Brachyspira intermedia]	Brachyspira intermedia	76.3	76.3	88%	4e-13	27.18%	212	WP_014488800.1



☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	75.9	75.9	99%	6e-13	28.51%	212	WP_008727222.1
☐	tia invasion determinant [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	70.9	70.9	99%	3e-11	27.93%	200	WP_157151890.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	70.9	70.9	99%	3e-11	27.48%	199	WP_013244609.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	70.1	70.1	99%	7e-11	27.03%	199	WP_219700345.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	69.7	69.7	99%	9e-11	27.03%	199	WP_219808853.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	69.7	69.7	99%	1e-10	27.03%	199	WP_157147203.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.9	68.9	99%	2e-10	27.03%	199	WP_041755546.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.9	68.9	99%	2e-10	26.58%	199	WP_041752824.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.9	68.9	99%	2e-10	27.03%	199	WP_157147848.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.2	68.2	99%	4e-10	26.58%	199	WP_115599729.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.2	68.2	99%	4e-10	27.03%	199	WP_147731684.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.2	68.2	99%	4e-10	26.58%	199	WP_157144235.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	67.4	67.4	99%	6e-10	26.13%	199	WP_219696600.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	67.0	67.0	99%	8e-10	26.13%	199	WP_157143467.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	67.0	67.0	99%	1e-09	25.68%	199	WP_219709749.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	67.0	67.0	99%	1e-09	26.13%	199	WP_157145250.1
☐	tia invasion determinant [Brachyspira pilosicoli WesB]	Brachyspira pilosicoli WesB	67.0	67.0	99%	1e-09	26.70%	198	CCG55985.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	66.6	66.6	99%	1e-09	26.13%	199	WP_101503086.1
☐	tia invasion determinant [Brachyspira pilosicoli P43/6/78]	Brachyspira pilosicoli P43/6/78	66.6	66.6	99%	1e-09	26.24%	198	AGA66599.1
☐	tia invasion determinant [Brachyspira pilosicoli]	Brachyspira pilosicoli	66.6	66.6	99%	2e-09	26.58%	199	WP_014936638.1
☐	outer membrane beta-barrel protein [Pseudodesulfovibrio sp.]	Pseudodesulfovibrio sp.	57.4	57.4	99%	5e-06	25.81%	230	MBI9081388.1
☐	TPA: outer membrane beta-barrel protein [Candidatus Mailhella merdigallinarum]	Candidatus Mailhella merdigallinarum	55.8	55.8	78%	2e-05	26.18%	242	HJA09222.1
☐	porin family protein [Desulfovibrionaceae bacterium]	Desulfovibrionaceae bacterium	55.5	55.5	78%	3e-05	26.18%	242	MBS5050541.1
☐	porin family protein [Enterobacter cloacae]	Enterobacter cloacae	54.3	54.3	89%	7e-05	25.70%	249	MBS7093442.1
☐	porin family protein [Desulfovibrionaceae bacterium]	Desulfovibrionaceae bacterium	49.7	49.7	74%	0.002	21.65%	222	MBG0789169.1
☐	porin family protein [Desulfovibrio sp. 6_1_46AFAA]	Desulfovibrio sp. 6_1_46AFAA	49.7	49.7	90%	0.002	23.47%	219	WP_009302179.1
☐	porin family protein [Desulfovibrio sp.]	Desulfovibrio sp.	48.5	48.5	90%	0.005	23.47%	219	MBS6830324.1
☐	porin family protein [Acinetobacter sp. MB5]	Acinetobacter sp. MB5	47.0	47.0	82%	0.017	27.59%	220	WP_111893837.1
☐	hypothetical protein A2051_06965 [Desulfovibrionales bacterium GWA2_65_9]	Desulfovibrionales bacterium GWA2_65_9	46.2	46.2	79%	0.033	26.32%	231	OGR34664.1

Threshold: 1.000 Window: 12



Emini Surface Accessibility Prediction Results

Input Sequences

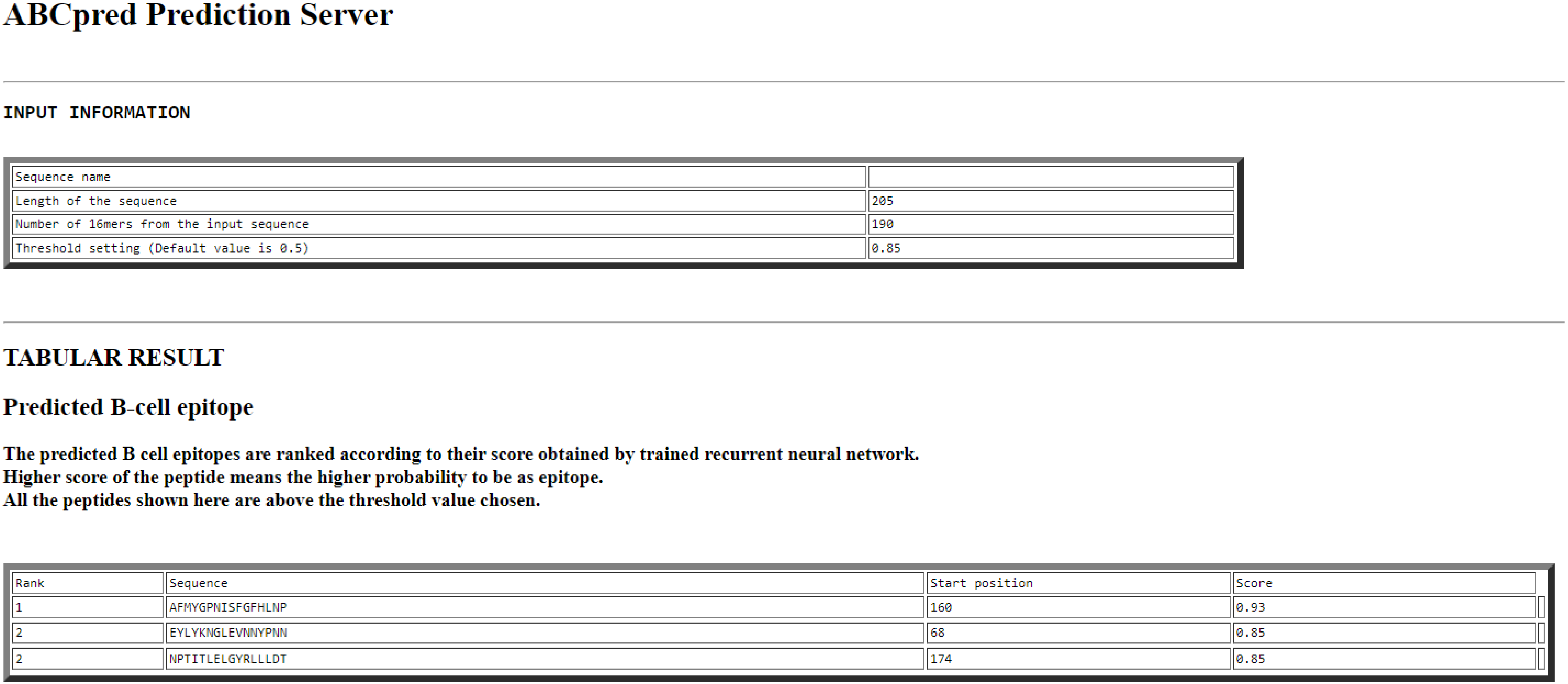
```
  1 MIKKILIIVV ICLSFANISY SFQNGVYISP KFIYSIKGNN NMFVGAGASI GYNFNILSKY
 61 SPIRVEFEYL YKNGLEVNNY PNNIDNINIH SMLFNAYYDI NLIYINYDGE ENNIYRNGKR
121 HIMTISLGFS LGGNIDYSLS SSFNEKFGLV KNYSYSDNFA FMYGPNISFG FHLNPTITLE
181 LGYRLLLDTA INLNHDVLLF MRLNF
```

Center position: 6 **Window size:** 12 **Threshold:** 1.000

Average: 1.000 **Minimum:** 0.004 **Maximum:** 10.676

MIKKILIIVVICLSFANISYSFQNGVYISPKFIYSIKGNNNMFVGAGASIGYNFNILSKYSPIRVEFEYLYKNGLEVNNYPNNI
DNINIHSMLFNAYYDINLIYINYDGEENNIYRNGKRHIMTISLGFSLGGNIDYSLSSSFNEKFGLVKNYSYSDNFAFMYGPNIS
FGFHLNPTITLELGYRLLLDTAINLNHDVLLFMRLNF

Threshold: 0.85 Window: 16



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	205
Number of 16mers from the input sequence	190
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

**The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.**

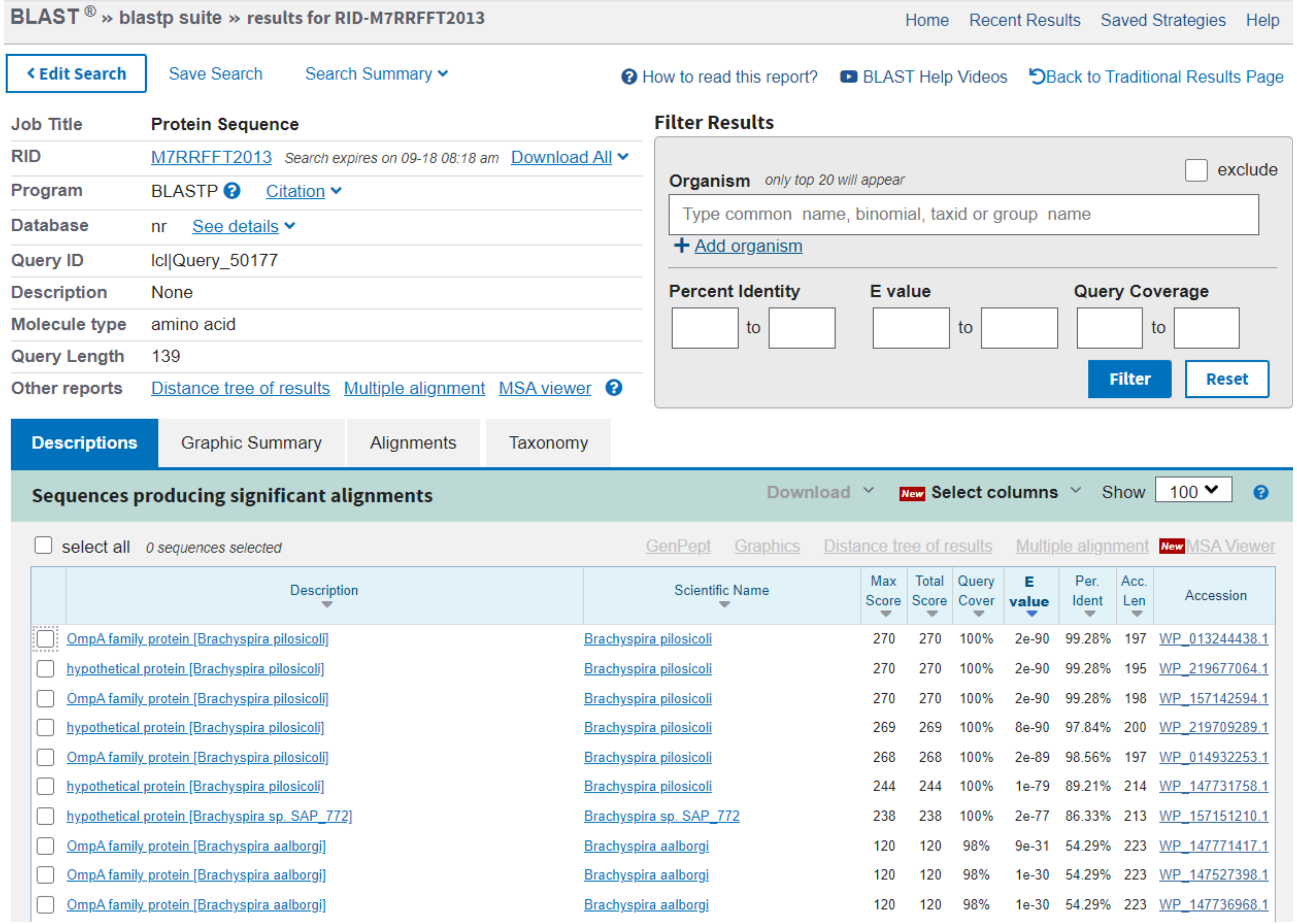
Rank	Sequence	Start position	Score
1	AFMYGPNISFGFHLNP	160	0.93
2	EYLYKNGLEVNNYPNN	68	0.85
2	NPTITLELGYRLLLDT	174	0.85

PROTEINA 7

```
>fig|6666666.171271.peg.2232
MIKKILIIVVICLSFANISYSFQNGVYISPKFIYSIKGNNNMFVGAGASIGYNFNILSKY
SPIRVEFEYLYKNGLEVNNYPNNIDNINIHSMLFNAYYDINLIYINYDGEENNIYRNGKR
HIMTISLGFSLGGNIDYSLSSSFNEKFGLVKNYSYSDNFAFMYGPNISFGFHLNPTITLE
LGYRLLLDTAINLNHDVLLFMRLNF
```

PROTEINA 8

```
>fig|6666666.171271.peg.2472
MKDPILFDSNSSVVNTNKYAETLDYLSLVLKSTNILNIYIEGHIDSSEVRYMNKNTVYNL
STTNNILYLYDRNNEVDLSYLRSLAVGDLLTDNDNKLKAIGLQNLIDYGTPEQNRRVEFV
IIENSNDMYMYTNYIYNLY
```



Job Title	**Protein Sequence**
RID	M7RRFFT2013 *Search expires on 09-18 08:18 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_50177
Description	None
Molecule type	amino acid
Query Length	139
Other reports	Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism *only top 20 will appear* ☐ exclude

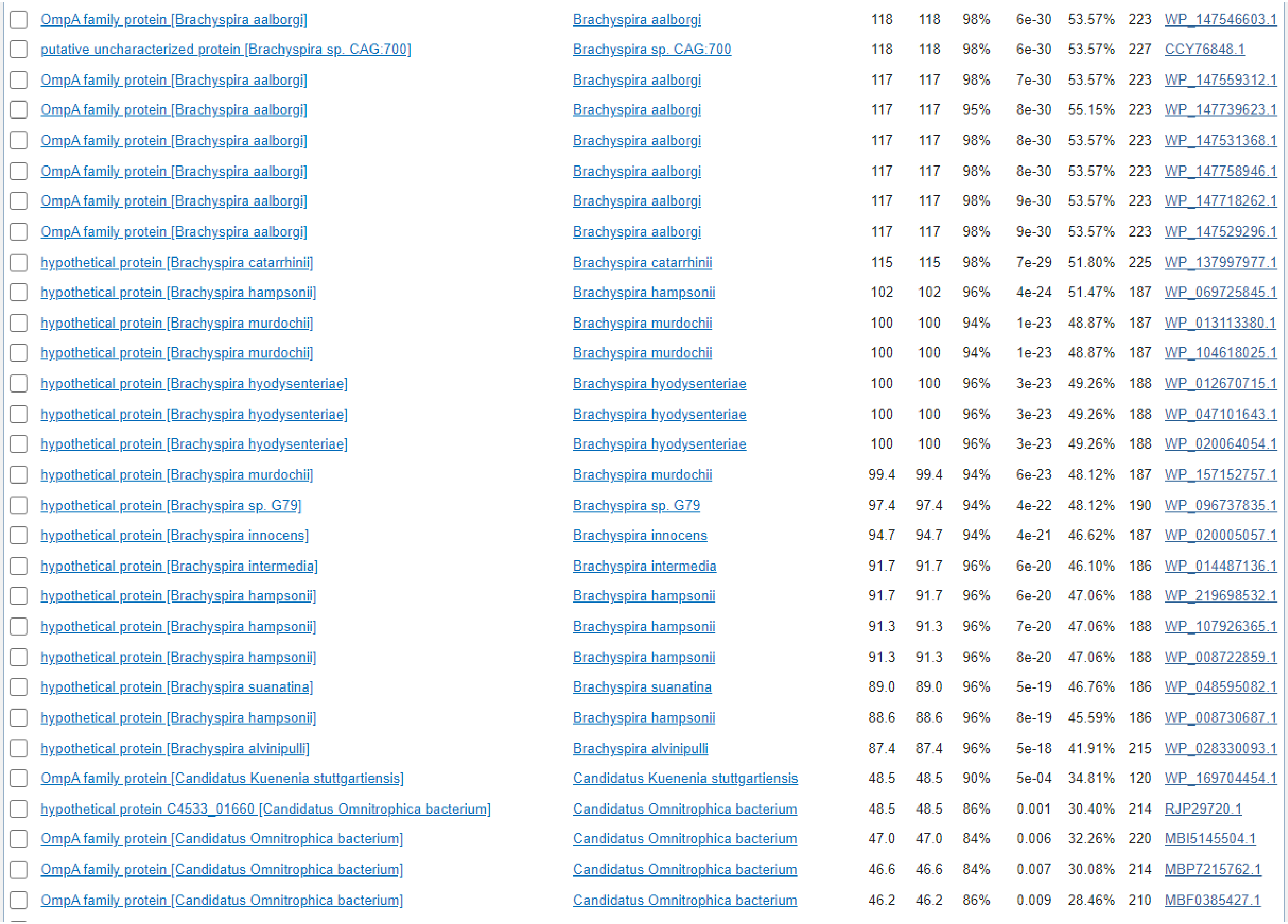
Type common name, binomial, taxid or group name

Percent Identity ☐ to ☐ **E value** ☐ to ☐ **Query Coverage** ☐ to ☐

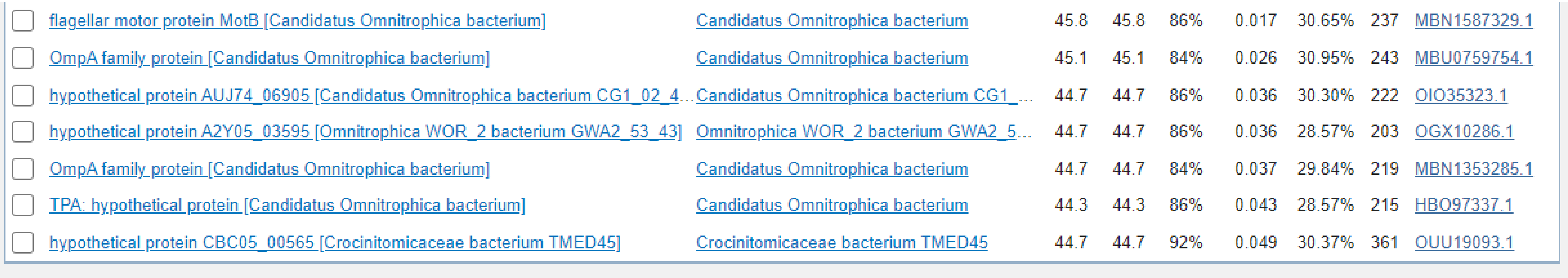
Sequences producing significant alignments Show 100

☐ select all *0 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☐	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	270	270	100%	2e-90	99.28%	197	WP_013244438.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	270	270	100%	2e-90	99.28%	195	WP_219677064.1
☐	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	270	270	100%	2e-90	99.28%	198	WP_157142594.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	269	269	100%	8e-90	97.84%	200	WP_219709289.1
☐	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	268	268	100%	2e-89	98.56%	197	WP_014932253.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	244	244	100%	1e-79	89.21%	214	WP_147731758.1
☐	hypothetical protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	238	238	100%	2e-77	86.33%	213	WP_157151210.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	120	120	98%	9e-31	54.29%	223	WP_147771417.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	120	120	98%	1e-30	54.29%	223	WP_147527398.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	120	120	98%	1e-30	54.29%	223	WP_147736968.1

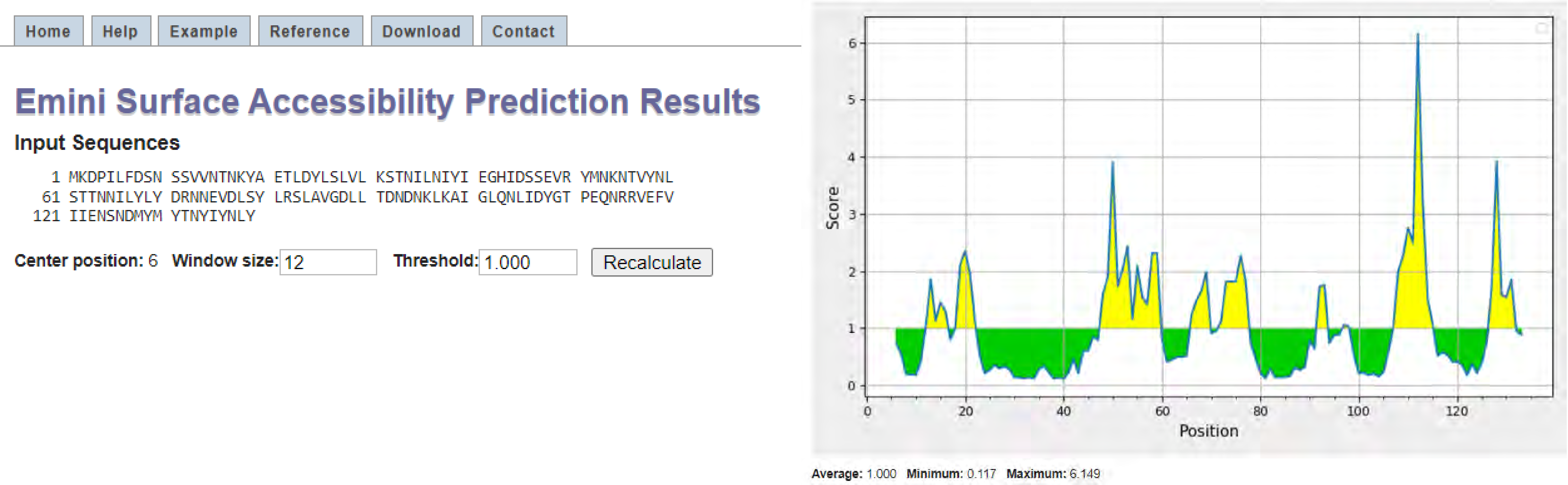


☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	118	118	98%	6e-30	53.57%	223	WP_147546603.1
☐	putative uncharacterized protein [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	118	118	98%	6e-30	53.57%	227	CCY76848.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	117	117	98%	7e-30	53.57%	223	WP_147559312.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	117	117	95%	8e-30	55.15%	223	WP_147739623.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	117	117	98%	8e-30	53.57%	223	WP_147531368.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	117	117	98%	8e-30	53.57%	223	WP_147758946.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	117	117	98%	9e-30	53.57%	223	WP_147718262.1
☐	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	117	117	98%	9e-30	53.57%	223	WP_147529296.1
☐	hypothetical protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	115	115	98%	7e-29	51.80%	225	WP_137997977.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	102	102	96%	4e-24	51.47%	187	WP_069725845.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	100	100	94%	1e-23	48.87%	187	WP_013113380.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	100	100	94%	1e-23	48.87%	187	WP_104618025.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	100	100	96%	3e-23	49.26%	188	WP_012670715.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	100	100	96%	3e-23	49.26%	188	WP_047101643.1
☐	hypothetical protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	100	100	96%	3e-23	49.26%	188	WP_020064054.1
☐	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	99.4	99.4	94%	6e-23	48.12%	187	WP_157152757.1
☐	hypothetical protein [Brachyspira sp. G79]	Brachyspira sp. G79	97.4	97.4	94%	4e-22	48.12%	190	WP_096737835.1
☐	hypothetical protein [Brachyspira innocens]	Brachyspira innocens	94.7	94.7	94%	4e-21	46.62%	187	WP_020005057.1
☐	hypothetical protein [Brachyspira intermedia]	Brachyspira intermedia	91.7	91.7	96%	6e-20	46.10%	186	WP_014487136.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	91.7	91.7	96%	6e-20	47.06%	188	WP_219698532.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	91.3	91.3	96%	7e-20	47.06%	188	WP_107926365.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	91.3	91.3	96%	8e-20	47.06%	188	WP_008722859.1
☐	hypothetical protein [Brachyspira suanatina]	Brachyspira suanatina	89.0	89.0	96%	5e-19	46.76%	186	WP_048595082.1
☐	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	88.6	88.6	96%	8e-19	45.59%	186	WP_008730687.1
☐	hypothetical protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	87.4	87.4	96%	5e-18	41.91%	215	WP_028330093.1
☐	OmpA family protein [Candidatus Kuenenia stuttgartiensis]	Candidatus Kuenenia stuttgartiensis	48.5	48.5	90%	5e-04	34.81%	120	WP_169704454.1
☐	hypothetical protein C4533_01660 [Candidatus Omnitrophica bacterium]	Candidatus Omnitrophica bacterium	48.5	48.5	86%	0.001	30.40%	214	RJP29720.1
☐	OmpA family protein [Candidatus Omnitrophica bacterium]	Candidatus Omnitrophica bacterium	47.0	47.0	84%	0.006	32.26%	220	MBI5145504.1
☐	OmpA family protein [Candidatus Omnitrophica bacterium]	Candidatus Omnitrophica bacterium	46.6	46.6	84%	0.007	30.08%	214	MBP7215762.1
☐	OmpA family protein [Candidatus Omnitrophica bacterium]	Candidatus Omnitrophica bacterium	46.2	46.2	86%	0.009	28.46%	210	MBF0385427.1



☐	flagellar motor protein MotB [Candidatus Omnitrophica bacterium]	Candidatus Omnitrophica bacterium	45.8	45.8	86%	0.017	30.65%	237	MBN1587329.1
☐	OmpA family protein [Candidatus Omnitrophica bacterium]	Candidatus Omnitrophica bacterium	45.1	45.1	84%	0.026	30.95%	243	MBU0759754.1
☐	hypothetical protein AUJ74_06905 [Candidatus Omnitrophica bacterium CG1_02_4…	Candidatus Omnitrophica bacterium CG1_…	44.7	44.7	86%	0.036	30.30%	222	OIO35323.1
☐	hypothetical protein A2Y05_03595 [Omnitrophica WOR_2 bacterium GWA2_53_43]	Omnitrophica WOR_2 bacterium GWA2_5…	44.7	44.7	86%	0.036	28.57%	203	OGX10286.1
☐	OmpA family protein [Candidatus Omnitrophica bacterium]	Candidatus Omnitrophica bacterium	44.7	44.7	84%	0.037	29.84%	219	MBN1353285.1
☐	TPA: hypothetical protein [Candidatus Omnitrophica bacterium]	Candidatus Omnitrophica bacterium	44.3	44.3	86%	0.043	28.57%	215	HBO97337.1
☐	hypothetical protein CBC05_00565 [Crocinitomicaceae bacterium TMED45]	Crocinitomicaceae bacterium TMED45	44.7	44.7	92%	0.049	30.37%	361	OUU19093.1

Threshold: 1.000 **Window: 12**



Emini Surface Accessibility Prediction Results

Input Sequences

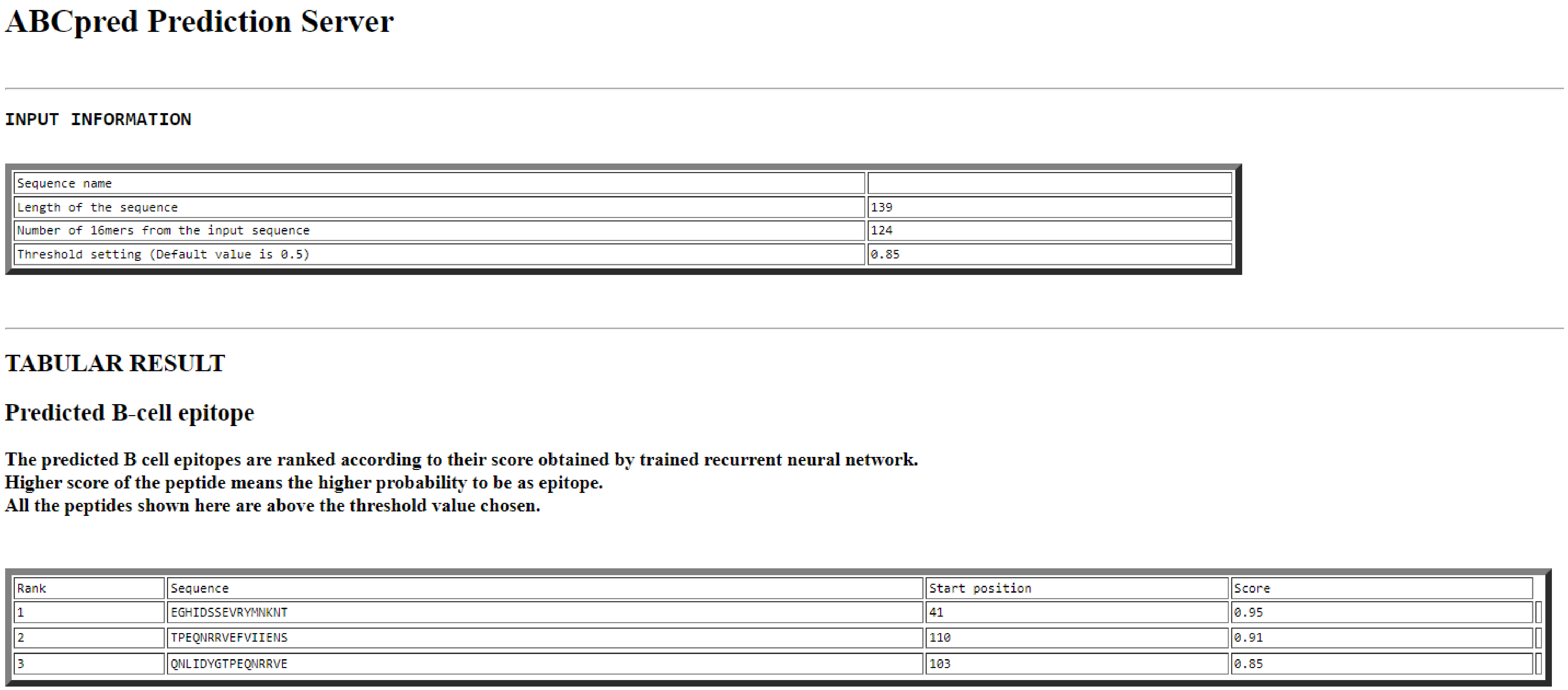
```
  1 MKDPILFDSN SSVVNTNKYA ETLDYLSLVL KSTNILNIYI EGHIDSSEVR YMNKNTVYNL
 61 STTNNILYLY DRNNEVDLSY LRSLAVGDLL TDNDNKLKAI GLQNLIDYGT PEQNRRVEFV
121 IIENSNDMYM YTNYIYNLY
```

Center position: 6 **Window size:** 12 **Threshold:** 1.000

Average: 1.000 **Minimum:** 0.117 **Maximum:** 6.149

MKDPILFDSNSSVVNTNKYAETLDYLSLVLKSTNILNIYIEGHIDSSEVRYMNKNTVYNLSTT
NNILYLYDRNNEVDLSYLRSLAVGDLLTDNDNKLKAIGLQNLIDYGTPEQNRRVEFVIIENSN
DMYMYTNYIYNLY

Threshold: 0.85 Window: 16



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	139
Number of 16mers from the input sequence	124
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

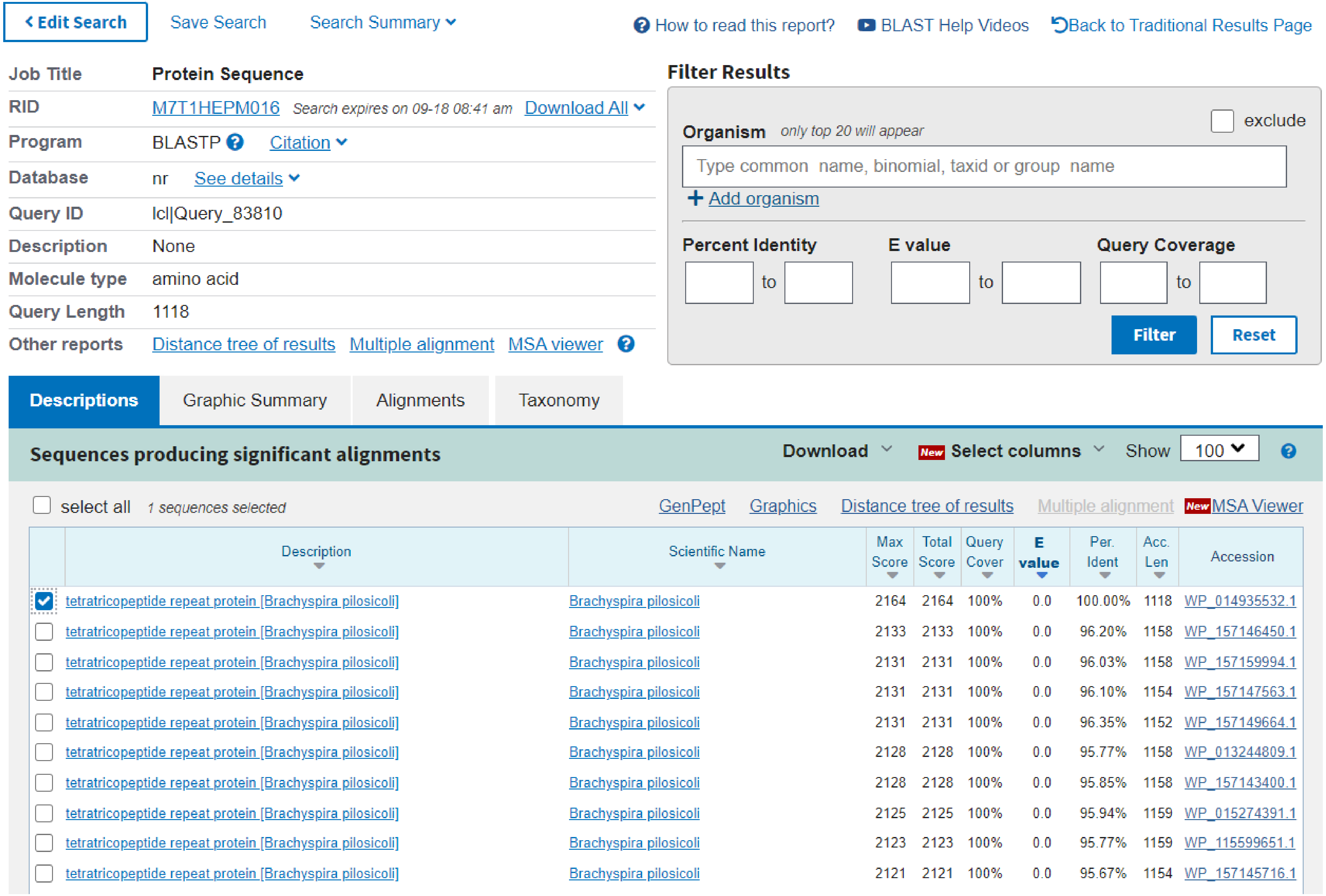
Rank	Sequence	Start position	Score
1	EGHIDSSEVRYMNKNT	41	0.95
2	TPEQNRRVEFVIIENS	110	0.91
3	QNLIDYGTPEQNRRVE	103	0.85

PROTEINA 8

```
>fig|6666666.171271.peg.2472
MKDPILFDSNSSVVNTNKYAETLDYLSLVLKSTNILNIYIEGHIDSSEVRYMNKNTVYN
LSTTNNILYLYDRNNEVDLSYLRSLAVGDLLTDNDNKLKAIGLQNLIDYGTPEQNRRVE
FVIIENSNDMYMYTNYIYNLY
```

PROTEINA 9

```
>fig|6666666.171271.peg.693
MPKIEDLERLGSLAFIIGNKNLPKELSQEDYNNFKSVFTDEYMANSTPNNDDDVPSIDDLDNLDNLDLPDDNTNDNLGLSDD
LGLPEELDTADNLDNNNTELDNLPDSTNDDLGLPDDLGLPEELNTADNLDNNNTELDNLPDSIDDDLGLPDDLGLPDDLDDI
KNDNKKLDNDTDLTNLDLPKDKELENKLNSEINDSYNSKLNNNIPDLPILDDLPLPESLDDYSNDSNDSIEETITDDIDNLA
DNLPDDLDDTLEEEIINNDSNLDDLDNLESILDDDTSEKEESKQEDTDNLDDLESILDDDTNEKEEPKQEDTDNLDDLESIL
DDDTSEKEEPKQEDTDNLDDLESILDDDTSEKEEPKQEDTDNLDDLDSILDDDTSEKEEPKQEDTDNLDDLDSILDDNAKEE
SNNNLETALDDDIKTQDADELENNIDNNSLESNNDNLMVENVAGNVRIIEEENTLPSPDSADSLGESKYEDVDKDINDDEVI
DNIKRLSPITRYHVLDAILNEKLSKNSMQKLLKALEKGESNEYITDFINNELGLSISDSRGGLLDIIPIPSSLKEYAKIIRI
AAIFLVLFVGVVLFSYQFIYKPVLANRYFKMGLENIYNSQFDEAERNFAKGDRLTPKKIKWYNKYAKEYIDRSAFDYALKKL
ETSVDIKPRNIDTRLLFGYYYRNKGEKELSEEDYNSGEELYNNLMTYTDKEKDLKRIYDDLGVLMISRAKTLVEPNYYNNAY
ENYREMINKFGDNVIPRKRVMLIKIYQDNYQDVKDLQNHINRLKNGYIDDDVYPKLAKYLLDKDDFYGARKLFEKLLAKYTN
NLESIVGYADYEARLKHYDRAKEILINSALPLYTSNPYNVGEEYVVYNMLGQIYYNLKEYGSAINNFKLALEKNSLYPDANFN
LANLYFYQDNDYKKAKEHYKIAYDNLAPDLRSDQLLYNLSWLYYLDGEYDLAFQGFNDLFYKNPDNSIVSYALGNSLLHLDR
ANLANGFYRNALNKALESRRDKFEMRTEKDFMFISYLASLHNNIGVSYAYNSVVSNKIENEQMAFKNFVVASEYFDQLRTSN
IDLDMAEKRTVNIDNQNIGASKYNMMAIQSKRNLKNSVIIDDYIPKTMFNLK
```

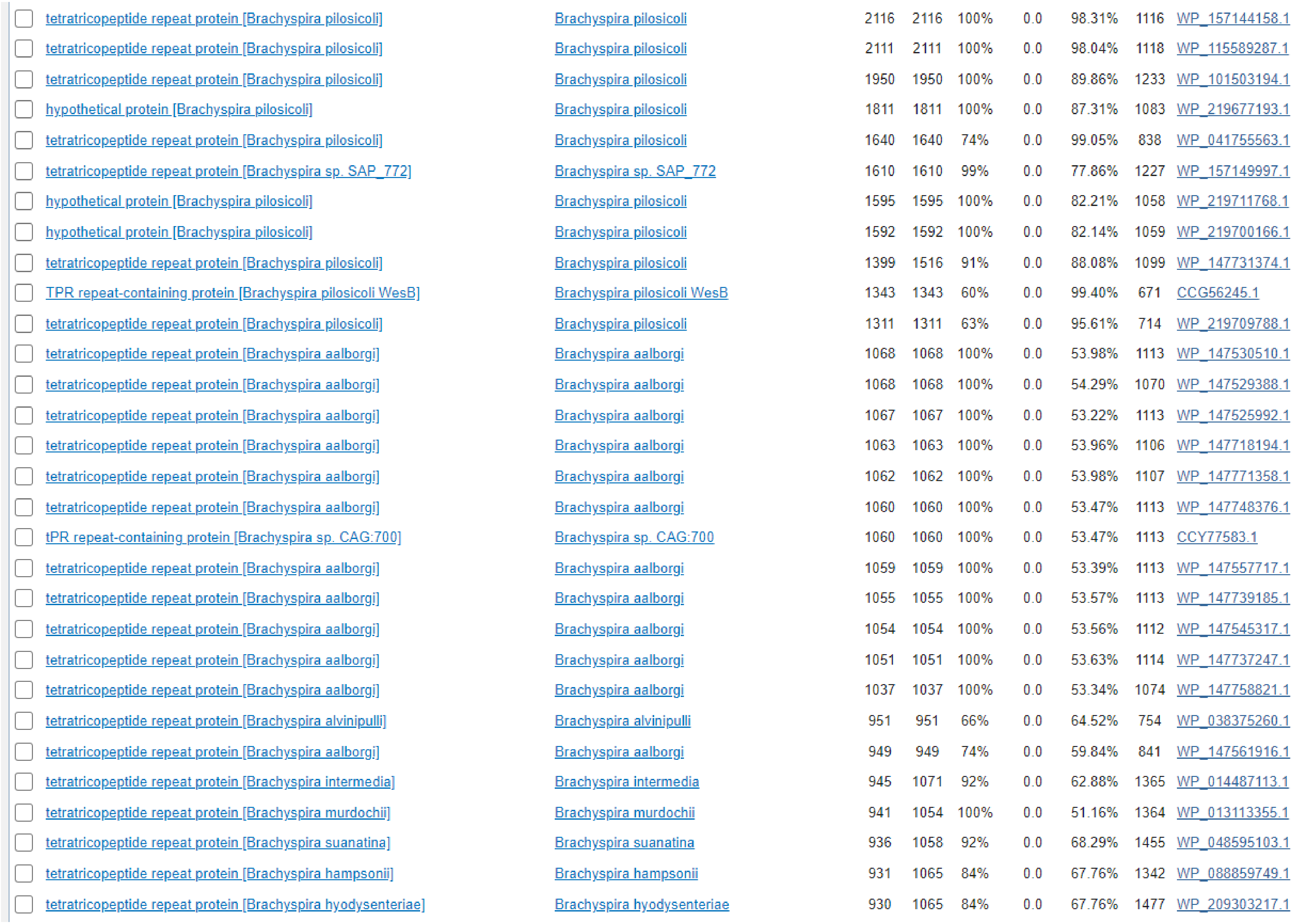


Job Title	Protein Sequence
RID	M7T1HEPM016 Search expires on 09-18 08:41 am Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_83810
Description	None
Molecule type	amino acid
Query Length	1118
Other reports	Distance tree of results Multiple alignment MSA viewer

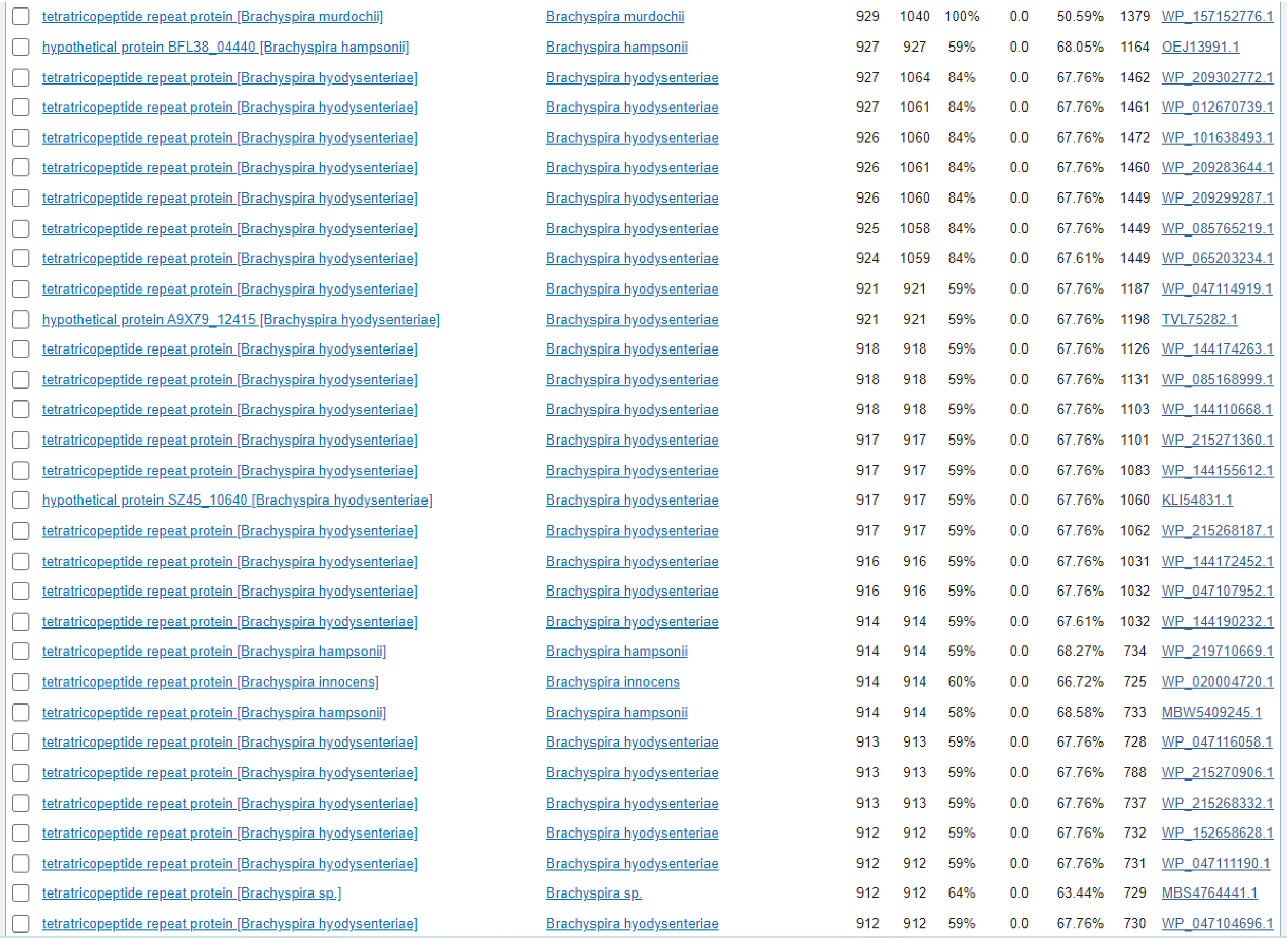
Sequences producing significant alignments

☐ select all *1 sequences selected*

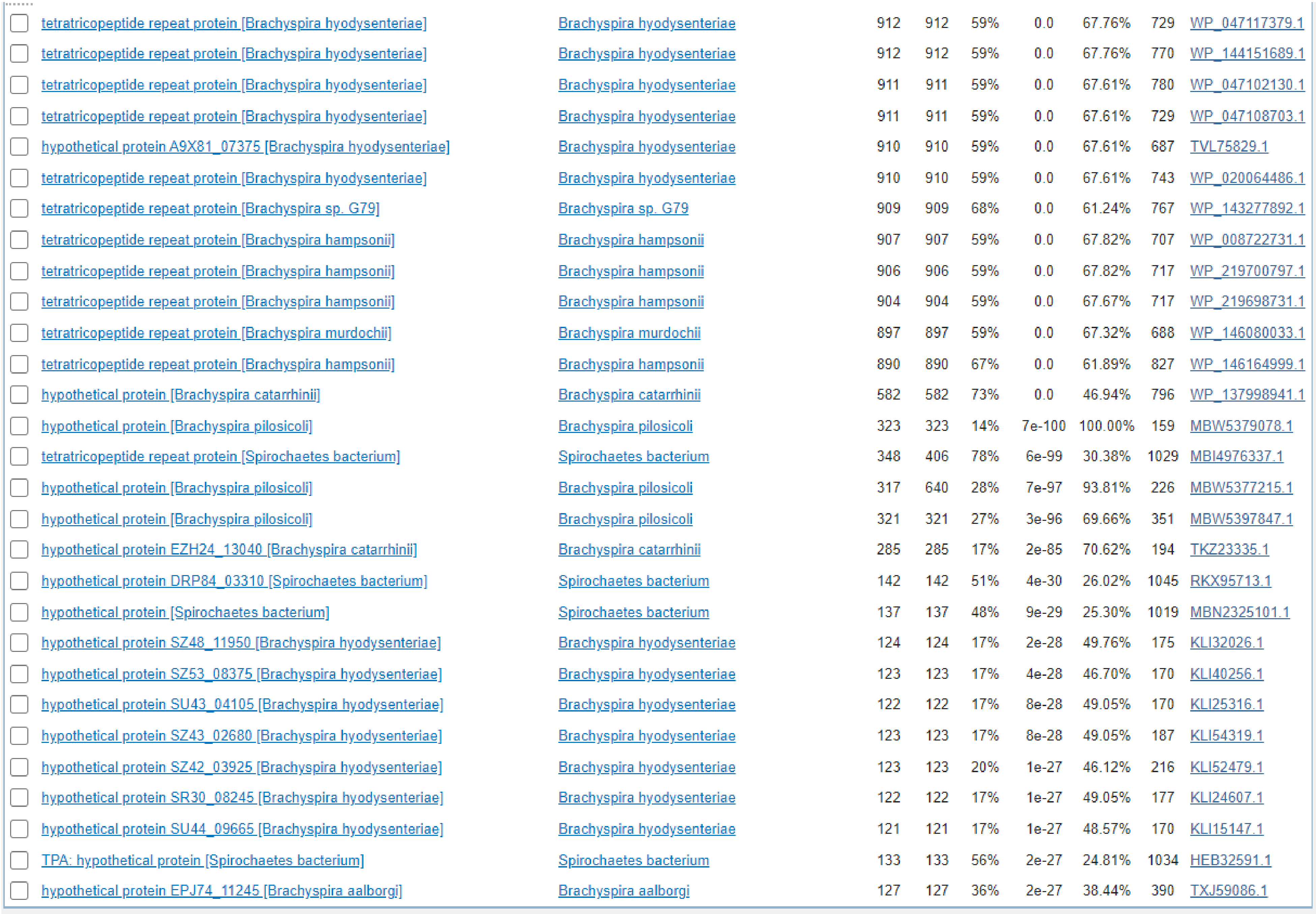
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2164	2164	100%	0.0	100.00%	1118	WP_014935532.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2133	2133	100%	0.0	96.20%	1158	WP_157146450.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2131	2131	100%	0.0	96.03%	1158	WP_157159994.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2131	2131	100%	0.0	96.10%	1154	WP_157147563.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2131	2131	100%	0.0	96.35%	1152	WP_157149664.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2128	2128	100%	0.0	95.77%	1158	WP_013244809.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2128	2128	100%	0.0	95.85%	1158	WP_157143400.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2125	2125	100%	0.0	95.94%	1159	WP_015274391.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2123	2123	100%	0.0	95.77%	1159	WP_115599651.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2121	2121	100%	0.0	95.67%	1154	WP_157145716.1



☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2116	2116	100%	0.0	98.31%	1116	WP_157144158.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	2111	2111	100%	0.0	98.04%	1118	WP_115589287.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1950	1950	100%	0.0	89.86%	1233	WP_101503194.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1811	1811	100%	0.0	87.31%	1083	WP_219677193.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1640	1640	74%	0.0	99.05%	838	WP_041755563.1
☐	tetratricopeptide repeat protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	1610	1610	99%	0.0	77.86%	1227	WP_157149997.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1595	1595	100%	0.0	82.21%	1058	WP_219711768.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1592	1592	100%	0.0	82.14%	1059	WP_219700166.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1399	1516	91%	0.0	88.08%	1099	WP_147731374.1
☐	TPR repeat-containing protein [Brachyspira pilosicoli WesB]	Brachyspira pilosicoli WesB	1343	1343	60%	0.0	99.40%	671	CCG56245.1
☐	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1311	1311	63%	0.0	95.61%	714	WP_219709788.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1068	1068	100%	0.0	53.98%	1113	WP_147530510.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1068	1068	100%	0.0	54.29%	1070	WP_147529388.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1067	1067	100%	0.0	53.22%	1113	WP_147525992.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1063	1063	100%	0.0	53.96%	1106	WP_147718194.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1062	1062	100%	0.0	53.98%	1107	WP_147771358.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1060	1060	100%	0.0	53.47%	1113	WP_147748376.1
☐	tPR repeat-containing protein [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	1060	1060	100%	0.0	53.47%	1113	CCY77583.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1059	1059	100%	0.0	53.39%	1113	WP_147557717.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1055	1055	100%	0.0	53.57%	1113	WP_147739185.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1054	1054	100%	0.0	53.56%	1112	WP_147545317.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1051	1051	100%	0.0	53.63%	1114	WP_147737247.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	1037	1037	100%	0.0	53.34%	1074	WP_147758821.1
☐	tetratricopeptide repeat protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	951	951	66%	0.0	64.52%	754	WP_038375260.1
☐	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	949	949	74%	0.0	59.84%	841	WP_147561916.1
☐	tetratricopeptide repeat protein [Brachyspira intermedia]	Brachyspira intermedia	945	1071	92%	0.0	62.88%	1365	WP_014487113.1
☐	tetratricopeptide repeat protein [Brachyspira murdochii]	Brachyspira murdochii	941	1054	100%	0.0	51.16%	1364	WP_013113355.1
☐	tetratricopeptide repeat protein [Brachyspira suanatina]	Brachyspira suanatina	936	1058	92%	0.0	68.29%	1455	WP_048595103.1
☐	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	931	1065	84%	0.0	67.76%	1342	WP_088859749.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	930	1065	84%	0.0	67.76%	1477	WP_209303217.1

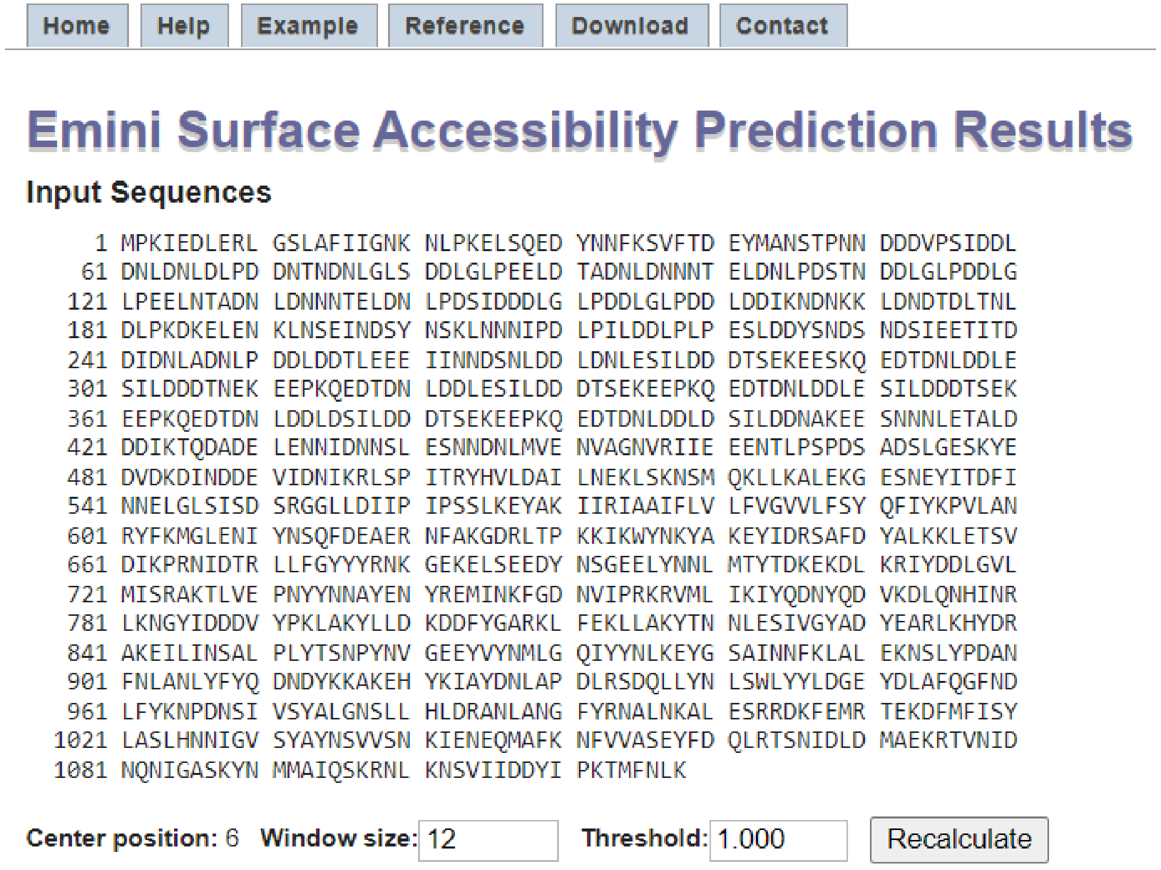


☐	tetratricopeptide repeat protein [Brachyspira murdochii]	Brachyspira murdochii	929	1040	100%	0.0	50.59%	1379	WP_157152776.1
☐	hypothetical protein BFL38_04440 [Brachyspira hampsonii]	Brachyspira hampsonii	927	927	59%	0.0	68.05%	1164	OEJ13991.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	927	1064	84%	0.0	67.76%	1462	WP_209302772.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	927	1061	84%	0.0	67.76%	1461	WP_012670739.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	926	1060	84%	0.0	67.76%	1472	WP_101638493.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	926	1061	84%	0.0	67.76%	1460	WP_209283644.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	926	1060	84%	0.0	67.76%	1449	WP_209299287.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	925	1058	84%	0.0	67.76%	1449	WP_085765219.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	924	1059	84%	0.0	67.61%	1449	WP_065203234.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	921	921	59%	0.0	67.76%	1187	WP_047114919.1
☐	hypothetical protein A9X79_12415 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	921	921	59%	0.0	67.76%	1198	TVL75282.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	918	918	59%	0.0	67.76%	1126	WP_144174263.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	918	918	59%	0.0	67.76%	1131	WP_085168999.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	918	918	59%	0.0	67.76%	1103	WP_144110668.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	917	917	59%	0.0	67.76%	1101	WP_215271360.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	917	917	59%	0.0	67.76%	1083	WP_144155612.1
☐	hypothetical protein SZ45_10640 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	917	917	59%	0.0	67.76%	1060	KLI54831.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	917	917	59%	0.0	67.76%	1062	WP_215268187.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	916	916	59%	0.0	67.76%	1031	WP_144172452.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	916	916	59%	0.0	67.76%	1032	WP_047107952.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	914	914	59%	0.0	67.61%	1032	WP_144190232.1
☐	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	914	914	59%	0.0	68.27%	734	WP_219710669.1
☐	tetratricopeptide repeat protein [Brachyspira innocens]	Brachyspira innocens	914	914	60%	0.0	66.72%	725	WP_020004720.1
☐	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	914	914	58%	0.0	68.58%	733	MBW5409245.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	913	913	59%	0.0	67.76%	728	WP_047116058.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	913	913	59%	0.0	67.76%	788	WP_215270906.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	913	913	59%	0.0	67.76%	737	WP_215268332.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	912	912	59%	0.0	67.76%	732	WP_152658628.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	912	912	59%	0.0	67.76%	731	WP_047111190.1
☐	tetratricopeptide repeat protein [Brachyspira sp.]	Brachyspira sp.	912	912	64%	0.0	63.44%	729	MBS4764441.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	912	912	59%	0.0	67.76%	730	WP_047104696.1



☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	912	912	59%	0.0	67.76%	729	WP_047117379.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	912	912	59%	0.0	67.76%	770	WP_144151689.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	911	911	59%	0.0	67.61%	780	WP_047102130.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	911	911	59%	0.0	67.61%	729	WP_047108703.1
☐	hypothetical protein A9X81_07375 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	910	910	59%	0.0	67.61%	687	TVL75829.1
☐	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	910	910	59%	0.0	67.61%	743	WP_020064486.1
☐	tetratricopeptide repeat protein [Brachyspira sp. G79]	Brachyspira sp. G79	909	909	68%	0.0	61.24%	767	WP_143277892.1
☐	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	907	907	59%	0.0	67.82%	707	WP_008722731.1
☐	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	906	906	59%	0.0	67.82%	717	WP_219700797.1
☐	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	904	904	59%	0.0	67.67%	717	WP_219698731.1
☐	tetratricopeptide repeat protein [Brachyspira murdochii]	Brachyspira murdochii	897	897	59%	0.0	67.32%	688	WP_146080033.1
☐	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	890	890	67%	0.0	61.89%	827	WP_146164999.1
☐	hypothetical protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	582	582	73%	0.0	46.94%	796	WP_137998941.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	323	323	14%	7e-100	100.00%	159	MBW5379078.1
☐	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	348	406	78%	6e-99	30.38%	1029	MBI4976337.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	317	640	28%	7e-97	93.81%	226	MBW5377215.1
☐	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	321	321	27%	3e-96	69.66%	351	MBW5397847.1
☐	hypothetical protein EZH24_13040 [Brachyspira catarrhinii]	Brachyspira catarrhinii	285	285	17%	2e-85	70.62%	194	TKZ23335.1
☐	hypothetical protein DRP84_03310 [Spirochaetes bacterium]	Spirochaetes bacterium	142	142	51%	4e-30	26.02%	1045	RKX95713.1
☐	hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	137	137	48%	9e-29	25.30%	1019	MBN2325101.1
☐	hypothetical protein SZ48_11950 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	124	124	17%	2e-28	49.76%	175	KLI32026.1
☐	hypothetical protein SZ53_08375 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	123	123	17%	4e-28	46.70%	170	KLI40256.1
☐	hypothetical protein SU43_04105 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	122	122	17%	8e-28	49.05%	170	KLI25316.1
☐	hypothetical protein SZ43_02680 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	123	123	17%	8e-28	49.05%	187	KLI54319.1
☐	hypothetical protein SZ42_03925 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	123	123	20%	1e-27	46.12%	216	KLI52479.1
☐	hypothetical protein SR30_08245 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	122	122	17%	1e-27	49.05%	177	KLI24607.1
☐	hypothetical protein SU44_09665 [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	121	121	17%	1e-27	48.57%	170	KLI15147.1
☐	TPA: hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	133	133	56%	2e-27	24.81%	1034	HEB32591.1
☐	hypothetical protein EPJ74_11245 [Brachyspira aalborgi]	Brachyspira aalborgi	127	127	36%	2e-27	38.44%	390	TXJ59086.1

Threshold: 1.000 Window: 12

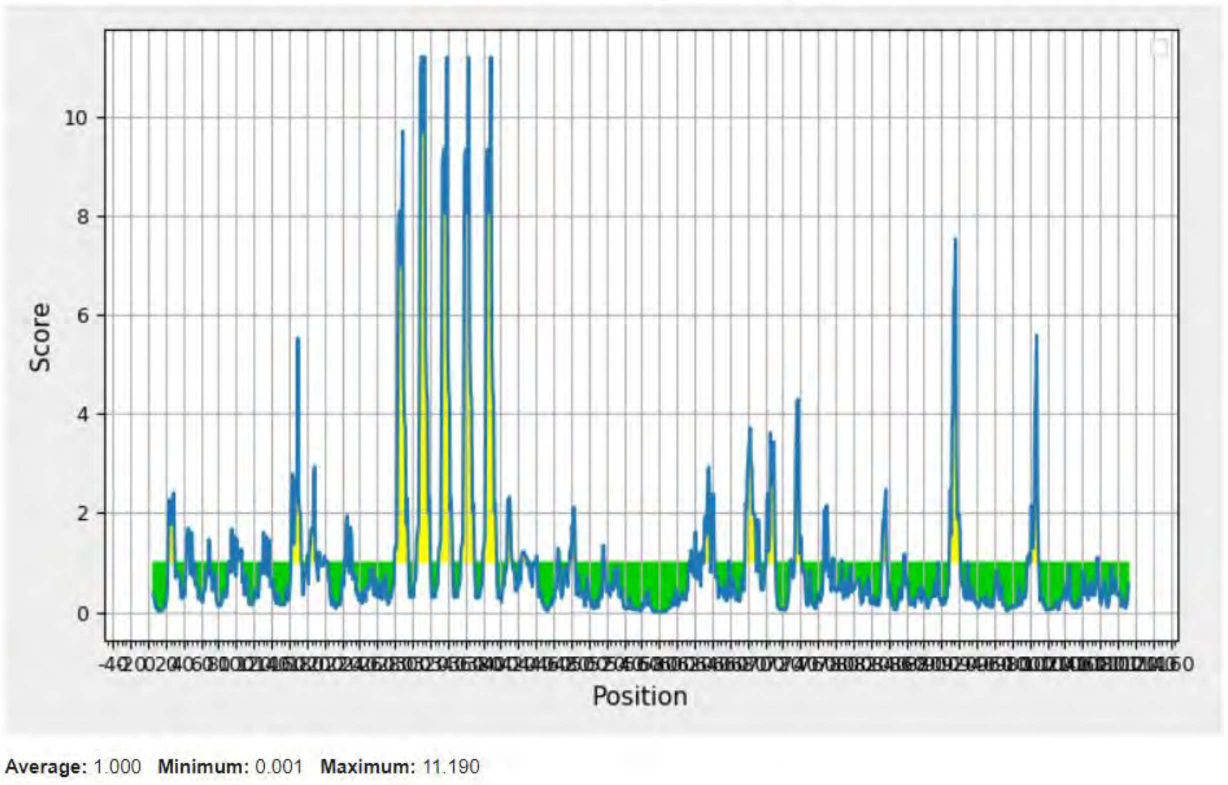


Emini Surface Accessibility Prediction Results

Input Sequences

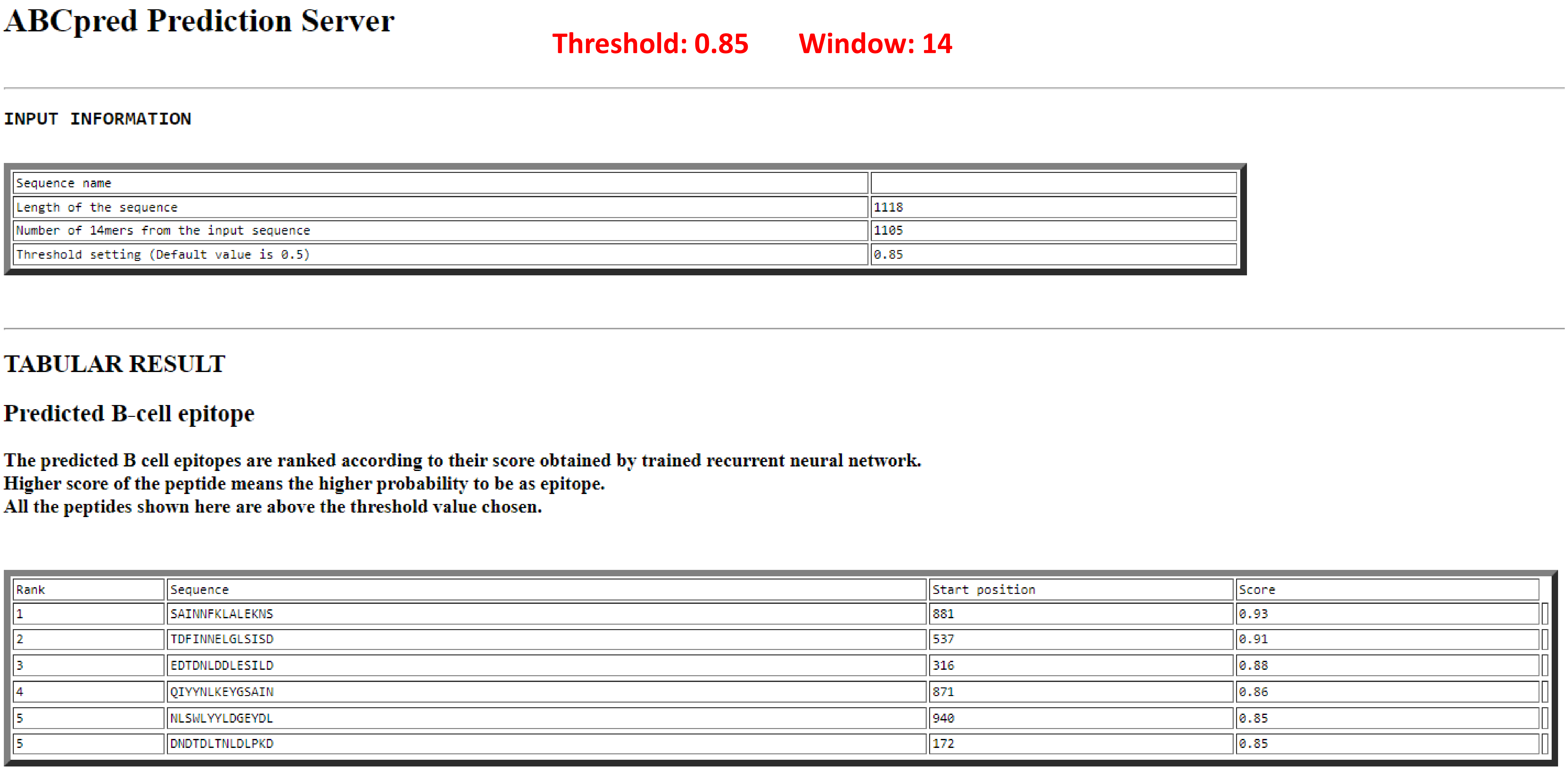
```
   1 MPKIEDLERL GSLAFIIGNK NLPKELSQED YNNFKSVFTD EYMANSTPNN DDDVPSIDDL
  61 DNLDNLDLPD DNTNDNLGLS DDLGLPEELD TADNLDNNNT ELDNLPDSTN DDLGLPDDLG
 121 LPEELNTADN LDNNNTELDN LPDSIDDDLG LPDDLGLPDD LDDIKNDNKK LDNDTDLTNL
 181 DLPKDKELEN KLNSEINDSY NSKLNNNIPD LPILDDLPLP ESLDDYSNDS NDSIEETITD
 241 DIDNLADNLP DDLDDTLEEE IINNDSNLDD LDNLESILDD DTSEKEESKQ EDTDNLDDLE
 301 SILDDDTNEK EEPKQEDTDN LDDLESILDD DTSEKEEPKQ EDTDNLDDLE SILDDDTSEK
 361 EEPKQEDTDN LDDLDSILDD DTSEKEEPKQ EDTDNLDDLD SILDDNAKEE SNNNLETALD
 421 DDIKTQDADE LENNIDNNSL ESNNDNLMVE NVAGNVRIIE EENTLPSPDS ADSLGESKYE
 481 DVDKDINDDE VIDNIKRLSP ITRYHVLDAI LNEKLSKNSM QKLLKALEKG ESNEYITDFI
 541 NNELGLSISD SRGGLLDIIP IPSSLKEYAK IIRIAAIFLV LFVGVVLFSY QFIYKPVLAN
 601 RYFKMGLENI YNSQFDEAER NFAKGDRLTP KKIKWYNKYA KEYIDRSAFD YALKKLETSV
 661 DIKPRNIDTR LLFGYYYRNK GEKELSEEDY NSGEELYNNL MTYTDKEKDL KRIYDDLGVL
 721 MISRAKTLVE PNYYNNAYEN YREMINKFGD NVIPRKRVML IKIYQDNYQD VKDLQNHINR
 781 LKNGYIDDDV YPKLAKYLLD KDDFYGARKL FEKLLAKYTN NLESIVGYAD YEARLKHYDR
 841 AKEILINSAL PLYTSNPYNV GEEYVYNMLG QIYYNLKEYG SAINNFKLAL EKNSLYPDAN
 901 FNLANLYFYQ DNDYKKAKEH YKIAYDNLAP DLRSDQLLYN LSWLYYLDGE YDLAFQGFND
 961 LFYKNPDNSI VSYALGNSLL HLDRANLANG FYRNALNKAL ESRRDKFEMR TEKDFMFISY
1021 LASLHNNIGV SYAYNSVVSN KIENEQMAFK NFVVASEYFD QLRTSNIDLD MAEKRTVNID
1081 NQNIGASKYN MMAIQSKRNL KNSVIIDDYI PKTMFNLK
```

Center position: 6 **Window size:** 12 **Threshold:** 1.000



Average: 1.000 **Minimum:** 0.001 **Maximum:** 11.190

MPKIEDLERLGSLAFIIGNKNLPKELSQEDYNNFKSVFTDEYMANSTPNNDDDVPSIDDLDNLDNLDLPDDNTNDNLGLSDDLGLPEELDTADNLDNNNTELDNLPDSTND
DLGLPDDLGLPEELNTADNLDNNNTELDNLPDSIDDDLGLPDDLGLPDDLDDIKNDNKKLDNDTDLTNLDLPKDKELENKLNSEINDSYNSKLNNNIPDLPILDDLPLPES
LDDYSNDSNDSIEETITDDIDNLADNLPDDLDDTLEEEIINNDSNLDDLDNLESILDDDTSEKEESKQEDTDNLDDLESILDDDTNEKEEPKQEDTDNLDDLESILDDDTS
EKEEPKQEDTDNLDDLESILDDDTSEKEEPKQEDTDNLDDLDSILDDDTSEKEEPKQEDTDNLDDLDSILDDNAKEESNNNLETALDDDIKTQDADELENNIDNNSLESNN
DNLMVENVAGNVRIIEEENTLPSPDSADSLGESKYEDVDKDINDDEVIDNIKRLSPITRYHVLDAILNEKLSKNSMQKLLKALEKGESNEYITDFINNELGLSISDSRGGL
LDIIPIPSSLKEYAKIIRIAAIFLVLFVGVVLFSYQFIYKPVLANRYFKMGLENIYNSQFDEAERNFAKGDRLTPKKIKWYNKYAKEYIDRSAFDYALKKLETSVDIKPRN
IDTRLLFGYYYRNKGEKELSEEDYNSGEELYNNLMTYTDKEKDLKRIYDDLGVLMISRAKTLVEPNYYNNAYENYREMINKFGDNVIPRKRVMLIKIYQDNYQDVKDLQNH
INRLKNGYIDDDVYPKLAKYLLDKDDFYGARKLFEKLLAKYTNNLESIVGYADYEARLKHYDRAKEILINSALPLYTSNPYNVGEEYVYNMLGQIYYNLKEYGSAINNFKL
ALEKNSLYPDANFNLANLYFYQDNDYKKAKEHYKIAYDNLAPDLRSDQLLYNLSWLYYLDGEYDLAFQGFNDLFYKNPDNSIVSYALGNSLLHLDRANLANGFYRNALNKA
LESRRDKFEMRTEKDFMFISYLASLHNNIGVSYAYNSVVSNKIENEQMAFKNFVVASEYFDQLRTSNIDLDMAEKRTVNIDNQNIGASKYNMMAIQSKRNLKNSVIIDDYI
PKTMFNLK



ABCpred Prediction Server

Threshold: 0.85 **Window: 14**

INPUT INFORMATION

Sequence name	
Length of the sequence	1118
Number of 14mers from the input sequence	1105
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

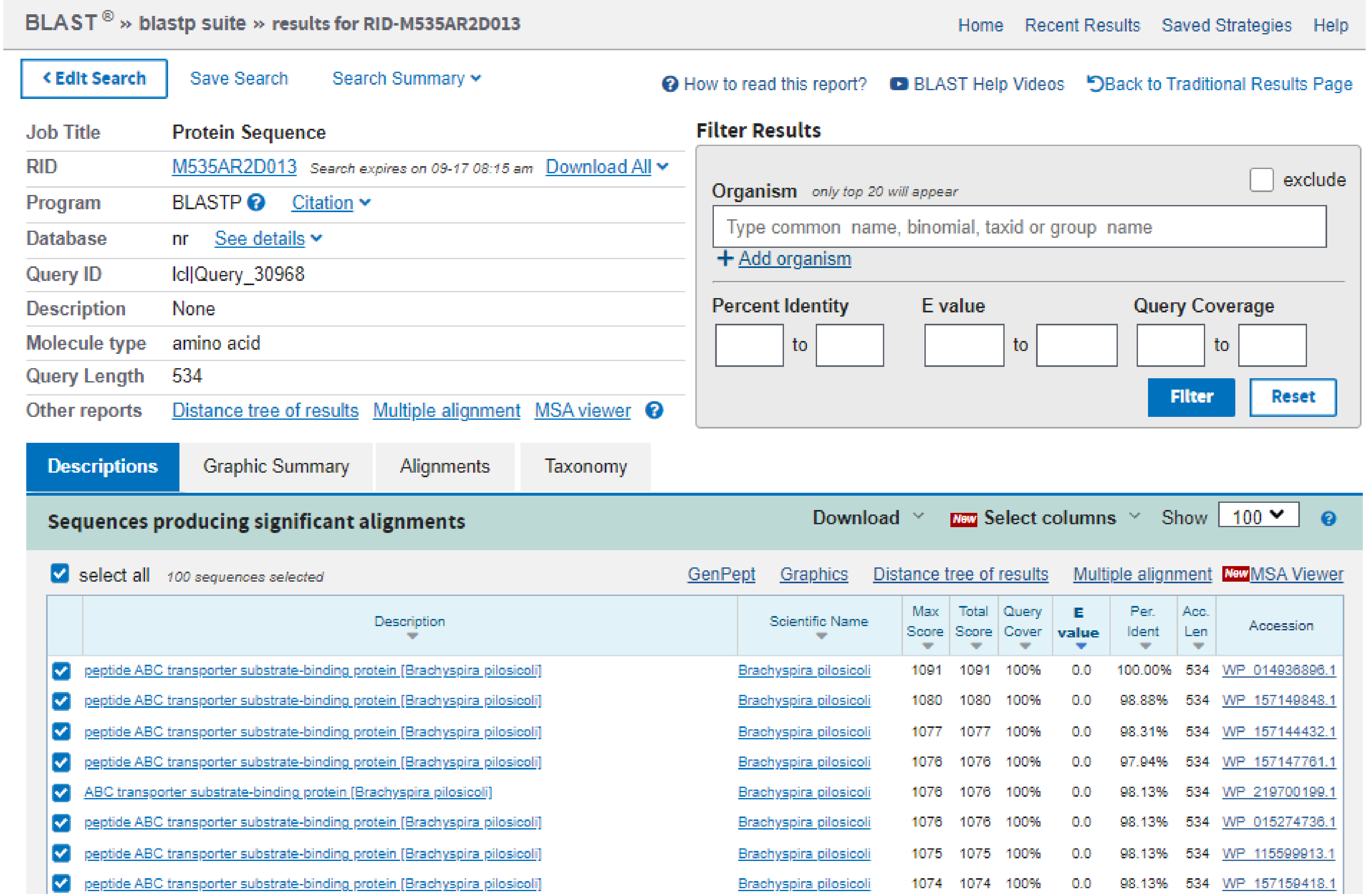
Rank	Sequence	Start position	Score
1	SAINNFKLALEKNS	881	0.93
2	TDFINNELGLSISD	537	0.91
3	EDTDNLDDLESILD	316	0.88
4	QIYYNLKEYGSAIN	871	0.86
5	NLSWLYYLDGEYDL	940	0.85
5	DNDTDLTNLDLPKD	172	0.85

PROTEINA 9

```
>fig|6666666.171271.peg.693
MPKIEDLERLGSLAFIIGNKNLPKELSQEDYNNFKSVFTDEYMANSTPNNDDDVPSIDDLDNLDNLDLPDDNTNDNLGLSDDLG
LPEELDTADNLDNNNTELDNLPDSTNDDLGLPDDLGLPEELNTADNLDNNNTELDNLPDSIDDDLGLPDDLGLPDDLDDIKNDN
KKLDNDTDLTNLDLPKDKELENKLNSEINDSYNSKLNNNIPDLPILDDLPLPESLDDYSNDSNDSIEETITDDIDNLADNLPDD
LDDTLEEEIINNDSNLDDLDNLESILDDDTSEKEESKQEDTDNLDDLESILDDDTNEKEEPKQEDTDNLDDLESILDDDTSEKE
EPKQEDTDNLDDLESILDDDTSEKEEPKQEDTDNLDDLDSILDDDTSEKEEPKQEDTDNLDDLDSILDDNAKEESNNNLETALD
DDIKTQDADELENNIDNNSLESNNDNLMVENVAGNVRIIEEENTLPSPDSADSLGESKYEDVDKDINDDEVIDNIKRLSPITRY
HVLDAILNEKLSKNSMQKLLKALEKGESNEYITDFINNELGLSISDSRGGLLDIIPIPSSLKEYAKIIRIAAIFLVLFVGVVLF
SYQFIYKPVLANRYFKMGLENIYNSQFDEAERNFAKGDRLTPKKIKWYNKYAKEYIDRSAFDYALKKLETSVDIKPRNIDTRLL
FGYYYRNKGEKELSEEDYNSGEELYNNLMTYTDKEKDLKRIYDDLGVLMISRAKTLVEPNYYNNAYENYREMINKFGDNVIPRK
RVMLIKIYQDNYQDVKDLQNHINRLKNGYIDDDVYPKLAKYLLDKDDFYGARKLFEKLLAKYTNNLESIVGYADYEARLKHYDR
AKEILINSALPLYTSNPYNVGEEYVYNMLGQIYYNLKEYGSAINNFKLALEKNSLYPDANFNLANLYFYQDNDYKKAKEHYKIA
YDNLAPDLRSDQLLYNLSWLYYLDGEYDLAFQGFNDLFYKNPDNSIVSYALGNSLLHLDRANLANGFYRNALNKALESRRDKFE
MRTEKDFMFISYLASLHNNIGVSYAYNSVVSNKIENEQMAFKNFVVASEYFDQLRTSNIDLDMAEKRTVNIDNQNIGASKYNMM
AIQSKRNLKNSVIIDDYIPKTMFNLK
```

PROTEINA 10

```
>fig|6666666.171271.peg.2613
MKKTIYIIFLILSIISCNNNNKTTSNNEISISLGGEPKTLDPTLNSLSFGSIYMIHFFEGLTKKDKNDEVTASMAKSWDISED
GLTYTFYLRDDAKWSDGEKVKAQDFEYALKRAADPKTAATYSHMLNVVKNGSLVISGKTNIDALGVKAIDDSTLEIVLENPTP
YFLEYLSVSSAYFPVRKDIVEKYGDDWSRNPETYIVNGAYVMTERKTDEKIVMEVNTNYYDKESIVAKKINVIIMSDSNTSLA
AIKRGDIQFSVIEAPLGEISSLIKENYILQEPAYGIYFLEINSKKGVLTNKNIRKALALAFDRNYIISNITKMNQTPAYAFVP
YGMKDGDGKDFRENGSNYLDLGSYDANIKEAKRLMELSGYTNGDNFPVLEIRTTPGYFTLICEAMQEMYKENLGIDVTIKSEE
YNETFQAMVEKNYDLARTGWTADYSDPLAMISFFSEVSAVNNSGFSSREFNDLLKFASSTTNTDERTKALHKAEDLIFDYMPI
IPIIYRMDPFMINPKLKGAIFNPLGRYRFHYAYLEK
```



Job Title	Protein Sequence
RID	M535AR2D013 *Search expires on 09-17 08:15 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_30968
Description	None
Molecule type	amino acid
Query Length	534
Other reports	Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism *only top 20 will appear* ☐ exclude

Type common name, binomial, taxid or group name

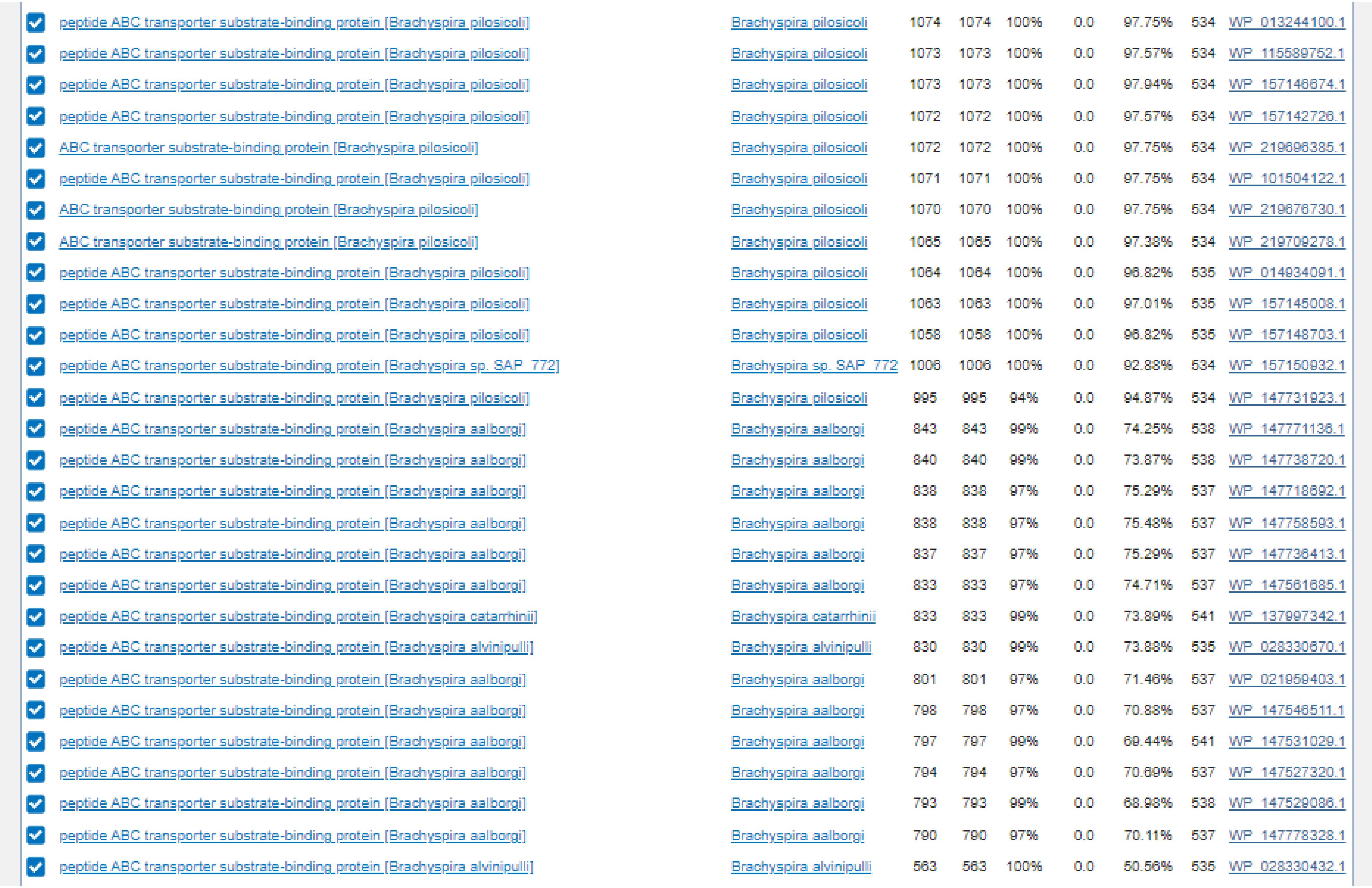
+ Add organism

Percent Identity ☐ to ☐ E value ☐ to ☐ Query Coverage ☐ to ☐

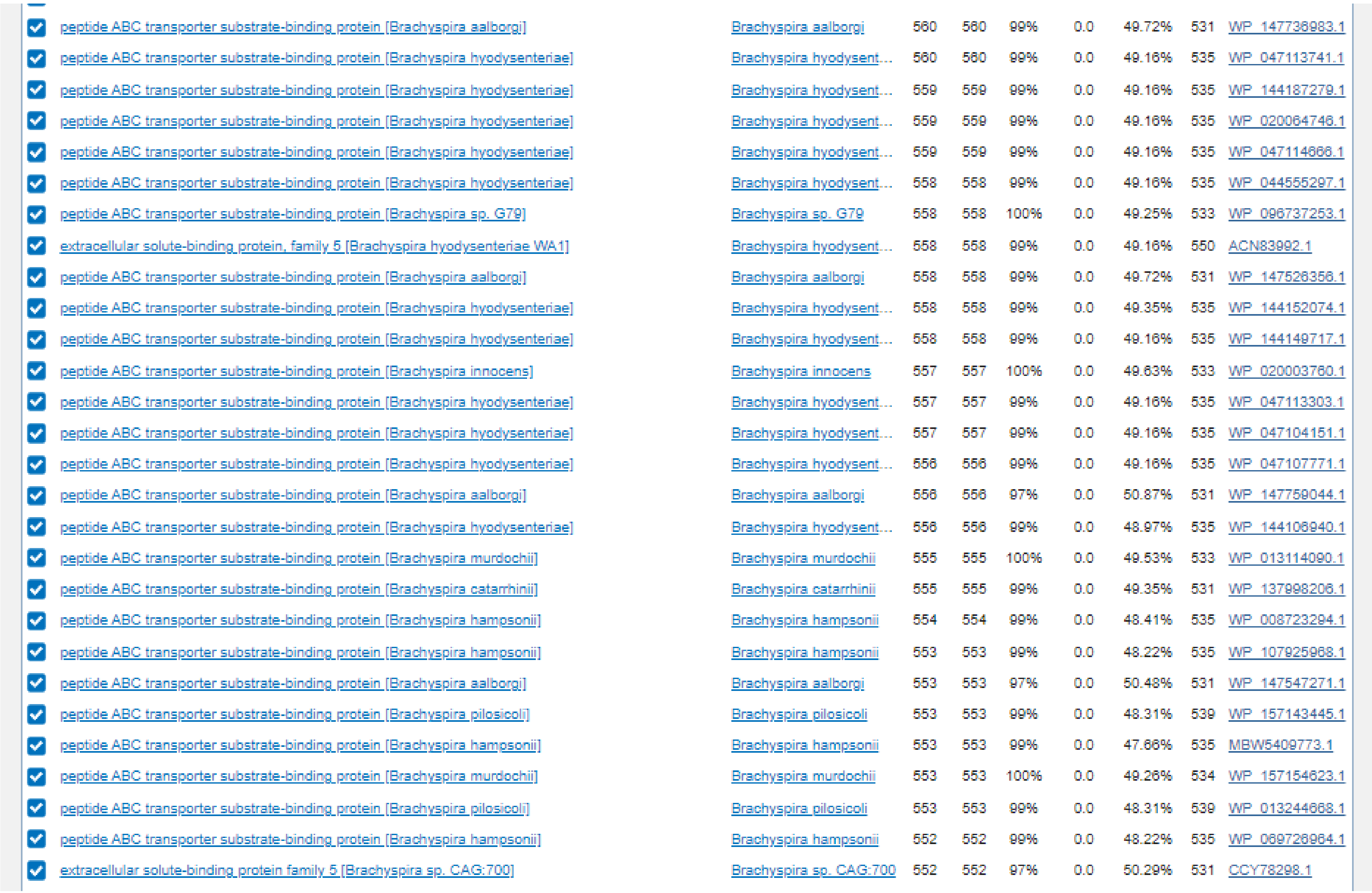
Sequences producing significant alignments

☑ select all *100 sequences selected*

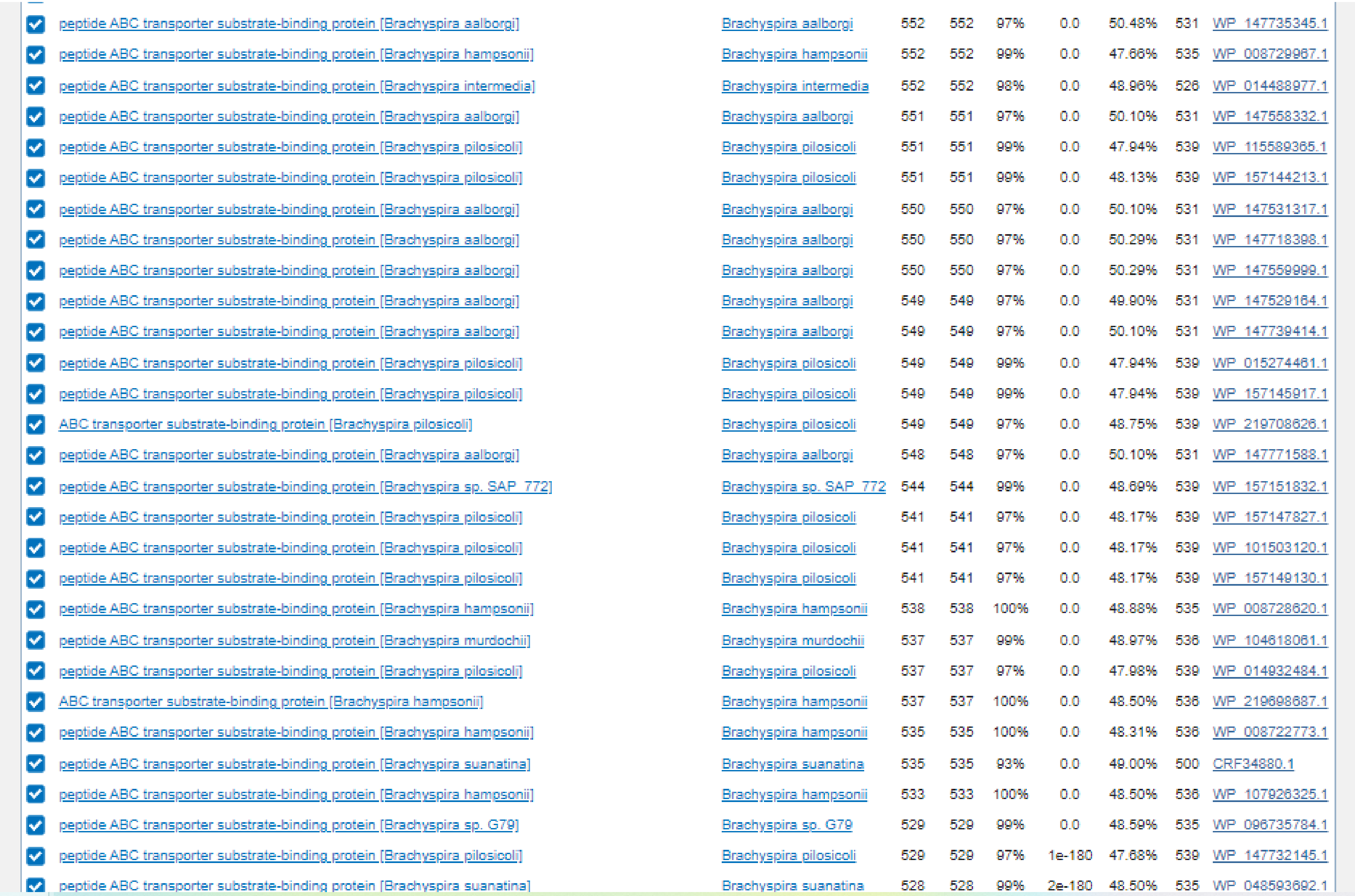
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1091	1091	100%	0.0	100.00%	534	WP_014936896.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1080	1080	100%	0.0	98.88%	534	WP_157149848.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1077	1077	100%	0.0	98.31%	534	WP_157144432.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1076	1076	100%	0.0	97.94%	534	WP_157147761.1
☑	ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1076	1076	100%	0.0	98.13%	534	WP_219700199.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1076	1076	100%	0.0	98.13%	534	WP_015274736.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1075	1075	100%	0.0	98.13%	534	WP_115599913.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1074	1074	100%	0.0	98.13%	534	WP_157159418.1



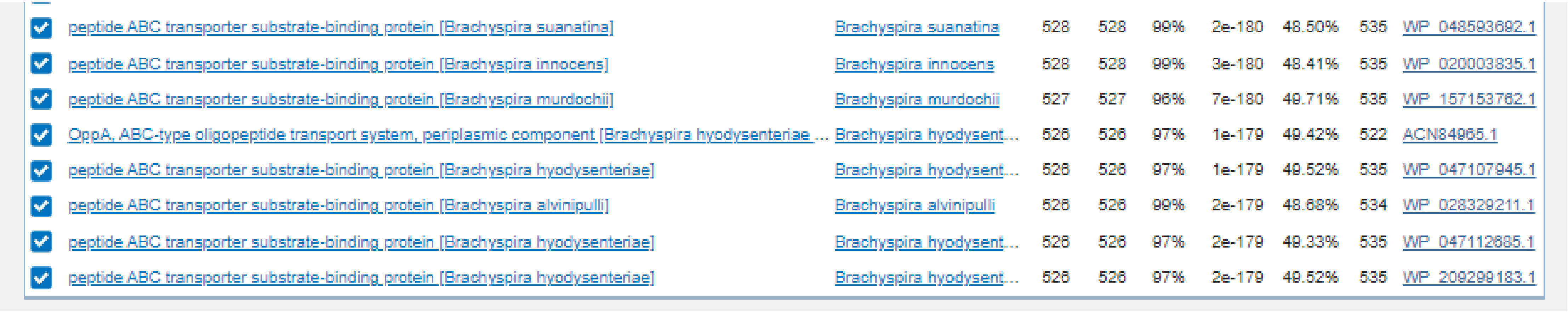
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1074	1074	100%	0.0	97.75%	534	WP_013244100.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1073	1073	100%	0.0	97.57%	534	WP_115589752.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1073	1073	100%	0.0	97.94%	534	WP_157146674.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1072	1072	100%	0.0	97.57%	534	WP_157142726.1
☑	ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1072	1072	100%	0.0	97.75%	534	WP_219696385.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1071	1071	100%	0.0	97.75%	534	WP_101504122.1
☑	ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1070	1070	100%	0.0	97.75%	534	WP_219676730.1
☑	ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1065	1065	100%	0.0	97.38%	534	WP_219709278.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1064	1064	100%	0.0	96.82%	535	WP_014934091.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1063	1063	100%	0.0	97.01%	535	WP_157145008.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	1058	1058	100%	0.0	96.82%	535	WP_157148703.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	1006	1006	100%	0.0	92.88%	534	WP_157150932.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	995	995	94%	0.0	94.87%	534	WP_147731923.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	843	843	99%	0.0	74.25%	538	WP_147771136.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	840	840	99%	0.0	73.87%	538	WP_147738720.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	838	838	97%	0.0	75.29%	537	WP_147718692.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	838	838	97%	0.0	75.48%	537	WP_147758593.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	837	837	97%	0.0	75.29%	537	WP_147736413.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	833	833	97%	0.0	74.71%	537	WP_147561685.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	833	833	99%	0.0	73.89%	541	WP_137997342.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	830	830	99%	0.0	73.88%	535	WP_028330670.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	801	801	97%	0.0	71.46%	537	WP_021959403.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	798	798	97%	0.0	70.88%	537	WP_147546511.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	797	797	99%	0.0	69.44%	541	WP_147531029.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	794	794	97%	0.0	70.69%	537	WP_147527320.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	793	793	99%	0.0	68.98%	538	WP_147529086.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	790	790	97%	0.0	70.11%	537	WP_147778328.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	563	563	100%	0.0	50.56%	535	WP_028330432.1



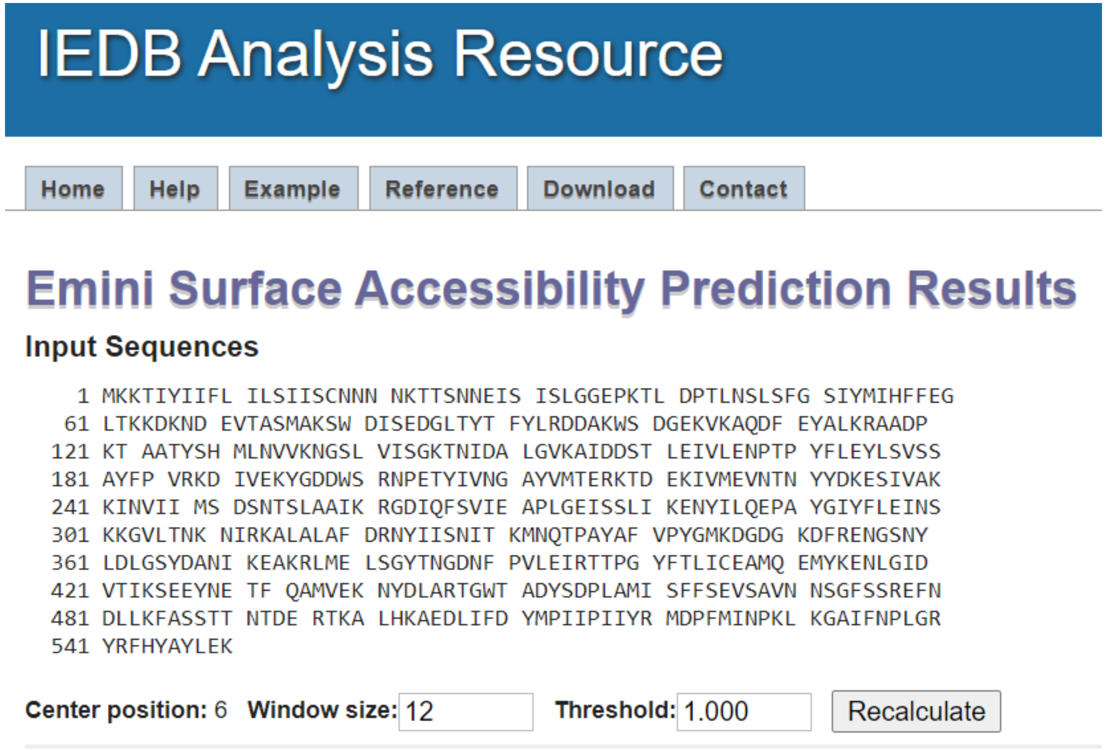
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	560	560	99%	0.0	49.72%	531	WP_147736983.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	560	560	99%	0.0	49.16%	535	WP_047113741.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	559	559	99%	0.0	49.16%	535	WP_144187279.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	559	559	99%	0.0	49.16%	535	WP_020064746.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	559	559	99%	0.0	49.16%	535	WP_047114666.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	558	558	99%	0.0	49.16%	535	WP_044555297.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira sp. G79]	Brachyspira sp. G79	558	558	100%	0.0	49.25%	533	WP_096737253.1
☑	extracellular solute-binding protein, family 5 [Brachyspira hyodysenteriae WA1]	Brachyspira hyodysent...	558	558	99%	0.0	49.16%	550	ACN83992.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	558	558	99%	0.0	49.72%	531	WP_147526356.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	558	558	99%	0.0	49.35%	535	WP_144152074.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	558	558	99%	0.0	49.16%	535	WP_144149717.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira innocens]	Brachyspira innocens	557	557	100%	0.0	49.63%	533	WP_020003760.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	557	557	99%	0.0	49.16%	535	WP_047113303.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	557	557	99%	0.0	49.16%	535	WP_047104151.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	556	556	99%	0.0	49.16%	535	WP_047107771.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	556	556	97%	0.0	50.87%	531	WP_147759044.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	556	556	99%	0.0	48.97%	535	WP_144106940.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira murdochii]	Brachyspira murdochii	555	555	100%	0.0	49.53%	533	WP_013114090.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	555	555	99%	0.0	49.35%	531	WP_137998206.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	554	554	99%	0.0	48.41%	535	WP_008723294.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	553	553	99%	0.0	48.22%	535	WP_107925968.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	553	553	97%	0.0	50.48%	531	WP_147547271.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	553	553	99%	0.0	48.31%	539	WP_157143445.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	553	553	99%	0.0	47.66%	535	MBW5409773.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira murdochii]	Brachyspira murdochii	553	553	100%	0.0	49.26%	534	WP_157154623.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	553	553	99%	0.0	48.31%	539	WP_013244668.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	552	552	99%	0.0	48.22%	535	WP_069726964.1
☑	extracellular solute-binding protein family 5 [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	552	552	97%	0.0	50.29%	531	CCY78298.1



☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	552	552	97%	0.0	50.48%	531	WP_147735345.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	552	552	99%	0.0	47.66%	535	WP_008729967.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira intermedia]	Brachyspira intermedia	552	552	98%	0.0	48.96%	526	WP_014488977.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	551	551	97%	0.0	50.10%	531	WP_147558332.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	551	551	99%	0.0	47.94%	539	WP_115589365.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	551	551	99%	0.0	48.13%	539	WP_157144213.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	550	550	97%	0.0	50.10%	531	WP_147531317.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	550	550	97%	0.0	50.29%	531	WP_147718398.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	550	550	97%	0.0	50.29%	531	WP_147559999.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	549	549	97%	0.0	49.90%	531	WP_147529164.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	549	549	97%	0.0	50.10%	531	WP_147739414.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	549	549	99%	0.0	47.94%	539	WP_015274461.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	549	549	99%	0.0	47.94%	539	WP_157145917.1
☑	ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	549	549	97%	0.0	48.75%	539	WP_219708626.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira aalborgi]	Brachyspira aalborgi	548	548	97%	0.0	50.10%	531	WP_147771588.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	544	544	99%	0.0	48.69%	539	WP_157151832.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	541	541	97%	0.0	48.17%	539	WP_157147827.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	541	541	97%	0.0	48.17%	539	WP_101503120.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	541	541	97%	0.0	48.17%	539	WP_157149130.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	538	538	100%	0.0	48.88%	535	WP_008728620.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira murdochii]	Brachyspira murdochii	537	537	99%	0.0	48.97%	536	WP_104618061.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	537	537	97%	0.0	47.98%	539	WP_014932484.1
☑	ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	537	537	100%	0.0	48.50%	536	WP_219698687.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	535	535	100%	0.0	48.31%	536	WP_008722773.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira suanatina]	Brachyspira suanatina	535	535	93%	0.0	49.00%	500	CRF34880.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hampsonii]	Brachyspira hampsonii	533	533	100%	0.0	48.50%	536	WP_107926325.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira sp. G79]	Brachyspira sp. G79	529	529	99%	0.0	48.59%	535	WP_096735784.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	529	529	97%	1e-180	47.68%	539	WP_147732145.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira suanatina]	Brachyspira suanatina	528	528	99%	2e-180	48.50%	535	WP_048593692.1



☑	peptide ABC transporter substrate-binding protein [Brachyspira suanatina]	Brachyspira suanatina	528	528	99%	2e-180	48.50%	535	WP_048593692.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira innocens]	Brachyspira innocens	528	528	99%	3e-180	48.41%	535	WP_020003835.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira murdochii]	Brachyspira murdochii	527	527	96%	7e-180	49.71%	535	WP_157153762.1
☑	OppA, ABC-type oligopeptide transport system, periplasmic component [Brachyspira hyodysenteriae ...	Brachyspira hyodysent...	526	526	97%	1e-179	49.42%	522	ACN84965.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	526	526	97%	1e-179	49.52%	535	WP_047107945.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	526	526	99%	2e-179	48.68%	534	WP_028329211.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	526	526	97%	2e-179	49.33%	535	WP_047112685.1
☑	peptide ABC transporter substrate-binding protein [Brachyspira hyodysenteriae]	Brachyspira hyodysent...	526	526	97%	2e-179	49.52%	535	WP_209299183.1

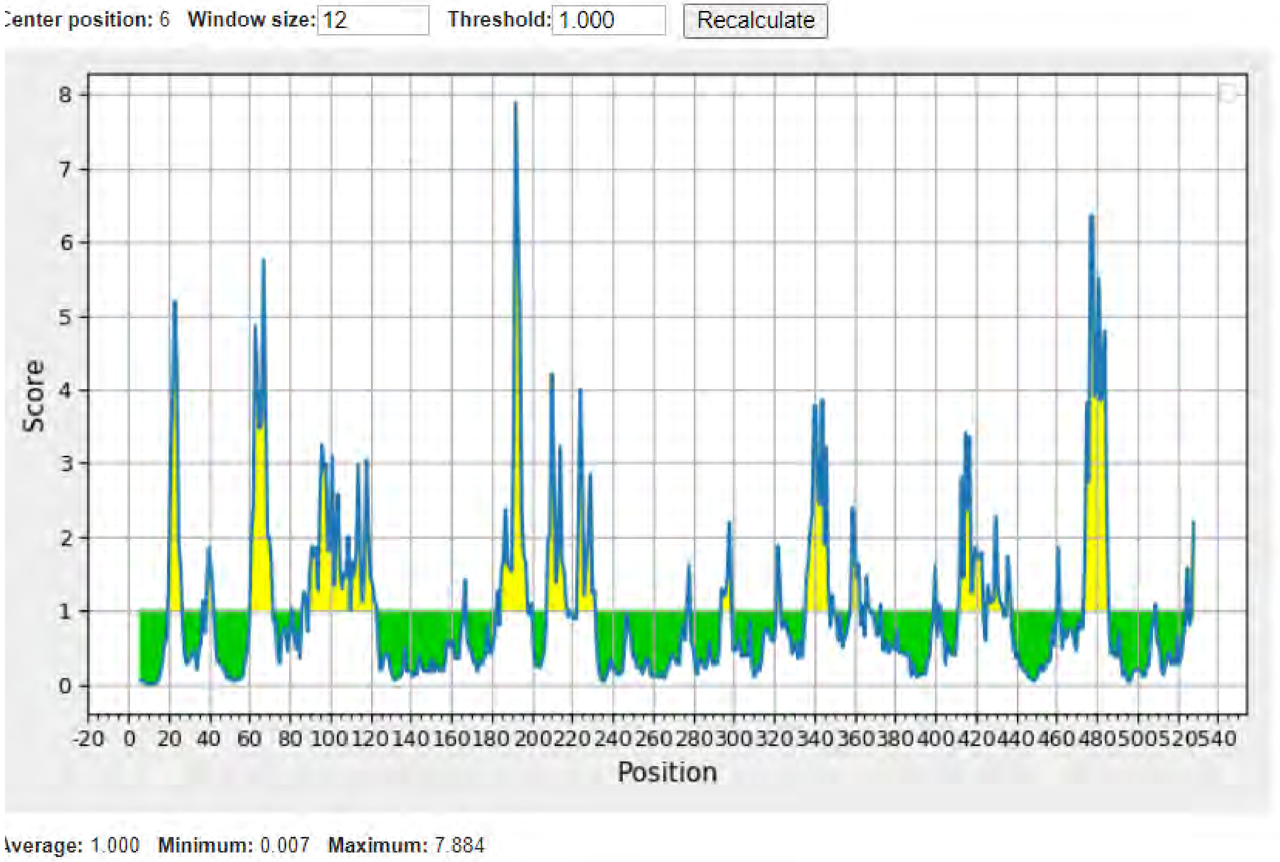


Emini Surface Accessibility Prediction Results

Input Sequences

```
  1 MKKTIYIIFL ILSIISCNNN NKTTSNNEIS ISLGGEPKTL DPTLNSLSFG SIYMIHFFEG
 61 LTKKDKND EVTASMAKSW DISEDGLTYT FYLRDDAKWS DGEKVKAQDF EYALKRAADP
121 KT AATYSH MLNVVKNGSL VISGKTNIDA LGVKAIDDST LEIVLENPTP YFLEYLSVSS
181 AYFP VRKD IVEKYGDDWS RNPETYIVNG AYVMTERKTD EKIVMEVNTN YYDKESIVAK
241 KINVII MS DSNTSLAAIK RGDIQFSVIE APLGEISSLI KENYILQEPA YGIYFLEINS
301 KKGVLTNK NIRKALALAF DRNYIISNIT KMNQTPAYAF VPYGMKDGDG KDFRENGSNY
361 LDLGSYDANI KEAKRLME LSGYTNGDNF PVLEIRTTPG YFTLICEAMQ EMYKENLGID
421 VTIKSEEYNE TF QAMVEK NYDLARTGWT ADYSDPLAMI SFFSEVSAVN NSGFSSREFN
481 DLLKFASSTT NTDE RTKA LHKAEDLIFD YMPIIPIIYR MDPFMINPKL KGAIFNPLGR
541 YRFHYAYLEK
```

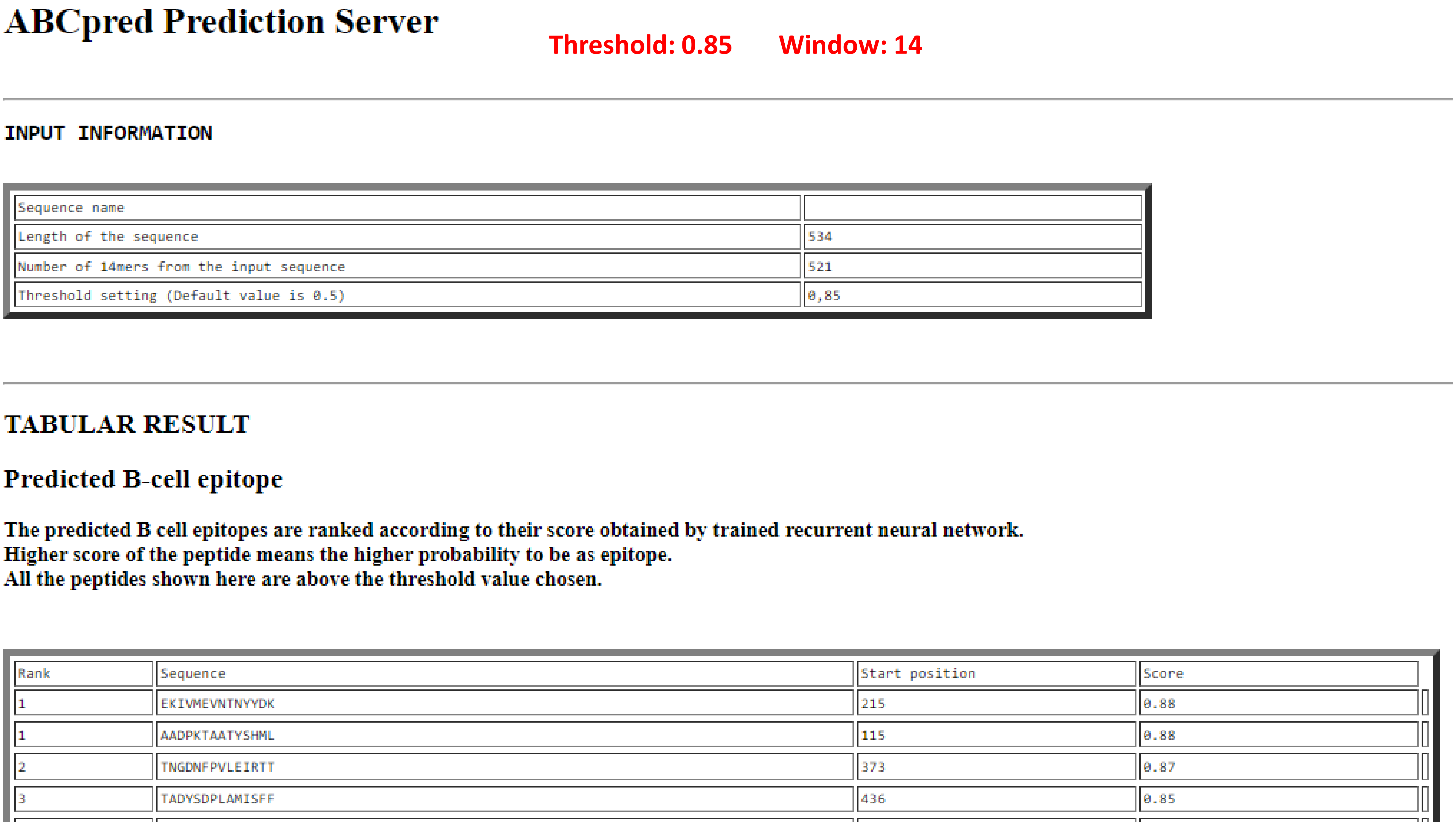
Center position: 6 **Window size:** 12 **Threshold:** 1.000



enter position: 6 **Window size:** 12 **Threshold:** 1.000

verage: 1.000 **Minimum:** 0.007 **Maximum:** 7.884

MKKTIYIIFLILSIISCNNNNKTTSNNEISISLGGEPKTLDPTLNSLSFGSIYMIHFFEGLTKKDKNDEVTASMAKSWDISE
DGLTYTFYLRDDAKWSDGEKVKAQDFEYALKRAADPKTAATYSHML NVVKNGSLVISGKTNIDALGVKAIDDSTLEIVLENP
TPYFLEYLSVSSAYFPVRKDIVEKYGDDWSRNPETYIVNGAYVMTERKTDEKIVMEVNTNYYDK ESIVAKKINVIIMSDSNT
SLAAIKRGDIQFSVIEAPLGEISSLIKENYILQEPAYGIYFLEINSKKGVLTNKNIRKALALAFDRNYIISNITKMNQTPAY
AFVPYGMKDGDGKDFRENGSNYLDLGSYDANIKEAKRLMELSGYTNGDNFPVLEIRTT PGYFTLICEAMQEMYKENLGIDVT
IKSEEYNETFQAMVEKNYDLARTGWTADYSDPLAMISFF SEVSAVNNSGFSSREFNDLLKFASSTTNTDERTKALHKAEDL
IFDYMPIIPIIYRMDPFMINPKLKGAIFNPLGRYRFHYAYLEK



ABCpred Prediction Server

Threshold: 0.85   Window: 14

INPUT INFORMATION

Sequence name	
Length of the sequence	534
Number of 14mers from the input sequence	521
Threshold setting (Default value is 0.5)	0,85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	EKIVMEVNTNYYDK	215	0.88
1	AADPKTAATYSHML	115	0.88
2	TNGDNFPVLEIRTT	373	0.87
3	TADYSDPLAMISFF	436	0.85

PROTEINA 10

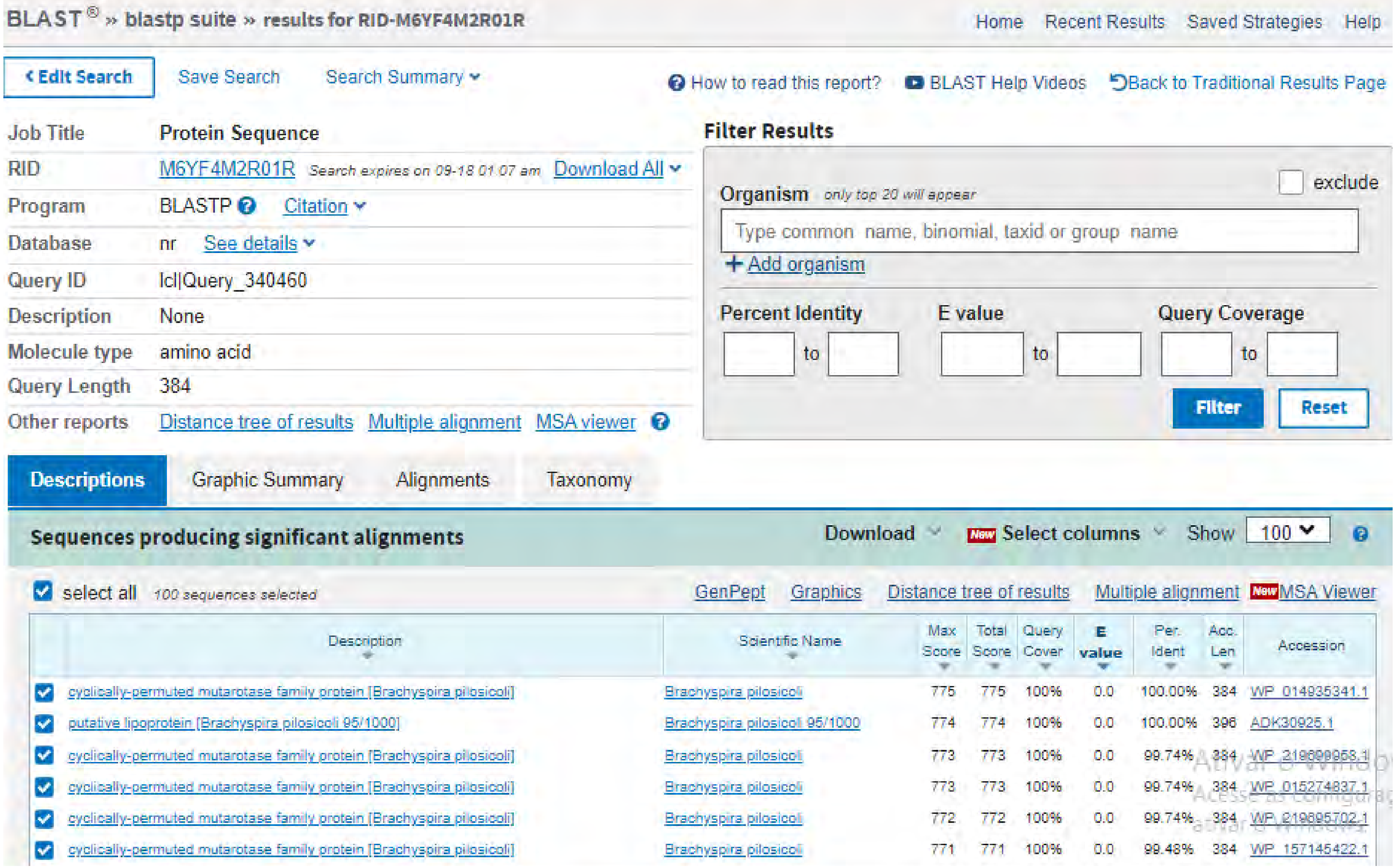
>fig|6666666.171271.peg.2613
MKKTIYIIFLILSIISCNNNNKTTSNNEISISLGGEPKTLDPTLNSLSFGSIYMIHFFEGLTKKDKNDEVTASMAKSWDISED
GLTYTFYLRDDAKWSDGEKVKAQDFEYALKRAADPKTAATYSHMLNVVKNGSLVISGKTNIDALGVKAIDDSTLEIVLENPTP
YFLEYLSVSSAYFPVRKDIVEKYGDDWSRNPETYIVNGAYVMTERKTDEKIVMEVNTNYYDKESIVAKKINVIIMSDSNTSLA
AIKRGDIQFSVIEAPLGEISSLIKENYILQEPAYGIYFLEINSKKGVLTNKNIRKALALAFDRNYIISNITKMNQTPAYAFVP
YGMKDGDGKDFRENGSNYLDLGSYDANIKEAKRLMELSGYTNGDNFPVLEIRTTPGYFTLICEAMQEMYKENLGIDVTIKSEE
YNETFQAMVEKNYDLARTGWTADYSDPLAMISFFSEVSAVNNSGFSSREFNDLLKFASSTTNTDE
RTKALHKAEDLIFDYMPIIPIIYRMDPFMINPKLKGAIFNPLGRYRFHYAYLEK

Predição combinada

>fig|6666666.171271.peg.2613
MKKTIYIIFLILSIISCNNNNKTTSNNEISISLGGEPKTLDPTLNSLSFGSIYMIHFFEGLTKKDKNDEVTASMAKSWDISED
GLTYTFYLRDDAKWSDGEKVKAQDFEYALKR**AADPKTAATYSHML**NVVKNGSLVISGKTNIDALGVKAIDDSTLEIVLENPTP
YFLEYLSVSSAYFPVRKDIVEKYGDDWSRNPETYIVNGAYV**MTERKTDEKIVMEVNTNYYDKESI**VAKKINVIIMSDSNTSLA
AIKRGDIQFSVIEAPLGEISSLIKENYILQEPAYGIYFLEINSKKGVLTNKNIRKALALAFDRNYIISNITKMNQTPAYAFVP
YGMKDGDGKDFRENGSNYLDLGSYDANIKEAKRLMELSGYTNGDNFPVLEIRTT PGYFTLICEAMQEMYKENLGIDVTIKSE
EYNETFQAMVEKNYDLARTGWTADYSDPLAMISFFSEVSAVNNSGFSSREFNDLLKFASSTTNTDERTKALHKAEDLIFDYMP
IIPIIYRMDPFMINPKLKGAIFNPLGRYRFHYAYLEK

PROTEINA 11

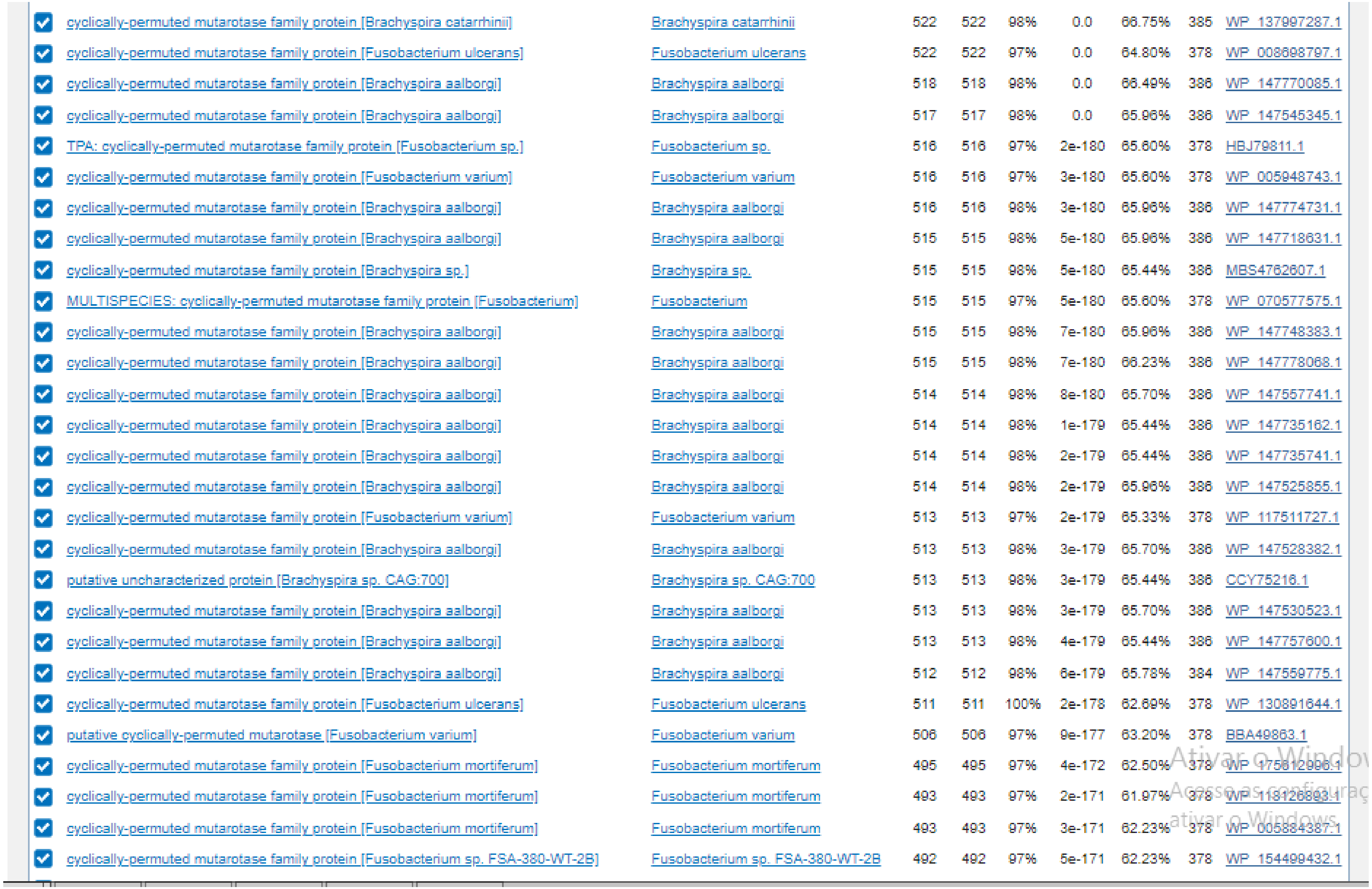
```
>fig|6666666.171271.peg.429
MKKLCLILSIIFAVSCSSNTTSSSSNVNVLDSKTDKKIVWEMGGRLPAQTGMDKNIGTAGLLYGSLENKYIVVGGGANFPEESV
LNGGAKKTYSDIYMLEDNNGVLEVVEHINWENELGYGASITTTNGIYYIGGSSNPEADDDILFITLKNNKLNVEKIGDLPFTLQ
NGVAVYKDNKLYIITGKQSGKGSDKVYEYDLATKETKELAPVPNQASRTQAVAQLLNGNIYVFSGGDATAYTDGYKYDFANNTW
EQVSDVALNNEGISLLGAVSVKLNEQEMLVIGGFNKAVYDDAVYNLGNLQEEALADFRAGYFGADPYEFDWNSKILIYNCESNT
WKTIGDVPFDAPCGEGLILIGNKIYSINGEIKPGVRTDKMYVGTIMAK
```



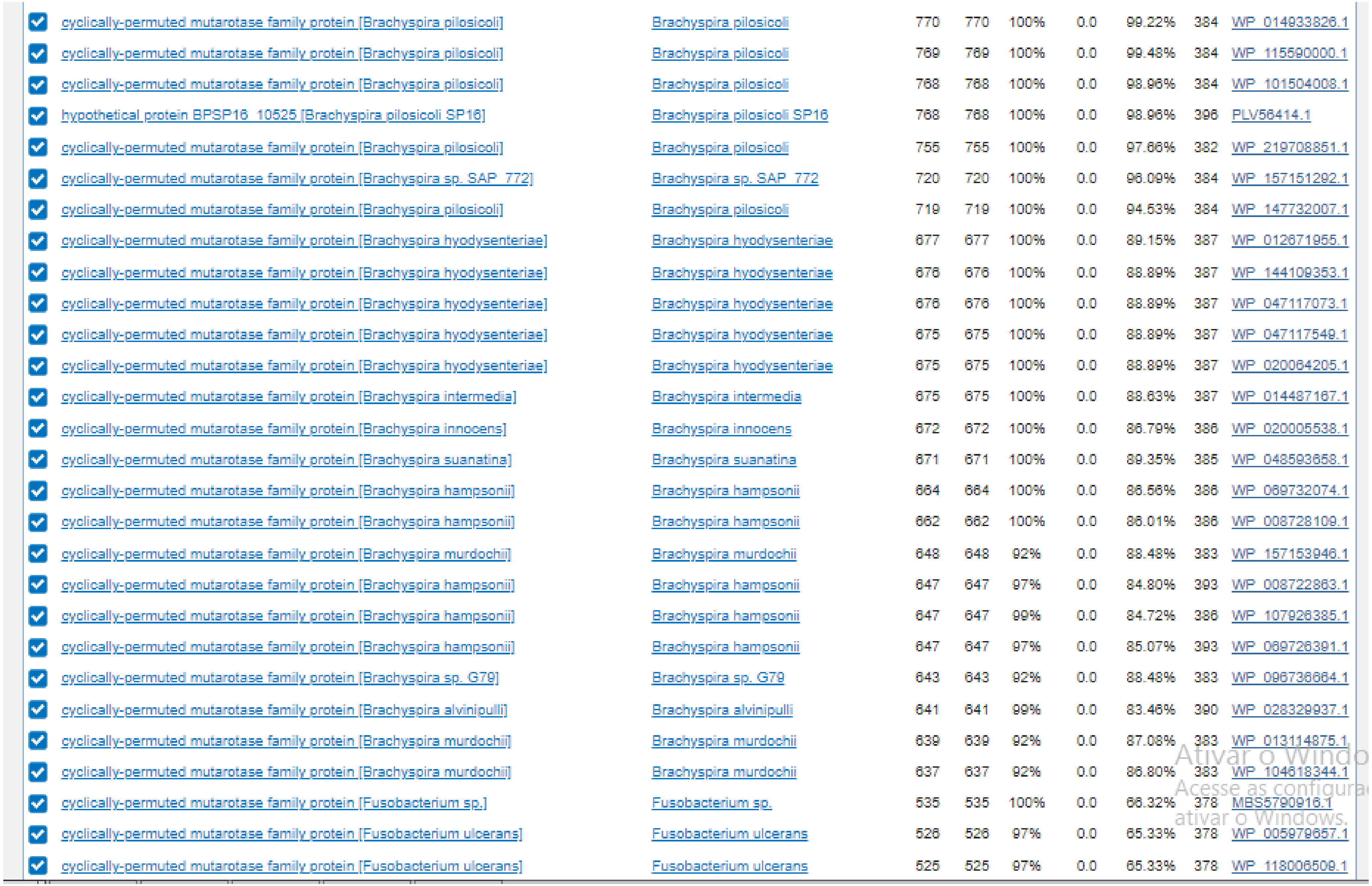
Job Title: Protein Sequence
RID: M6YF4M2R01R *Search expires on 09-18 01:07 am* Download All
Program: BLASTP Citation
Database: nr See details
Query ID: lcl|Query_340460
Description: None
Molecule type: amino acid
Query Length: 384
Other reports: Distance tree of results Multiple alignment MSA viewer

Sequences producing significant alignments

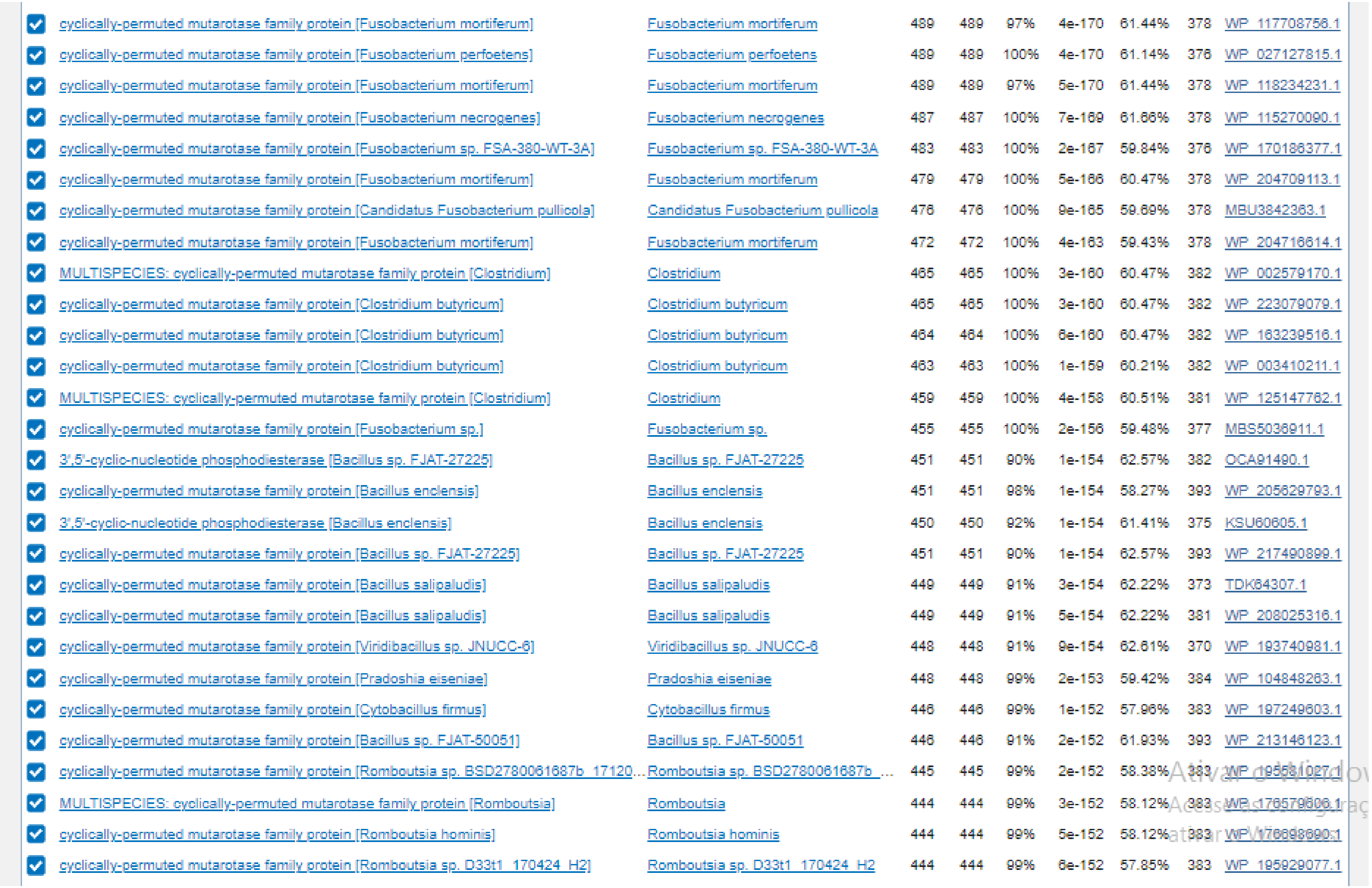
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	775	775	100%	0.0	100.00%	384	WP_014935341.1
☑	putative lipoprotein [Brachyspira pilosicoli 95/1000]	Brachyspira pilosicoli 95/1000	774	774	100%	0.0	100.00%	396	ADK30925.1
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	773	773	100%	0.0	99.74%	384	WP_219698958.1
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	773	773	100%	0.0	99.74%	384	WP_015274837.1
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	772	772	100%	0.0	99.74%	384	WP_219695702.1
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	771	771	100%	0.0	99.48%	384	WP_157145422.1



☑	cyclically-permuted mutarotase family protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	522	522	98%	0.0	66.75%	385	WP_137997287.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium ulcerans]	Fusobacterium ulcerans	522	522	97%	0.0	64.80%	378	WP_008698797.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	518	518	98%	0.0	66.49%	386	WP_147770085.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	517	517	98%	0.0	65.96%	386	WP_147545345.1
☑	TPA: cyclically-permuted mutarotase family protein [Fusobacterium sp.]	Fusobacterium sp.	516	516	97%	2e-180	65.60%	378	HBJ79811.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium varium]	Fusobacterium varium	516	516	97%	3e-180	65.60%	378	WP_005948743.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	516	516	98%	3e-180	65.96%	386	WP_147774731.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	515	515	98%	5e-180	65.96%	386	WP_147718631.1
☑	cyclically-permuted mutarotase family protein [Brachyspira sp.]	Brachyspira sp.	515	515	98%	5e-180	65.44%	386	MBS4762607.1
☑	MULTISPECIES: cyclically-permuted mutarotase family protein [Fusobacterium]	Fusobacterium	515	515	97%	5e-180	65.60%	378	WP_070577575.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	515	515	98%	7e-180	65.96%	386	WP_147748383.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	515	515	98%	7e-180	66.23%	386	WP_147778068.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	514	514	98%	8e-180	65.70%	386	WP_147557741.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	514	514	98%	1e-179	65.44%	386	WP_147735162.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	514	514	98%	2e-179	65.44%	386	WP_147735741.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	514	514	98%	2e-179	65.96%	386	WP_147525855.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium varium]	Fusobacterium varium	513	513	97%	2e-179	65.33%	378	WP_117511727.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	513	513	98%	3e-179	65.70%	386	WP_147528382.1
☑	putative uncharacterized protein [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	513	513	98%	3e-179	65.44%	386	CCY75216.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	513	513	98%	3e-179	65.70%	386	WP_147530523.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	513	513	98%	4e-179	65.44%	386	WP_147757600.1
☑	cyclically-permuted mutarotase family protein [Brachyspira aalborgi]	Brachyspira aalborgi	512	512	98%	6e-179	65.78%	384	WP_147559775.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium ulcerans]	Fusobacterium ulcerans	511	511	100%	2e-178	62.69%	378	WP_130891644.1
☑	putative cyclically-permuted mutarotase [Fusobacterium varium]	Fusobacterium varium	506	506	97%	9e-177	63.20%	378	BBA49863.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium mortiferum]	Fusobacterium mortiferum	495	495	97%	4e-172	62.50%	378	WP_175612996.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium mortiferum]	Fusobacterium mortiferum	493	493	97%	2e-171	61.97%	378	WP_118126893.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium mortiferum]	Fusobacterium mortiferum	493	493	97%	3e-171	62.23%	378	WP_005884387.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium sp. FSA-380-WT-2B]	Fusobacterium sp. FSA-380-WT-2B	492	492	97%	5e-171	62.23%	378	WP_154499432.1

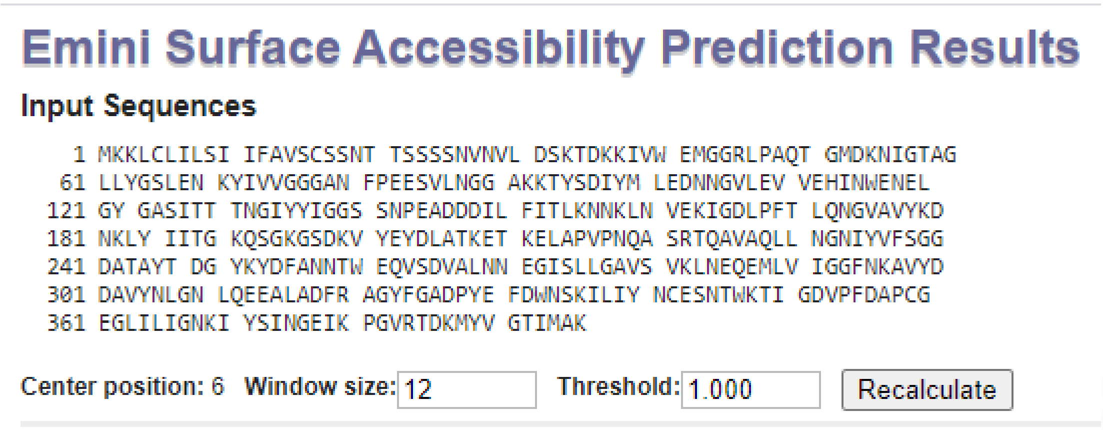


☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	770	770	100%	0.0	99.22%	384	WP_014933826.1
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	769	769	100%	0.0	99.48%	384	WP_115590000.1
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	768	768	100%	0.0	98.96%	384	WP_101504008.1
☑	hypothetical protein BPSP16_10525 [Brachyspira pilosicoli SP16]	Brachyspira pilosicoli SP16	768	768	100%	0.0	98.96%	396	PLV56414.1
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	755	755	100%	0.0	97.66%	382	WP_219708851.1
☑	cyclically-permuted mutarotase family protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	720	720	100%	0.0	96.09%	384	WP_157151292.1
☑	cyclically-permuted mutarotase family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	719	719	100%	0.0	94.53%	384	WP_147732007.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	677	677	100%	0.0	89.15%	387	WP_012671955.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	676	676	100%	0.0	88.89%	387	WP_144109353.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	676	676	100%	0.0	88.89%	387	WP_047117073.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	675	675	100%	0.0	88.89%	387	WP_047117549.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	675	675	100%	0.0	88.89%	387	WP_020064205.1
☑	cyclically-permuted mutarotase family protein [Brachyspira intermedia]	Brachyspira intermedia	675	675	100%	0.0	88.63%	387	WP_014487167.1
☑	cyclically-permuted mutarotase family protein [Brachyspira innocens]	Brachyspira innocens	672	672	100%	0.0	86.79%	386	WP_020005538.1
☑	cyclically-permuted mutarotase family protein [Brachyspira suanatina]	Brachyspira suanatina	671	671	100%	0.0	89.35%	385	WP_048593658.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hampsonii]	Brachyspira hampsonii	664	664	100%	0.0	86.56%	386	WP_069732074.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hampsonii]	Brachyspira hampsonii	662	662	100%	0.0	86.01%	386	WP_008728109.1
☑	cyclically-permuted mutarotase family protein [Brachyspira murdochii]	Brachyspira murdochii	648	648	92%	0.0	88.48%	383	WP_157153946.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hampsonii]	Brachyspira hampsonii	647	647	97%	0.0	84.80%	393	WP_008722863.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hampsonii]	Brachyspira hampsonii	647	647	99%	0.0	84.72%	386	WP_107926385.1
☑	cyclically-permuted mutarotase family protein [Brachyspira hampsonii]	Brachyspira hampsonii	647	647	97%	0.0	85.07%	393	WP_069726391.1
☑	cyclically-permuted mutarotase family protein [Brachyspira sp. G79]	Brachyspira sp. G79	643	643	92%	0.0	88.48%	383	WP_096736664.1
☑	cyclically-permuted mutarotase family protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	641	641	99%	0.0	83.46%	390	WP_028329937.1
☑	cyclically-permuted mutarotase family protein [Brachyspira murdochii]	Brachyspira murdochii	639	639	92%	0.0	87.08%	383	WP_013114875.1
☑	cyclically-permuted mutarotase family protein [Brachyspira murdochii]	Brachyspira murdochii	637	637	92%	0.0	86.80%	383	WP_104618344.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium sp.]	Fusobacterium sp.	535	535	100%	0.0	66.32%	378	MBS5790916.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium ulcerans]	Fusobacterium ulcerans	526	526	97%	0.0	65.33%	378	WP_005979657.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium ulcerans]	Fusobacterium ulcerans	525	525	97%	0.0	65.33%	378	WP_118006509.1



☑	cyclically-permuted mutarotase family protein [Fusobacterium mortiferum]	Fusobacterium mortiferum	489	489	97%	4e-170	61.44%	378	WP_117708756.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium perfoetens]	Fusobacterium perfoetens	489	489	100%	4e-170	61.14%	376	WP_027127815.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium mortiferum]	Fusobacterium mortiferum	489	489	97%	5e-170	61.44%	378	WP_118234231.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium necrogenes]	Fusobacterium necrogenes	487	487	100%	7e-169	61.66%	378	WP_115270090.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium sp. FSA-380-WT-3A]	Fusobacterium sp. FSA-380-WT-3A	483	483	100%	2e-167	59.84%	376	WP_170186377.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium mortiferum]	Fusobacterium mortiferum	479	479	100%	5e-166	60.47%	378	WP_204709113.1
☑	cyclically-permuted mutarotase family protein [Candidatus Fusobacterium pullicola]	Candidatus Fusobacterium pullicola	476	476	100%	9e-165	59.69%	378	MBU3842363.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium mortiferum]	Fusobacterium mortiferum	472	472	100%	4e-163	59.43%	378	WP_204716614.1
☑	MULTISPECIES: cyclically-permuted mutarotase family protein [Clostridium]	Clostridium	465	465	100%	3e-160	60.47%	382	WP_002579170.1
☑	cyclically-permuted mutarotase family protein [Clostridium butyricum]	Clostridium butyricum	465	465	100%	3e-160	60.47%	382	WP_223079079.1
☑	cyclically-permuted mutarotase family protein [Clostridium butyricum]	Clostridium butyricum	464	464	100%	6e-160	60.47%	382	WP_163239516.1
☑	cyclically-permuted mutarotase family protein [Clostridium butyricum]	Clostridium butyricum	463	463	100%	1e-159	60.21%	382	WP_003410211.1
☑	MULTISPECIES: cyclically-permuted mutarotase family protein [Clostridium]	Clostridium	459	459	100%	4e-158	60.51%	381	WP_125147762.1
☑	cyclically-permuted mutarotase family protein [Fusobacterium sp.]	Fusobacterium sp.	455	455	100%	2e-156	59.48%	377	MBS5036911.1
☑	3',5'-cyclic-nucleotide phosphodiesterase [Bacillus sp. FJAT-27225]	Bacillus sp. FJAT-27225	451	451	90%	1e-154	62.57%	382	OCA91490.1
☑	cyclically-permuted mutarotase family protein [Bacillus enclensis]	Bacillus enclensis	451	451	98%	1e-154	58.27%	393	WP_205629793.1
☑	3',5'-cyclic-nucleotide phosphodiesterase [Bacillus enclensis]	Bacillus enclensis	450	450	92%	1e-154	61.41%	375	KSU60605.1
☑	cyclically-permuted mutarotase family protein [Bacillus sp. FJAT-27225]	Bacillus sp. FJAT-27225	451	451	90%	1e-154	62.57%	393	WP_217490899.1
☑	cyclically-permuted mutarotase family protein [Bacillus salipaludis]	Bacillus salipaludis	449	449	91%	3e-154	62.22%	373	TDK64307.1
☑	cyclically-permuted mutarotase family protein [Bacillus salipaludis]	Bacillus salipaludis	449	449	91%	5e-154	62.22%	381	WP_208025316.1
☑	cyclically-permuted mutarotase family protein [Viridibacillus sp. JNUCC-6]	Viridibacillus sp. JNUCC-6	448	448	91%	9e-154	62.61%	370	WP_193740981.1
☑	cyclically-permuted mutarotase family protein [Pradoshia eiseniae]	Pradoshia eiseniae	448	448	99%	2e-153	59.42%	384	WP_104848263.1
☑	cyclically-permuted mutarotase family protein [Cytobacillus firmus]	Cytobacillus firmus	446	446	99%	1e-152	57.96%	383	WP_197249603.1
☑	cyclically-permuted mutarotase family protein [Bacillus sp. FJAT-50051]	Bacillus sp. FJAT-50051	446	446	91%	2e-152	61.93%	393	WP_213146123.1
☑	cyclically-permuted mutarotase family protein [Romboutsia sp. BSD2780061687b_17120...	Romboutsia sp. BSD2780061687b_...	445	445	99%	2e-152	58.38%	383	WP_195581027.1
☑	MULTISPECIES: cyclically-permuted mutarotase family protein [Romboutsia]	Romboutsia	444	444	99%	3e-152	58.12%	383	WP_176579606.1
☑	cyclically-permuted mutarotase family protein [Romboutsia hominis]	Romboutsia hominis	444	444	99%	5e-152	58.12%	383	WP_176698690.1
☑	cyclically-permuted mutarotase family protein [Romboutsia sp. D33t1_170424_H2]	Romboutsia sp. D33t1_170424_H2	444	444	99%	6e-152	57.85%	383	WP_195929077.1

☑	cyclically-permuted mutarotase family protein [Lysinibacillus contaminans]	Lysinibacillus contaminans	443	443	99%	1e-151	57.81%	381	WP_053583965.1
☑	cyclically-permuted mutarotase family protein [Cytobacillus firmus]	Cytobacillus firmus	442	442	99%	2e-151	57.70%	383	WP_197216242.1
☑	cyclically-permuted mutarotase family protein [Clostridium tarantellae]	Clostridium tarantellae	442	442	99%	5e-151	56.70%	389	WP_152891584.1
☑	cyclically-permuted mutarotase family protein [Bacillus velezensis]	Bacillus velezensis	441	441	90%	8e-151	61.49%	381	WP_172771062.1
☑	cyclically-permuted mutarotase family protein [Lysinibacillus sp. JNUCC-52]	Lysinibacillus sp. JNUCC-52	441	441	90%	1e-150	61.49%	381	QPQ36256.1
☑	cyclically-permuted mutarotase family protein [Romboutsia sp. 1001713B170131_17050...	Romboutsia sp. 1001713B170131_...	441	441	99%	1e-150	58.38%	383	WP_195938280.1
☑	MULTISPECIES: cyclically-permuted mutarotase family protein [unclassified Fusobacteri...	unclassified Fusobacterium	440	440	100%	1e-150	56.48%	378	WP_211493280.1
☑	MULTISPECIES: cyclically-permuted mutarotase family protein [unclassified Fusobacteri...	unclassified Fusobacterium	439	439	99%	3e-150	55.73%	378	WP_101473419.1
☑	cyclically-permuted mutarotase family protein [Bacillus sp. FJAT-18017]	Bacillus sp. FJAT-18017	439	439	99%	5e-150	58.42%	393	WP_197282592.1

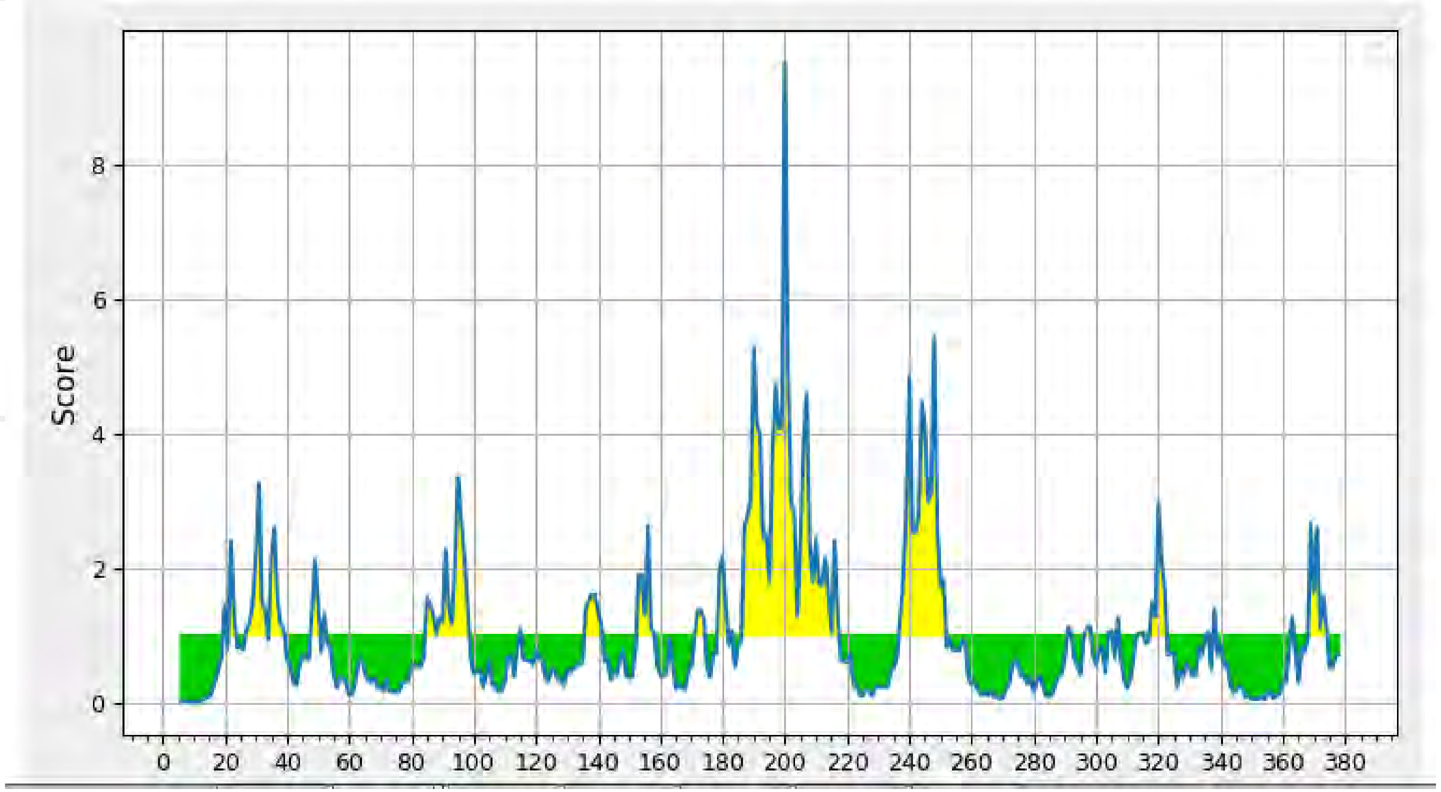


Emini Surface Accessibility Prediction Results

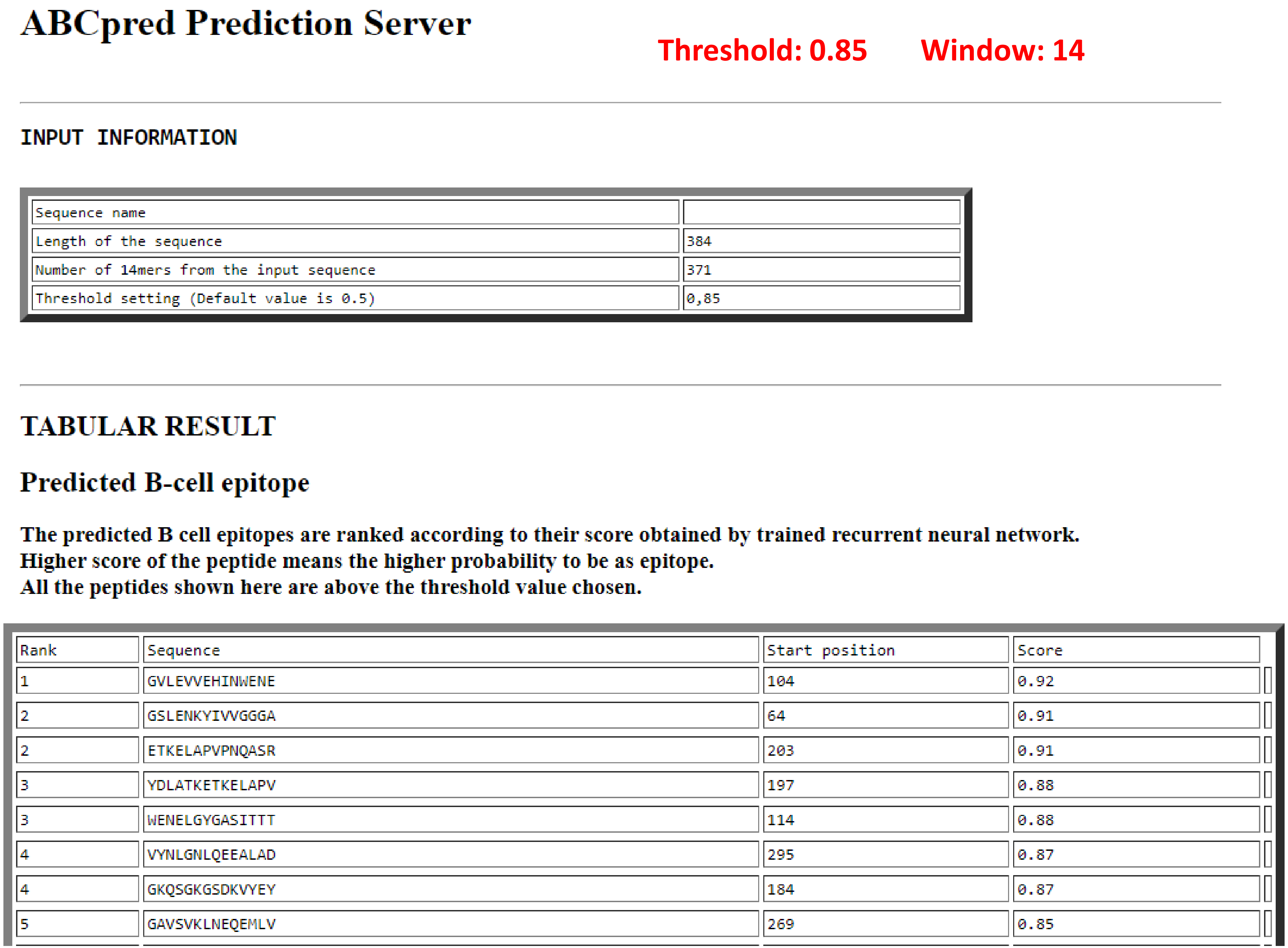
Input Sequences

```
  1 MKKLCLILSI IFAVSCSSNT TSSSSNVNVL DSKTDKKIVW EMGGRLPAQT GMDKNIGTAG
 61 LLYGSLEN KYIVVGGGAN FPEESVLNGG AKKTYSDIYM LEDNNGVLEV VEHINWENEL
121 GY GASITT TNGIYYIGGS SNPEADDDIL FITLKNNKLN VEKIGDLPFT LQNGVAVYKD
181 NKLY IITG KQSGKGSDKV YEYDLATKET KELAPVPNQA SRTQAVAQLL NGNIYVFSGG
241 DATAYT DG YKYDFANNTW EQVSDVALNN EGISLLGAVS VKLNEQEMLV IGGFNKAVYD
301 DAVYNLGN LQEEALADFR AGYFGADPYE FDWNSKILIY NCESNTWKTI GDVPFDAPCG
361 EGLILIGNKI YSINGEIK PGVRTDKMYV GTIMAK
```

Center position: 6 Window size: 12 Threshold: 1.000



```
>fig|6666666.171271.peg.429
MKKLCLILSIIFAVSCSSNTTSSSSNVNVLDSKTDKKIVWEMGGRLPAQTGMDKNIGTAGLLYGSLENKYIVVGG
GANFPEESVLNGGAKKTYSDIYMLEDNNGVLEVVEHINWENELGYGASITTTNGIYYIGGSSNPEADDDILFITL
KNNKLNVEKIGDLPFTLQNGVAVYKDNKLYIITGKQSGKGSDKVYEYDLATKETKELAPVPNQASRTQAVAQLLN
GNIYVFSGGDATAYTDGYKYDFANNTWEQVSDVALNNEGISLLGAVSVKLNEQEMLVIGGFNKAVYDDAVYNLGN
LQEEALADFRAGYFGADPYEFDWNSKILIYNCESNTWKTIGDVPFDAPCGEGLILIGNKIYSINGEIKPGVRTDK
MYVGTIMAK
```



ABCpred Prediction Server

Threshold: 0.85 Window: 14

INPUT INFORMATION

Sequence name	
Length of the sequence	384
Number of 14mers from the input sequence	371
Threshold setting (Default value is 0.5)	0,85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	GVLEVVEHINWENE	104	0.92
2	GSLENKYIVVGGGA	64	0.91
2	ETKELAPVPNQASR	203	0.91
3	YDLATKETKELAPV	197	0.88
3	WENELGYGASITTT	114	0.88
4	VYNLGNLQEEALAD	295	0.87
4	GKQSGKGSDKVYEY	184	0.87
5	GAVSVKLNEQEMLV	269	0.85

PROTEINA 11

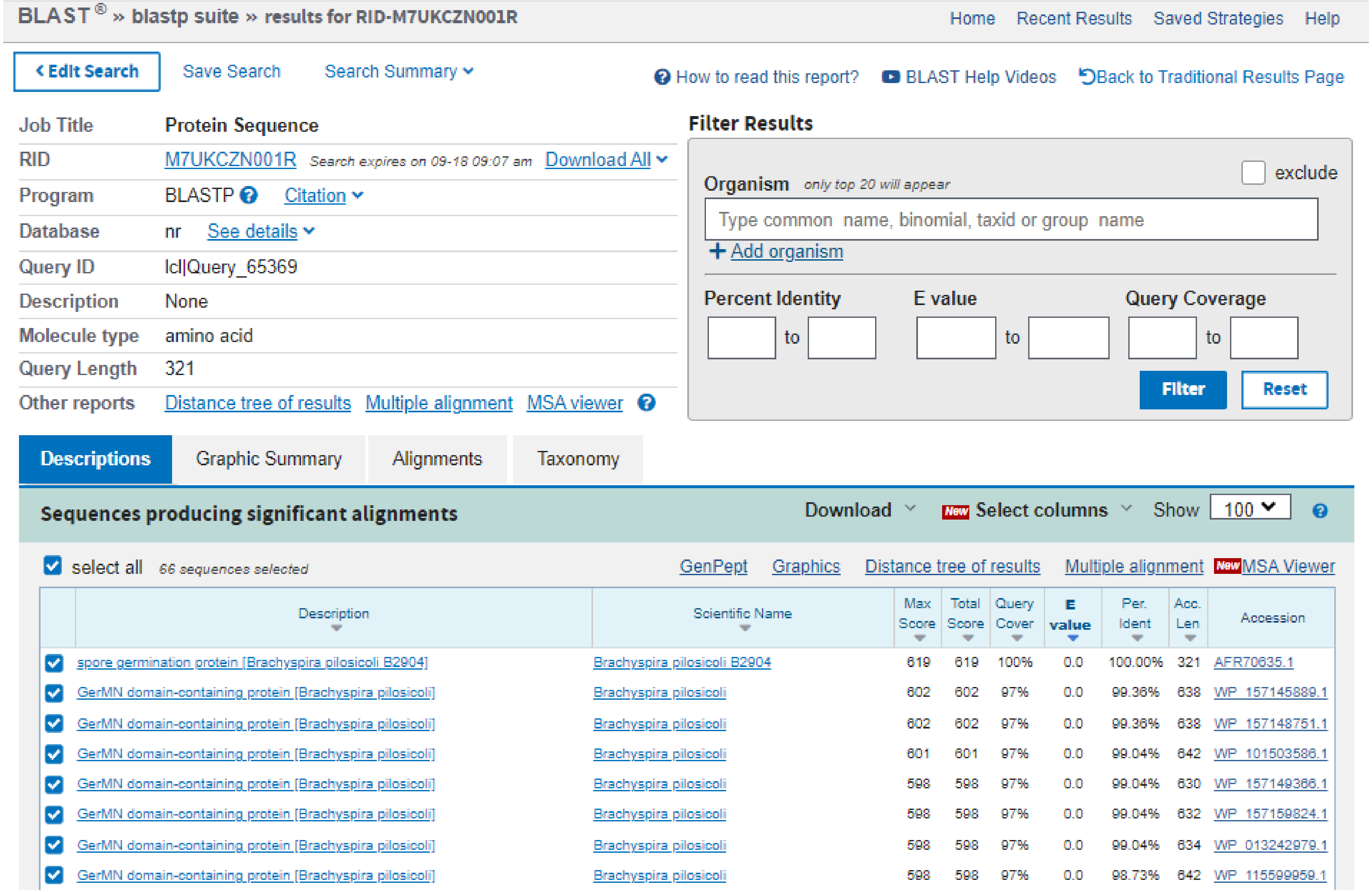
>fig|6666666.171271.peg.429
MKKLCLILSIIFAVSCSSNTTSSSSNVNVLDSKTDKKIVWEMGGRLPAQTGMDKNIGTAGLLYGSLENKYIVVGG
GANFPEESVLNGGAKKTYSDIYMLEDNNGVLEVVEHINWENELGYGASITTTNGIYYIGGSSNPEADDDILFITL
KNNKLNVEKIGDLPFTLQNGVAVYKDNKLYIITGKQSGKGSDKVYEYDLATKETKELAPVPNQASRTQAVAQLLN
GNIYVFSGGDATAYTDGYKYDFANNTWEQVSDVALNNEGISLLGAVSVKLNEQEMLVIGGFNKAVYDDAVYNLGN
LQEEALADFRAGYFGADPYEFDWNSKILIYNCESNTWKTIGDVPFDAPCGEGLILIGNKIYSINGEIKPGVRTDK
MYVGTIMAK

Predição combinada

>fig|6666666.171271.peg.429
MKKLCLILSIIFAVSCSSNTTSSSSNVNVLDSKTDKKIVWEMGGRLPAQTGMDKNIGTAGLLYGSLENKYIVVGG
GANFPEESVLNGGAKKTYSDIYMLEDNNGVLEVVEHINWENELGYGASITTTNGIYYIGGSSNPEADDDILFITL
KNNKLNVEKIGDLPFTLQNGVAVYKDNKLYIITGKQSGK**GSDKVYEYDLATKETKELAPVPNQASR**TQAVAQLLN
GNIYVFSGGDATAYTDGYKYDFANNTWEQVSDVALNNEGISLLGAVSVKLNEQEMLVIGGFNKAVYDDAVYNLGN
LQEEALADFRAGYFGADPYEFDWNSKILIYNCESNTWKTIGDVPFDAPCGEGLILIGNKIYSINGEIKPGVRTDK
MYVGTIMAK

PROTEINA 12

```
>fig|6666666.171271.peg.1294
MPRYEQLKAKSKGISYTRRIRSEDKEFNFKKPIIISVSFILLVSILFTVIKKYSPMVDIAVKDFFSINHREALTLETTGSEE
ENKISFLDNVPLFNFFIKSNTNETLSIMAYETNSMLETSVNTQNTNSMQNNSTITRESLSVFFNNNQNNQLNNTKDIEEQKD
NNIENTEEQNINNIVNDSYNYIQEMIQQNRGVNNNNNNNTINENNNLENNNLNNLTEEKNNYLEKVTNSINNKTSDEKIAAN
NSNISSSIFYDILKPKENTTRDIKTMRPATTTYSSTPPSYMRNNNEPKEKYNTNNYNYYFREDKKKKIIIIILEKE
```

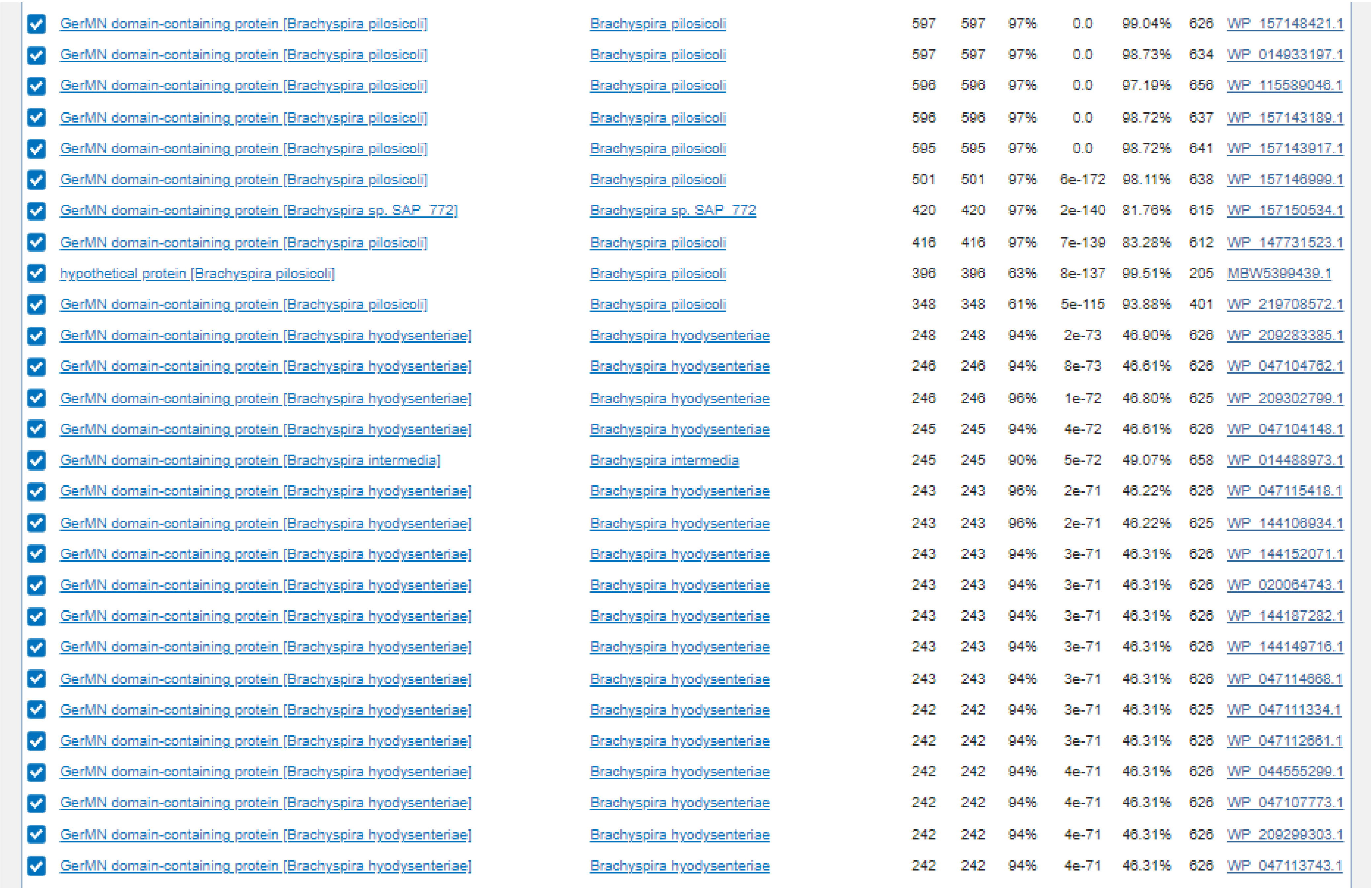


Job Title: Protein Sequence
RID: M7UKCZN001R *Search expires on 09-18 09:07 am* Download All
Program: BLASTP Citation
Database: nr See details
Query ID: lcl|Query_65369
Description: None
Molecule type: amino acid
Query Length: 321
Other reports: Distance tree of results Multiple alignment MSA viewer

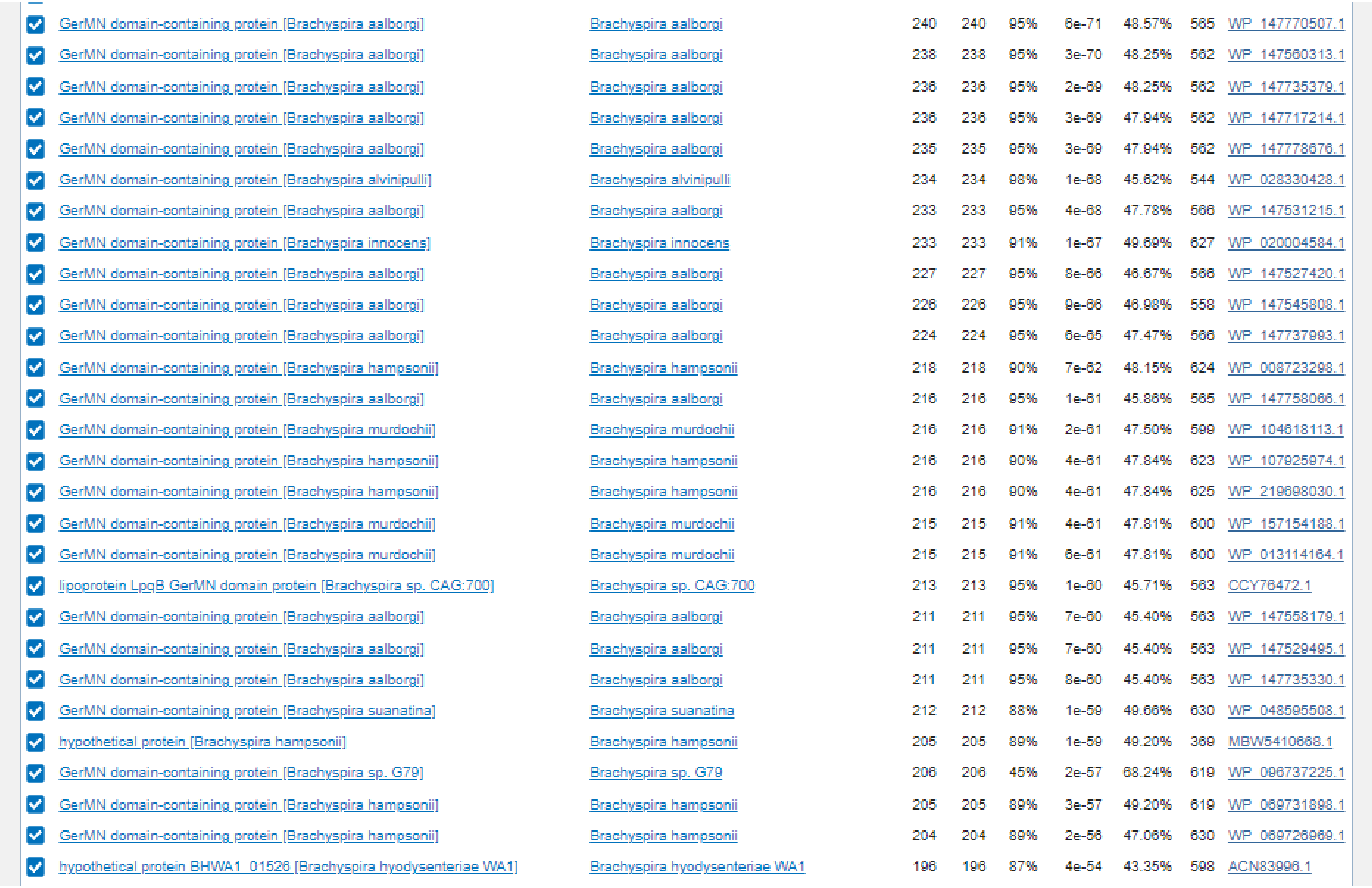
Sequences producing significant alignments

☑ select all *66 sequences selected*

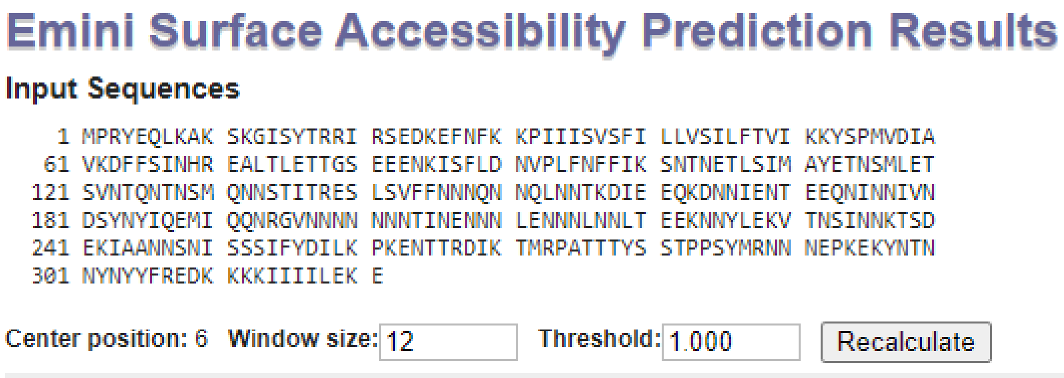
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	spore germination protein [Brachyspira pilosicoli B2904]	Brachyspira pilosicoli B2904	619	619	100%	0.0	100.00%	321	AFR70635.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	602	602	97%	0.0	99.36%	638	WP_157145889.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	602	602	97%	0.0	99.36%	638	WP_157148751.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	601	601	97%	0.0	99.04%	642	WP_101503586.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	598	598	97%	0.0	99.04%	630	WP_157149366.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	598	598	97%	0.0	99.04%	632	WP_157159824.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	598	598	97%	0.0	99.04%	634	WP_013242979.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	598	598	97%	0.0	98.73%	642	WP_115599959.1



☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	597	597	97%	0.0	99.04%	626	WP_157148421.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	597	597	97%	0.0	98.73%	634	WP_014933197.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	596	596	97%	0.0	97.19%	656	WP_115589046.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	596	596	97%	0.0	98.72%	637	WP_157143189.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	595	595	97%	0.0	98.72%	641	WP_157143917.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	501	501	97%	6e-172	98.11%	638	WP_157146999.1
☑	GerMN domain-containing protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	420	420	97%	2e-140	81.76%	615	WP_157150534.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	416	416	97%	7e-139	83.28%	612	WP_147731523.1
☑	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	396	396	63%	8e-137	99.51%	205	MBW5399439.1
☑	GerMN domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	348	348	61%	5e-115	93.88%	401	WP_219708572.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	248	248	94%	2e-73	46.90%	626	WP_209283385.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	246	246	94%	8e-73	46.61%	626	WP_047104762.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	246	246	96%	1e-72	46.80%	625	WP_209302799.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	245	245	94%	4e-72	46.61%	626	WP_047104148.1
☑	GerMN domain-containing protein [Brachyspira intermedia]	Brachyspira intermedia	245	245	90%	5e-72	49.07%	658	WP_014488973.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	243	243	96%	2e-71	46.22%	626	WP_047115418.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	243	243	96%	2e-71	46.22%	625	WP_144106934.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	243	243	94%	3e-71	46.31%	626	WP_144152071.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	243	243	94%	3e-71	46.31%	626	WP_020064743.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	243	243	94%	3e-71	46.31%	626	WP_144187282.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	243	243	94%	3e-71	46.31%	626	WP_144149716.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	243	243	94%	3e-71	46.31%	626	WP_047114668.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	242	242	94%	3e-71	46.31%	625	WP_047111334.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	242	242	94%	3e-71	46.31%	626	WP_047112661.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	242	242	94%	4e-71	46.31%	626	WP_044555299.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	242	242	94%	4e-71	46.31%	626	WP_047107773.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	242	242	94%	4e-71	46.31%	626	WP_209299303.1
☑	GerMN domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	242	242	94%	4e-71	46.31%	626	WP_047113743.1



☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	240	240	95%	6e-71	48.57%	565	WP_147770507.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	238	238	95%	3e-70	48.25%	562	WP_147560313.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	236	236	95%	2e-69	48.25%	562	WP_147735379.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	236	236	95%	3e-69	47.94%	562	WP_147717214.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	235	235	95%	3e-69	47.94%	562	WP_147778676.1
☑	GerMN domain-containing protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	234	234	98%	1e-68	45.62%	544	WP_028330428.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	233	233	95%	4e-68	47.78%	566	WP_147531215.1
☑	GerMN domain-containing protein [Brachyspira innocens]	Brachyspira innocens	233	233	91%	1e-67	49.69%	627	WP_020004584.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	227	227	95%	8e-66	46.67%	566	WP_147527420.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	226	226	95%	9e-66	46.98%	558	WP_147545808.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	224	224	95%	6e-65	47.47%	566	WP_147737993.1
☑	GerMN domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	218	218	90%	7e-62	48.15%	624	WP_008723298.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	216	216	95%	1e-61	45.86%	565	WP_147758066.1
☑	GerMN domain-containing protein [Brachyspira murdochii]	Brachyspira murdochii	216	216	91%	2e-61	47.50%	599	WP_104618113.1
☑	GerMN domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	216	216	90%	4e-61	47.84%	623	WP_107925974.1
☑	GerMN domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	216	216	90%	4e-61	47.84%	625	WP_219698030.1
☑	GerMN domain-containing protein [Brachyspira murdochii]	Brachyspira murdochii	215	215	91%	4e-61	47.81%	600	WP_157154188.1
☑	GerMN domain-containing protein [Brachyspira murdochii]	Brachyspira murdochii	215	215	91%	6e-61	47.81%	600	WP_013114164.1
☑	lipoprotein LpqB GerMN domain protein [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	213	213	95%	1e-60	45.71%	563	CCY76472.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	211	211	95%	7e-60	45.40%	563	WP_147558179.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	211	211	95%	7e-60	45.40%	563	WP_147529495.1
☑	GerMN domain-containing protein [Brachyspira aalborgi]	Brachyspira aalborgi	211	211	95%	8e-60	45.40%	563	WP_147735330.1
☑	GerMN domain-containing protein [Brachyspira suanatina]	Brachyspira suanatina	212	212	88%	1e-59	49.66%	630	WP_048595508.1
☑	hypothetical protein [Brachyspira hampsonii]	Brachyspira hampsonii	205	205	89%	1e-59	49.20%	369	MBW5410668.1
☑	GerMN domain-containing protein [Brachyspira sp. G79]	Brachyspira sp. G79	206	206	45%	2e-57	68.24%	619	WP_096737225.1
☑	GerMN domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	205	205	89%	3e-57	49.20%	619	WP_069731898.1
☑	GerMN domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	204	204	89%	2e-56	47.06%	630	WP_069726969.1
☑	hypothetical protein BHWA1_01526 [Brachyspira hyodysenteriae WA1]	Brachyspira hyodysenteriae WA1	196	196	87%	4e-54	43.35%	598	ACN83996.1

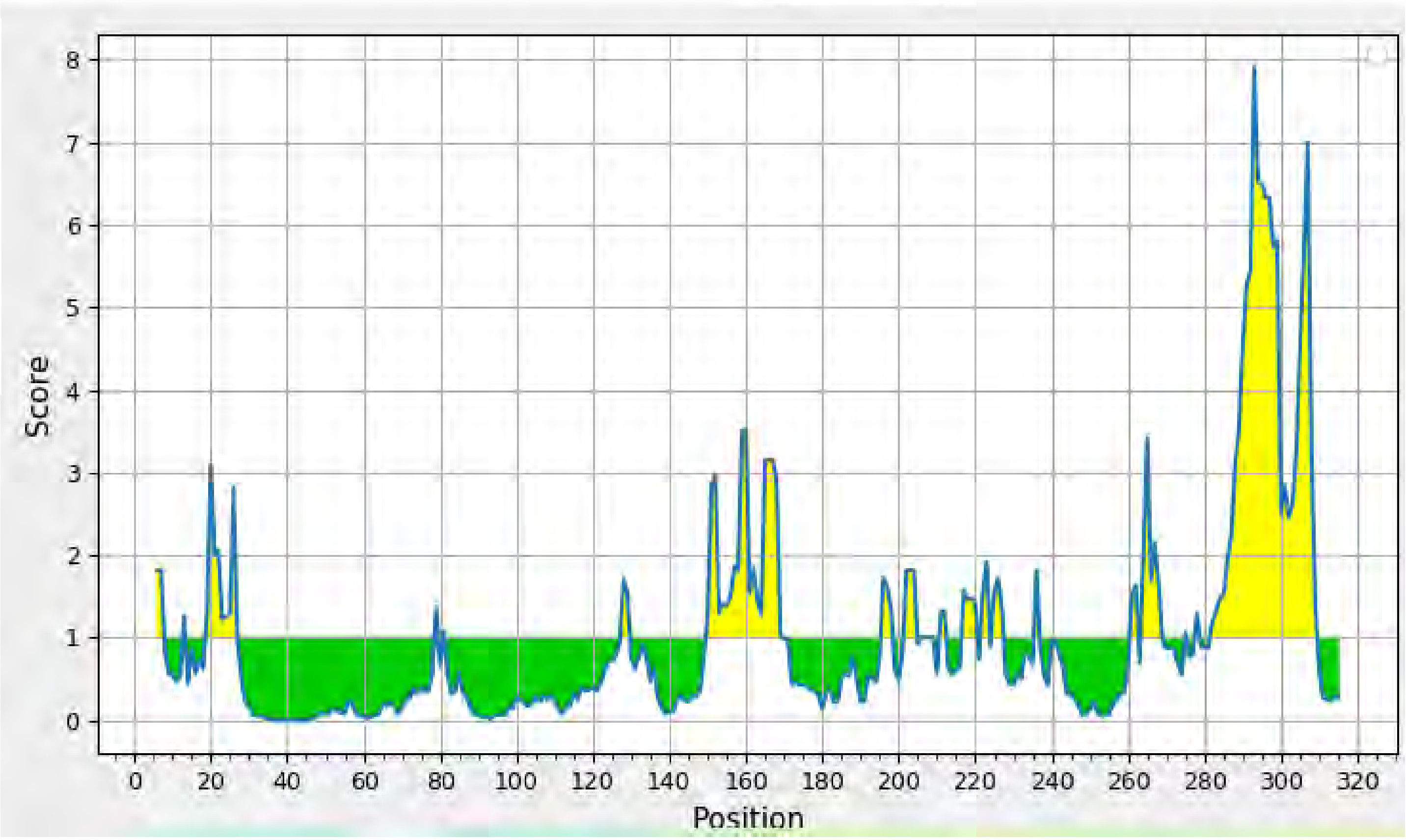


Emini Surface Accessibility Prediction Results

Input Sequences

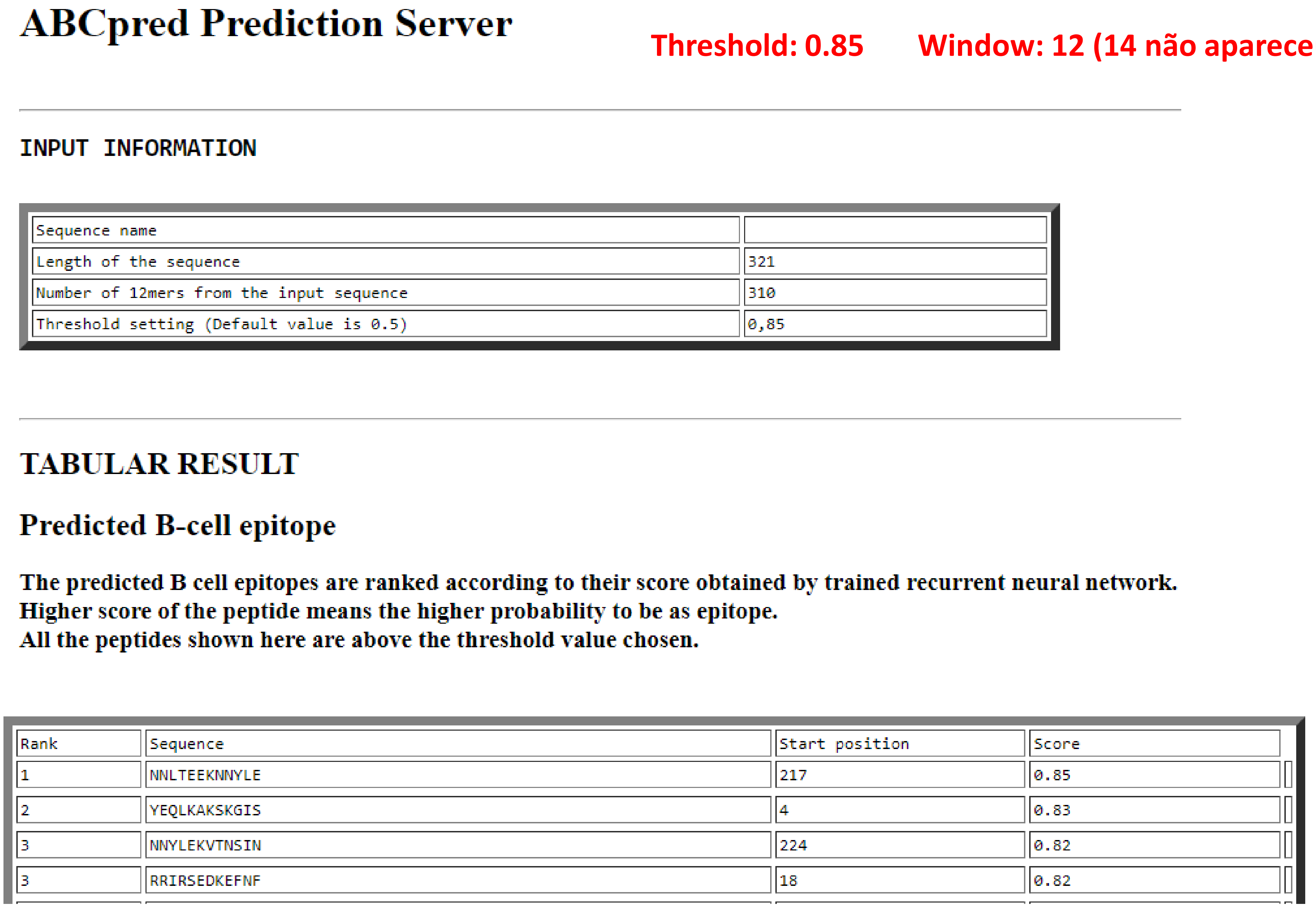
```
  1 MPRYEQLKAK SKGISYTRRI RSEDKEFNFK KPIIISVSFI LLVSILFTVI KKYSPMVDIA
 61 VKDFFSINHR EALTLETTGS EEENKISFLD NVPLFNFFIK SNTNETLSIM AYETNSMLET
121 SVNTQNTNSM QNNSTITRES LSVFFNNNQN NQLNNTKDIE EQKDNNIENT EEQNINNIVN
181 DSYNYIQEMI QQNRGVNNNN NNNTINENNN LENNNLNNLT EEKNNYLEKV TNSINNKTSD
241 EKIAANNSNI SSSIFYDILK PKENTTRDIK TMRPATTTYS STPPSYMRNN NEPKEKYNTN
301 NYNYYFREDK KKKIIIILEK E
```

Center position: 6 Window size: 12 Threshold: 1.000



>fig|6666666.171271.peg.1294
MPRYEQLKAKSKGISYTRRIRSEDKEFNFKKPIIISVSFILLVSILFTVIKKYSPMVDIAVKDFFSINHREALTLETTGSEE
ENKISFLDNVPLFNFFIKSNTNETLSIMAYETNSMLETSVNTQNTNSMQNNSTITRESLSVFFNNNQNNQLNNTKDIEEQKD
NNIENTEEQNINNIVNDSYNYIQEMIQQNRGVNNNNNNNTINENNNLENNNLNNLTEEKNNYLEKVTNSINNKTSDEKIAAN
NSNISSSIFYDILKPKENTTRDIKTMRPATTTYSSTPPSYMRNNNEPKEKYNTNNYNYYFREDKKKKIIIILEKE

Threshold: 0.85 **Window: 12 (14 não apareceu nada)**



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	321
Number of 12mers from the input sequence	310
Threshold setting (Default value is 0.5)	0,85

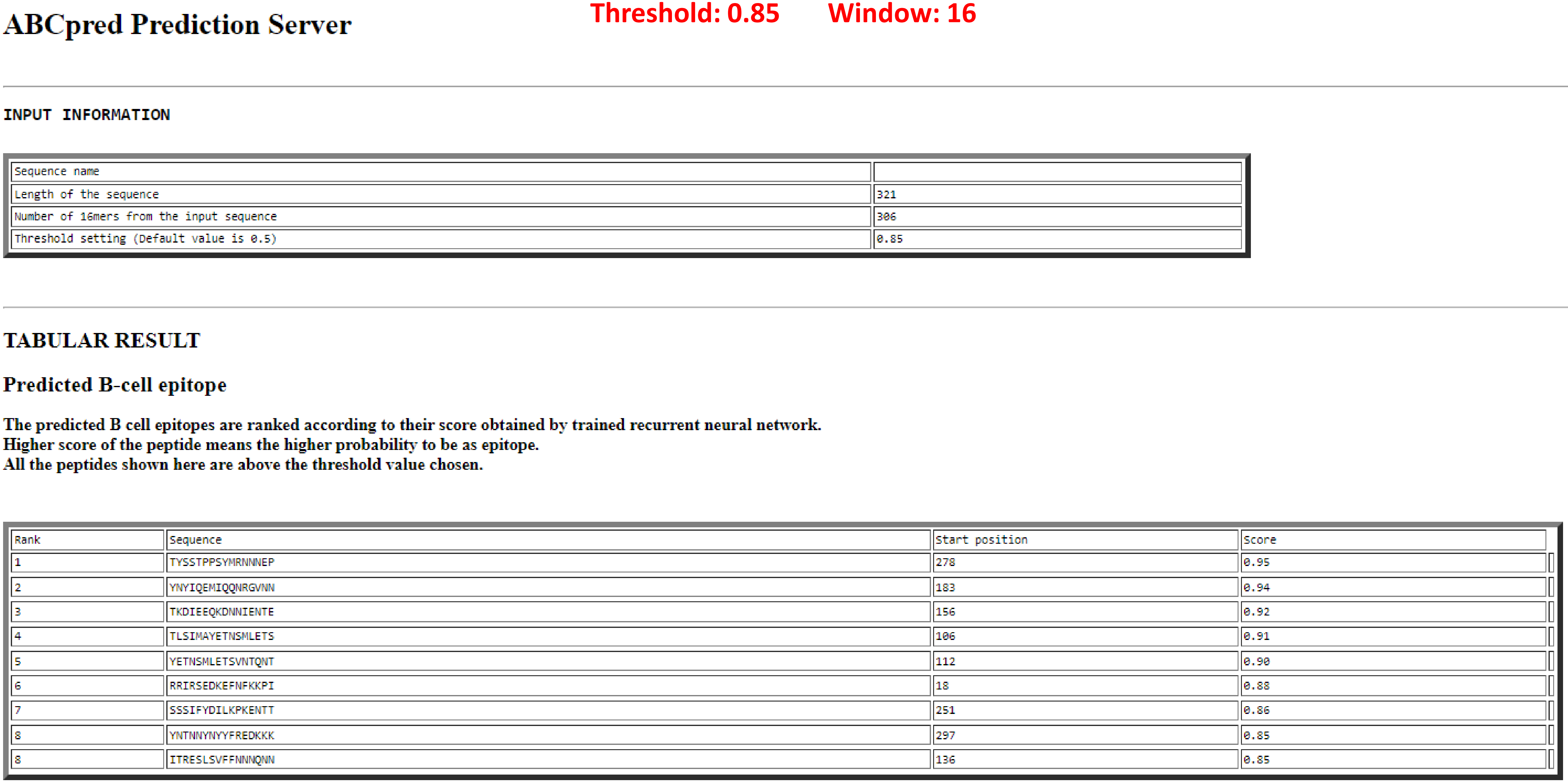
TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	NNLTEEKNNYLE	217	0.85
2	YEQLKAKSKGIS	4	0.83
3	NNYLEKVTNSIN	224	0.82
3	RRIRSEDKEFNF	18	0.82

Threshold: 0.85 **Window: 16**



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	321
Number of 16mers from the input sequence	306
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	TYSSTPPSYMRNNNEP	278	0.95
2	YNYIQEMIQQNRGVNN	183	0.94
3	TKDIEEQKDNNIENTE	156	0.92
4	TLSIMAYETNSMLETS	106	0.91
5	YETNSMLETSVNTQNT	112	0.90
6	RRIRSEDKEFNFKKPI	18	0.88
7	SSSIFYDILKPKENTT	251	0.86
8	YNTNNYNYYFREDKKK	297	0.85
8	ITRESLSVFFNNNQNN	136	0.85

PROTEINA 12

>fig|6666666.171271.peg.1294
MPRYEQLKAKSKGISYTRRIRSEDKEFNFKKPIIISVSFILLVSILFTVIKKYSPMVDIAVKDFFSINHREALTLETTGSEE
ENKISFLDNVPLFNFFIKSNTNETLSIMAYETNSMLETSVNTQNTNSMQNNSTITRESLSVFFNNNQNNQLNNTKDIEEQKD
NNIENTEEQNINNIVNDSYNYIQEMIQQNRGVNNNNNNNTINENNNLENNNLNNLTEEKNNYLEKVTNSINNKTSDEKIAAN
NSNISSSIFYDILKPKENTTRDIKTMRPATTTYSSTPPSYMRNNNEPKEKYNTNNYNYYFREDKKKKIIIILEKE

Predição combinada

abcPred Threshold: 0.85

Window: 12 (14 não apareceu nada)

>fig|6666666.171271.peg.1294
MPRYEQLKAKSKGISYTRRIRSEDKEFNFKKPIIISVSFILLVSILFTVIKKYSPMVDIAVKDFFSINHREALTLETTGSEE
ENKISFLDNVPLFNFFIKSNTNETLSIMAYETNSMLETSVNTQNTNSMQNNSTITRESLSVFFNNNQNNQLNNTKDIEEQKD
NNIENTEEQNINNIVNDSYNYIQEMIQQNRGVNNNNNNNTINENNNLENNNL**NNLTEEKNNYLE**KVTNSINNKTSDEKIAAN
NSNISSSIFYDILKPKENTTRDIKTMRPATTTYSSTPPSYMRNNNEPKEKYNTNNYNYYFREDKKKKIIIILEKE

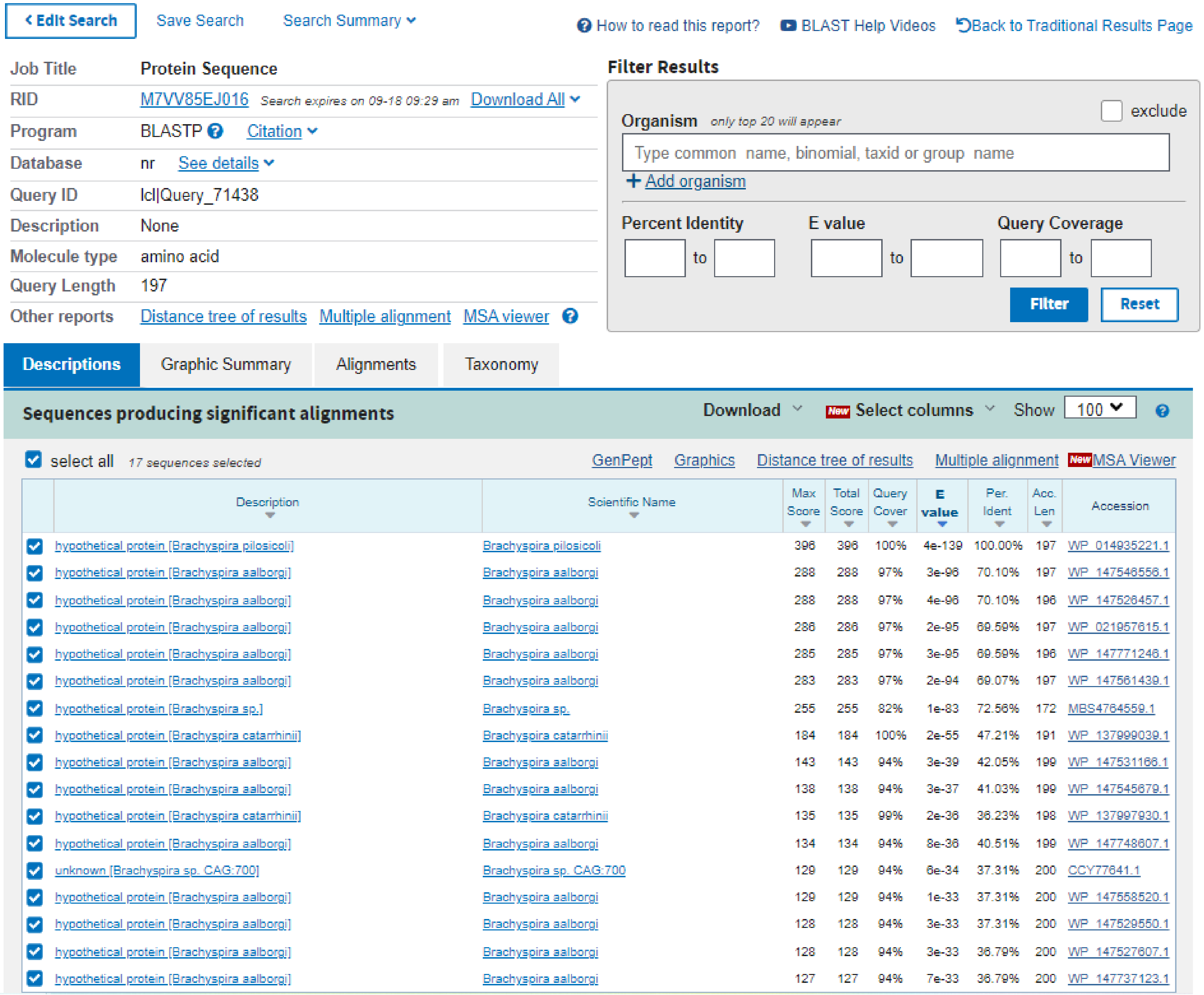
abcPred Threshold: 0.85

Window: 16

>fig|6666666.171271.peg.1294
MPRYEQLKAKSKGISYTRRIRSEDKEFNFKKPIIISVSFILLVSILFTVIKKYSPMVDIAVKDFFSINHREALTLETTGSEE
ENKISFLDNVPLFNFFIKSNTNETLSIMAYETNSMLETSVNTQNTNSMQNNSTITRESLSVFFNNNQNNQLNNTKDIEEQKD
NNIENTEEQNINNIVNDSYNYIQEMIQQNRGVNNNNNNNTINENNNLENNNLNNLTEEKNNYLEKVTNSINNKTSDEKIAAN
NSNISSSIFYDILKPKENTTRDIKTMRPATTTYSSTPPSYMRNNNEPKEKYNTNNYNYYFREDKKKKIIIILEKE

PROTEINA 13

```
>fig|6666666.171271.peg.235
MKNRILLILFLILVSFSFAYPKKMVLTLACLPPEGNMNDDAKLSYVTAVETAFTDAGHLVADRQRLDKLMKEVLLQQTSGMV
DETTAAAEAGKVMKVKYLVAVIVDKWDEEQVNSAASARAAANMIGSFLGNSQTTVSSGDSDLITVEKVRVSVKVIDVETSFV
LASGVGQGKLKDDPSKITKKIVKDLEKQLKKRL
```

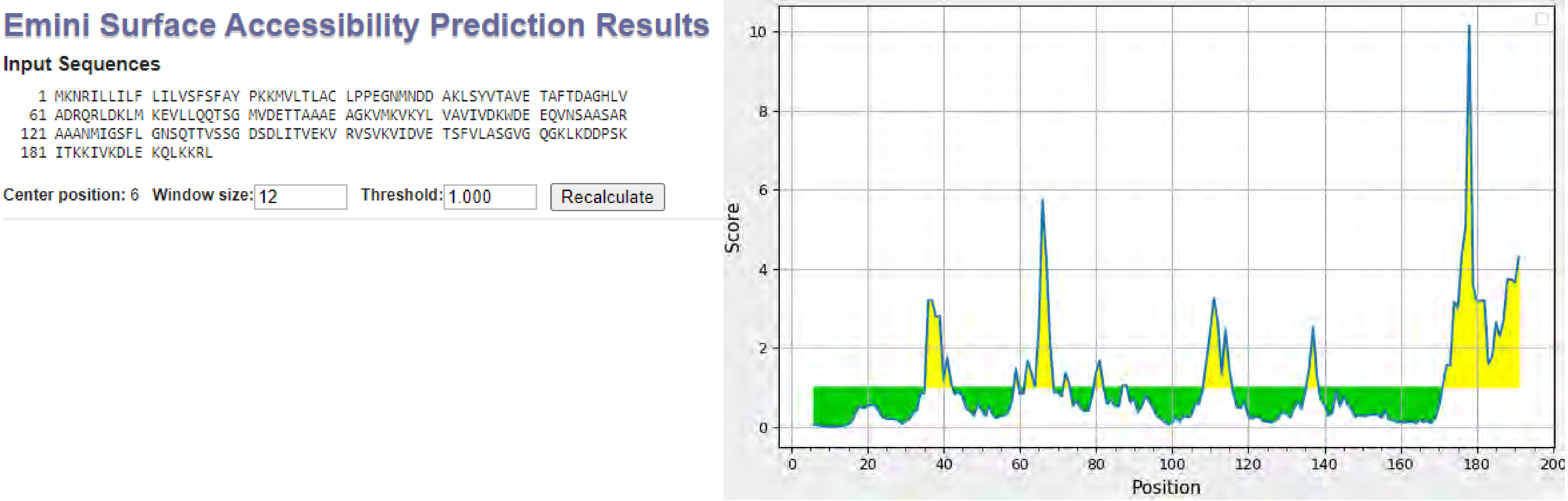


Job Title	Protein Sequence
RID	M7VV85EJ016 *Search expires on 09-18 09:29 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_71438
Description	None
Molecule type	amino acid
Query Length	197
Other reports	Distance tree of results Multiple alignment MSA viewer

Sequences producing significant alignments

☑ select all *17 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hypothetical protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	396	396	100%	4e-139	100.00%	197	WP_014935221.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	288	288	97%	3e-96	70.10%	197	WP_147546556.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	288	288	97%	4e-96	70.10%	196	WP_147526457.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	286	286	97%	2e-95	69.59%	197	WP_021957615.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	285	285	97%	3e-95	69.59%	196	WP_147771246.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	283	283	97%	2e-94	69.07%	197	WP_147561439.1
☑	hypothetical protein [Brachyspira sp.]	Brachyspira sp.	255	255	82%	1e-83	72.56%	172	MBS4764559.1
☑	hypothetical protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	184	184	100%	2e-55	47.21%	191	WP_137999039.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	143	143	94%	3e-39	42.05%	199	WP_147531166.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	138	138	94%	3e-37	41.03%	199	WP_147545679.1
☑	hypothetical protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	135	135	99%	2e-36	36.23%	198	WP_137997930.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	134	134	94%	8e-36	40.51%	199	WP_147748607.1
☑	unknown [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	129	129	94%	6e-34	37.31%	200	CCY77641.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	129	129	94%	1e-33	37.31%	200	WP_147558520.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	128	128	94%	3e-33	37.31%	200	WP_147529550.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	128	128	94%	3e-33	36.79%	200	WP_147527607.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	127	127	94%	7e-33	36.79%	200	WP_147737123.1



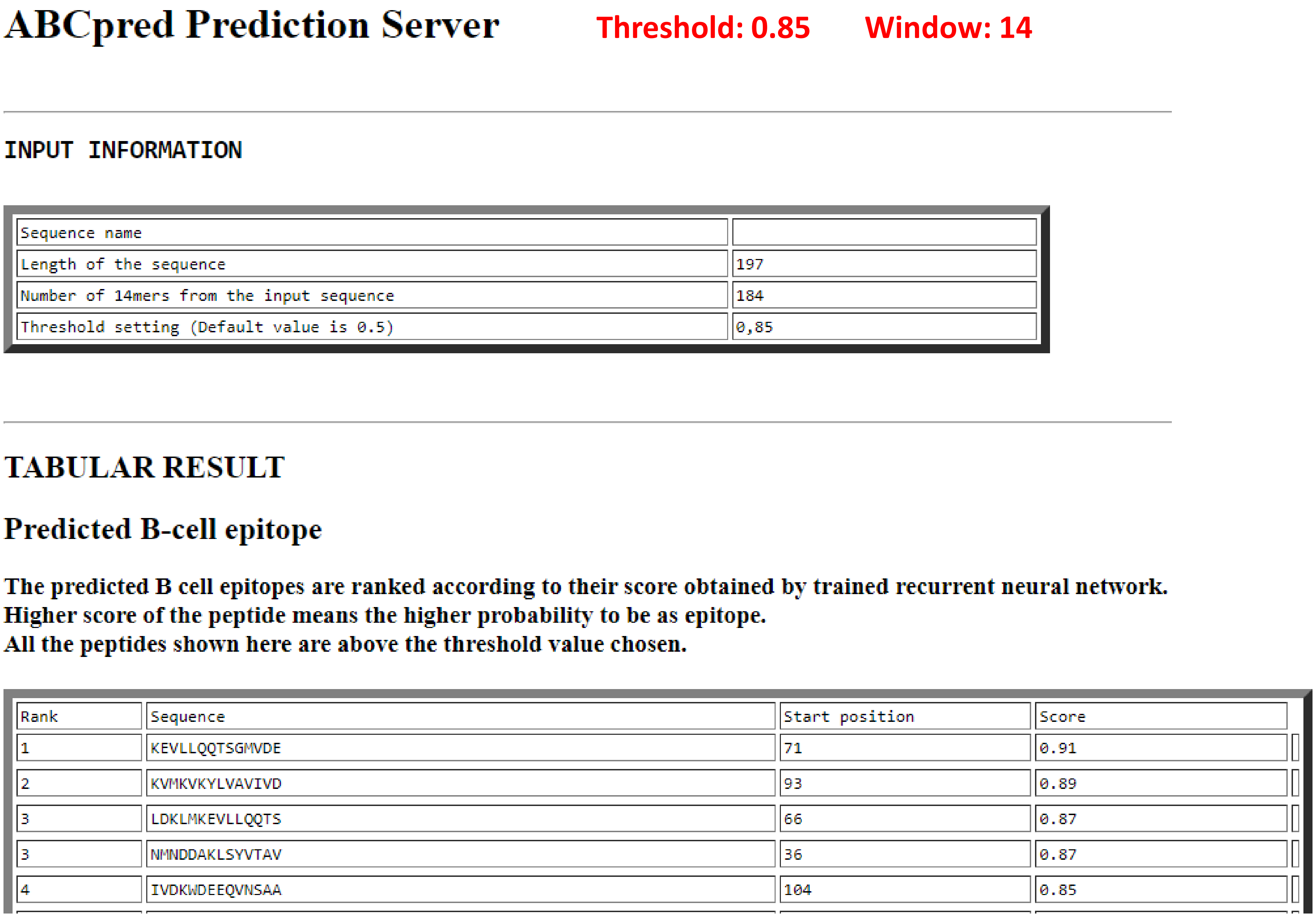
Emini Surface Accessibility Prediction Results

Input Sequences

```
    1 MKNRILLILF LILVSFSFAY PKKMVLTLAC LPPEGNMNDD AKLSYVTAVE TAFTDAGHLV
   61 ADRQRLDKLM KEVLLQQTSG MVDETTAAAE AGKVMKVKYL VAVIVDKWDE EQVNSAASAR
  121 AAANMIGSFL GNSQTTVSSG DSDLITVEKV RVSVKVIDVE TSFVLASGVG QGKLKDDPSK
  181 ITKKIVKDLE KQLKKRL
```

Center position: 6 Window size: 12 Threshold: 1.000

```
>fig|6666666.171271.peg.235
MKNRILLILFLILVSFSFAYPKKMVLTLACLPPEGNMNDDAKLSYVTAVETAFTDAGHLVADRQRLDKLMKEVLLQQTSGMV
DETTAAAEAGKVMKVKYLVAVIVDKWDEEQVNSAASARAAANMIGSFLGNSQTTVSSGDSDLITVEKVRVSVKVIDVETSFV
LASGVGQGKLKDDPSKITKKIVKDLEKQLKKRL
```



ABCpred Prediction Server

Threshold: 0.85 **Window: 14**

INPUT INFORMATION

Sequence name	
Length of the sequence	197
Number of 14mers from the input sequence	184
Threshold setting (Default value is 0.5)	0,85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	KEVLLQQTSGMVDE	71	0.91
2	KVMKVKYLVAVIVD	93	0.89
3	LDKLMKEVLLQQTS	66	0.87
3	NMNDDAKLSYVTAV	36	0.87
4	IVDKWDEEQVNSAA	104	0.85

PROTEINA 13

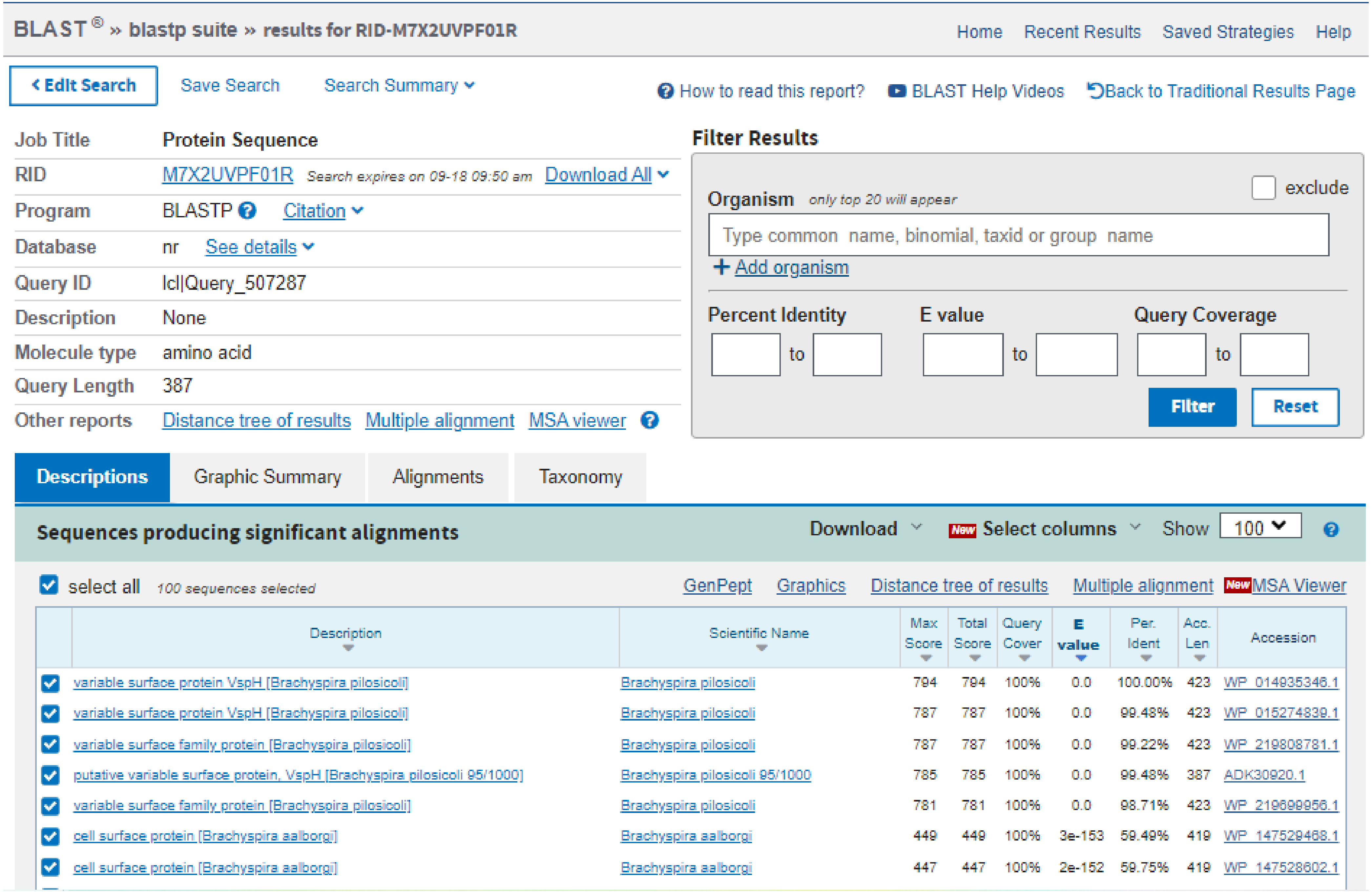
>fig|6666666.171271.peg.235
MKNRILLILFLILVSFSFAYPKKMVLTLACLPPEGNMNDDAKLSYVTAVETAFTDAGHLVADRQRLDKLMKEVLLQQTSGMV
DETTAAAEAGKVMKVKYLVAVIVDKWDEEQVNSAASARAAANMIGSFLGNSQTTVSSGDSDLITVEKVRVSVKVIDVETSFV
LASGVGQGKLKDDPSKITKKIVKDLEKQLKKRL

Predição combinada

>fig|6666666.171271.peg.235
MKNRILLILFLILVSFSFAYPKKMVLTLACLPPEG**NMNDDAKLSYVTAV**ETAFTDAGHLVA**DRQRLDKLMKEVLLQQTSGM**V
DETTAAAEAG**KVMKVKYLVAVIVDKWDEEQVNSAA**SARAAANMIGSFLGNSQTTVSSGDSDLITVEKVRVSVKVIDVETSFV
LASGVGQGKLKDDPSKITKKIVKDLEKQLKKRL

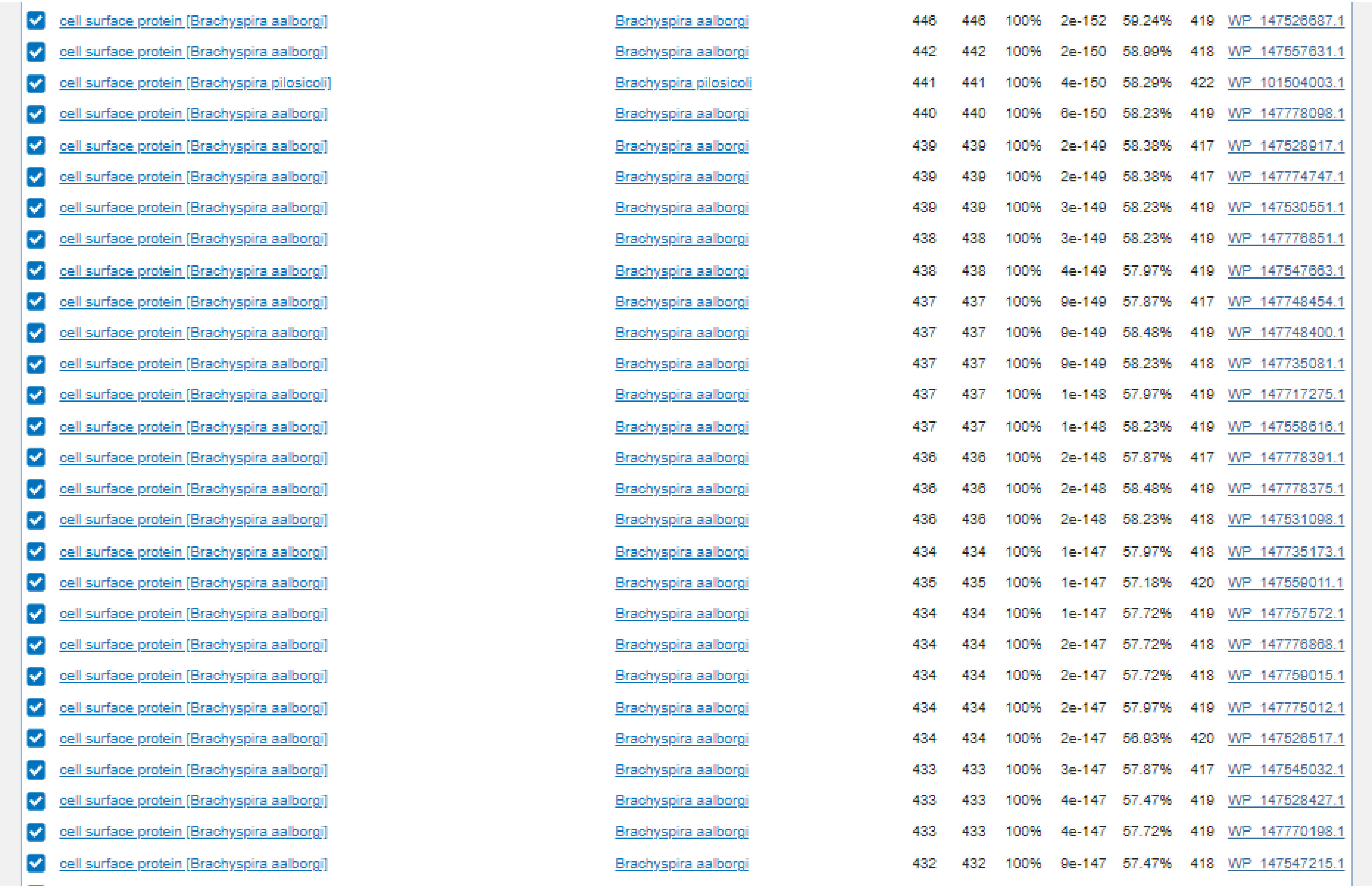
PROTEINA 13

```
>fig|6666666.171271.peg.434
MRIRTDRLGVLAGPRNWRFVAGLTGANIASGLILHNTGAPNTQQENTENNDKKGVDKFVPSALVAFGYDSDLFGIAAGYEFT
WKSPTYMVHTPILHMTALNDSFRINIPISIGVGQKSYVNDKSLKGTMVISTAIEGRYYFAEDIPALSHLRFYFNYGNSTIKA
LDFKDASFTQQSVGGEFRMYFKILTENIKIEPIFRVRFDAALATTYKNIDEANRGSILDSYAVSAKGFIPDDPGGTGANIAA
GGANASGTLQGGYIASIPSGYYAKEPYRLGLAIPVGFTATSADENISFYFEPALSLTIVNAKEIYTFGQHAWEDVASRHRRT
NPFYAFGYVVYAELYIRPVKNLEWYTELQTGGSTVAGDLSTASSTTIVFNASTGITWYF
```

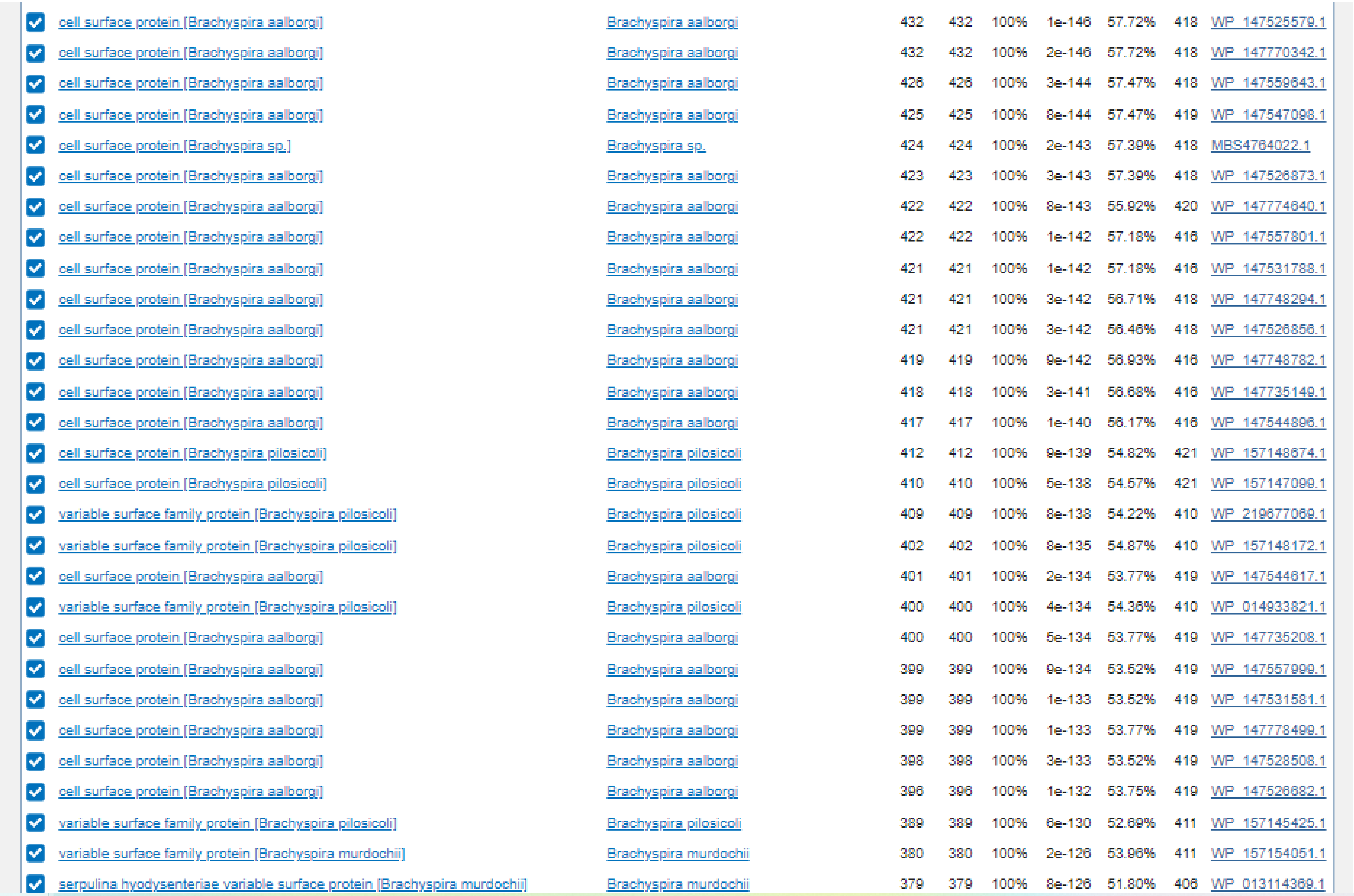


Job Title	Protein Sequence
RID	M7X2UVPF01R *Search expires on 09-18 09:50 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_507287
Description	None
Molecule type	amino acid
Query Length	387
Other reports	Distance tree of results Multiple alignment MSA viewer

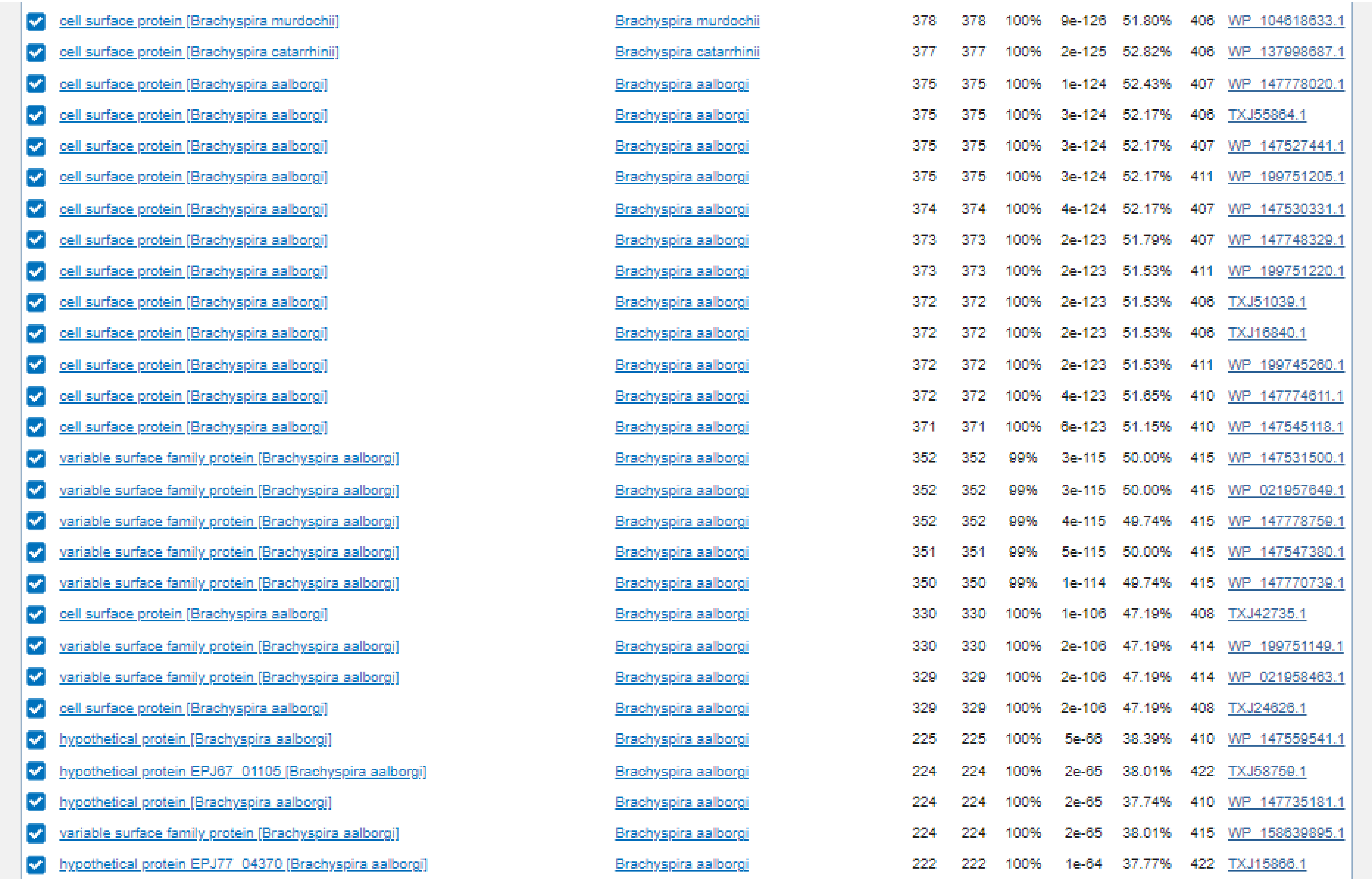
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	variable surface protein VspH [Brachyspira pilosicoli]	Brachyspira pilosicoli	794	794	100%	0.0	100.00%	423	WP_014935346.1
☑	variable surface protein VspH [Brachyspira pilosicoli]	Brachyspira pilosicoli	787	787	100%	0.0	99.48%	423	WP_015274839.1
☑	variable surface family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	787	787	100%	0.0	99.22%	423	WP_219808781.1
☑	putative variable surface protein, VspH [Brachyspira pilosicoli 95/1000]	Brachyspira pilosicoli 95/1000	785	785	100%	0.0	99.48%	387	ADK30920.1
☑	variable surface family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	781	781	100%	0.0	98.71%	423	WP_219699956.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	449	449	100%	3e-153	59.49%	419	WP_147529468.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	447	447	100%	2e-152	59.75%	419	WP_147528602.1



☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	446	446	100%	2e-152	59.24%	419	WP_147526687.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	442	442	100%	2e-150	58.99%	418	WP_147557631.1
☑	cell surface protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	441	441	100%	4e-150	58.29%	422	WP_101504003.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	440	440	100%	6e-150	58.23%	419	WP_147778098.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	439	439	100%	2e-149	58.38%	417	WP_147528917.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	439	439	100%	2e-149	58.38%	417	WP_147774747.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	439	439	100%	3e-149	58.23%	419	WP_147530551.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	438	438	100%	3e-149	58.23%	419	WP_147776851.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	438	438	100%	4e-149	57.97%	419	WP_147547663.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	437	437	100%	9e-149	57.87%	417	WP_147748454.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	437	437	100%	9e-149	58.48%	419	WP_147748400.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	437	437	100%	9e-149	58.23%	418	WP_147735081.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	437	437	100%	1e-148	57.97%	419	WP_147717275.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	437	437	100%	1e-148	58.23%	419	WP_147558616.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	436	436	100%	2e-148	57.87%	417	WP_147778391.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	436	436	100%	2e-148	58.48%	419	WP_147778375.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	436	436	100%	2e-148	58.23%	418	WP_147531098.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	434	434	100%	1e-147	57.97%	418	WP_147735173.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	435	435	100%	1e-147	57.18%	420	WP_147559011.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	434	434	100%	1e-147	57.72%	419	WP_147757572.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	434	434	100%	2e-147	57.72%	418	WP_147776868.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	434	434	100%	2e-147	57.72%	418	WP_147759015.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	434	434	100%	2e-147	57.97%	419	WP_147775012.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	434	434	100%	2e-147	56.93%	420	WP_147526517.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	433	433	100%	3e-147	57.87%	417	WP_147545032.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	433	433	100%	4e-147	57.47%	419	WP_147528427.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	433	433	100%	4e-147	57.72%	419	WP_147770198.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	432	432	100%	9e-147	57.47%	418	WP_147547215.1

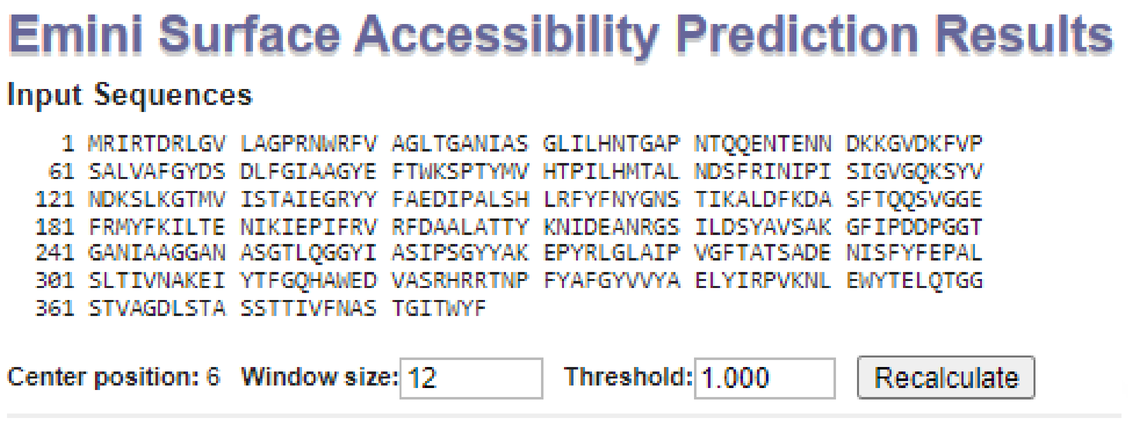


☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	432	432	100%	1e-146	57.72%	418	WP_147525579.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	432	432	100%	2e-146	57.72%	418	WP_147770342.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	426	426	100%	3e-144	57.47%	418	WP_147559643.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	425	425	100%	8e-144	57.47%	419	WP_147547098.1
☑	cell surface protein [Brachyspira sp.]	Brachyspira sp.	424	424	100%	2e-143	57.39%	418	MBS4764022.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	423	423	100%	3e-143	57.39%	418	WP_147526873.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	422	422	100%	8e-143	55.92%	420	WP_147774640.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	422	422	100%	1e-142	57.18%	416	WP_147557801.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	421	421	100%	1e-142	57.18%	416	WP_147531788.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	421	421	100%	3e-142	56.71%	418	WP_147748294.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	421	421	100%	3e-142	56.46%	418	WP_147526856.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	419	419	100%	9e-142	56.93%	416	WP_147748782.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	418	418	100%	3e-141	56.68%	416	WP_147735149.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	417	417	100%	1e-140	56.17%	416	WP_147544896.1
☑	cell surface protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	412	412	100%	9e-139	54.82%	421	WP_157148674.1
☑	cell surface protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	410	410	100%	5e-138	54.57%	421	WP_157147099.1
☑	variable surface family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	409	409	100%	8e-138	54.22%	410	WP_219677069.1
☑	variable surface family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	402	402	100%	8e-135	54.87%	410	WP_157148172.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	401	401	100%	2e-134	53.77%	419	WP_147544617.1
☑	variable surface family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	400	400	100%	4e-134	54.36%	410	WP_014933821.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	400	400	100%	5e-134	53.77%	419	WP_147735208.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	399	399	100%	9e-134	53.52%	419	WP_147557999.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	399	399	100%	1e-133	53.52%	419	WP_147531581.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	399	399	100%	1e-133	53.77%	419	WP_147778499.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	398	398	100%	3e-133	53.52%	419	WP_147528508.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	396	396	100%	1e-132	53.75%	419	WP_147526682.1
☑	variable surface family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	389	389	100%	6e-130	52.69%	411	WP_157145425.1
☑	variable surface family protein [Brachyspira murdochii]	Brachyspira murdochii	380	380	100%	2e-126	53.96%	411	WP_157154051.1
☑	serpulina hyodysenteriae variable surface protein [Brachyspira murdochii]	Brachyspira murdochii	379	379	100%	8e-126	51.80%	406	WP_013114369.1



☑	cell surface protein [Brachyspira murdochii]	Brachyspira murdochii	378	378	100%	9e-126	51.80%	406	WP_104618633.1
☑	cell surface protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	377	377	100%	2e-125	52.82%	406	WP_137998687.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	375	375	100%	1e-124	52.43%	407	WP_147778020.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	375	375	100%	3e-124	52.17%	406	TXJ55864.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	375	375	100%	3e-124	52.17%	407	WP_147527441.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	375	375	100%	3e-124	52.17%	411	WP_199751205.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	374	374	100%	4e-124	52.17%	407	WP_147530331.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	373	373	100%	2e-123	51.79%	407	WP_147748329.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	373	373	100%	2e-123	51.53%	411	WP_199751220.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	372	372	100%	2e-123	51.53%	406	TXJ51039.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	372	372	100%	2e-123	51.53%	406	TXJ16840.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	372	372	100%	2e-123	51.53%	411	WP_199745260.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	372	372	100%	4e-123	51.65%	410	WP_147774611.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	371	371	100%	6e-123	51.15%	410	WP_147545118.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	352	352	99%	3e-115	50.00%	415	WP_147531500.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	352	352	99%	3e-115	50.00%	415	WP_021957649.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	352	352	99%	4e-115	49.74%	415	WP_147778759.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	351	351	99%	5e-115	50.00%	415	WP_147547380.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	350	350	99%	1e-114	49.74%	415	WP_147770739.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	330	330	100%	1e-106	47.19%	408	TXJ42735.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	330	330	100%	2e-106	47.19%	414	WP_199751149.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	329	329	100%	2e-106	47.19%	414	WP_021958463.1
☑	cell surface protein [Brachyspira aalborgi]	Brachyspira aalborgi	329	329	100%	2e-106	47.19%	408	TXJ24626.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	225	225	100%	5e-66	38.39%	410	WP_147559541.1
☑	hypothetical protein EPJ67_01105 [Brachyspira aalborgi]	Brachyspira aalborgi	224	224	100%	2e-65	38.01%	422	TXJ58759.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	224	224	100%	2e-65	37.74%	410	WP_147735181.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	224	224	100%	2e-65	38.01%	415	WP_158639895.1
☑	hypothetical protein EPJ77_04370 [Brachyspira aalborgi]	Brachyspira aalborgi	222	222	100%	1e-64	37.77%	422	TXJ15866.1

☑	hypothetical protein EPJ76_10720 [Brachyspira aalborgi]	Brachyspira aalborgi	222	222	100%	1e-64	37.77%	422	TXJ53872.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	221	221	100%	2e-64	37.77%	415	WP_158640422.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	221	221	100%	2e-64	37.77%	415	WP_021958549.1
☑	hypothetical protein EPJ81_08215 [Brachyspira aalborgi]	Brachyspira aalborgi	221	221	100%	5e-64	37.53%	422	TXJ39085.1
☑	variable surface family protein [Brachyspira aalborgi]	Brachyspira aalborgi	220	220	100%	6e-64	37.53%	415	WP_158636827.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	219	219	100%	9e-64	37.96%	410	WP_147526197.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	219	219	100%	1e-63	37.44%	412	WP_147557317.1
☑	hypothetical protein [Brachyspira aalborgi]	Brachyspira aalborgi	219	219	100%	1e-63	37.96%	410	WP_147770082.1

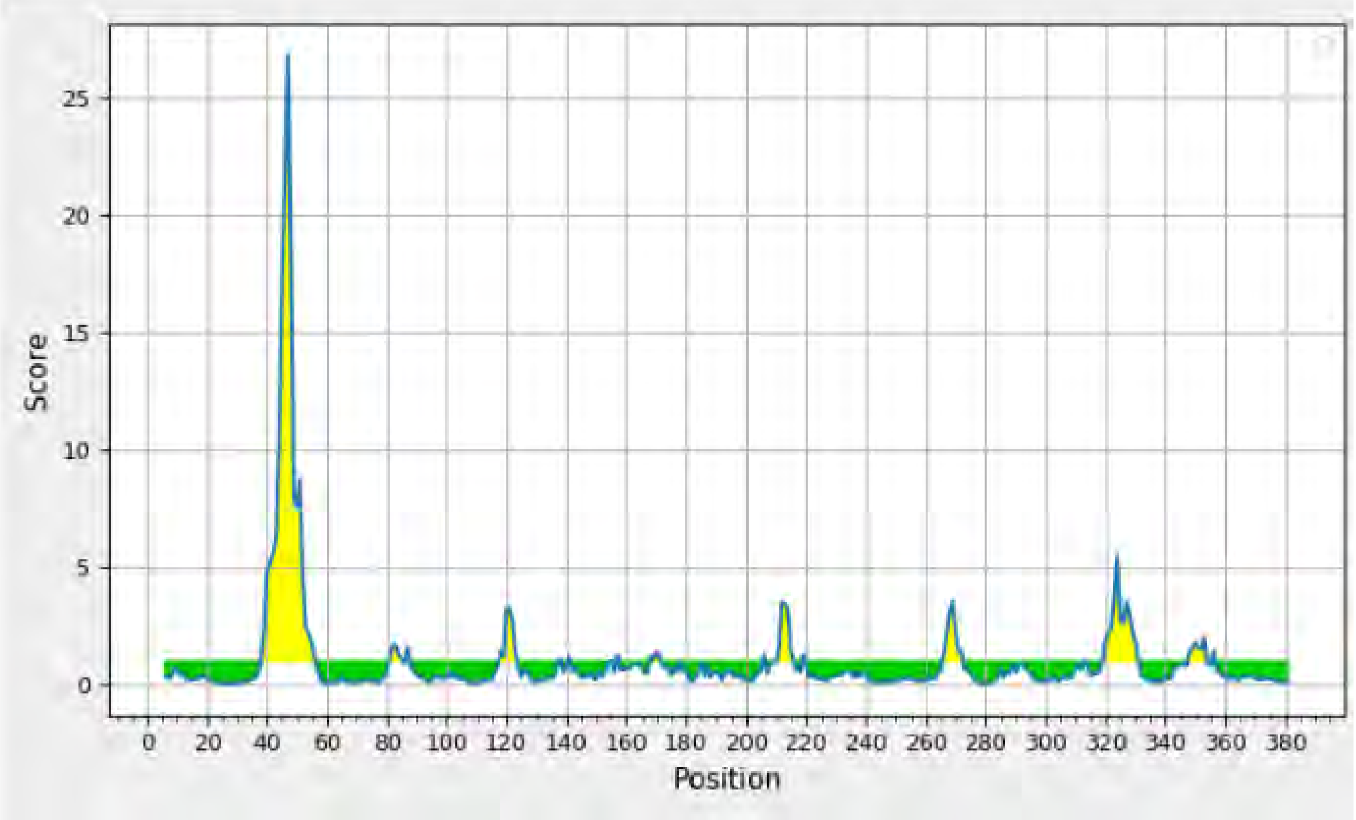


Emini Surface Accessibility Prediction Results

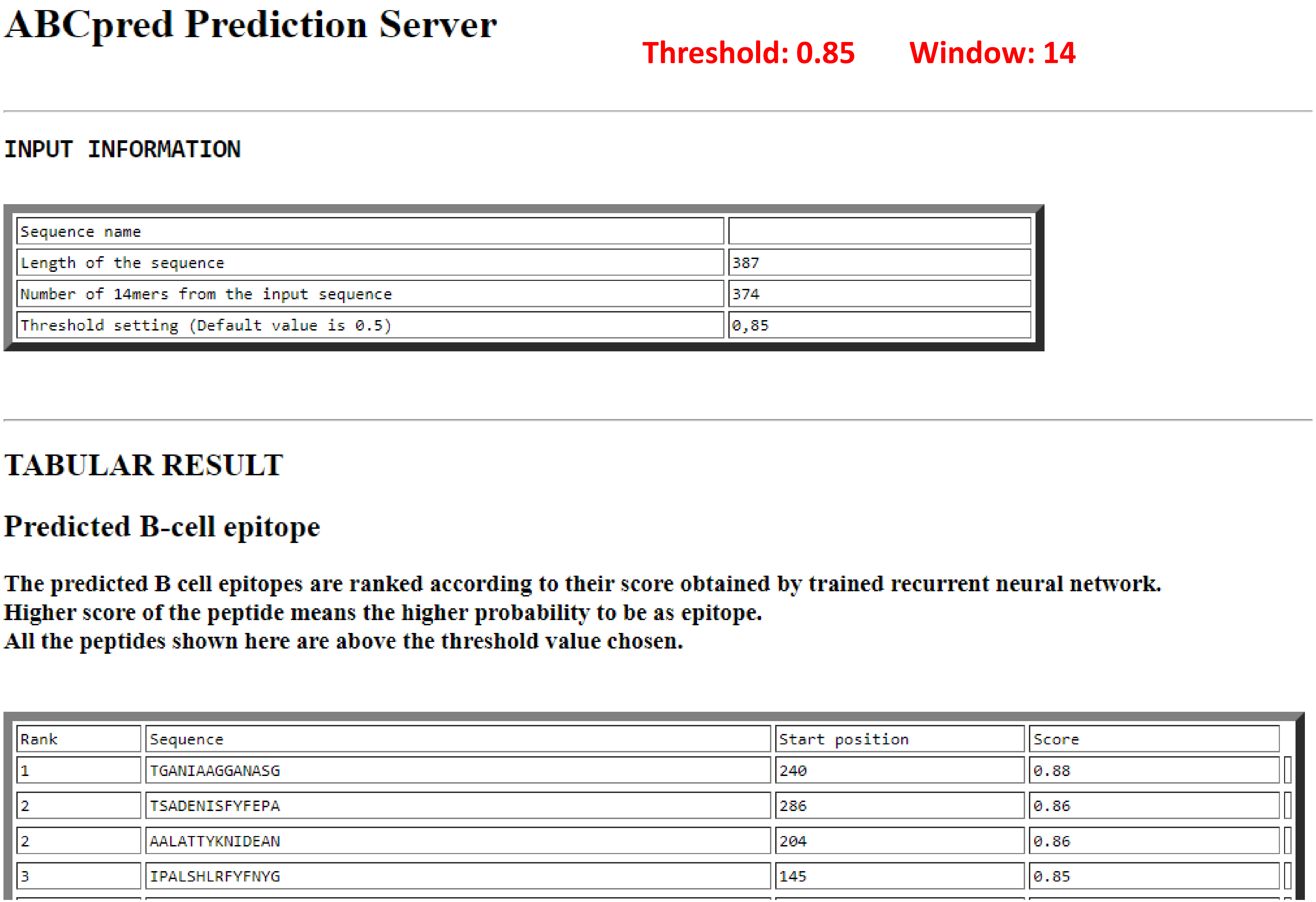
Input Sequences

```
  1 MRIRTDRLGV LAGPRNWRFV AGLTGANIAS GLILHNTGAP NTQQENTENN DKKGVDKFVP
 61 SALVAFGYDS DLFGIAAGYE FTWKSPTYMV HTPILHMTAL NDSFRINIPI SIGVGQKSYV
121 NDKSLKGTMV ISTAIEGRYY FAEDIPALSH LRFYFNYGNS TIKALDFKDA SFTQQSVGGE
181 FRMYFKILTE NIKIEPIFRV RFDAALATTY KNIDEANRGS ILDSYAVSAK GFIPDDPGGT
241 GANIAAGGAN ASGTLQGGYI ASIPSGYYAK EPYRLGLAIP VGFTATSADE NISFYFEPAL
301 SLTIVNAKEI YTFGQHAWED VASRHRRTNP FYAFGYVVYA ELYIRPVKNL EWYTELQTGG
361 STVAGDLSTA SSTTIVFNAS TGITWYF
```

Center position: 6 Window size: 12 Threshold: 1.000



>fig|6666666.171271.peg.434
MRIRTDRLGVLAGPRNWRFVAGLTGANIASGLILHNTGAPNTQQENTENNDKKGVDKFVPSALVAFGYDSDLFGIAAGYEFT
WKSPTYMVHTPILHMTALNDSFRINIPISIGVGQKSYVNDKSLKGTMVISTAIEGRYYFAEDIPALSHLRFYFNYGNSTIKA
LDFKDASFTQQSVGGEFRMYFKILTENIKIEPIFRVRFDAALATTYKNIDEANRGSILDSYAVSAKGFIPDDPGGTGANIAA
GGANASGTLQGGYIASIPSGYYAKEPYRLGLAIPVGFTATSADENISFYFEPALSLTIVNAKEIYTFGQHAWEDVASRHRRT
NPFYAFGYVVYAELYIRPVKNLEWYTELQTGGSTVAGDLSTASSTTIVFNASTGITWYF



ABCpred Prediction Server

Threshold: 0.85 Window: 14

INPUT INFORMATION

Sequence name	
Length of the sequence	387
Number of 14mers from the input sequence	374
Threshold setting (Default value is 0.5)	0,85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	TGANIAAGGANASG	240	0.88
2	TSADENISFYFEPA	286	0.86
2	AALATTYKNIDEAN	204	0.86
3	IPALSHLRFYFNYG	145	0.85

PROTEINA 14

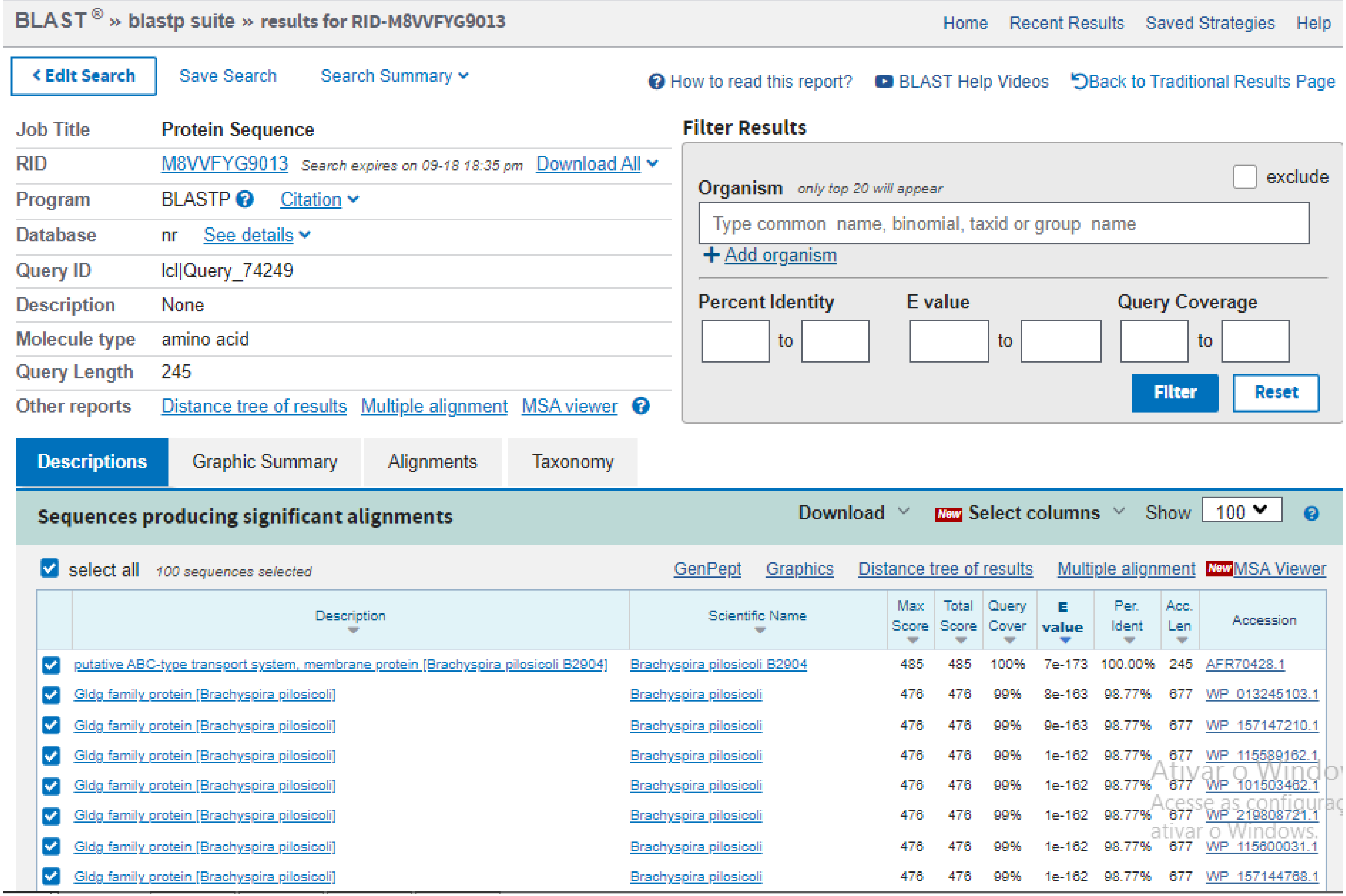
>fig|6666666.171271.peg.434
MRIRTDRLGVLAGPRNWRFVAGLTGANIASGLILHNTGAPNTQQENTENNDKKGVDKFVPSALVAFGYDSDLFGIAAGYEFT
WKSPTYMVHTPILHMTALNDSFRINIPISIGVGQKSYVNDKSLKGTMVISTAIEGRYYFAEDIPALSHLRFYFNYGNSTIKA
LDFKDASFTQQSVGGEFRMYFKILTENIKIEPIFRVRFDAALATTYKNIDEANRGSILDSYAVSAKGFIPDDPGGTGANIAA
GGANASGTLQGGYIASIPSGYYAKEPYRLGLAIPVGFTATSADENISFYFEPALSLTIVNAKEIYTFGQHAWEDVASRHRRT
NPFYAFGYVVYAELYIRPVKNLEWYTELQTGGSTVAGDLSTASSTTIVFNASTGITWYF

Predição combinada

>fig|6666666.171271.peg.434
MRIRTDRLGVLAGPRNWRFVAGLTGANIASGLILHNTGAPNTQQENTENNDKKGVDKFVPSALVAFGYDSDLFGIAAGYEFT
WKSPTYMVHTPILHMTALNDSFRINIPISIGVGQKSYVNDKSLKGTMVISTAIEGRYYFAEDIPALSHLRFYFNYGNSTIKA
LDFKDASFTQQSVGGEFRMYFKILTENIKIEPIFRVRFD**AALATTYKNIDEANRG**SILDSYAVSAKGFIPDDPGGTGANIAA
GGANASGTLQGGYIASIPSGYYAKEPYRLGLAIPVGFTATSADENISFYFEPALSLTIVNAKEIYTFGQHAWEDVASRHRRT
NPFYAFGYVVYAELYIRPVKNLEWYTELQTGGSTVAGDLSTASSTTIVFNASTGITWYF

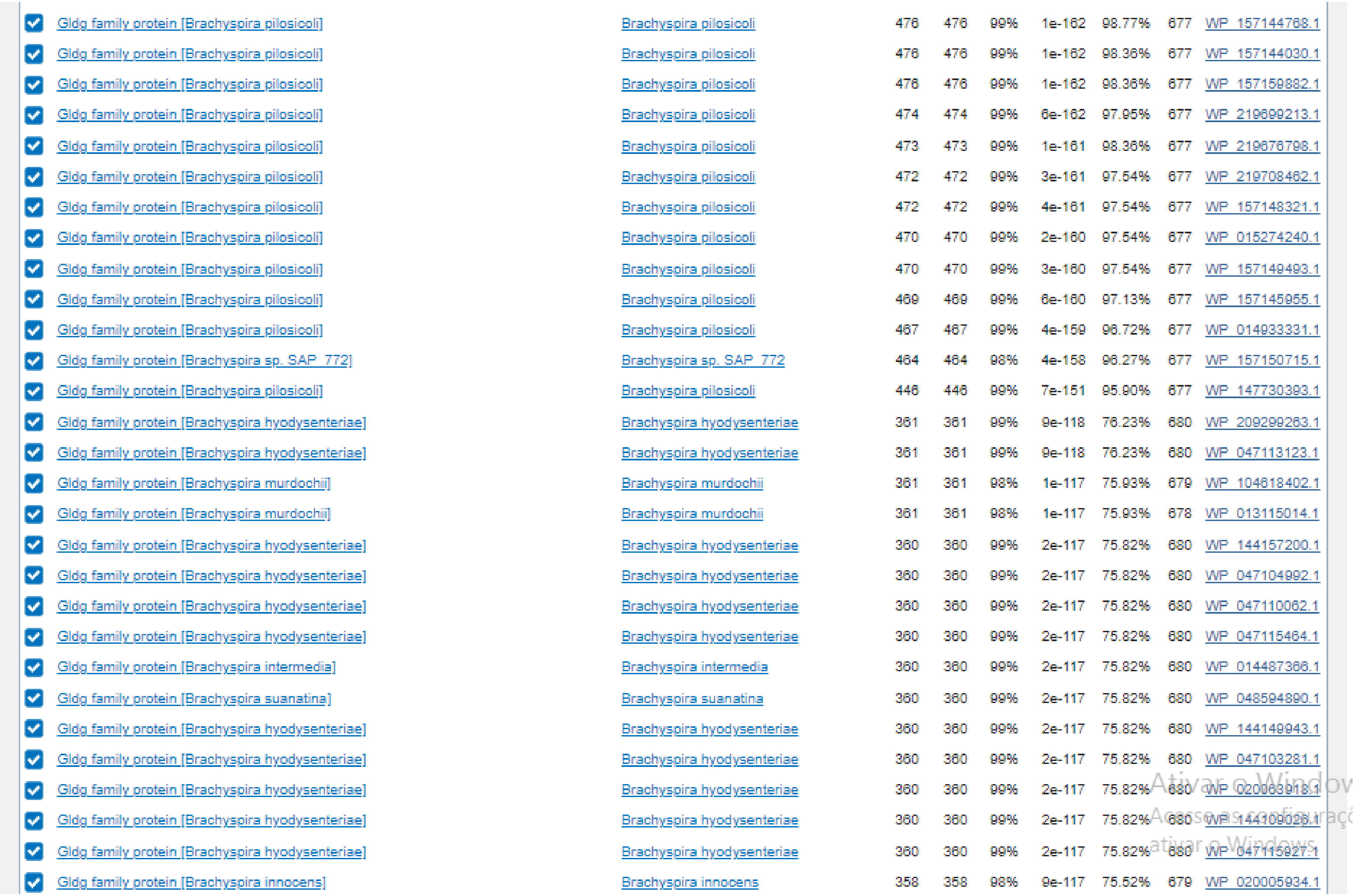
PROTEINA 15

```
>fig|6666666.171271.peg.1083
MTKRKDRIITFIFVLVIIVLINAIVNQFTPFIDLTKDKVYSLSSGSKSLVKSLKEPLSVKFFLTPNLPPPFSTYEKYIKDLF
AEYKSAAGKNISFEIIDASTNTIVANQYGITSTQINVLEKDQTSSKIAYMGLAFIYGDSIESIPFVRSTEGLEYNIDTIIRK
LIDKNDKLSRLENNLNVYYISSPEVYELLPIGAIELIPDSIMQAVTEANKNLMNKVVFTHVDMSSPNQENEDIIKNLILKN
```

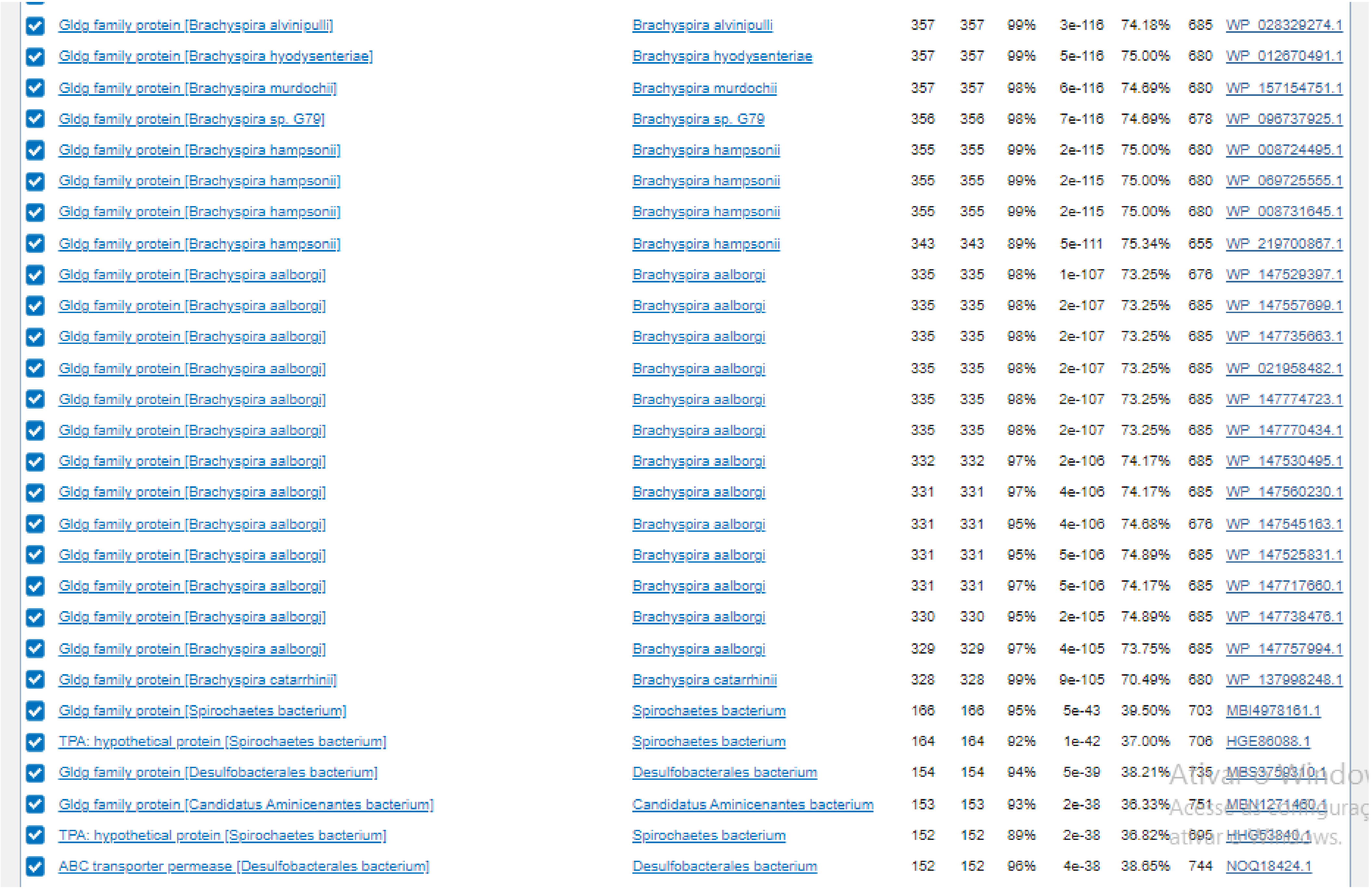


Job Title	Protein Sequence
RID	M8VVFYG9013 Search expires on 09-18 18:35 pm Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_74249
Description	None
Molecule type	amino acid
Query Length	245
Other reports	Distance tree of results Multiple alignment MSA viewer

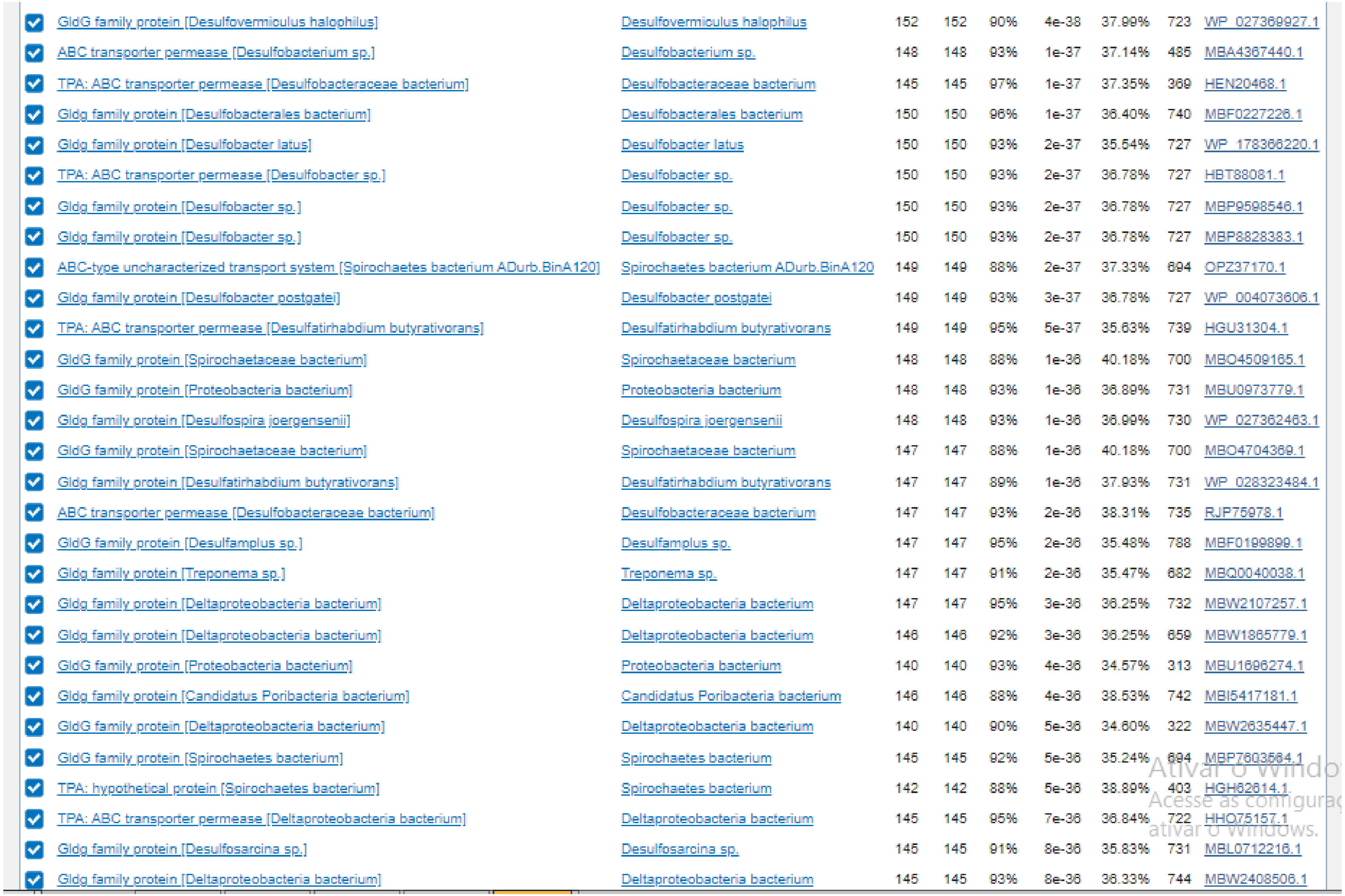
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	putative ABC-type transport system, membrane protein [Brachyspira pilosicoli B2904]	Brachyspira pilosicoli B2904	485	485	100%	7e-173	100.00%	245	AFR70428.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	8e-163	98.77%	677	WP_013245103.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	9e-163	98.77%	677	WP_157147210.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	1e-162	98.77%	677	WP_115589162.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	1e-162	98.77%	677	WP_101503462.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	1e-162	98.77%	677	WP_219808721.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	1e-162	98.77%	677	WP_115600031.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	1e-162	98.77%	677	WP_157144768.1



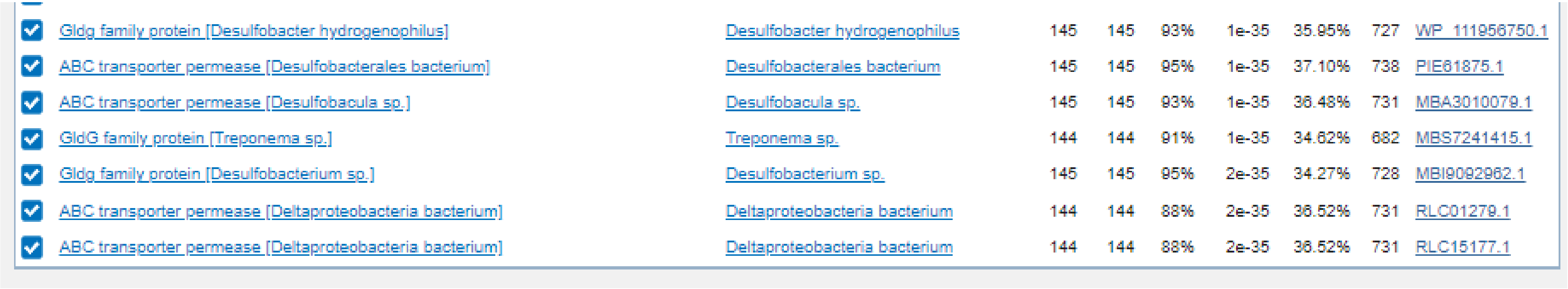
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	1e-162	98.77%	677	WP_157144768.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	1e-162	98.36%	677	WP_157144030.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	476	476	99%	1e-162	98.36%	677	WP_157159882.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	474	474	99%	6e-162	97.95%	677	WP_219699213.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	473	473	99%	1e-161	98.36%	677	WP_219676798.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	472	472	99%	3e-161	97.54%	677	WP_219708462.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	472	472	99%	4e-161	97.54%	677	WP_157148321.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	470	470	99%	2e-160	97.54%	677	WP_015274240.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	470	470	99%	3e-160	97.54%	677	WP_157149493.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	469	469	99%	6e-160	97.13%	677	WP_157145955.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	467	467	99%	4e-159	96.72%	677	WP_014933331.1
☑	Gldg family protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	464	464	98%	4e-158	96.27%	677	WP_157150715.1
☑	Gldg family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	446	446	99%	7e-151	95.90%	677	WP_147730393.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	361	361	99%	9e-118	76.23%	680	WP_209299263.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	361	361	99%	9e-118	76.23%	680	WP_047113123.1
☑	Gldg family protein [Brachyspira murdochii]	Brachyspira murdochii	361	361	98%	1e-117	75.93%	679	WP_104618402.1
☑	Gldg family protein [Brachyspira murdochii]	Brachyspira murdochii	361	361	98%	1e-117	75.93%	678	WP_013115014.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_144157200.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_047104992.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_047110062.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_047115464.1
☑	Gldg family protein [Brachyspira intermedia]	Brachyspira intermedia	360	360	99%	2e-117	75.82%	680	WP_014487366.1
☑	Gldg family protein [Brachyspira suanatina]	Brachyspira suanatina	360	360	99%	2e-117	75.82%	680	WP_048594890.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_144149943.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_047103281.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_020063918.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_144109026.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	360	360	99%	2e-117	75.82%	680	WP_047115927.1
☑	Gldg family protein [Brachyspira innocens]	Brachyspira innocens	358	358	98%	9e-117	75.52%	679	WP_020005934.1



☑	Gldg family protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	357	357	99%	3e-116	74.18%	685	WP_028329274.1
☑	Gldg family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	357	357	99%	5e-116	75.00%	680	WP_012670491.1
☑	Gldg family protein [Brachyspira murdochii]	Brachyspira murdochii	357	357	98%	6e-116	74.69%	680	WP_157154751.1
☑	Gldg family protein [Brachyspira sp. G79]	Brachyspira sp. G79	356	356	98%	7e-116	74.69%	678	WP_096737925.1
☑	Gldg family protein [Brachyspira hampsonii]	Brachyspira hampsonii	355	355	99%	2e-115	75.00%	680	WP_008724495.1
☑	Gldg family protein [Brachyspira hampsonii]	Brachyspira hampsonii	355	355	99%	2e-115	75.00%	680	WP_069725555.1
☑	Gldg family protein [Brachyspira hampsonii]	Brachyspira hampsonii	355	355	99%	2e-115	75.00%	680	WP_008731645.1
☑	Gldg family protein [Brachyspira hampsonii]	Brachyspira hampsonii	343	343	89%	5e-111	75.34%	655	WP_219700867.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	335	335	98%	1e-107	73.25%	676	WP_147529397.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	335	335	98%	2e-107	73.25%	685	WP_147557699.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	335	335	98%	2e-107	73.25%	685	WP_147735663.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	335	335	98%	2e-107	73.25%	685	WP_021958482.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	335	335	98%	2e-107	73.25%	685	WP_147774723.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	335	335	98%	2e-107	73.25%	685	WP_147770434.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	332	332	97%	2e-106	74.17%	685	WP_147530495.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	331	331	97%	4e-106	74.17%	685	WP_147560230.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	331	331	95%	4e-106	74.68%	676	WP_147545163.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	331	331	95%	5e-106	74.89%	685	WP_147525831.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	331	331	97%	5e-106	74.17%	685	WP_147717660.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	330	330	95%	2e-105	74.89%	685	WP_147738476.1
☑	Gldg family protein [Brachyspira aalborgi]	Brachyspira aalborgi	329	329	97%	4e-105	73.75%	685	WP_147757994.1
☑	Gldg family protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	328	328	99%	9e-105	70.49%	680	WP_137998248.1
☑	Gldg family protein [Spirochaetes bacterium]	Spirochaetes bacterium	166	166	95%	5e-43	39.50%	703	MBI4978161.1
☑	TPA: hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	164	164	92%	1e-42	37.00%	706	HGE86088.1
☑	Gldg family protein [Desulfobacterales bacterium]	Desulfobacterales bacterium	154	154	94%	5e-39	38.21%	735	MBS3759310.1
☑	Gldg family protein [Candidatus Aminicenantes bacterium]	Candidatus Aminicenantes bacterium	153	153	93%	2e-38	36.33%	751	MBN1271460.1
☑	TPA: hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	152	152	89%	2e-38	36.82%	695	HHG53840.1
☑	ABC transporter permease [Desulfobacterales bacterium]	Desulfobacterales bacterium	152	152	96%	4e-38	38.65%	744	NOQ18424.1



☑	GldG family protein [Desulfovermiculus halophilus]	Desulfovermiculus halophilus	152	152	90%	4e-38	37.99%	723	WP_027369927.1
☑	ABC transporter permease [Desulfobacterium sp.]	Desulfobacterium sp.	148	148	93%	1e-37	37.14%	485	MBA4367440.1
☑	TPA: ABC transporter permease [Desulfobacteraceae bacterium]	Desulfobacteraceae bacterium	145	145	97%	1e-37	37.35%	369	HEN20468.1
☑	Gldg family protein [Desulfobacterales bacterium]	Desulfobacterales bacterium	150	150	96%	1e-37	36.40%	740	MBF0227226.1
☑	Gldg family protein [Desulfobacter latus]	Desulfobacter latus	150	150	93%	2e-37	35.54%	727	WP_178366220.1
☑	TPA: ABC transporter permease [Desulfobacter sp.]	Desulfobacter sp.	150	150	93%	2e-37	36.78%	727	HBT88081.1
☑	Gldg family protein [Desulfobacter sp.]	Desulfobacter sp.	150	150	93%	2e-37	36.78%	727	MBP9598546.1
☑	Gldg family protein [Desulfobacter sp.]	Desulfobacter sp.	150	150	93%	2e-37	36.78%	727	MBP8828383.1
☑	ABC-type uncharacterized transport system [Spirochaetes bacterium ADurb.BinA120]	Spirochaetes bacterium ADurb.BinA120	149	149	88%	2e-37	37.33%	694	OPZ37170.1
☑	Gldg family protein [Desulfobacter postgatei]	Desulfobacter postgatei	149	149	93%	3e-37	36.78%	727	WP_004073606.1
☑	TPA: ABC transporter permease [Desulfatirhabdium butyrativorans]	Desulfatirhabdium butyrativorans	149	149	95%	5e-37	35.63%	739	HGU31304.1
☑	GldG family protein [Spirochaetaceae bacterium]	Spirochaetaceae bacterium	148	148	88%	1e-36	40.18%	700	MBO4509165.1
☑	GldG family protein [Proteobacteria bacterium]	Proteobacteria bacterium	148	148	93%	1e-36	36.89%	731	MBU0973779.1
☑	Gldg family protein [Desulfospira joergensenii]	Desulfospira joergensenii	148	148	93%	1e-36	36.99%	730	WP_027362463.1
☑	GldG family protein [Spirochaetaceae bacterium]	Spirochaetaceae bacterium	147	147	88%	1e-36	40.18%	700	MBO4704369.1
☑	Gldg family protein [Desulfatirhabdium butyrativorans]	Desulfatirhabdium butyrativorans	147	147	89%	1e-36	37.93%	731	WP_028323484.1
☑	ABC transporter permease [Desulfobacteraceae bacterium]	Desulfobacteraceae bacterium	147	147	93%	2e-36	38.31%	735	RJP75978.1
☑	GldG family protein [Desulfamplus sp.]	Desulfamplus sp.	147	147	95%	2e-36	35.48%	788	MBF0199899.1
☑	Gldg family protein [Treponema sp.]	Treponema sp.	147	147	91%	2e-36	35.47%	682	MBQ0040038.1
☑	Gldg family protein [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	147	147	95%	3e-36	36.25%	732	MBW2107257.1
☑	Gldg family protein [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	146	146	92%	3e-36	36.25%	659	MBW1865779.1
☑	GldG family protein [Proteobacteria bacterium]	Proteobacteria bacterium	140	140	93%	4e-36	34.57%	313	MBU1696274.1
☑	Gldg family protein [Candidatus Poribacteria bacterium]	Candidatus Poribacteria bacterium	146	146	88%	4e-36	38.53%	742	MBI5417181.1
☑	GldG family protein [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	140	140	90%	5e-36	34.60%	322	MBW2635447.1
☑	GldG family protein [Spirochaetes bacterium]	Spirochaetes bacterium	145	145	92%	5e-36	35.24%	694	MBP7603564.1
☑	TPA: hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	142	142	88%	5e-36	38.89%	403	HGH62614.1
☑	TPA: ABC transporter permease [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	145	145	95%	7e-36	36.84%	722	HHO75157.1
☑	Gldg family protein [Desulfosarcina sp.]	Desulfosarcina sp.	145	145	91%	8e-36	35.83%	731	MBL0712216.1
☑	Gldg family protein [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	145	145	93%	8e-36	36.33%	744	MBW2408506.1



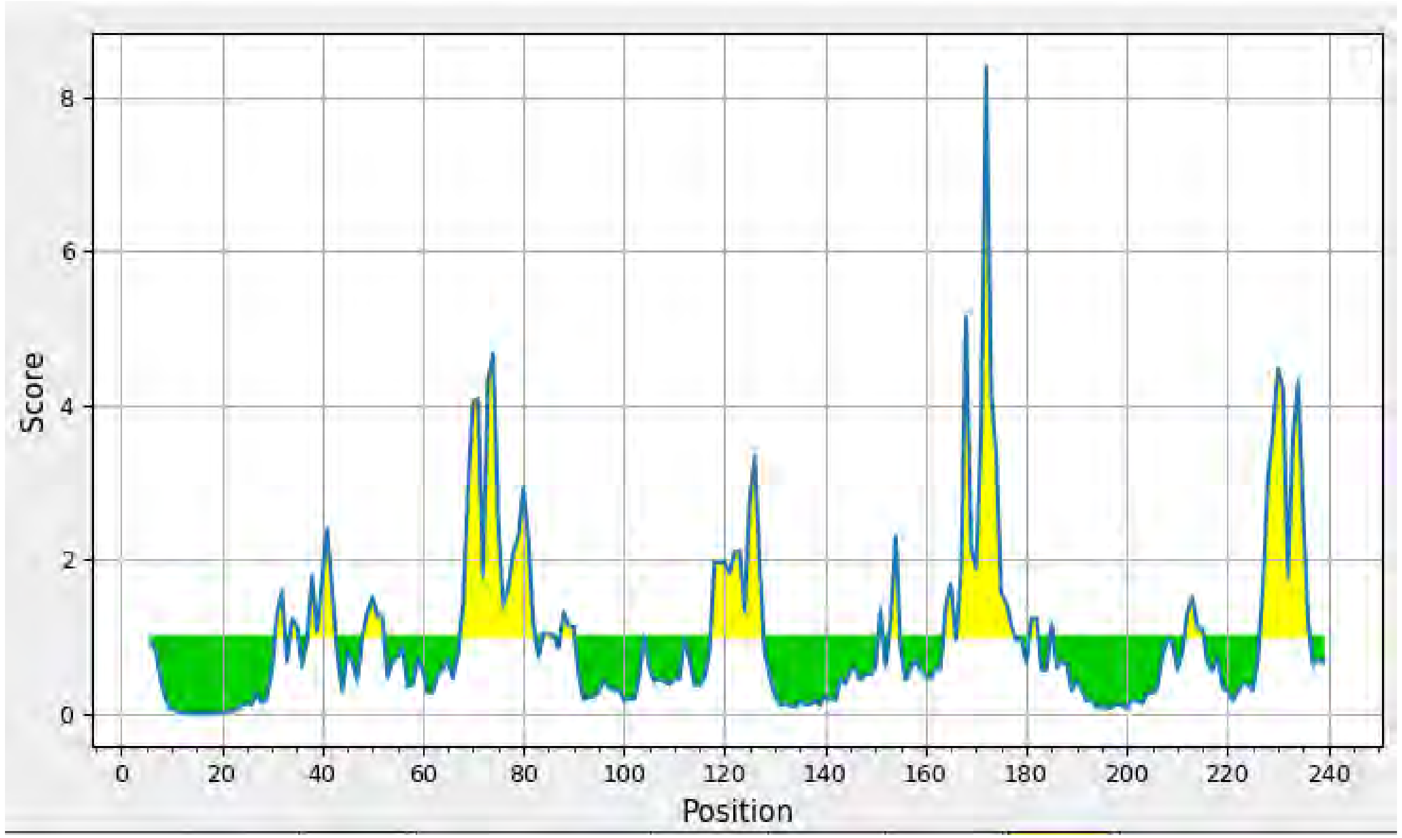
☑	Gldg family protein [Desulfobacter hydrogenophilus]	Desulfobacter hydrogenophilus	145	145	93%	1e-35	35.95%	727	WP_111956750.1
☑	ABC transporter permease [Desulfobacterales bacterium]	Desulfobacterales bacterium	145	145	95%	1e-35	37.10%	738	PIE61875.1
☑	ABC transporter permease [Desulfobacula sp.]	Desulfobacula sp.	145	145	93%	1e-35	36.48%	731	MBA3010079.1
☑	GldG family protein [Treponema sp.]	Treponema sp.	144	144	91%	1e-35	34.62%	682	MBS7241415.1
☑	Gldg family protein [Desulfobacterium sp.]	Desulfobacterium sp.	145	145	95%	2e-35	34.27%	728	MBI9092962.1
☑	ABC transporter permease [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	144	144	88%	2e-35	36.52%	731	RLC01279.1
☑	ABC transporter permease [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	144	144	88%	2e-35	36.52%	731	RLC15177.1

Emini Surface Accessibility Prediction Results

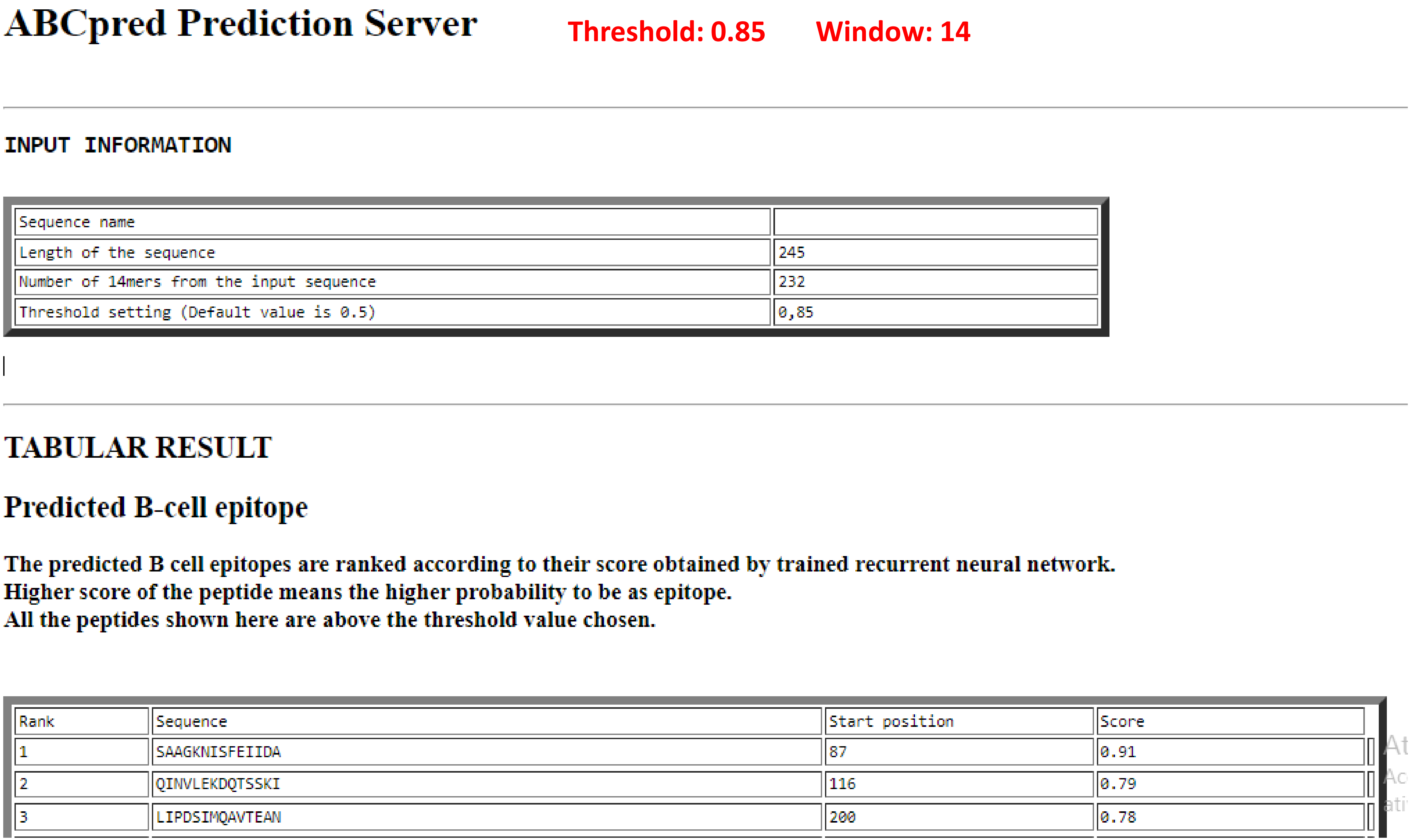
Input Sequences

```
   1 MTKRKDRIIT FIFVLVIIVL INAIVNQFTP FIDLTKDKVY SLSSGSKSLV KSLKEPLSVK
  61 FFLTPNLP PPFSTYEKYI KDLFAEYKSA AGKNISFEII DASTNTIVAN QYGITSTQIN
 121 VL EKDQTS SKIAYMGLAF IYGDSIESIP FVRSTEGLEY NIDTIIRKLI DKNDKLSRLE
 181 NNLN VYYI SSPEVYELLP IGAIELIPDS IMQAVTEANK NLMNKVVFTH VDMSSPNQEN
 241 EDIIKN LI LKN
```

Center position: 6 Window size: 12 Threshold: 1.000



```
>fig|6666666.171271.peg.1083
MTKRKDRIITFIFVLVIIVLINAIVNQFTPFIDLTKDKVYSLSSGSKSLVKSLKEPLSVKFFLTPNLPPPFSTYEKYIKDLF
AEYKSAAGKNISFEIIDASTNTIVANQYGITSTQINVLEKDQTSSKIAYMGLAFIYGDSIESIPFVRSTEGLEYNIDTIIRK
LIDKNDKLSRLENNLNVYYISSPEVYELLPIGAIELIPDSIMQAVTEANKNLMNKVVFTHVDMSSPNQENEDIIKNLILKN
```



ABCpred Prediction Server

Threshold: 0.85 **Window: 14**

INPUT INFORMATION

Sequence name	
Length of the sequence	245
Number of 14mers from the input sequence	232
Threshold setting (Default value is 0.5)	0,85

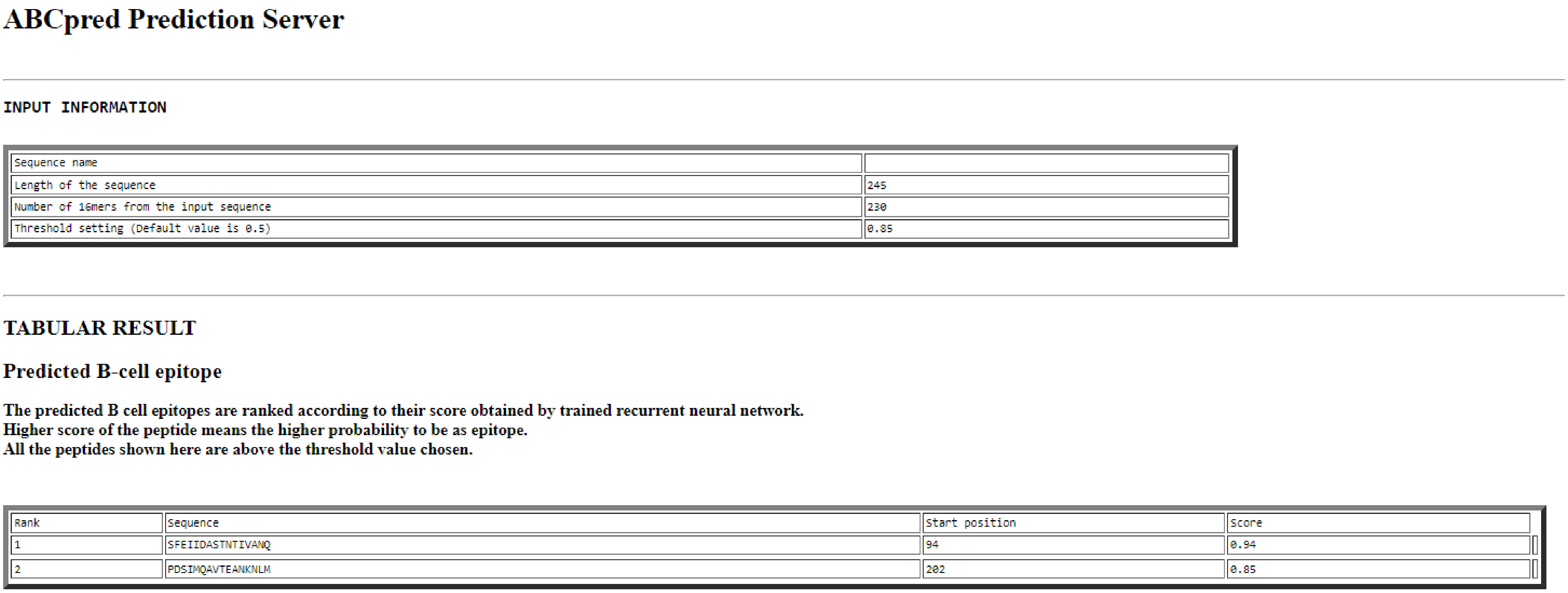
TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	SAAGKNISFEIIDA	87	0.91
2	QINVLEKDQTSSKI	116	0.79
3	LIPDSIMQAVTEAN	200	0.78

Threshold: 0.85 Window: 16



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	245
Number of 16mers from the input sequence	230
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	SFEIIDASTNTIVANQ	94	0.94
2	PDSIMQAVTEANKNLM	202	0.85

PROTEINA 15

\>fig|6666666.171271.peg.1083
MTKRKDRIITFIFVLVIIVLINAIVNQFTPFIDLTKDKVYSLSSGSKSLVKSLKEPLSVKFFLTPNLPPPFSTYEKYIKDLF
AEYKSAAGKNISFEIIDASTNTIVANQYGITSTQINVLEKDQTSSKIAYMGLAFIYGDSIESIPFVRSTEGLEYNIDTIIRK
LIDKNDKLSRLENNLNVYYISSPEVYELLPIGAIELIPDSIMQAVTEANKNLMNKVVFTHVDMSSPNQENEDIIKNLILKN

Predição combinada AbcPred Threshold: 0.85 Window: 14

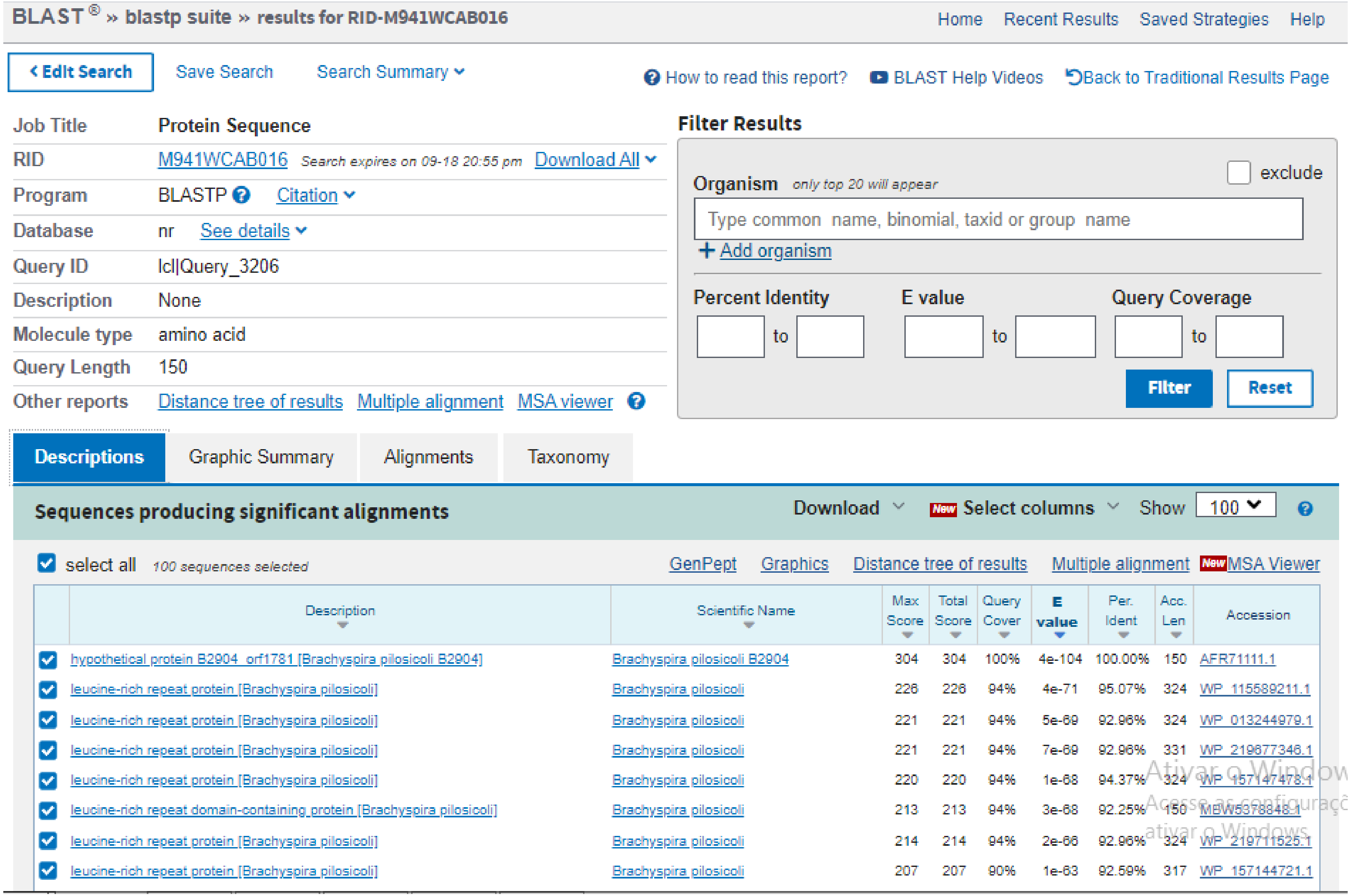
\>fig|6666666.171271.peg.1083
MTKRKDRIITFIFVLVIIVLINAIVNQFTPFIDLTKDKVYSLSSGSKSLVKSLKEPLSVKFFLTPNLPPPFSTYEKYIKDLF
A**EYKSAAGKNISFEIIDA**STNTIVANQYGITSTQINVLEKDQTSSKIAYMGLAFIYGDSIESIPFVRSTEGLEYNIDTIIRK
LIDKNDKLSRLENNLNVYYISSPEVYELLPIGAIELIPDSIMQAVTEANKNLMNKVVFTHVDMSSPNQENEDIIKNLILKN

Predição combinada AbcPred Threshold: 0.85 Window: 16

\>fig|6666666.171271.peg.1083
MTKRKDRIITFIFVLVIIVLINAIVNQFTPFIDLTKDKVYSLSSGSKSLVKSLKEPLSVKFFLTPNLPPPFSTYEKYIKDLF
AEYKSAAGKNI**SFEIIDASTNTIVANQ**YGITSTQINVLEKDQTSSKIAYMGLAFIYGDSIESIPFVRSTEGLEYNIDTIIRK
LIDKNDKLSRLENNLNVYYISSPEVYELLPIGAIELI**PDSIMQAVTEANKNLM**NKVVFTHVDMSSPNQENEDIIKNLILKN

PROTEINA 16

```
>fig|6666666.171271.peg.1772
MYKKILLIMLCFLAAMACSSPSNPDNTNNGDIVNGGGSGNGGGSGNTGDGGSTGDGGNTDIPWTEIAPPLPVLDEEAIKYGI
DISQEDSVIKEQIRTKIQQYNKDKGGYKVIFIGTPKSEYTQQSSLAKLVIDIAEELYKYKKYKYRNRY
```



Job Title	Protein Sequence
RID	M941WCAB016 *Search expires on 09-18 20:55 pm* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_3206
Description	None
Molecule type	amino acid
Query Length	150
Other reports	Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism *only top 20 will appear* ☐ exclude

Type common name, binomial, taxid or group name

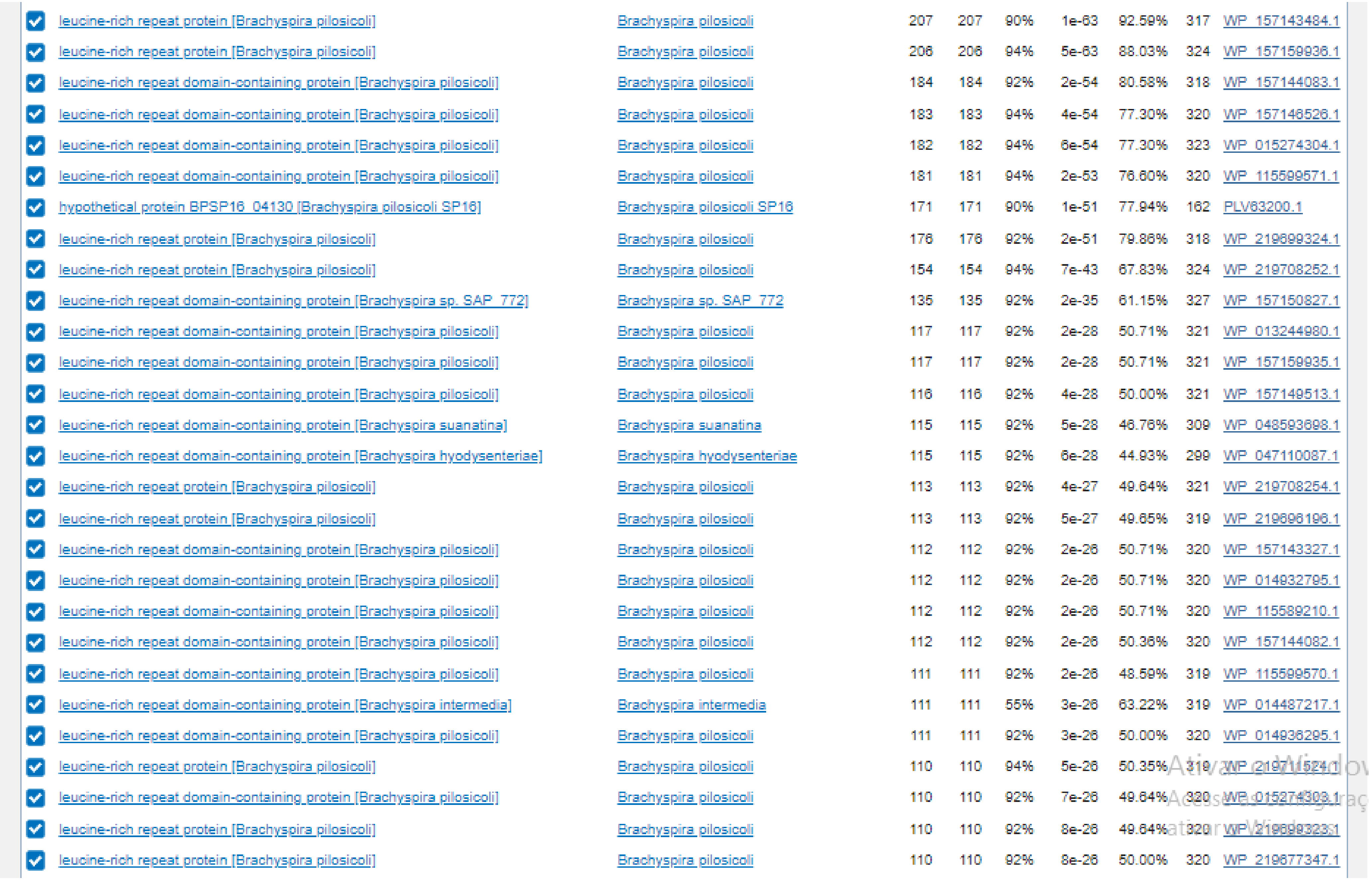
+ Add organism

Percent Identity ☐ to ☐ E value ☐ to ☐ Query Coverage ☐ to ☐

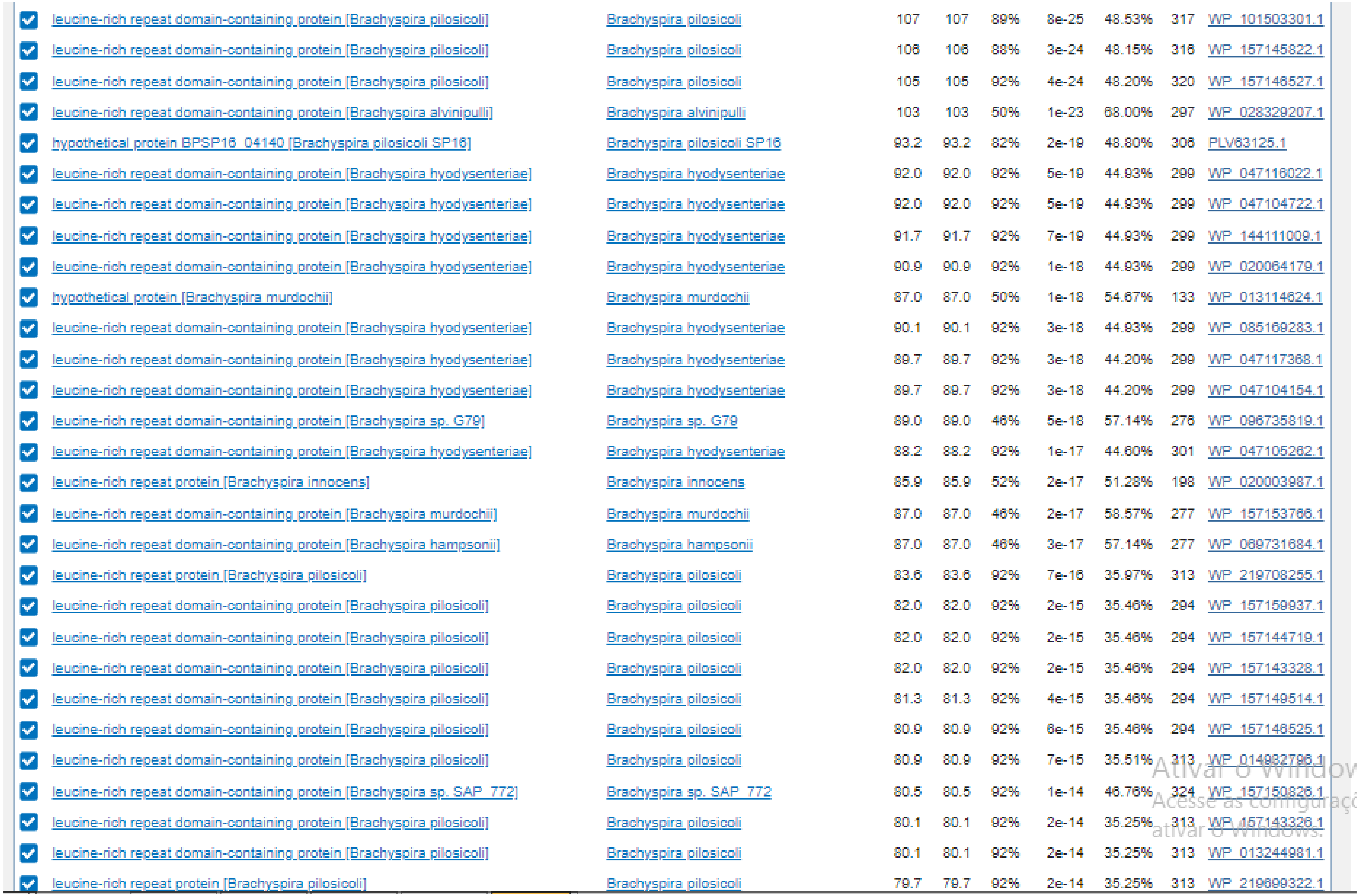
Sequences producing significant alignments

☑ select all *100 sequences selected*

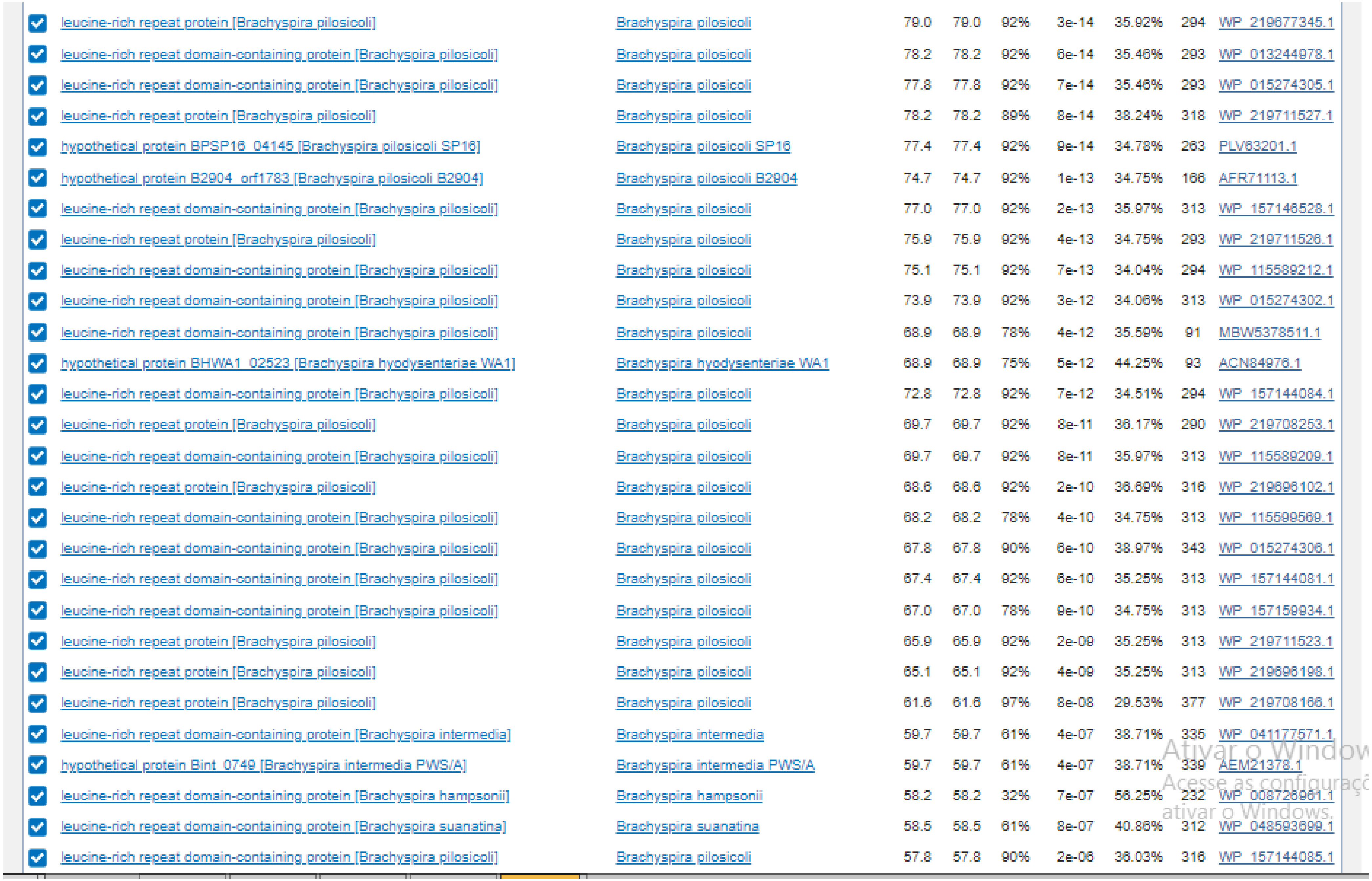
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hypothetical protein B2904_orf1781 [Brachyspira pilosicoli B2904]	Brachyspira pilosicoli B2904	304	304	100%	4e-104	100.00%	150	AFR71111.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	226	226	94%	4e-71	95.07%	324	WP_115589211.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	221	221	94%	5e-69	92.96%	324	WP_013244979.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	221	221	94%	7e-69	92.96%	331	WP_219677346.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	220	220	94%	1e-68	94.37%	324	WP_157147478.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	213	213	94%	3e-68	92.25%	150	MBW5378848.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	214	214	94%	2e-66	92.96%	324	WP_219711525.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	207	207	90%	1e-63	92.59%	317	WP_157144721.1



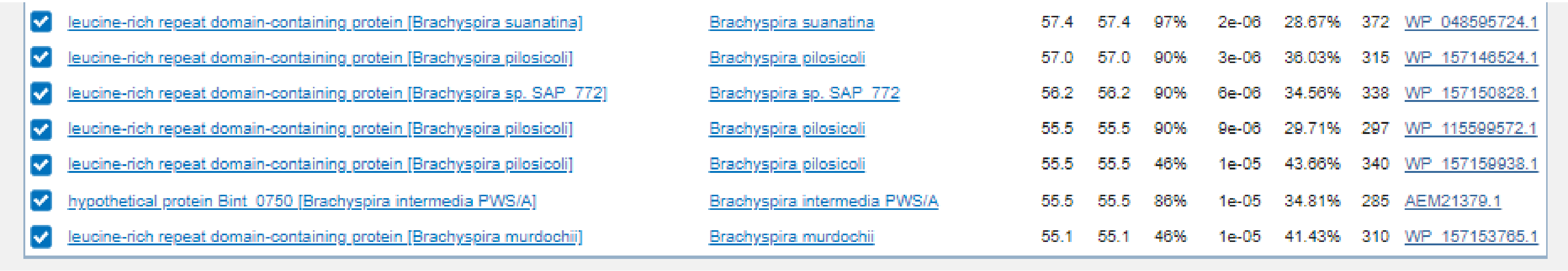
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	207	207	90%	1e-63	92.59%	317	WP_157143484.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	206	206	94%	5e-63	88.03%	324	WP_157159936.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	184	184	92%	2e-54	80.58%	318	WP_157144083.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	183	183	94%	4e-54	77.30%	320	WP_157146526.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	182	182	94%	6e-54	77.30%	323	WP_015274304.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	181	181	94%	2e-53	76.60%	320	WP_115599571.1
☑	hypothetical protein BPSP16_04130 [Brachyspira pilosicoli SP16]	Brachyspira pilosicoli SP16	171	171	90%	1e-51	77.94%	162	PLV63200.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	176	176	92%	2e-51	79.86%	318	WP_219699324.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	154	154	94%	7e-43	67.83%	324	WP_219708252.1
☑	leucine-rich repeat domain-containing protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	135	135	92%	2e-35	61.15%	327	WP_157150827.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	117	117	92%	2e-28	50.71%	321	WP_013244980.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	117	117	92%	2e-28	50.71%	321	WP_157159935.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	116	116	92%	4e-28	50.00%	321	WP_157149513.1
☑	leucine-rich repeat domain-containing protein [Brachyspira suanatina]	Brachyspira suanatina	115	115	92%	5e-28	46.76%	309	WP_048593698.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	115	115	92%	6e-28	44.93%	299	WP_047110087.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	113	113	92%	4e-27	49.64%	321	WP_219708254.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	113	113	92%	5e-27	49.65%	319	WP_219696196.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	112	112	92%	2e-26	50.71%	320	WP_157143327.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	112	112	92%	2e-26	50.71%	320	WP_014932795.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	112	112	92%	2e-26	50.71%	320	WP_115589210.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	112	112	92%	2e-26	50.36%	320	WP_157144082.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	111	111	92%	2e-26	48.59%	319	WP_115599570.1
☑	leucine-rich repeat domain-containing protein [Brachyspira intermedia]	Brachyspira intermedia	111	111	55%	3e-26	63.22%	319	WP_014487217.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	111	111	92%	3e-26	50.00%	320	WP_014936295.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	110	110	94%	5e-26	50.35%	319	WP_219711524.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	110	110	92%	7e-26	49.64%	320	WP_015274303.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	110	110	92%	8e-26	49.64%	320	WP_219699323.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	110	110	92%	8e-26	50.00%	320	WP_219677347.1



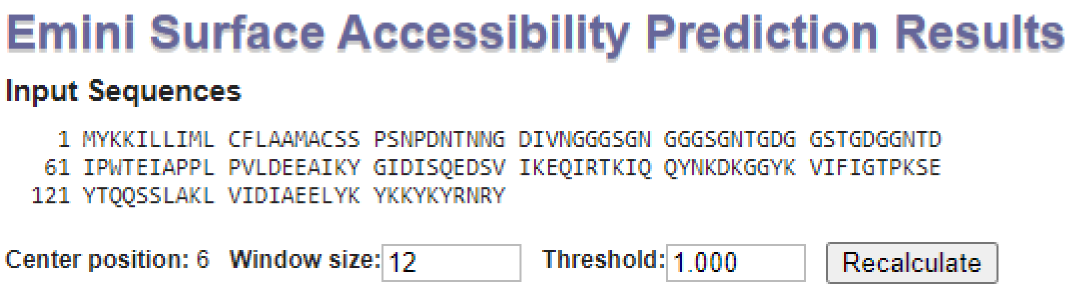
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	107	107	89%	8e-25	48.53%	317	WP_101503301.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	106	106	88%	3e-24	48.15%	316	WP_157145822.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	105	105	92%	4e-24	48.20%	320	WP_157146527.1
☑	leucine-rich repeat domain-containing protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	103	103	50%	1e-23	68.00%	297	WP_028329207.1
☑	hypothetical protein BPSP16_04140 [Brachyspira pilosicoli SP16]	Brachyspira pilosicoli SP16	93.2	93.2	82%	2e-19	48.80%	306	PLV63125.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	92.0	92.0	92%	5e-19	44.93%	299	WP_047116022.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	92.0	92.0	92%	5e-19	44.93%	299	WP_047104722.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	91.7	91.7	92%	7e-19	44.93%	299	WP_144111009.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	90.9	90.9	92%	1e-18	44.93%	299	WP_020064179.1
☑	hypothetical protein [Brachyspira murdochii]	Brachyspira murdochii	87.0	87.0	50%	1e-18	54.67%	133	WP_013114624.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	90.1	90.1	92%	3e-18	44.93%	299	WP_085169283.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	89.7	89.7	92%	3e-18	44.20%	299	WP_047117368.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	89.7	89.7	92%	3e-18	44.20%	299	WP_047104154.1
☑	leucine-rich repeat domain-containing protein [Brachyspira sp. G79]	Brachyspira sp. G79	89.0	89.0	46%	5e-18	57.14%	276	WP_096735819.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	88.2	88.2	92%	1e-17	44.60%	301	WP_047105262.1
☑	leucine-rich repeat protein [Brachyspira innocens]	Brachyspira innocens	85.9	85.9	52%	2e-17	51.28%	198	WP_020003987.1
☑	leucine-rich repeat domain-containing protein [Brachyspira murdochii]	Brachyspira murdochii	87.0	87.0	46%	2e-17	58.57%	277	WP_157153766.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	87.0	87.0	46%	3e-17	57.14%	277	WP_069731684.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	83.6	83.6	92%	7e-16	35.97%	313	WP_219708255.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	82.0	82.0	92%	2e-15	35.46%	294	WP_157159937.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	82.0	82.0	92%	2e-15	35.46%	294	WP_157144719.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	82.0	82.0	92%	2e-15	35.46%	294	WP_157143328.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	81.3	81.3	92%	4e-15	35.46%	294	WP_157149514.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	80.9	80.9	92%	6e-15	35.46%	294	WP_157146525.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	80.9	80.9	92%	7e-15	35.51%	313	WP_014932796.1
☑	leucine-rich repeat domain-containing protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	80.5	80.5	92%	1e-14	46.76%	324	WP_157150826.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	80.1	80.1	92%	2e-14	35.25%	313	WP_157143326.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	80.1	80.1	92%	2e-14	35.25%	313	WP_013244981.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	79.7	79.7	92%	2e-14	35.25%	313	WP_219699322.1



☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	79.0	79.0	92%	3e-14	35.92%	294	WP_219677345.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	78.2	78.2	92%	6e-14	35.46%	293	WP_013244978.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	77.8	77.8	92%	7e-14	35.46%	293	WP_015274305.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	78.2	78.2	89%	8e-14	38.24%	318	WP_219711527.1
☑	hypothetical protein BPSP16_04145 [Brachyspira pilosicoli SP16]	Brachyspira pilosicoli SP16	77.4	77.4	92%	9e-14	34.78%	263	PLV63201.1
☑	hypothetical protein B2904_orf1783 [Brachyspira pilosicoli B2904]	Brachyspira pilosicoli B2904	74.7	74.7	92%	1e-13	34.75%	166	AFR71113.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	77.0	77.0	92%	2e-13	35.97%	313	WP_157146528.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	75.9	75.9	92%	4e-13	34.75%	293	WP_219711526.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	75.1	75.1	92%	7e-13	34.04%	294	WP_115589212.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	73.9	73.9	92%	3e-12	34.06%	313	WP_015274302.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.9	68.9	78%	4e-12	35.59%	91	MBW5378511.1
☑	hypothetical protein BHWA1_02523 [Brachyspira hyodysenteriae WA1]	Brachyspira hyodysenteriae WA1	68.9	68.9	75%	5e-12	44.25%	93	ACN84976.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	72.8	72.8	92%	7e-12	34.51%	294	WP_157144084.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	69.7	69.7	92%	8e-11	36.17%	290	WP_219708253.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	69.7	69.7	92%	8e-11	35.97%	313	WP_115589209.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.6	68.6	92%	2e-10	36.69%	316	WP_219696102.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	68.2	68.2	78%	4e-10	34.75%	313	WP_115599569.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	67.8	67.8	90%	6e-10	38.97%	343	WP_015274306.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	67.4	67.4	92%	6e-10	35.25%	313	WP_157144081.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	67.0	67.0	78%	9e-10	34.75%	313	WP_157159934.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	65.9	65.9	92%	2e-09	35.25%	313	WP_219711523.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	65.1	65.1	92%	4e-09	35.25%	313	WP_219696198.1
☑	leucine-rich repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	61.6	61.6	97%	8e-08	29.53%	377	WP_219708166.1
☑	leucine-rich repeat domain-containing protein [Brachyspira intermedia]	Brachyspira intermedia	59.7	59.7	61%	4e-07	38.71%	335	WP_041177571.1
☑	hypothetical protein Bint_0749 [Brachyspira intermedia PWS/A]	Brachyspira intermedia PWS/A	59.7	59.7	61%	4e-07	38.71%	339	AEM21378.1
☑	leucine-rich repeat domain-containing protein [Brachyspira hampsonii]	Brachyspira hampsonii	58.2	58.2	32%	7e-07	56.25%	232	WP_008726961.1
☑	leucine-rich repeat domain-containing protein [Brachyspira suanatina]	Brachyspira suanatina	58.5	58.5	61%	8e-07	40.86%	312	WP_048593699.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	57.8	57.8	90%	2e-06	36.03%	316	WP_157144085.1



☑	leucine-rich repeat domain-containing protein [Brachyspira suanatina]	Brachyspira suanatina	57.4	57.4	97%	2e-06	28.67%	372	WP_048595724.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	57.0	57.0	90%	3e-06	36.03%	315	WP_157146524.1
☑	leucine-rich repeat domain-containing protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	56.2	56.2	90%	6e-06	34.56%	338	WP_157150828.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	55.5	55.5	90%	9e-06	29.71%	297	WP_115599572.1
☑	leucine-rich repeat domain-containing protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	55.5	55.5	46%	1e-05	43.66%	340	WP_157159938.1
☑	hypothetical protein Bint_0750 [Brachyspira intermedia PWS/A]	Brachyspira intermedia PWS/A	55.5	55.5	86%	1e-05	34.81%	285	AEM21379.1
☑	leucine-rich repeat domain-containing protein [Brachyspira murdochii]	Brachyspira murdochii	55.1	55.1	46%	1e-05	41.43%	310	WP_157153765.1

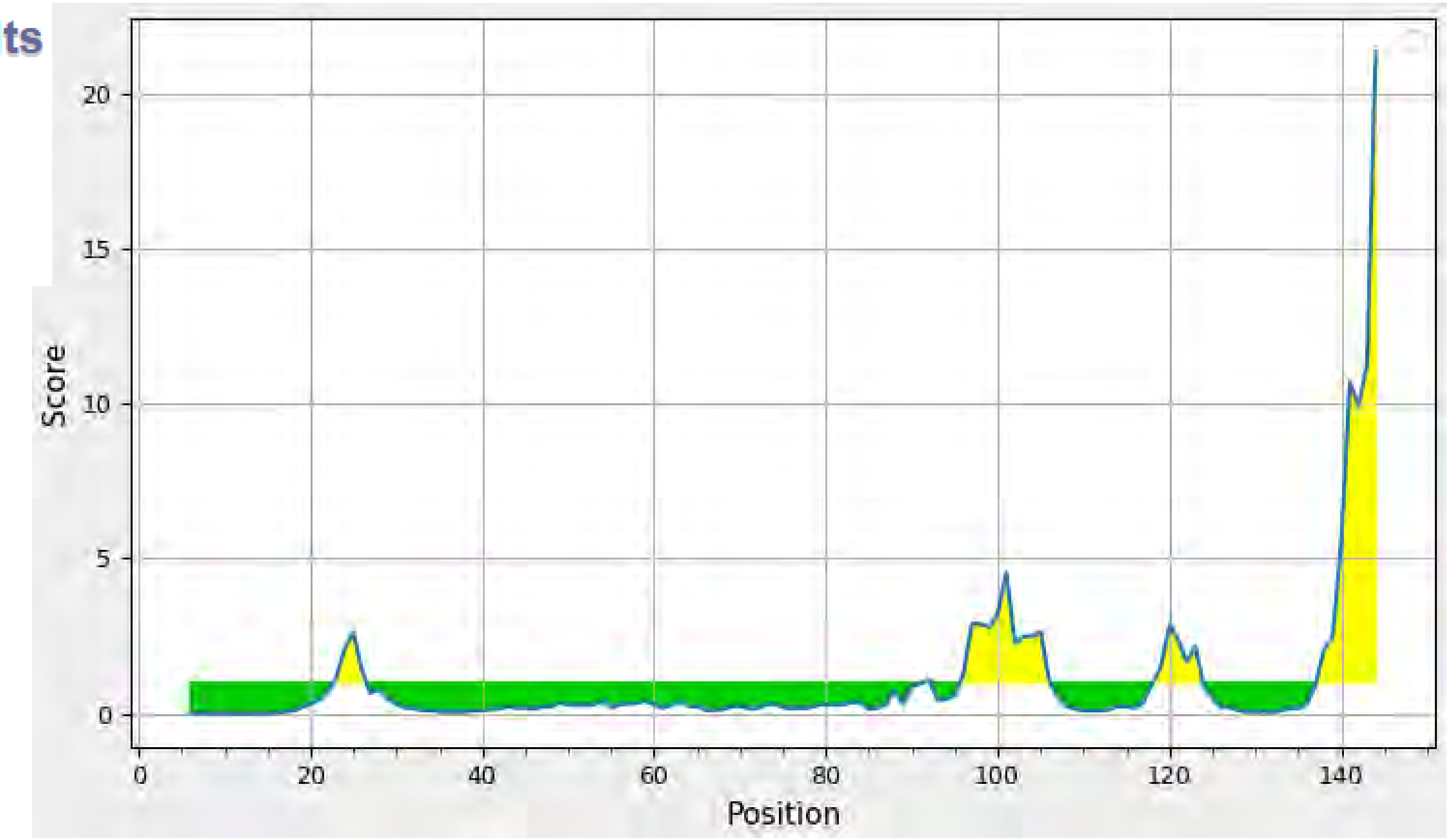


Emini Surface Accessibility Prediction Results

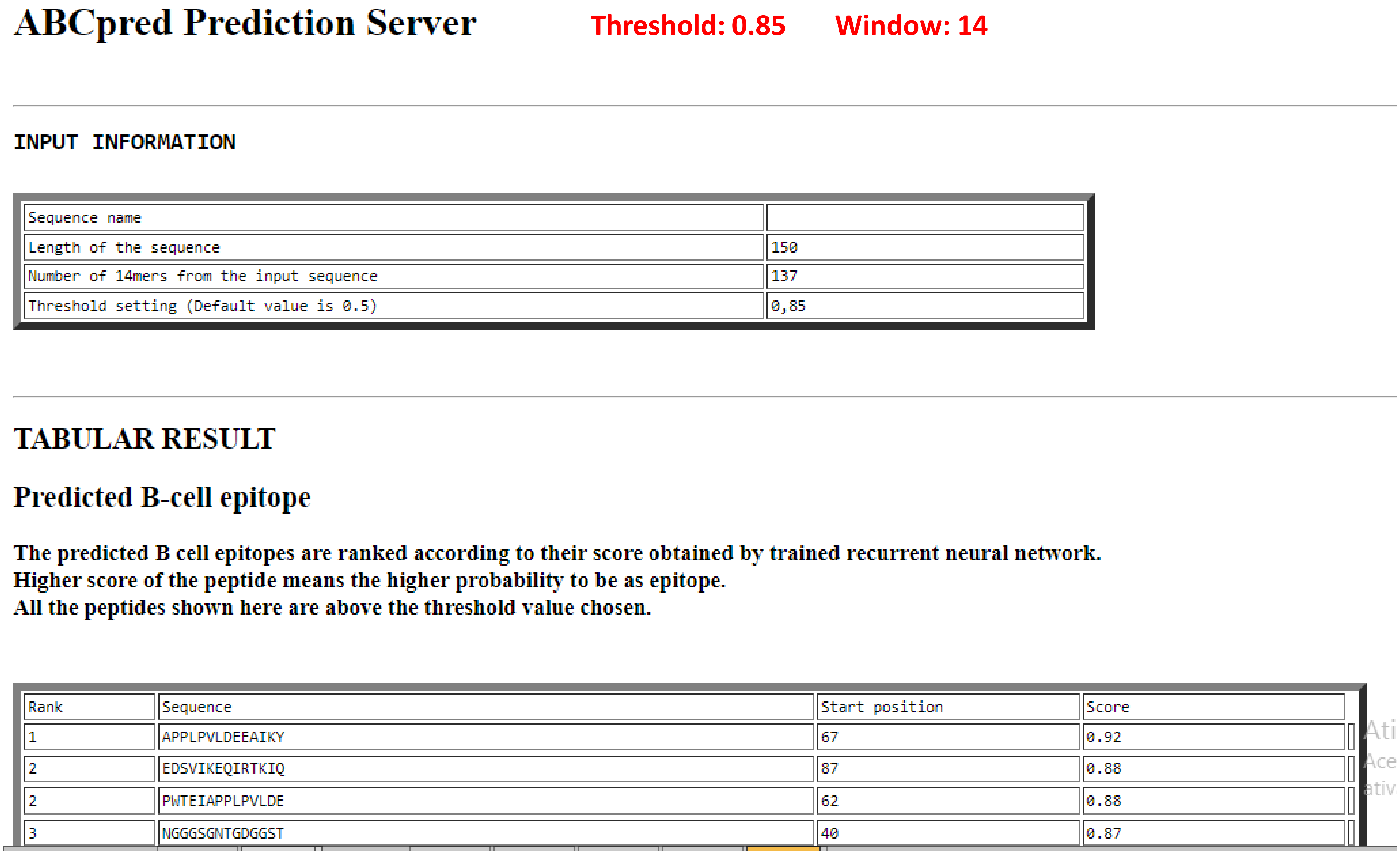
Input Sequences

```
  1 MYKKILLIML CFLAAMACSS PSNPDNTNNG DIVNGGGSGN GGGSGNTGDG GSTGDGGNTD
 61 IPWTEIAPPL PVLDEEAIKY GIDISQEDSV IKEQIRTKIQ QYNKDKGGYK VIFIGTPKSE
121 YTQQSSLAKL VIDIAEELYK YKKYKYRNRY
```

Center position: 6 **Window size:** 12 **Threshold:** 1.000



>fig|6666666.171271.peg.1772
MYKKILLIMLCFLAAMACSSPSNPDNTNNGDIVNGGGSGNGGGSGNTGDGGSTGDGGNTDIPWTEIAPPLPVLDEEAIKYGI
DISQEDSVIKEQIRTKIQQYNKDKGGYKVIFIGTPKSEYTQQSSLAKLVIDIAEELYKYKKYKYRNRY



ABCpred Prediction Server

Threshold: 0.85 **Window: 14**

INPUT INFORMATION

Sequence name	
Length of the sequence	150
Number of 14mers from the input sequence	137
Threshold setting (Default value is 0.5)	0,85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	APPLPVLDEEAIKY	67	0.92
2	EDSVIKEQIRTKIQ	87	0.88
2	PWTEIAPPLPVLDE	62	0.88
3	NGGGSGNTGDGGST	40	0.87

PROTEINA 16

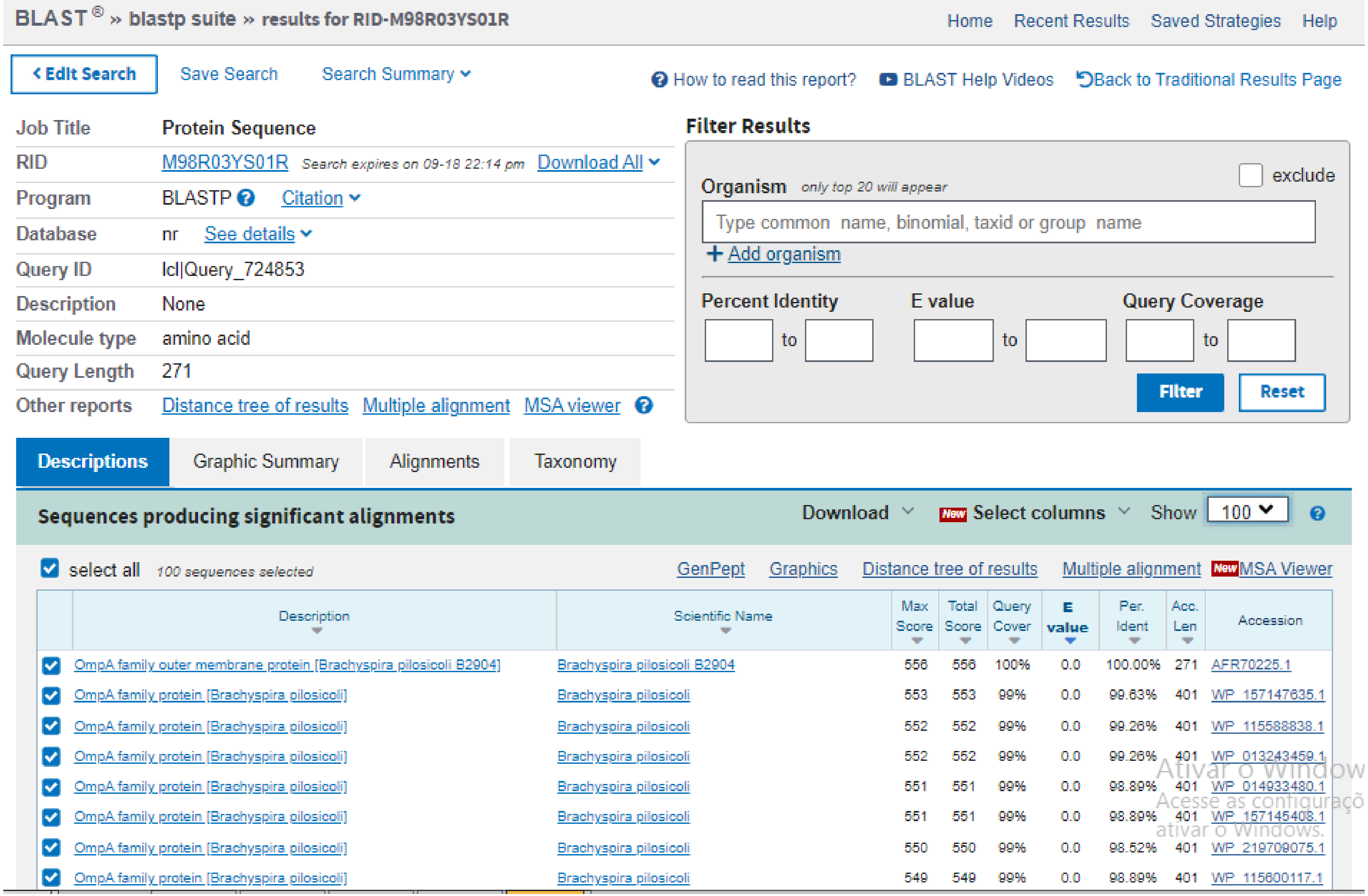
>fig|6666666.171271.peg.1772
MYKKILLIMLCFLAAMACSSPSNPDNTNNGDIVNGGGSGNGGGSGNTGDGGSTGDGGNTDIPWTEIAPPLPVLDEEAIKYGI
DISQEDSVIKEQIRTKIQQYNKDKGGYKVIFIGTPKSEYTQQSSLAKLVIDIAEELYKYKKYKYRNRY

Predição combinada

>fig|6666666.171271.peg.1772
MYKKILLIMLCFLAAMACSSPSNPDNTNNGDIVNGGGSGNGGGSGNTGDGGSTGDGGNTDIPWTEIAPPLPVLDEEAIKYGI
DIS**QEDSVIKEQIRTKIQQYNKDK**GGYKVIFIGTPKSEYTQQSSLAKLVIDIAEELYKYKKYKYRNRY

PROTEINA 17

```
>fig|6666666.171271.peg.878
MSKIKFILILTIFIFNISYTQTISHKFFWNLKVGERIESVKTADVEYYENGLLKKTYKERNIVDLTVIAIAPKGGYRVSGVF
KIFRLYDGNSVFHLEEEYSSDFIIHTNGKFEVPYNYFMPNVRHIPTFPDKEISLTHSWNSEAMEIVKVNNAPNLAMALSADY
LFANIETNENNDPLAVIQYHIMTDKDLLQAGLSRNGYPERIYGFNYGTFLWDMNKNIPVSQTERYQILFGYGKNLSHLSLQY
KMNIISTYEIYSTITEEENELNRKN
```

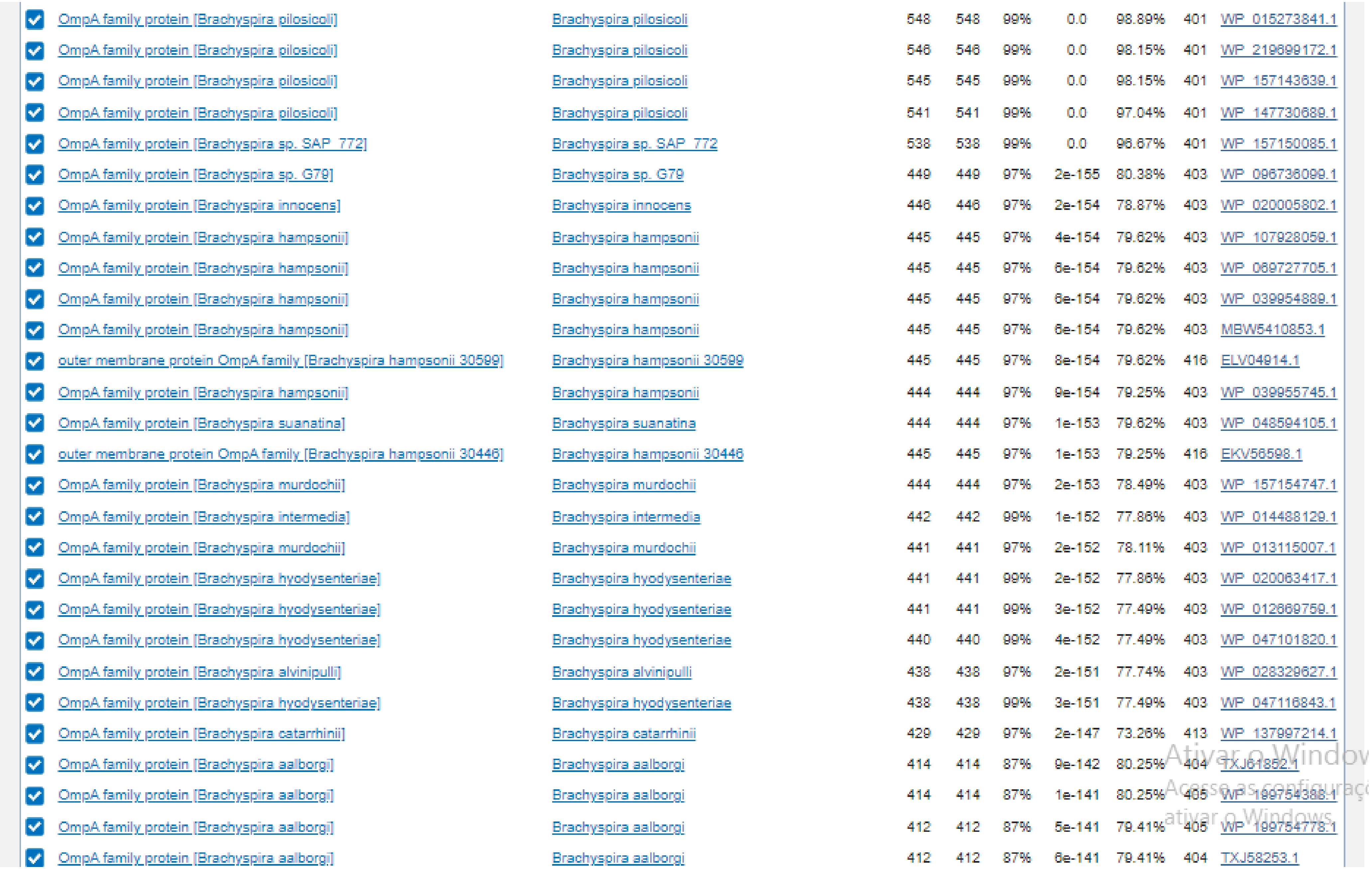


Job Title	Protein Sequence
RID	M98R03YS01R *Search expires on 09-18 22:14 pm* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_724853
Description	None
Molecule type	amino acid
Query Length	271
Other reports	Distance tree of results Multiple alignment MSA viewer

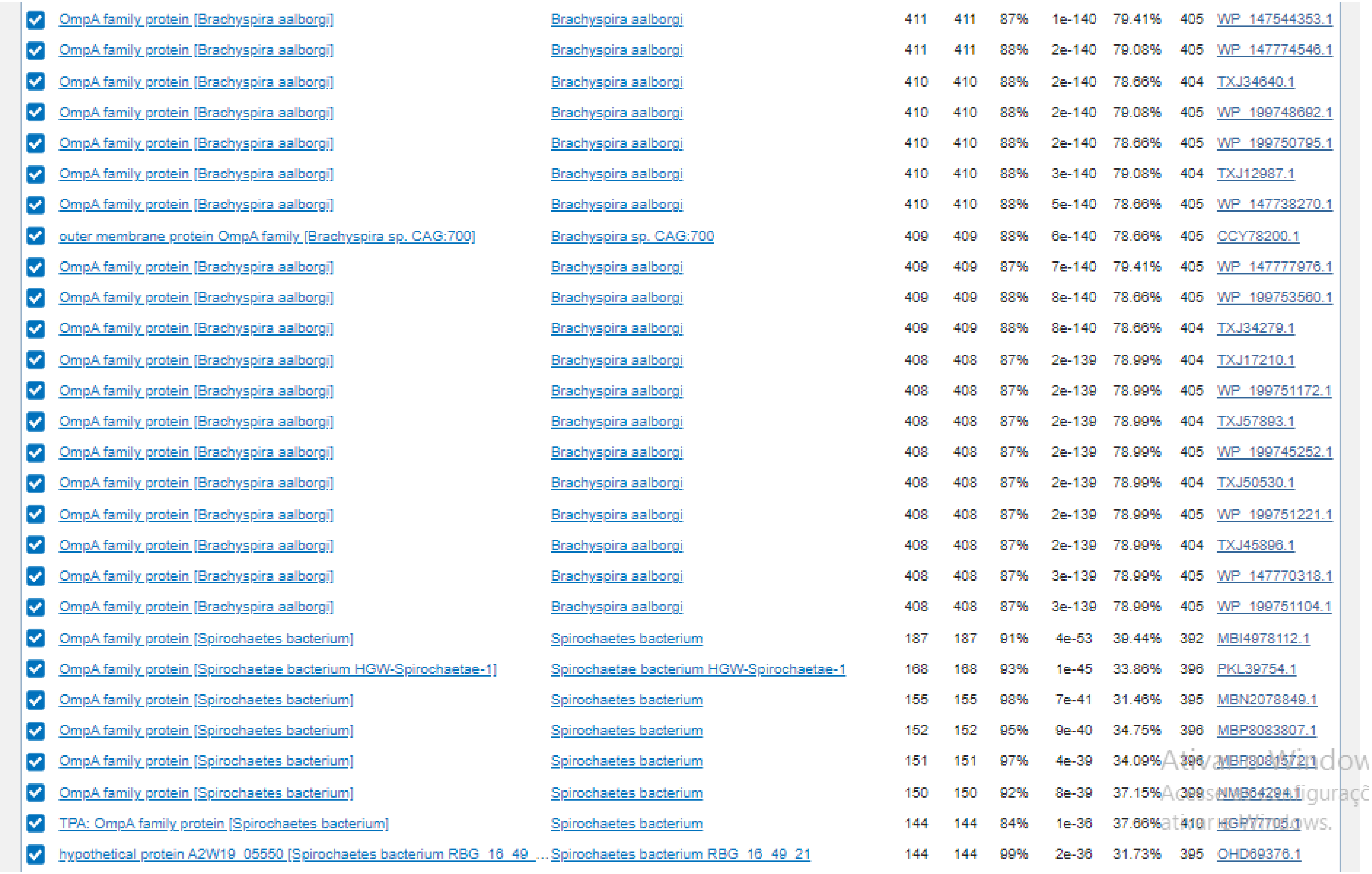
Sequences producing significant alignments

☑ select all *100 sequences selected*

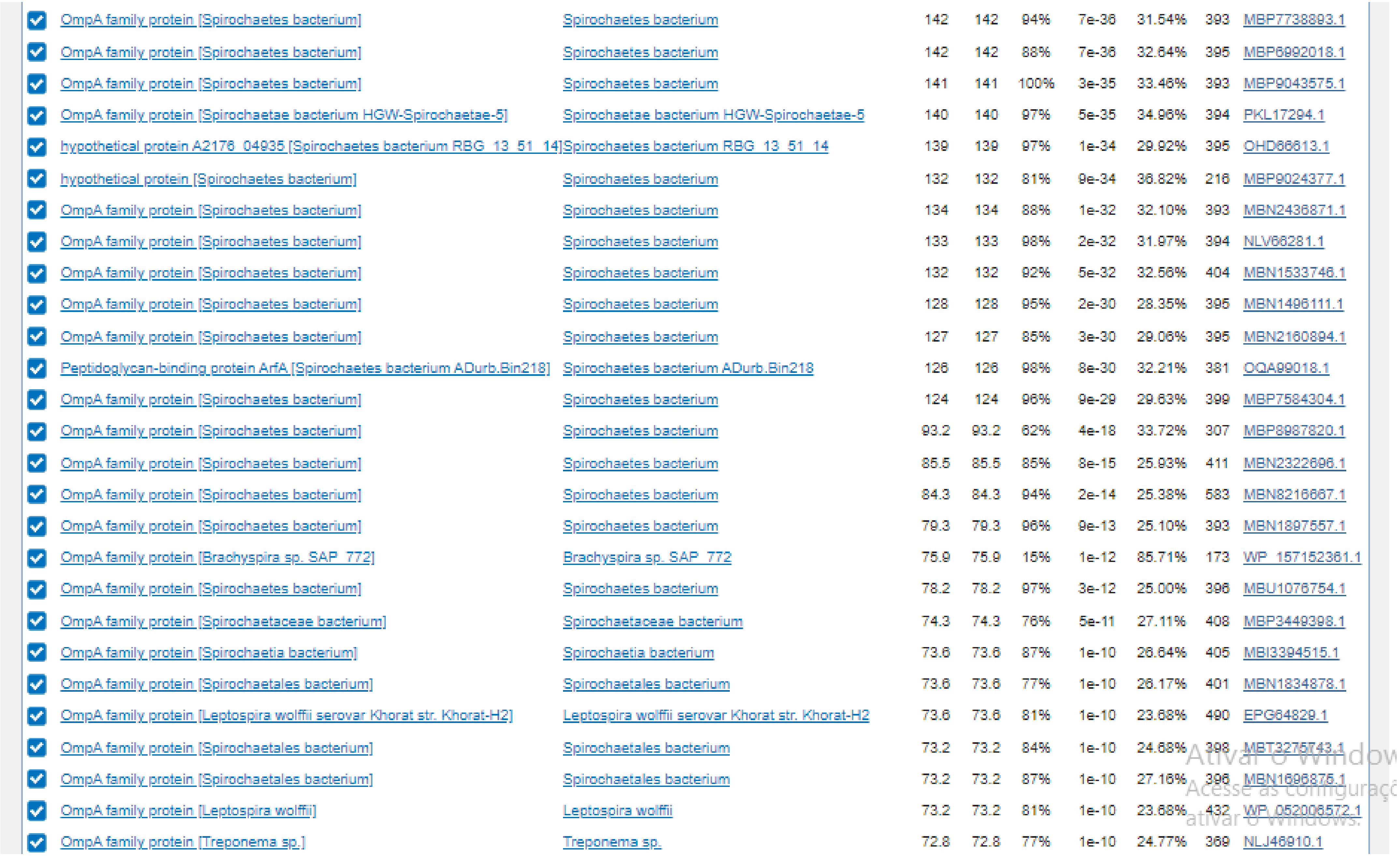
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	OmpA family outer membrane protein [Brachyspira pilosicoli B2904]	Brachyspira pilosicoli B2904	556	556	100%	0.0	100.00%	271	AFR70225.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	553	553	99%	0.0	99.63%	401	WP_157147635.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	552	552	99%	0.0	99.26%	401	WP_115588838.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	552	552	99%	0.0	99.26%	401	WP_013243459.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	551	551	99%	0.0	98.89%	401	WP_014933480.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	551	551	99%	0.0	98.89%	401	WP_157145408.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	550	550	99%	0.0	98.52%	401	WP_219709075.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	549	549	99%	0.0	98.89%	401	WP_115600117.1



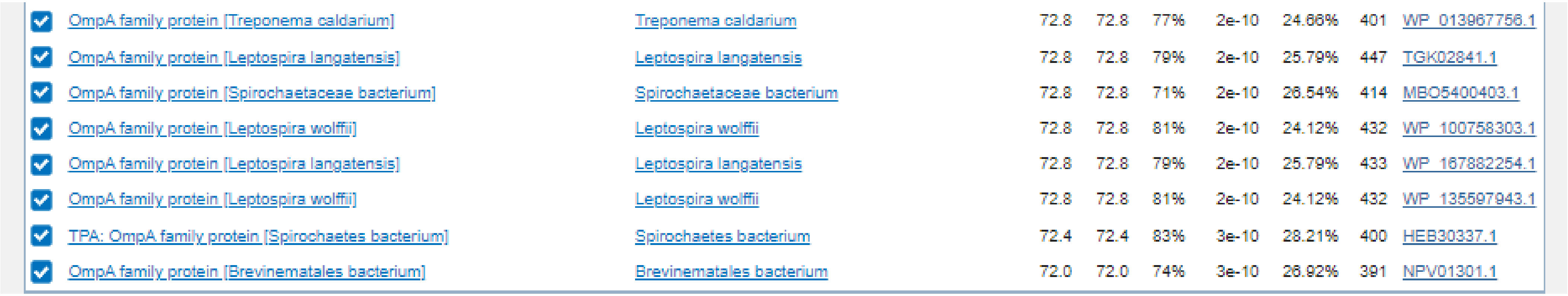
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	548	548	99%	0.0	98.89%	401	WP_015273841.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	546	546	99%	0.0	98.15%	401	WP_219699172.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	545	545	99%	0.0	98.15%	401	WP_157143639.1
☑	OmpA family protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	541	541	99%	0.0	97.04%	401	WP_147730689.1
☑	OmpA family protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	538	538	99%	0.0	96.67%	401	WP_157150085.1
☑	OmpA family protein [Brachyspira sp. G79]	Brachyspira sp. G79	449	449	97%	2e-155	80.38%	403	WP_096736099.1
☑	OmpA family protein [Brachyspira innocens]	Brachyspira innocens	446	446	97%	2e-154	78.87%	403	WP_020005802.1
☑	OmpA family protein [Brachyspira hampsonii]	Brachyspira hampsonii	445	445	97%	4e-154	79.62%	403	WP_107928059.1
☑	OmpA family protein [Brachyspira hampsonii]	Brachyspira hampsonii	445	445	97%	6e-154	79.62%	403	WP_069727705.1
☑	OmpA family protein [Brachyspira hampsonii]	Brachyspira hampsonii	445	445	97%	6e-154	79.62%	403	WP_039954889.1
☑	OmpA family protein [Brachyspira hampsonii]	Brachyspira hampsonii	445	445	97%	6e-154	79.62%	403	MBW5410853.1
☑	outer membrane protein OmpA family [Brachyspira hampsonii 30599]	Brachyspira hampsonii 30599	445	445	97%	8e-154	79.62%	416	ELV04914.1
☑	OmpA family protein [Brachyspira hampsonii]	Brachyspira hampsonii	444	444	97%	9e-154	79.25%	403	WP_039955745.1
☑	OmpA family protein [Brachyspira suanatina]	Brachyspira suanatina	444	444	97%	1e-153	79.62%	403	WP_048594105.1
☑	outer membrane protein OmpA family [Brachyspira hampsonii 30446]	Brachyspira hampsonii 30446	445	445	97%	1e-153	79.25%	416	EKV56598.1
☑	OmpA family protein [Brachyspira murdochii]	Brachyspira murdochii	444	444	97%	2e-153	78.49%	403	WP_157154747.1
☑	OmpA family protein [Brachyspira intermedia]	Brachyspira intermedia	442	442	99%	1e-152	77.86%	403	WP_014488129.1
☑	OmpA family protein [Brachyspira murdochii]	Brachyspira murdochii	441	441	97%	2e-152	78.11%	403	WP_013115007.1
☑	OmpA family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	441	441	99%	2e-152	77.86%	403	WP_020063417.1
☑	OmpA family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	441	441	99%	3e-152	77.49%	403	WP_012669759.1
☑	OmpA family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	440	440	99%	4e-152	77.49%	403	WP_047101820.1
☑	OmpA family protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	438	438	97%	2e-151	77.74%	403	WP_028329627.1
☑	OmpA family protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	438	438	99%	3e-151	77.49%	403	WP_047116843.1
☑	OmpA family protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	429	429	97%	2e-147	73.26%	413	WP_137997214.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	414	414	87%	9e-142	80.25%	404	TXJ61852.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	414	414	87%	1e-141	80.25%	405	WP_199754388.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	412	412	87%	5e-141	79.41%	405	WP_199754778.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	412	412	87%	6e-141	79.41%	404	TXJ58253.1



☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	411	411	87%	1e-140	79.41%	405	WP_147544353.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	411	411	88%	2e-140	79.08%	405	WP_147774546.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	410	410	88%	2e-140	78.66%	404	TXJ34640.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	410	410	88%	2e-140	79.08%	405	WP_199748692.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	410	410	88%	2e-140	78.66%	405	WP_199750795.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	410	410	88%	3e-140	79.08%	404	TXJ12987.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	410	410	88%	5e-140	78.66%	405	WP_147738270.1
☑	outer membrane protein OmpA family [Brachyspira sp. CAG:700]	Brachyspira sp. CAG:700	409	409	88%	6e-140	78.66%	405	CCY78200.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	409	409	87%	7e-140	79.41%	405	WP_147777976.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	409	409	88%	8e-140	78.66%	405	WP_199753560.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	409	409	88%	8e-140	78.66%	404	TXJ34279.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	2e-139	78.99%	404	TXJ17210.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	2e-139	78.99%	405	WP_199751172.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	2e-139	78.99%	404	TXJ57893.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	2e-139	78.99%	405	WP_199745252.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	2e-139	78.99%	404	TXJ50530.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	2e-139	78.99%	405	WP_199751221.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	2e-139	78.99%	404	TXJ45896.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	3e-139	78.99%	405	WP_147770318.1
☑	OmpA family protein [Brachyspira aalborgi]	Brachyspira aalborgi	408	408	87%	3e-139	78.99%	405	WP_199751104.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	187	187	91%	4e-53	39.44%	392	MBI4978112.1
☑	OmpA family protein [Spirochaetae bacterium HGW-Spirochaetae-1]	Spirochaetae bacterium HGW-Spirochaetae-1	168	168	93%	1e-45	33.86%	396	PKL39754.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	155	155	98%	7e-41	31.46%	395	MBN2078849.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	152	152	95%	9e-40	34.75%	396	MBP8083807.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	151	151	97%	4e-39	34.09%	396	MBP8081572.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	150	150	92%	8e-39	37.15%	399	NMB64294.1
☑	TPA: OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	144	144	84%	1e-36	37.66%	410	HGP77705.1
☑	hypothetical protein A2W19_05550 [Spirochaetes bacterium RBG_16_49_...	Spirochaetes bacterium RBG_16_49_21	144	144	99%	2e-36	31.73%	395	OHD69376.1



☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	142	142	94%	7e-36	31.54%	393	MBP7738893.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	142	142	88%	7e-36	32.64%	395	MBP6992018.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	141	141	100%	3e-35	33.46%	393	MBP9043575.1
☑	OmpA family protein [Spirochaetae bacterium HGW-Spirochaetae-5]	Spirochaetae bacterium HGW-Spirochaetae-5	140	140	97%	5e-35	34.96%	394	PKL17294.1
☑	hypothetical protein A2176_04935 [Spirochaetes bacterium RBG_13_51_14]	Spirochaetes bacterium RBG_13_51_14	139	139	97%	1e-34	29.92%	395	OHD66613.1
☑	hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	132	132	81%	9e-34	36.82%	216	MBP9024377.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	134	134	88%	1e-32	32.10%	393	MBN2436871.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	133	133	98%	2e-32	31.97%	394	NLV66281.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	132	132	92%	5e-32	32.56%	404	MBN1533746.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	128	128	95%	2e-30	28.35%	395	MBN1496111.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	127	127	85%	3e-30	29.06%	395	MBN2160894.1
☑	Peptidoglycan-binding protein ArfA [Spirochaetes bacterium ADurb.Bin218]	Spirochaetes bacterium ADurb.Bin218	126	126	98%	8e-30	32.21%	381	OQA99018.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	124	124	96%	9e-29	29.63%	399	MBP7584304.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	93.2	93.2	62%	4e-18	33.72%	307	MBP8987820.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	85.5	85.5	85%	8e-15	25.93%	411	MBN2322696.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	84.3	84.3	94%	2e-14	25.38%	583	MBN8216667.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	79.3	79.3	96%	9e-13	25.10%	393	MBN1897557.1
☑	OmpA family protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	75.9	75.9	15%	1e-12	85.71%	173	WP_157152361.1
☑	OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	78.2	78.2	97%	3e-12	25.00%	396	MBU1076754.1
☑	OmpA family protein [Spirochaetaceae bacterium]	Spirochaetaceae bacterium	74.3	74.3	76%	5e-11	27.11%	408	MBP3449398.1
☑	OmpA family protein [Spirochaetia bacterium]	Spirochaetia bacterium	73.6	73.6	87%	1e-10	26.64%	405	MBI3394515.1
☑	OmpA family protein [Spirochaetales bacterium]	Spirochaetales bacterium	73.6	73.6	77%	1e-10	26.17%	401	MBN1834878.1
☑	OmpA family protein [Leptospira wolffii serovar Khorat str. Khorat-H2]	Leptospira wolffii serovar Khorat str. Khorat-H2	73.6	73.6	81%	1e-10	23.68%	490	EPG64829.1
☑	OmpA family protein [Spirochaetales bacterium]	Spirochaetales bacterium	73.2	73.2	84%	1e-10	24.68%	398	MBT3275743.1
☑	OmpA family protein [Spirochaetales bacterium]	Spirochaetales bacterium	73.2	73.2	87%	1e-10	27.16%	396	MBN1696875.1
☑	OmpA family protein [Leptospira wolffii]	Leptospira wolffii	73.2	73.2	81%	1e-10	23.68%	432	WP_052006572.1
☑	OmpA family protein [Treponema sp.]	Treponema sp.	72.8	72.8	77%	1e-10	24.77%	369	NLJ46910.1



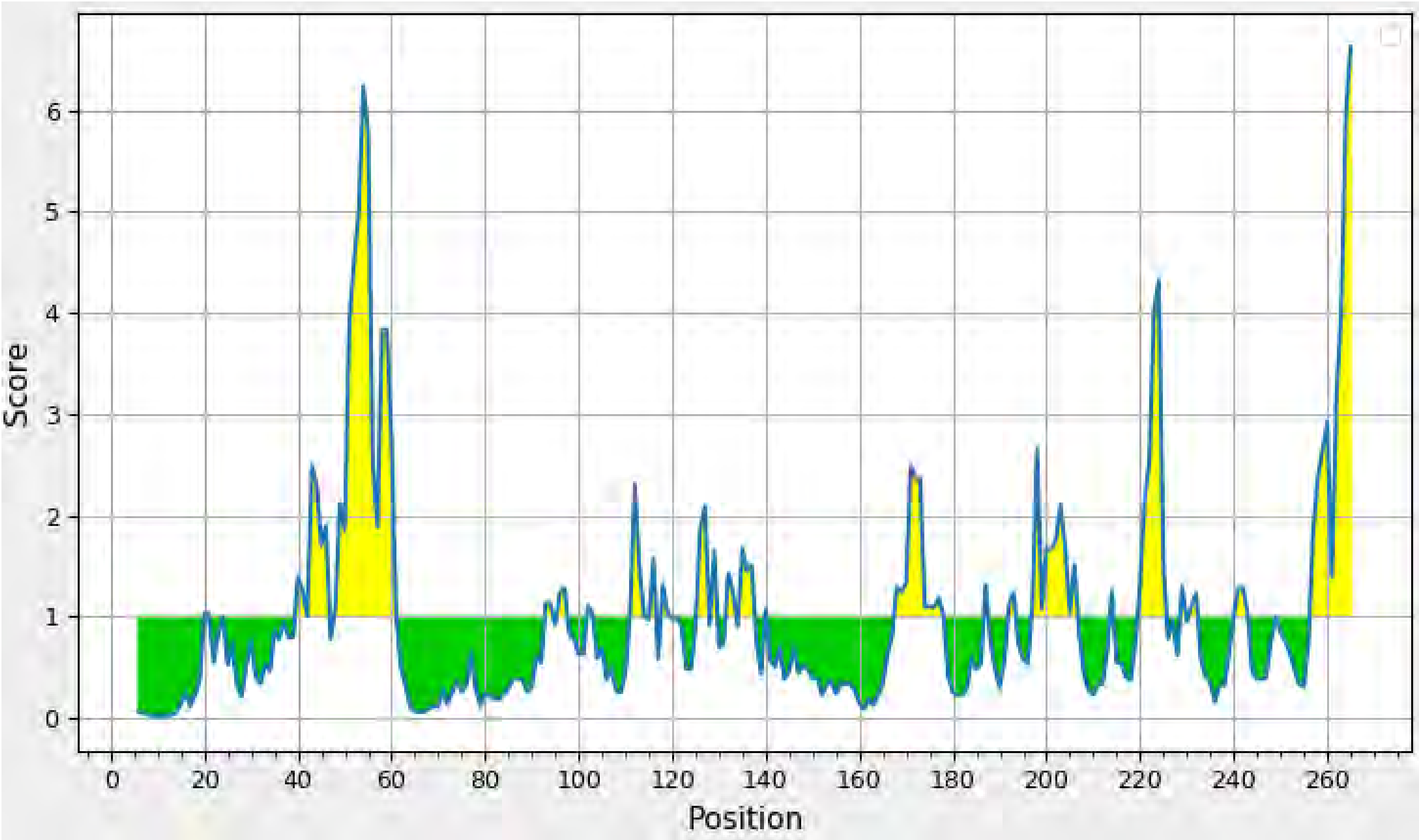
☑	OmpA family protein [Treponema caldarium]	Treponema caldarium	72.8	72.8	77%	2e-10	24.66%	401	WP_013967756.1
☑	OmpA family protein [Leptospira langatensis]	Leptospira langatensis	72.8	72.8	79%	2e-10	25.79%	447	TGK02841.1
☑	OmpA family protein [Spirochaetaceae bacterium]	Spirochaetaceae bacterium	72.8	72.8	71%	2e-10	26.54%	414	MBO5400403.1
☑	OmpA family protein [Leptospira wolffii]	Leptospira wolffii	72.8	72.8	81%	2e-10	24.12%	432	WP_100758303.1
☑	OmpA family protein [Leptospira langatensis]	Leptospira langatensis	72.8	72.8	79%	2e-10	25.79%	433	WP_167882254.1
☑	OmpA family protein [Leptospira wolffii]	Leptospira wolffii	72.8	72.8	81%	2e-10	24.12%	432	WP_135597943.1
☑	TPA: OmpA family protein [Spirochaetes bacterium]	Spirochaetes bacterium	72.4	72.4	83%	3e-10	28.21%	400	HEB30337.1
☑	OmpA family protein [Brevinematales bacterium]	Brevinematales bacterium	72.0	72.0	74%	3e-10	26.92%	391	NPV01301.1

Emini Surface Accessibility Prediction Results

Input Sequences

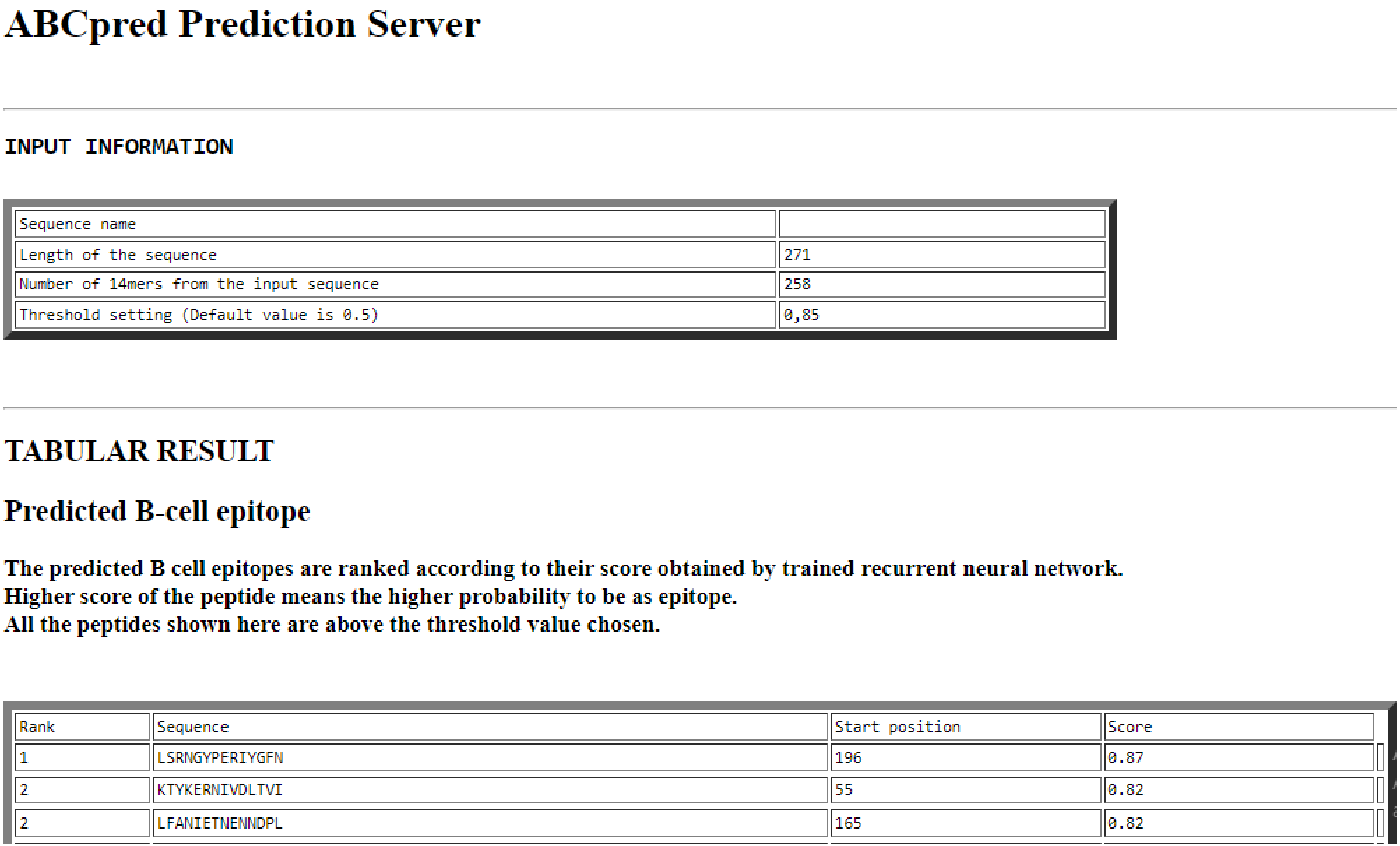
```
  1 MSKIKFILIL TIFIFNISYT QTISHKFFWN LKVGERIESV KTADVEYYEN GLLKKTYKER
 61 NIVDLTVIAI APKGGYRVSG VFKIFRLYDG NSVFHLEEEY SSDFIIHTNG KFEVPYNYFM
121 PNVRHIPTFP DKEISLTHSW NSEAMEIVKV NNAPNLAMAL SADYLFANIE TNENNDPLAV
181 IQYHIMTDKD LLQAGLSRNG YPERIYGFNY GTFLWDMNKN IPVSQTERYQ ILFGYGKNLS
241 HLSLQYKMNI ISTYEIYSTI TEEENELNRK N
```

Center position: 6 Window size: 12 Threshold: 1.000



```
>fig|6666666.171271.peg.878
MSKIKFILILTIFIFNISYTQTISHKFFWNLKVGERIESVKTADVEYYENGLLKKTYKERNIVDLTVIAIAPKGGYRVSGVF
KIFRLYDGNSVFHLEEEYSSDFIIHTNGKFEVPYNYFMPNVRHIPTFPDKEISLTHSWNSEAMEIVKVNNAPNLAMALSADY
LFANIETNENNDPLAVIQYHIMTDKDLLQAGLSRNGYPERIYGFNYGTFLWDMNKNIPVSQTERYQILFGYGKNLSHLSLQY
KMNIISTYEIYSTITEEENELNRKN
```

Threshold: 0.85 Window: 14



ABCpred Prediction Server

INPUT INFORMATION

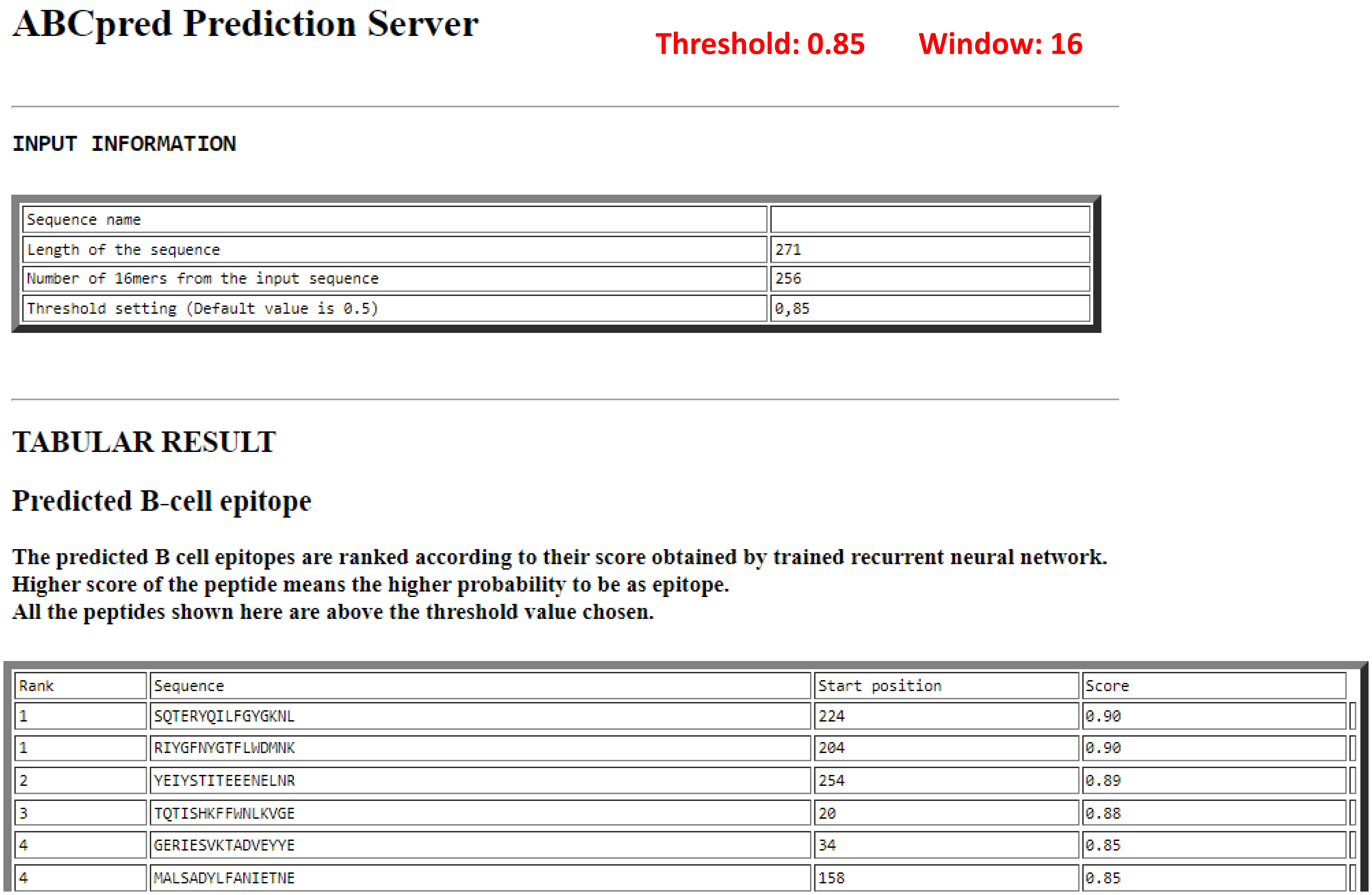
Sequence name	
Length of the sequence	271
Number of 14mers from the input sequence	258
Threshold setting (Default value is 0.5)	0,85

TABULAR RESULT

Predicted B-cell epitope

**The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.**

Rank	Sequence	Start position	Score
1	LSRNGYPERIYGFN	196	0.87
2	KTYKERNIVDLTVI	55	0.82
2	LFANIETNENNDPL	165	0.82



ABCpred Prediction Server

Threshold: 0.85   Window: 16

INPUT INFORMATION

Sequence name	
Length of the sequence	271
Number of 16mers from the input sequence	256
Threshold setting (Default value is 0.5)	0,85

TABULAR RESULT

Predicted B-cell epitope

**The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.**

Rank	Sequence	Start position	Score
1	SQTERYQILFGYGKNL	224	0.90
1	RIYGFNYGTFLWDMNK	204	0.90
2	YEIYSTITEEENELNR	254	0.89
3	TQTISHKFFWNLKVGE	20	0.88
4	GERIESVKTADVEYYE	34	0.85
4	MALSADYLFANIETNE	158	0.85

PROTEINA 17

>fig|6666666.171271.peg.878
MSKIKFILILTIFIFNISYTQTISHKFFWNLKVGERIESVKTADVEYYENGLLKKTYKERNIVDLTVIAIAPKGGYRVSGVF
KIFRLYDGNSVFHLEEEYSSDFIIHTNGKFEVPYNYFMPNVRHIPTFPDKEISLTHSWNSEAMEIVKVNNAPNLAMALSADY
LFANIETNENNDPLAVIQYHIMTDKDLLQAGLSRNGYPERIYGFNYGTFLWDMNKNIPVSQTERYQILFGYGKNLSHLSLQY
KMNIISTYEIYSTITEEENELNRKN

Predição combinada Threshold: 0.85 Window: 14

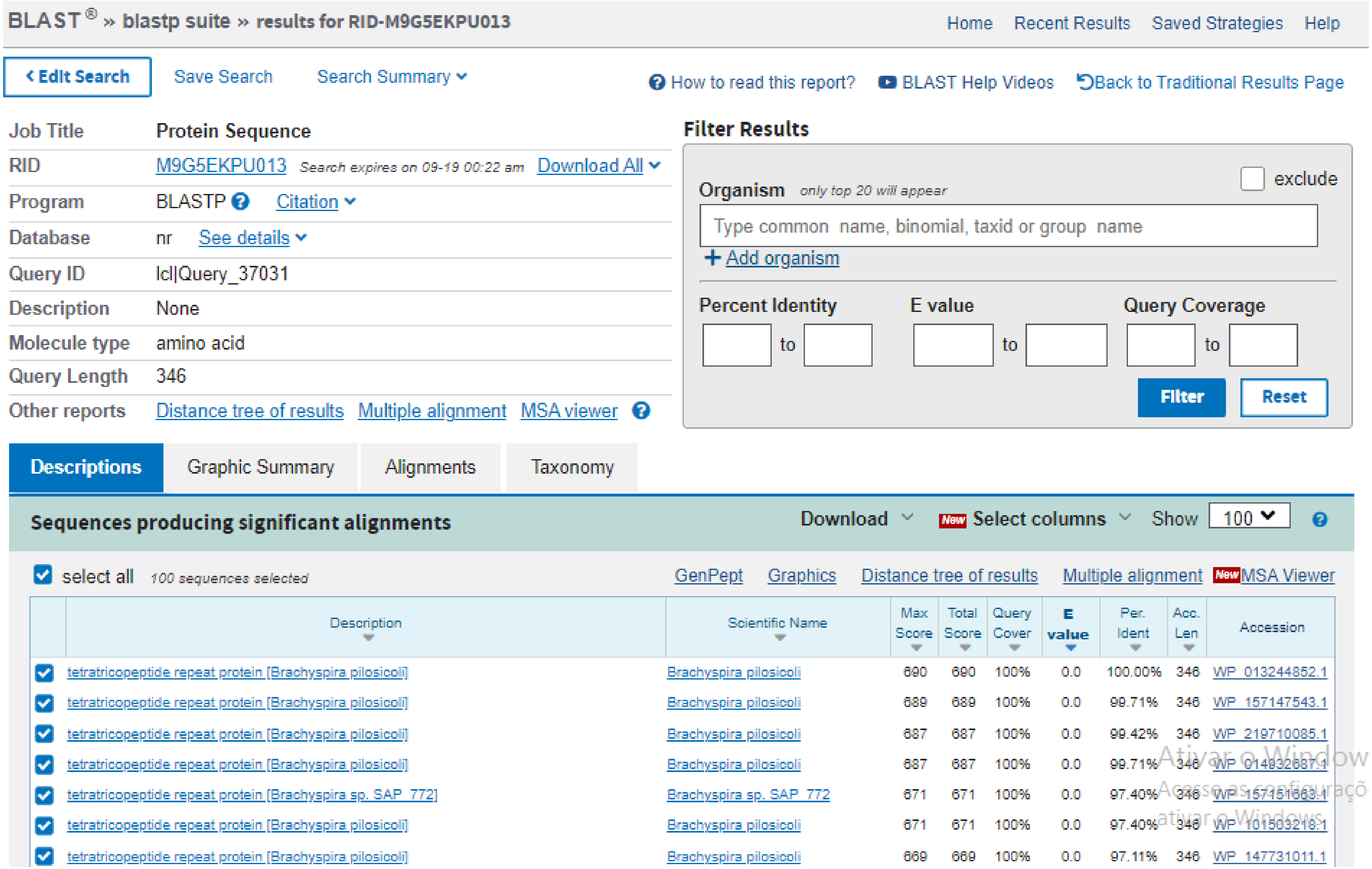
>fig|6666666.171271.peg.878
MSKIKFILILTIFIFNISYTQTISHKFFWNLKVGERIESVKTADVEYYENGLLKKTYKERNIVDLTVIAIAPKGGYRVSGVF
KIFRLYDGNSVFHLEEEYSSDFIIHTNGKFEVPYNYFMPNVRHIPTFPDKEISLTHSWNSEAMEIVKVNNAPNLAMALSADY
LFANIETNENNDPLAVIQYHIMTDKDLLQAGLSRNGYPERIYGFNYGTFLWDMNKNIPVSQTERYQILFGYGKNLSHLSLQY
KMNIISTYEIYSTITEEENELNRKN

Predição combinada Threshold: 0.85 Window: 16

>fig|6666666.171271.peg.878
MSKIKFILILTIFIFNISYTQTISHKFFWNLKVGERIESVKTADVEYYENGLLKKTYKERNIVDLTVIAIAPKGGYRVSGVF
KIFRLYDGNSVFHLEEEYSSDFIIHTNGKFEVPYNYFMPNVRHIPTFPDKEISLTHSWNSEAMEIVKVNNAPNLA**MALSADY**
LFANIETNENNDPLAVIQYHIMTDKDLLQAGLSRNGYPERIYGFNYGTFLWDMNKNIPVSQTERYQILFGYGKNLSHLSLQY
KMNIISTYEIYSTITEEENELNRKN

PROTEINA 18

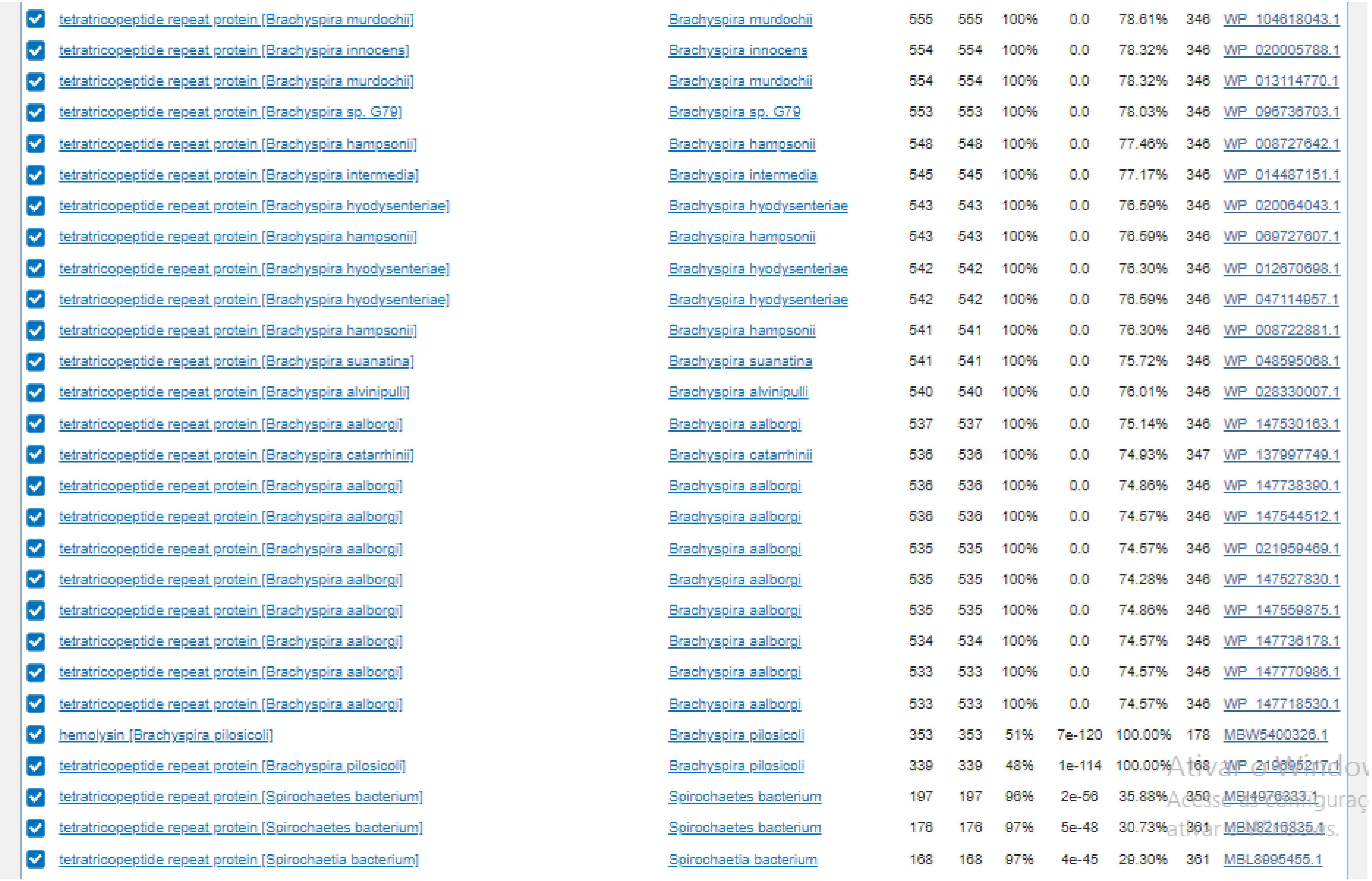
```
>fig|6666666.171271.peg.1917
MKTYAAVLASVITVVAILIGVFITKVSTLSSPERYFQKGKRYYELENYNEAINNLNEYLSIDSRSKPVSNVAESYFIVADSL
KKMKNYNLAKNRLSEIIDGVGFEAYQLDAIIAYADIARLQNSADQYIIAKLQNNLKPADKSLASTINMQYGYQLFFEKKYGE
ALSYFLRSDGELAVLGRARVYFAMNEYDRAFEIYEDFLKYYNTSIYYNEVSRTYLIQVPAIAHRMYVQKNYVKARMYYNKIA
TLFPRTKYQEEALFKIGESYYNEKNYNSAVDYFNRVRLNNVYTLDAEALLYIGLSYFKVGRYSDSYKALDTFVNTYPDNPNV
SRAKDYMAALQETLLAIN
```



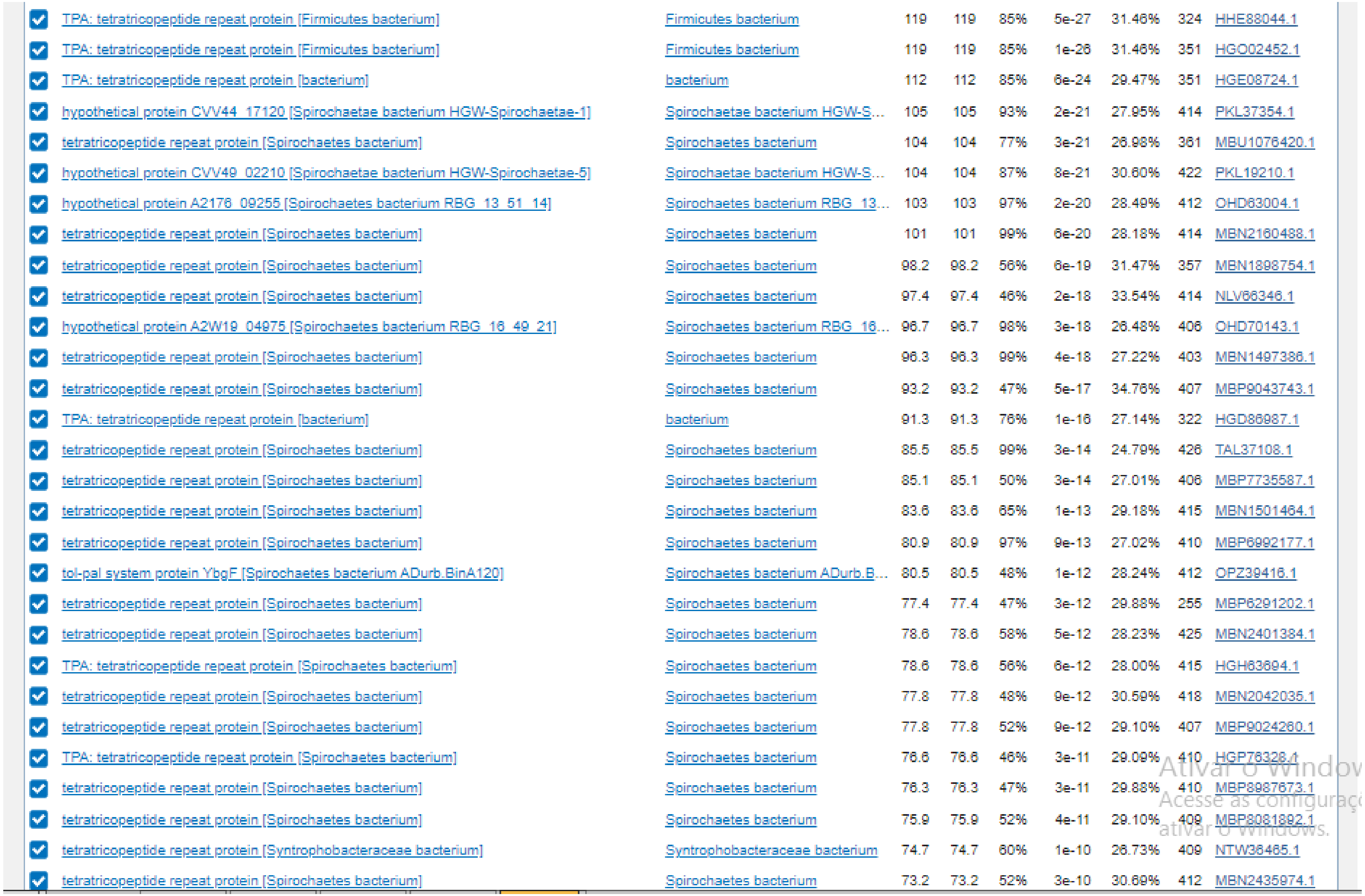
Job Title	Protein Sequence
RID	M9G5EKPU013 *Search expires on 09-19 00:22 am* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_37031
Description	None
Molecule type	amino acid
Query Length	346
Other reports	Distance tree of results Multiple alignment MSA viewer

Sequences producing significant alignments

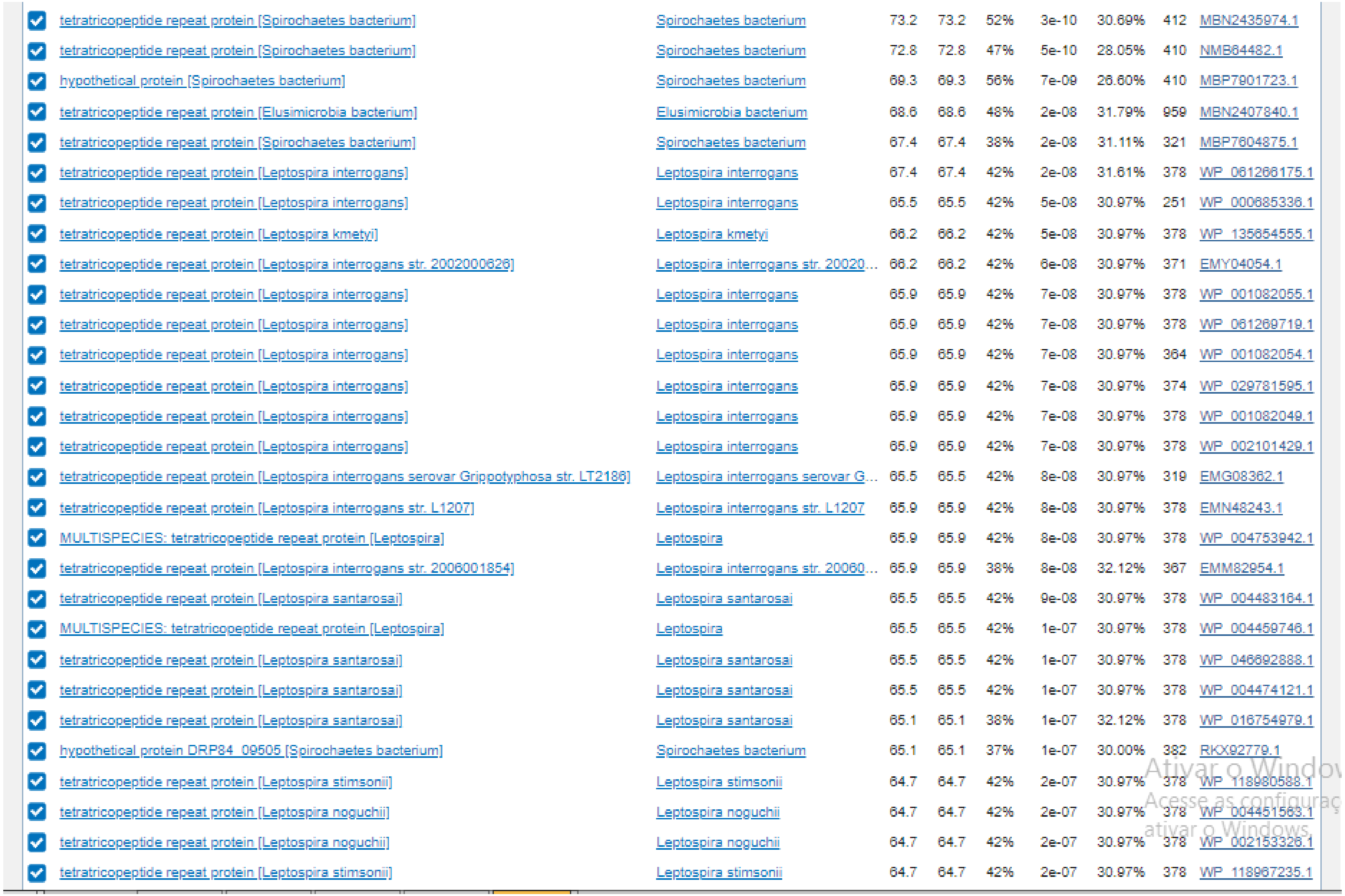
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	690	690	100%	0.0	100.00%	346	WP_013244852.1
☑	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	689	689	100%	0.0	99.71%	346	WP_157147543.1
☑	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	687	687	100%	0.0	99.42%	346	WP_219710085.1
☑	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	687	687	100%	0.0	99.71%	346	WP_014932687.1
☑	tetratricopeptide repeat protein [Brachyspira sp. SAP_772]	Brachyspira sp. SAP_772	671	671	100%	0.0	97.40%	346	WP_157151663.1
☑	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	671	671	100%	0.0	97.40%	346	WP_101503216.1
☑	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	669	669	100%	0.0	97.11%	346	WP_147731011.1



☑	tetratricopeptide repeat protein [Brachyspira murdochii]	Brachyspira murdochii	555	555	100%	0.0	78.61%	346	WP_104618043.1
☑	tetratricopeptide repeat protein [Brachyspira innocens]	Brachyspira innocens	554	554	100%	0.0	78.32%	346	WP_020005788.1
☑	tetratricopeptide repeat protein [Brachyspira murdochii]	Brachyspira murdochii	554	554	100%	0.0	78.32%	346	WP_013114770.1
☑	tetratricopeptide repeat protein [Brachyspira sp. G79]	Brachyspira sp. G79	553	553	100%	0.0	78.03%	346	WP_096736703.1
☑	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	548	548	100%	0.0	77.46%	346	WP_008727642.1
☑	tetratricopeptide repeat protein [Brachyspira intermedia]	Brachyspira intermedia	545	545	100%	0.0	77.17%	346	WP_014487151.1
☑	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	543	543	100%	0.0	76.59%	346	WP_020064043.1
☑	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	543	543	100%	0.0	76.59%	346	WP_069727607.1
☑	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	542	542	100%	0.0	76.30%	346	WP_012670698.1
☑	tetratricopeptide repeat protein [Brachyspira hyodysenteriae]	Brachyspira hyodysenteriae	542	542	100%	0.0	76.59%	346	WP_047114957.1
☑	tetratricopeptide repeat protein [Brachyspira hampsonii]	Brachyspira hampsonii	541	541	100%	0.0	76.30%	346	WP_008722881.1
☑	tetratricopeptide repeat protein [Brachyspira suanatina]	Brachyspira suanatina	541	541	100%	0.0	75.72%	346	WP_048595068.1
☑	tetratricopeptide repeat protein [Brachyspira alvinipulli]	Brachyspira alvinipulli	540	540	100%	0.0	76.01%	346	WP_028330007.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	537	537	100%	0.0	75.14%	346	WP_147530163.1
☑	tetratricopeptide repeat protein [Brachyspira catarrhinii]	Brachyspira catarrhinii	536	536	100%	0.0	74.93%	347	WP_137997749.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	536	536	100%	0.0	74.86%	346	WP_147738390.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	536	536	100%	0.0	74.57%	346	WP_147544512.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	535	535	100%	0.0	74.57%	346	WP_021959469.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	535	535	100%	0.0	74.28%	346	WP_147527830.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	535	535	100%	0.0	74.86%	346	WP_147559875.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	534	534	100%	0.0	74.57%	346	WP_147736178.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	533	533	100%	0.0	74.57%	346	WP_147770986.1
☑	tetratricopeptide repeat protein [Brachyspira aalborgi]	Brachyspira aalborgi	533	533	100%	0.0	74.57%	346	WP_147718530.1
☑	hemolysin [Brachyspira pilosicoli]	Brachyspira pilosicoli	353	353	51%	7e-120	100.00%	178	MBW5400326.1
☑	tetratricopeptide repeat protein [Brachyspira pilosicoli]	Brachyspira pilosicoli	339	339	48%	1e-114	100.00%	168	WP_219695217.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	197	197	96%	2e-56	35.88%	350	MBI4976333.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	176	176	97%	5e-48	30.73%	361	MBN8216835.1
☑	tetratricopeptide repeat protein [Spirochaetia bacterium]	Spirochaetia bacterium	168	168	97%	4e-45	29.30%	361	MBL8995455.1



☑	TPA: tetratricopeptide repeat protein [Firmicutes bacterium]	Firmicutes bacterium	119	119	85%	5e-27	31.46%	324	HHE88044.1
☑	TPA: tetratricopeptide repeat protein [Firmicutes bacterium]	Firmicutes bacterium	119	119	85%	1e-26	31.46%	351	HGO02452.1
☑	TPA: tetratricopeptide repeat protein [bacterium]	bacterium	112	112	85%	6e-24	29.47%	351	HGE08724.1
☑	hypothetical protein CVV44_17120 [Spirochaetae bacterium HGW-Spirochaetae-1]	Spirochaetae bacterium HGW-S...	105	105	93%	2e-21	27.95%	414	PKL37354.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	104	104	77%	3e-21	26.98%	361	MBU1076420.1
☑	hypothetical protein CVV49_02210 [Spirochaetae bacterium HGW-Spirochaetae-5]	Spirochaetae bacterium HGW-S...	104	104	87%	8e-21	30.60%	422	PKL19210.1
☑	hypothetical protein A2176_09255 [Spirochaetes bacterium RBG_13_51_14]	Spirochaetes bacterium RBG_13...	103	103	97%	2e-20	28.49%	412	OHD63004.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	101	101	99%	6e-20	28.18%	414	MBN2160488.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	98.2	98.2	56%	6e-19	31.47%	357	MBN1898754.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	97.4	97.4	46%	2e-18	33.54%	414	NLV66346.1
☑	hypothetical protein A2W19_04975 [Spirochaetes bacterium RBG_16_49_21]	Spirochaetes bacterium RBG_16...	96.7	96.7	98%	3e-18	26.48%	406	OHD70143.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	96.3	96.3	99%	4e-18	27.22%	403	MBN1497386.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	93.2	93.2	47%	5e-17	34.76%	407	MBP9043743.1
☑	TPA: tetratricopeptide repeat protein [bacterium]	bacterium	91.3	91.3	76%	1e-16	27.14%	322	HGD86987.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	85.5	85.5	99%	3e-14	24.79%	426	TAL37108.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	85.1	85.1	50%	3e-14	27.01%	406	MBP7735587.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	83.6	83.6	65%	1e-13	29.18%	415	MBN1501464.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	80.9	80.9	97%	9e-13	27.02%	410	MBP6992177.1
☑	tol-pal system protein YbgF [Spirochaetes bacterium ADurb.BinA120]	Spirochaetes bacterium ADurb.B...	80.5	80.5	48%	1e-12	28.24%	412	OPZ39416.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	77.4	77.4	47%	3e-12	29.88%	255	MBP6291202.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	78.6	78.6	58%	5e-12	28.23%	425	MBN2401384.1
☑	TPA: tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	78.6	78.6	56%	6e-12	28.00%	415	HGH63694.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	77.8	77.8	48%	9e-12	30.59%	418	MBN2042035.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	77.8	77.8	52%	9e-12	29.10%	407	MBP9024260.1
☑	TPA: tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	76.6	76.6	46%	3e-11	29.09%	410	HGP76328.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	76.3	76.3	47%	3e-11	29.88%	410	MBP8987673.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	75.9	75.9	52%	4e-11	29.10%	409	MBP8081892.1
☑	tetratricopeptide repeat protein [Syntrophobacteraceae bacterium]	Syntrophobacteraceae bacterium	74.7	74.7	60%	1e-10	26.73%	409	NTW36465.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	73.2	73.2	52%	3e-10	30.69%	412	MBN2435974.1



☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	73.2	73.2	52%	3e-10	30.69%	412	MBN2435974.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	72.8	72.8	47%	5e-10	28.05%	410	NMB64482.1
☑	hypothetical protein [Spirochaetes bacterium]	Spirochaetes bacterium	69.3	69.3	56%	7e-09	26.60%	410	MBP7901723.1
☑	tetratricopeptide repeat protein [Elusimicrobia bacterium]	Elusimicrobia bacterium	68.6	68.6	48%	2e-08	31.79%	959	MBN2407840.1
☑	tetratricopeptide repeat protein [Spirochaetes bacterium]	Spirochaetes bacterium	67.4	67.4	38%	2e-08	31.11%	321	MBP7604875.1
☑	tetratricopeptide repeat protein [Leptospira interrogans]	Leptospira interrogans	67.4	67.4	42%	2e-08	31.61%	378	WP_061266175.1
☑	tetratricopeptide repeat protein [Leptospira interrogans]	Leptospira interrogans	65.5	65.5	42%	5e-08	30.97%	251	WP_000685336.1
☑	tetratricopeptide repeat protein [Leptospira kmetyi]	Leptospira kmetyi	66.2	66.2	42%	5e-08	30.97%	378	WP_135654555.1
☑	tetratricopeptide repeat protein [Leptospira interrogans str. 2002000626]	Leptospira interrogans str. 20020...	66.2	66.2	42%	6e-08	30.97%	371	EMY04054.1
☑	tetratricopeptide repeat protein [Leptospira interrogans]	Leptospira interrogans	65.9	65.9	42%	7e-08	30.97%	378	WP_001082055.1
☑	tetratricopeptide repeat protein [Leptospira interrogans]	Leptospira interrogans	65.9	65.9	42%	7e-08	30.97%	378	WP_061269719.1
☑	tetratricopeptide repeat protein [Leptospira interrogans]	Leptospira interrogans	65.9	65.9	42%	7e-08	30.97%	364	WP_001082054.1
☑	tetratricopeptide repeat protein [Leptospira interrogans]	Leptospira interrogans	65.9	65.9	42%	7e-08	30.97%	374	WP_029781595.1
☑	tetratricopeptide repeat protein [Leptospira interrogans]	Leptospira interrogans	65.9	65.9	42%	7e-08	30.97%	378	WP_001082049.1
☑	tetratricopeptide repeat protein [Leptospira interrogans]	Leptospira interrogans	65.9	65.9	42%	7e-08	30.97%	378	WP_002101429.1
☑	tetratricopeptide repeat protein [Leptospira interrogans serovar Grippotyphosa str. LT2186]	Leptospira interrogans serovar G...	65.5	65.5	42%	8e-08	30.97%	319	EMG08362.1
☑	tetratricopeptide repeat protein [Leptospira interrogans str. L1207]	Leptospira interrogans str. L1207	65.9	65.9	42%	8e-08	30.97%	378	EMN48243.1
☑	MULTISPECIES: tetratricopeptide repeat protein [Leptospira]	Leptospira	65.9	65.9	42%	8e-08	30.97%	378	WP_004753942.1
☑	tetratricopeptide repeat protein [Leptospira interrogans str. 2006001854]	Leptospira interrogans str. 20060...	65.9	65.9	38%	8e-08	32.12%	367	EMM82954.1
☑	tetratricopeptide repeat protein [Leptospira santarosai]	Leptospira santarosai	65.5	65.5	42%	9e-08	30.97%	378	WP_004483164.1
☑	MULTISPECIES: tetratricopeptide repeat protein [Leptospira]	Leptospira	65.5	65.5	42%	1e-07	30.97%	378	WP_004459746.1
☑	tetratricopeptide repeat protein [Leptospira santarosai]	Leptospira santarosai	65.5	65.5	42%	1e-07	30.97%	378	WP_046692888.1
☑	tetratricopeptide repeat protein [Leptospira santarosai]	Leptospira santarosai	65.5	65.5	42%	1e-07	30.97%	378	WP_004474121.1
☑	tetratricopeptide repeat protein [Leptospira santarosai]	Leptospira santarosai	65.1	65.1	38%	1e-07	32.12%	378	WP_016754979.1
☑	hypothetical protein DRP84_09505 [Spirochaetes bacterium]	Spirochaetes bacterium	65.1	65.1	37%	1e-07	30.00%	382	RKX92779.1
☑	tetratricopeptide repeat protein [Leptospira stimsonii]	Leptospira stimsonii	64.7	64.7	42%	2e-07	30.97%	378	WP_118980588.1
☑	tetratricopeptide repeat protein [Leptospira noguchii]	Leptospira noguchii	64.7	64.7	42%	2e-07	30.97%	378	WP_004451563.1
☑	tetratricopeptide repeat protein [Leptospira noguchii]	Leptospira noguchii	64.7	64.7	42%	2e-07	30.97%	378	WP_002153326.1
☑	tetratricopeptide repeat protein [Leptospira stimsonii]	Leptospira stimsonii	64.7	64.7	42%	2e-07	30.97%	378	WP_118967235.1

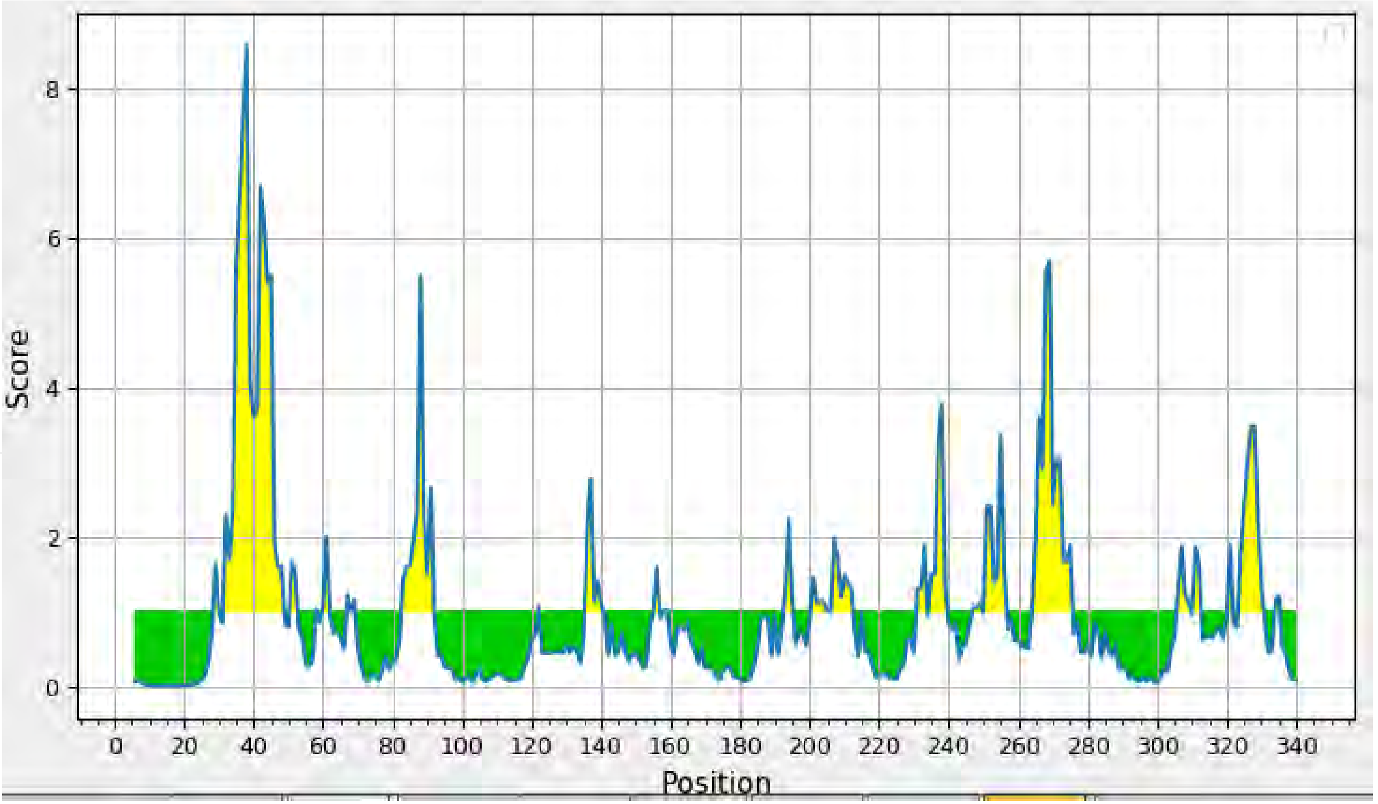
☑	tetratricopeptide repeat protein [Leptospira stimsonii]	Leptospira stimsonii	64.7	64.7	42%	2e-07	30.97%	378	WP_118967235.1
☑	tetratricopeptide repeat protein [Leptospira noguchii]	Leptospira noguchii	64.3	64.3	42%	2e-07	30.97%	378	WP_004419645.1
☑	tetratricopeptide repeat protein [Leptospira noguchii]	Leptospira noguchii	64.3	64.3	42%	2e-07	30.97%	378	WP_002179858.1
☑	hypothetical protein B2G50_06435 [Leptospira interrogans serovar Canicola]	Leptospira interrogans serovar C...	64.3	64.3	43%	2e-07	30.62%	378	ASV08686.1
☑	tetratricopeptide repeat protein [Firmicutes bacterium]	Firmicutes bacterium	65.1	118	85%	3e-07	23.76%	966	MQY53097.1
☑	tetratricopeptide repeat protein [Balneolaceae bacterium]	Balneolaceae bacterium	64.7	64.7	82%	3e-07	27.00%	914	MBN2731182.1
☑	tetratricopeptide repeat protein [Leptospira sp. 201903070]	Leptospira sp. 201903070	63.5	63.5	42%	5e-07	30.32%	378	WP_205281477.1
☑	tol-pal system protein YbgF [Fibrobacter sp.]	Fibrobacter sp.	62.8	62.8	32%	5e-07	29.46%	266	NLW33285.1
☑	tetratricopeptide repeat protein [Leptospira sp. 201903071]	Leptospira sp. 201903071	63.5	63.5	42%	5e-07	30.32%	378	WP_205275055.1

Emini Surface Accessibility Prediction Results

Input Sequences

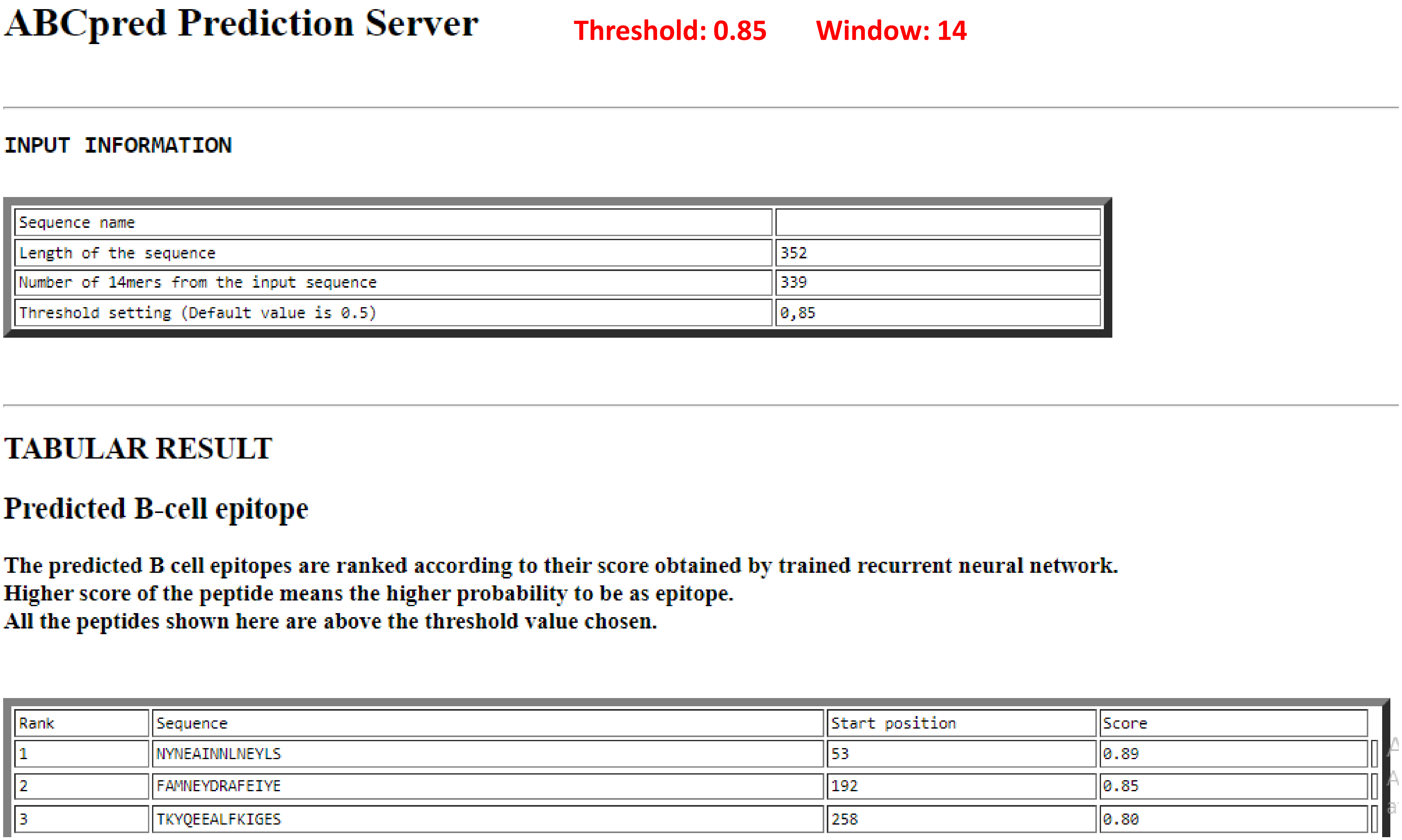
```
  1 MKTYAAVLAS VITVVAILIG VFITKVSTLS SPERYFQKGK RYYELENYNE AINNLNEYLS
 61 IDSRSKPV SNVAESYFIV ADSLKKMKNY NLAKNRLSEI IDGVGFEAYQ LDAIIAYADI
121 AR LQNSAD QYIIAKLQNN LKPADKSLAS TINMQYGYQL FFEKKYGEAL SYFLRSDGEL
181 AVLG RARV YFAMNEYDRA FEIYEDFLKY YNTSIYYNEV SRTYLIQVPA IAHRMYVQKN
241 YVKARM YY NKIATLFPRT KYQEEALFKI GESYYNEKNY NSAVDYFNRV RLNNVYTLDA
301 EALLYIGL SYFKVGRYSD SYKALDTFVN TYPDNPNVSR AKDYMAALQE TLLAIN
```

Center position: 6 **Window size:** 12 **Threshold:** 1.000



>fig|6666666.171271.peg.1917
MKTYAAVLASVITVVAILIGVFITKVSTLSSPERYFQKGKRYYELENYNEAINNLNEYLSIDSRSKPVSNVAESYFIVADSL
KKMKNYNLAKNRLSEIIDGVGFEAYQLDAIIAYADIARLQNSADQYIIAKLQNNLKPADKSLASTINMQYGYQL
FFEKKYGEALSYFLRSDGELAVLGRARVYFAMNEYDRAFEIYEDFLKYYNTSIYYNEVSRTYLIQVPAIAHRMYVQKNYVKA
RMYYNKIATLFPRTKYQEEALFKIGESYYNEKNYNSAVDYFNRVRLNNVYTLDAEALLYIGLSYFKVGRYSDSYKALDTFVN
TYPDNPNVSRAKDYMAALQETLLAIN

Threshold: 0.85 **Window: 14**



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	352
Number of 14mers from the input sequence	339
Threshold setting (Default value is 0.5)	0,85

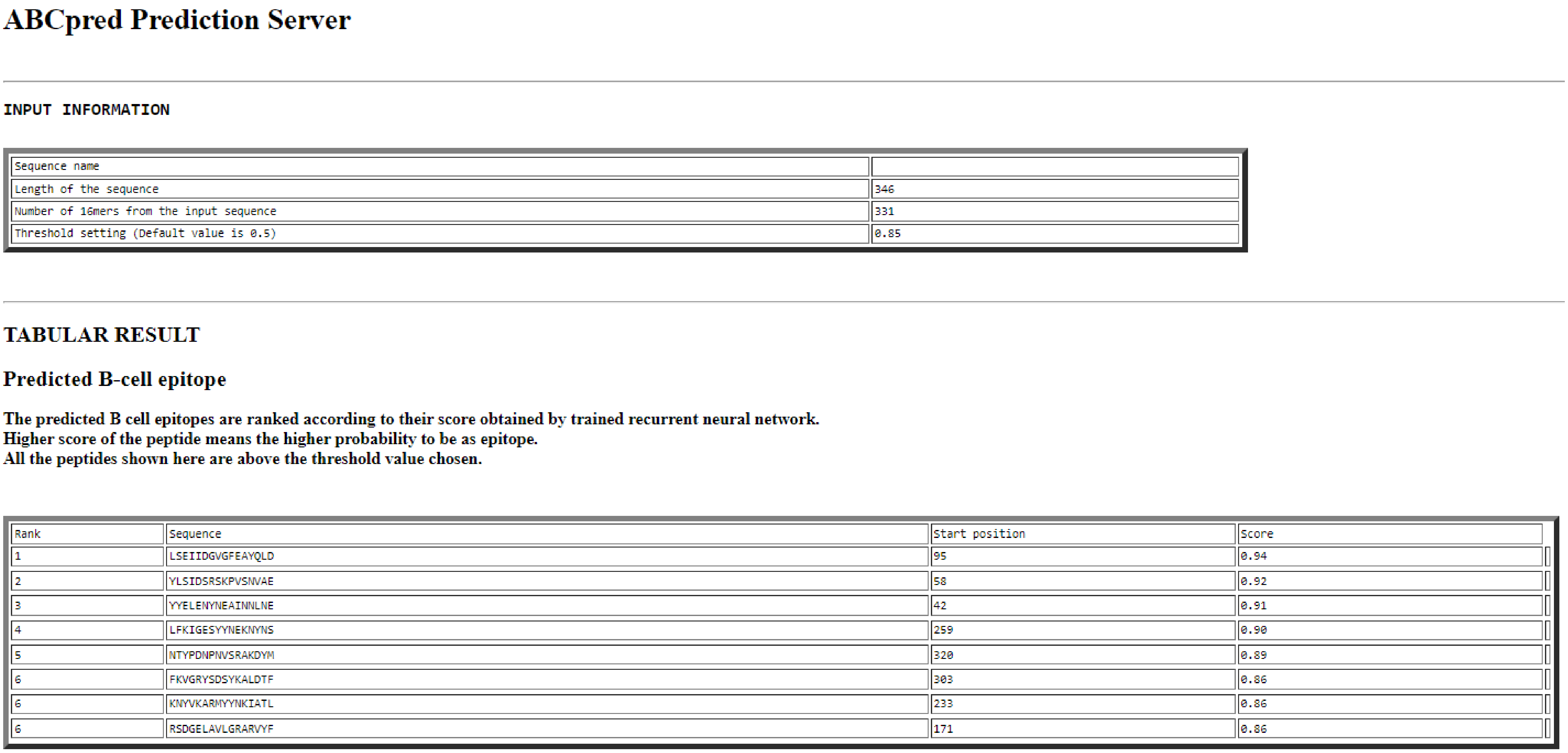
TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	NYNEAINNLNEYLS	53	0.89
2	FAMNEYDRAFEIYE	192	0.85
3	TKYQEEALFKIGES	258	0.80

Threshold: 0.85 Window: 16



ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	346
Number of 16mers from the input sequence	331
Threshold setting (Default value is 0.5)	0.85

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score
1	LSEIIDGVGFEAYQLD	95	0.94
2	YLSIDSRSKPVSNVAE	58	0.92
3	YYELENYNEAINNLNE	42	0.91
4	LFKIGESYYNEKNYNS	259	0.90
5	NTYPDNPNVSRAKDYM	320	0.89
6	FKVGRYSDSYKALDTF	303	0.86
6	KNYVKARMYYNKIATL	233	0.86
6	RSDGELAVLGRARVYF	171	0.86

PROTEINA 18

>fig|6666666.171271.peg.1917
MKTYAAVLASVITVVAILIGVFITKVSTLSSPERYFQKGKRYYELENYNEAINNLNEYLSIDSRSKPVSNVAESYFIVADSL
KKMKNYNLAKNRLSEIIDGVGFEAYQLDAIIAYADIARLQNSADQYIIAKLQNNLKPADKSLASTINMQYGYQLFFEKKYGE
ALSYFLRSDGELAVLGRARVYFAMNEYDRAFEIYEDFLKYYNTSIYYNEVSRTYLIQVPAIAHRMYVQKNYVKARMYYNKIA
TLFPRTKYQEEALFKIGESYYNEKNYNSAVDYFNRVRLNNVYTLDAEALLYIGLSYFKVGRYSDSYKALDTFVNTYPDNPNV
SRAKDYMAALQETLLAIN

Predição combinada AbcPred Threshold: 0.85 Window: 14

>fig|6666666.171271.peg.1917
MKTYAAVLASVITVVAILIGVFITKVSTLSSPERYFQKGKRYYELENYNEAINNLNEYLSIDSRSKPVSNVAESYFIVADSL
KKMKNYNLAKNRLSEIIDGVGFEAYQLDAIIAYADIARLQNSADQYIIAKLQNNLKPADKSLASTINMQYGYQLFFEKKYGE
ALSYFLRSDGELAVLGRARVYFAMNEYDRAFEIYEDFLKYYNTSIYYNEVSRTYLIQVPAIAHRMYVQKNYVKARMYYNKIA
TLFPRTKYQEEALFKIGESYYNEKNYNSAVDYFNRVRLNNVYTLDAEALLYIGLSYFKVGRYSDSYKALDTFVNTYPDNPNV
SRAKDYMAALQETLLAIN

Predição combinada AbcPred Threshold: 0.85 Window: 16

>fig|6666666.171271.peg.1917
MKTYAAVLASVITVVAILIGVFITKVSTLSSPERYFQKGKRYYELENYNEAINNLNEYLSIDSRSKPVSNVAESYFIVADSL
KKMKNYNLAKNRLSEIIDGVGFEAYQLDAIIAYADIARLQNSADQYIIAKLQNNLKPADKSLASTINMQYGYQLFFEKKYGE
ALSYFLRSDGELAVLGRARVYFAMNEYDRAFEIYEDFLKYYNTSIYYNEVSRTYLIQVPAIAHRMYVQKNYVKARMYYNKIA
TLFPRTKYQEEA**LFKIGESYYNEKNYNSA**VDYFNRVRLNNVYTLDAEALLYIGLSYFKVGRYSDSYKALDTFVNTYPDNPNV
SRAKDYMAALQETLLAIN

EPITOPOS ESCOLHIDOS:

PROTEINA 1: YIQNNNKEYMDMNKIK

PROTEINA 2: KKASTAPGGEGPTKEDEVKPP

PROTEINA 3: GGLEPPKEEDNTAGK

PROTEINA 4: EIYKDIANAPEEYKHTY

PROTEINA 5: LFPKYYKVQYRKVG

PROTEINA 6: GLTKNTRFKVYS

PROTEINA 7: PIRVEFEYLYKNGLEVNNYPNNID

PROTEINA 8: EGHIDSSEVRYMNKNTVYN

PROTEINA 9: DDTSEKEEPKQEDTDNLDDLDSILD

PROTEINA 10: MTERKTDEKIVMEVNTNYYDKESI

PROTEINA 11: GKQSGKGSDKVYEYDLATKETKELAPVPNQASR

PROTEINA 12: TPPSYMRNNNEP

PROTEINA 13: DRQRLDKLMKEVLLQQTSGMVDE

PROTEINA 14: AALATTYKNIDEANRG

PROTEINA 15: EYKSAAGKNISFEIIDA

PROTEINA 16: QEDSVIKEQIRTKIQQYNKDK

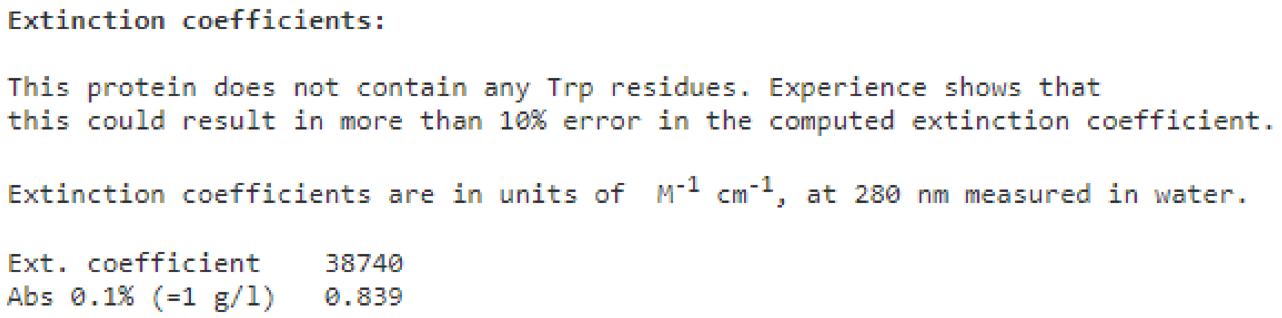
PROTEINA 17: MALSADYLFANIETNENNDPL

PROTEINA 18: LFKIGESYYNEKNYNSA

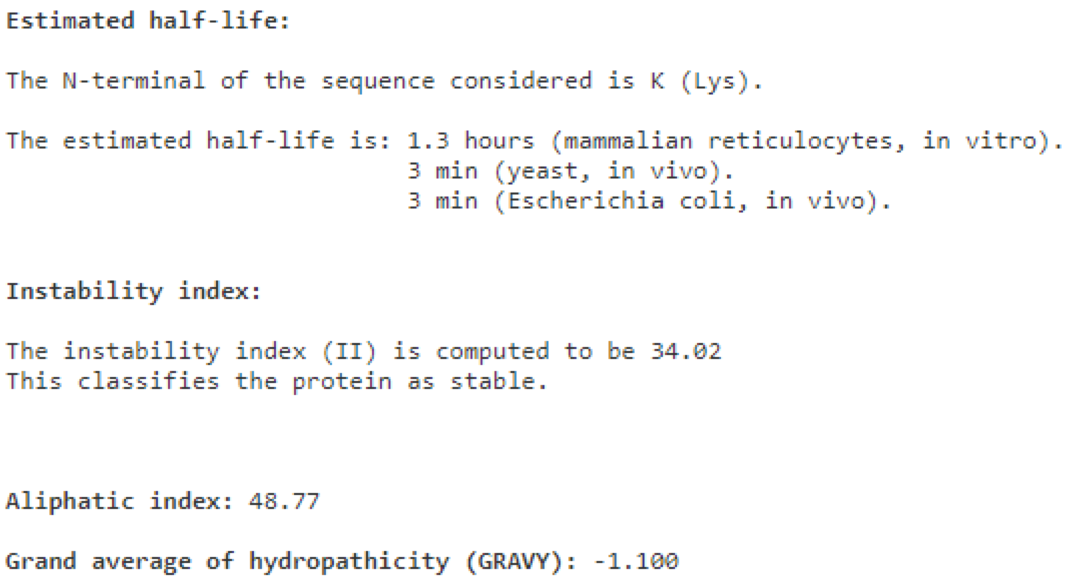
PROTEÍNA QUIMERA: 2-3-8-7-13-15-6-10-11-14-9-1-17-18-16-4-5-12

KKASTAPGGEGPTKEDEVKPPGPGPGGGLEPPKEEDNTAGKGPGPGEGHIDSSEVRYMNKNTVYNGPGPGPIRVEFEYLYKNGLE
VNNYPNNIDGPGPGDRQRLDKLMKEVLLQQTSGMVDEGPGPGEYKSAAGKNISFEIIDAGPGPGGLTKNTRFKVYSGPGPGMTER
KTDEKIVMEVNTNYYDKESIGPGPGGKQSGKGSDKVYEYDLATKETKELAPVPNQASRGPGPGAALATTYKNIDEANRGGPGPGD
DTSEKEEPKQEDTDNLDDLDSILDGPGPGYIQNNNKEYMDMNKIKGPGPGMALSADYLFANIETNENNDPLGPGPGLFKIGESYY
NEKNYNSAGPGPGQEDSVIKEQIRTKIQQYNKDKGPGPGEIYKDIANAPEEYKHTYGPGPGLFPKYYKVQYRKVGGPGPGTPPSY
MRNNNEP

Boa solubilidade em água (Pepcalc)



```
Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that
this could result in more than 10% error in the computed extinction coefficient.

Extinction coefficients are in units of  M-1 cm-1, at 280 nm measured in water.

Ext. coefficient    38740
Abs 0.1% (=1 g/l)   0.839
```



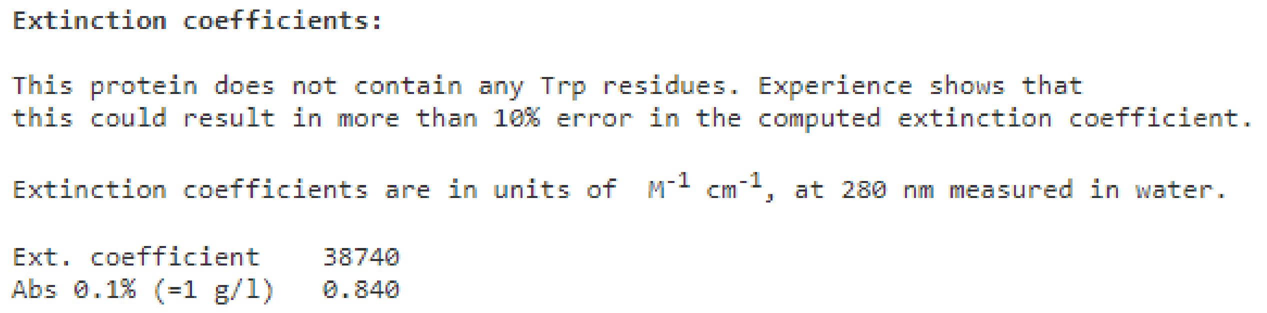
```
Estimated half-life:

The N-terminal of the sequence considered is K (Lys).

The estimated half-life is: 1.3 hours (mammalian reticulocytes, in vitro).
                            3 min (yeast, in vivo).
                            3 min (Escherichia coli, in vivo).


Instability index:

The instability index (II) is computed to be 34.02
This classifies the protein as stable.


Aliphatic index: 48.77

Grand average of hydropathicity (GRAVY): -1.100
```

Simlaridade apenas com *Brachyspira* no Blast-p

PROTEÍNA QUIMERA: 2-8-3-7-13-15-14-10-6-11-9-17-1-4-5-18-16-12

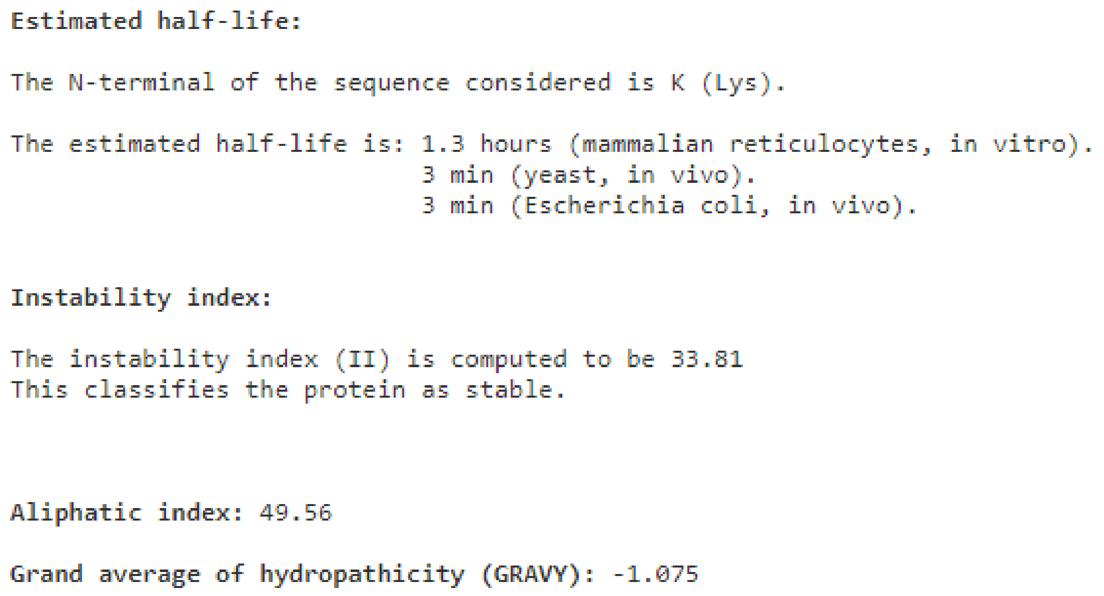
```
KKASTAPGGEGPTKEDEVKPPGPGPGEGHIDSSEVRYMNKNTVYNGPGPGGGLEPPKEEDNTAGKGPGPGPIRVEFEYLYKNGLE
VNNYPNNIDGPGPGDRQRLDKLMKEVLLQQTSGMVDEGPGPGEYKSAAGKNISFEIIDAGPGPGEYKSAAGKNISFEIIDAGPGP
GMTERKTDEKIVMEVNTNYYDKESIGPGPGGLTKNTRFKVYGPGPGGKQSGKGSDKVYEYDLATKETKELAPVPNQASGPGPGDD
TSEKEEPKQEDTDNLDDLDSILDGPGPGMALSADYLFANIETNENNDPLGPGPGYIQNNNKEYMDMNKIKGPGPGEIYKDIANAP
EEYKHTYGPGPGLFPKYYKVQYRKVGGPGPGLFKIGESYYNEKNYNSAGPGPGQEDSVIKEQIRTKIQQYNKDKGPGPGTPPSYM
RNNNEP
```

Boa solubilidade em água (Pepcalc)



```
Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that
this could result in more than 10% error in the computed extinction coefficient.

Extinction coefficients are in units of  M-1 cm-1, at 280 nm measured in water.

Ext. coefficient    38740
Abs 0.1% (=1 g/l)   0.840
```

Simlaridade apenas com *Brachyspira Canaripox* e *Chiloscyllium* no Blast-p



```
Estimated half-life:

The N-terminal of the sequence considered is K (Lys).

The estimated half-life is: 1.3 hours (mammalian reticulocytes, in vitro).
                            3 min (yeast, in vivo).
                            3 min (Escherichia coli, in vivo).


Instability index:

The instability index (II) is computed to be 33.81
This classifies the protein as stable.



Aliphatic index: 49.56

Grand average of hydropathicity (GRAVY): -1.075
```