http://www.cbs.dtu.dk/services/TMHMM/
TMHMM Server v. 2.0
Prediction of transmembrane helices in proteins

AndersKrogh, BjörnLarsson12 Gunnarvon Heijne2 Erik L.LSonnhammer3
Predicting transmembrane protein topology with a hidden markov model: application to complete genomes1 Volume 305, Issue 3, 19 January 2001, Pages 567-580 J Mol Biol
https://doi.org/10.1006/jmbi.2000.4315

Labyrinthin entered:
http://www.cbs.dtu.dk/cgi-bin/webface2.fcgi?jobid=6104619D000067650C139F31&wait=20

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# WEBSEQUENCE Length: 255
# WEBSEQUENCE Number of predicted TMHs:  0
# WEBSEQUENCE Exp number of AAs in TMHs: 2.5038
# WEBSEQUENCE Exp number, first 60 AAs:  2.5038
# WEBSEQUENCE Total prob of N-in:        0.14531
WEBSEQUENCE TMHMM2.0      outside      1   255
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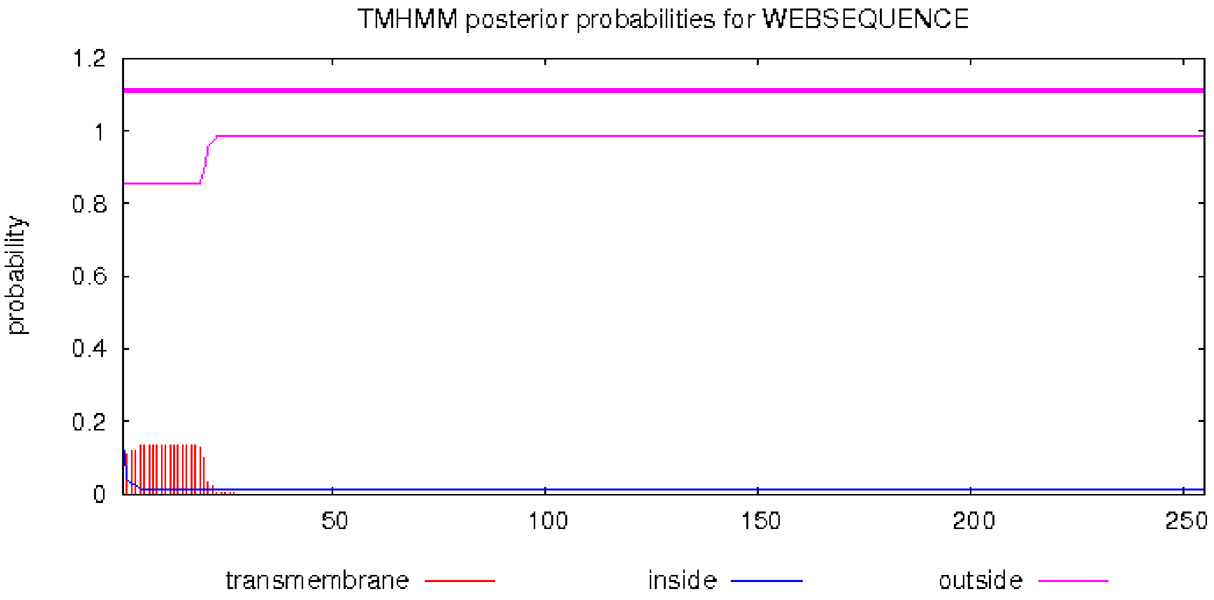

WEBSEQUENCE

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3 I	0.02760	0.11771	0.85468
4 A	0.02760	0.11785	0.85454
5 L	0.01190	0.13376	0.85434
6 L	0.01190	0.13377	0.85433
7 G	0.01173	0.13393	0.85433
8 V	0.01173	0.13393	0.85433
9 W	0.01173	0.13394	0.85433
10 T	0.01173	0.13394	0.85433
11 S	0.01173	0.13394	0.85433
12 V	0.01172	0.13394	0.85433
13 A	0.01172	0.13394	0.85433
14 V	0.01172	0.13394	0.85433
15 V	0.01172	0.13394	0.85433
16 W	0.01172	0.13394	0.85433
17 F	0.01172	0.13337	0.8549
18 D	0.01172	0.13142	0.85686
19 L	0.01173	0.13088	0.8574
20 V	0.01175	0.10105	0.8872
21 D	0.01184	0.02965	0.95851
22 Y	0.01185	0.02066	0.96748
23 E	0.01195	0.00269	0.98536
24 E	0.01196	0.00199	0.98605
25 V	0.01196	0.00118	0.98685
26 L	0.01197	0.00090	0.98713
27 G	0.01202	0.00069	0.9873
28 K	0.01207	0.00001	0.98792
29 L	0.01207	0.00001	0.98792
30 G	0.01207	0.00001	0.98792
31 I	0.01207	0.00001	0.98792
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33 D	0.01207	0.00000	0.98793
34 A	0.01207	0.00000	0.98793
35 D	0.01207	0.00000	0.98793
36 G	0.01207	0.00000	0.98793
37 D	0.01207	0.00000	0.98793
38 G	0.01207	0.00000	0.98793
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41 D	0.01207	0.00000	0.98793
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43 D	0.01207	0.00000	0.98793
44 D	0.01207	0.00000	0.98793
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46 K	0.01207	0.00000	0.98793

47 V	0.01207	0.00000	0.98793
48 L	0.01207	0.00000	0.98793
49 L	0.01207	0.00000	0.98793
50 G	0.01207	0.00000	0.98793
51 L	0.01207	0.00000	0.98793
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57 S	0.01207	0.00000	0.98793
58 E	0.01207	0.00000	0.98793
59 P	0.01207	0.00000	0.98793
60 A	0.01207	0.00000	0.98793
61 V	0.01207	0.00000	0.98793
62 P	0.01207	0.00000	0.98793
63 P	0.01207	0.00000	0.98793
64 E	0.01207	0.00000	0.98793
65 E	0.01207	0.00000	0.98793
66 A	0.01207	0.00000	0.98793
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71 E	0.01207	0.00000	0.98793
72 P	0.01207	0.00000	0.98793
73 E	0.01207	0.00000	0.98793
74 E	0.01207	0.00000	0.98793
75 Q	0.01207	0.00000	0.98793
76 V	0.01207	0.00000	0.98793
77 P	0.01207	0.00000	0.98793
78 V	0.01207	0.00000	0.98793
79 E	0.01207	0.00000	0.98793
80 A	0.01207	0.00000	0.98793
81 E	0.01207	0.00000	0.98793
82 P	0.01207	0.00000	0.98793
83 Q	0.01207	0.00000	0.98793
84 N	0.01207	0.00000	0.98793
85 I	0.01207	0.00000	0.98793
86 E	0.01207	0.00000	0.98793
87 D	0.01207	0.00000	0.98793
88 E	0.01207	0.00000	0.98793
89 A	0.01207	0.00000	0.98793
90 K	0.01207	0.00000	0.98793
91 E	0.01207	0.00000	0.98793
92 Q	0.01207	0.00000	0.98793
93 I	0.01207	0.00000	0.98793
94 Q	0.01207	0.00000	0.98793
95 S	0.01207	0.00000	0.98793

96 L	0.01207	0.00000	0.98793
97 L	0.01207	0.00000	0.98793
98 H	0.01207	0.00000	0.98793
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100 M	0.01207	0.00000	0.98793
101 V	0.01207	0.00000	0.98793
102 H	0.01207	0.00000	0.98793
103 A	0.01207	0.00000	0.98793
104 E	0.01207	0.00000	0.98793
105 H	0.01207	0.00000	0.98793
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117 P	0.01207	0.00000	0.98793
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145 V	0.01207	0.00000	0.98793
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176 E	0.01207	0.00000	0.98793
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184 V	0.01207	0.00000	0.98793
185 V	0.01207	0.00000	0.98793
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190 L	0.01207	0.00000	0.98793
191 H	0.01207	0.00000	0.98793
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205 Q	0.01207	0.00000	0.98793
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213 N	0.01207	0.00000	0.98793
214 E	0.01207	0.00000	0.98793
215 G	0.01207	0.00000	0.98793
216 I	0.01207	0.00000	0.98793
217 E	0.01207	0.00000	0.98793
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219 T	0.01207	0.00000	0.98793
220 E	0.01207	0.00000	0.98793
221 V	0.01207	0.00000	0.98793
222 T	0.01207	0.00000	0.98793
223 A	0.01207	0.00000	0.98793
224 P	0.01207	0.00000	0.98793
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250 E	0.01207	0.00000	0.98793
251 V	0.01207	0.00000	0.98793
252 P	0.01207	0.00000	0.98793
253 P	0.01207	0.00000	0.98793
254 D	0.01207	0.00000	0.98793
255 T	0.01207	0.00000	0.98793

https://tmdas.bioinfo.se/DAS/
TMHMM Server v. 2.0
Prediction of transmembrane helices in proteins

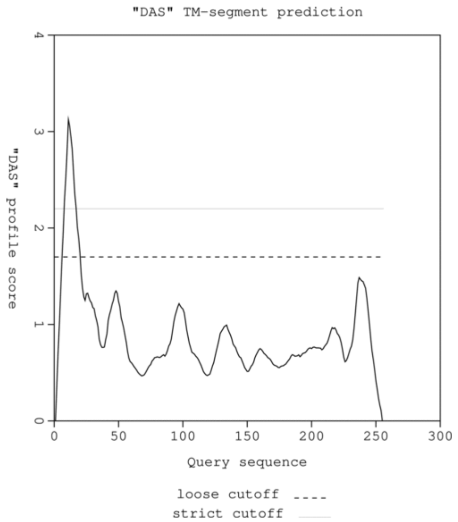
https://tmdas.bioinfo.se/cgi-bin/tmdas.cgi
"DAS" - Transmembrane Prediction server

M. Cserzo, E. Wallin, I. Simon, G. von Heijne and A. Elofsson: Prediction of transmembrane alpha-helices in procariotic membrane proteins: the Dense Alignment Surface method; Prot. Eng. vol. 10, no. 6, 673-676, 1997

Labyrinthin:

Potential transmembrane segments

Start	Stop	Length	~	Cutoff
7	20	14	~	1.7
8	17	10	~	2.2



Omasits U, Ahrens CH, Müller S, Wollscheid B. Protter: interactive protein feature visualization and integration with experimental proteomic data. Bioinformatics. 2014 Mar 15;30(6):884-6. doi: 10.1093/bioinformatics/btt607. Epub 2013 Oct 24. PMID: 24162465.

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http://tmkinkpredictor.mbi.ucla.edu/

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http://www.proteus2.ca/proteus2/

Montgomerie S, Cruz JA, Shrivastava S, Arndt D, Berjanskii M, Wishart DS. PROTEUS2: a web server for comprehensive protein structure prediction and structure-based annotation. Nucleic Acids Res. 2008 Jul 1;36(Web Server issue):W202-9. Epub 2008 May 15.

It employs PSIPred, JNET, and TRANSSEC to produce a consensus “Jury”

Labyrinthin

PROTEUS2 prediction (ID=4724994) complete

Summary:

- Time of Submission: 15:38:17 Jul 30, 2021
- Sequence Name: None given
- Number of residues read in: 255
- Sequence does not contain a transmembrane helicle region.
- Sequence does not contain a signal peptide.
- No homolog was found
- Number of sequence alignments used for ab-initio predictions: **15**
- Overall confidence value: 73.2%
- Predicted % Helix content: 30 % (76 residues)
- Predicted % Beta sheet content: 5 % (12 residues)
- Predicted % Coil content: 65 % (167 residues)
- Predicted % Signal peptide content: 0 % (0 residues)
- Predicted % membrane content: 0 % (0 residues)
- Homology modelling failed, see below. (MB: No other protein current found)

Legend:

```
H = Helix
E = Beta Strand
C = Coil
T = Membrane helix
B = Membrane strand
S = Signal peptide
c = Cleavage site
Line 1 = sequence (single letter IUPAC code, 60 characters per line)
Line 2 = secondary structure (H, E or C)
Line 3 = confidence score (0-9, 0 = low, 9 = high)
```

Predicted Complete Secondary Structure:

```
A '*' character above the overall prediction indicates the homolog's structure was
used at this residue.
  1   MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA 60
      CCECHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCHHHHHHHHHHHHCCCCCCC
      844357889999999988888888876546767788887764699999998756887777

 61   VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
      CCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHCCCCHHHHCCCCCCCC
      767777766665556788886799999999999999999988648874555556788777

121   PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS 180
      CCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHCCCCCCCC
      777654345655687655468876556676654545665667877455555545678877

181   SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV 240
      CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEECCCCCCCCCCCCHHHHHHHC
      776666666678865566667788777778887588887467777778876467899765

241   SIFPVEEQQEVPPDT 255
      CCCCCCCCCCCCCCC
      666776677777788
```

Predicted Signal Peptide Structure (only showing first 60 residues):

No signal peptide found

Predicted Transmembrane Structure:

No transmembrane region found

Detailed Prediction Information:

Proteus2 uses a "Jury of Experts" approach involving predictions from PSIPRED (Jones, 1999), JNET (Barton et al., 2000), TRANSSEC (a locally developed tool), and structural alignment (XALIGN). Following is the predicted secondary structure from each component.

PSIPRED

```
  1   MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA 60
      CEEEHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCHHHHHHHHHHCCCCCCC
      944356689899999998866899987646545788887665445665434446887888

 61   VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
      CCCCCCCCCCCHHHHCCCCCCHHHHHHHHHHHHHHHHHHHHHHHCCCHHHHHHHCCCCCC
      898777766786886877788544679999999999999887554555556666688889

121   PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS 180
      CCCCHHHEEEEECCCHHHHHCCCCCCHHHHCCHHHHHHHHHCCCCHHHHHHHHHCCCCCC
      875545434444565455556887544555444444566655786568988765568887

181   SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV 240
      CCCCCHHHHHCCCHHHCCHHCCCCCCCCCCCCCCCEEEEECCCCCCCCCCCCHHHHHHHH
      775444566567655543443456656586555775776556788888665455545443

241   SIFPVEEQQEVPPDT 255
      CCCCCHHCCCCCCCC
      334445546888899
```

JNET

```
  1   MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA 60
      CHHHHEEEEEEEEEEEECHHHHHHCCCCCCCCCCCCCCHHHHHHHHHHHCCCCCCCCCCC
      812110233346666411011430343144546689411344468864035778999998

 61   VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
      CCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHCCCCCCCHHHHHCCCCCCCCC
      888989943998877776770223567899999888875147556311332434898999

121   PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS 180
      CCCCCEECCCCCCCCCCCCCCCCEEECCCCEEEEECCCCCCCCCCCCCCCCCCCCCCCCC
      988413402335678866667822200110122311245778998763000478899933

181   SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV 240
      CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEECCCCCCCCCCCCCEEEEEEEECC
      374421112269947520125587765689931136614566899999812356775200

241   SIFPVEEQQEVPPDT 255
      EECCCCCCCCCCCCC
      214467888999999
```

TRANSSEC

```
   1  MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA 60
      CCCCCCCCCCCCCCCCCCCCCCCCEEEEEEECCCCCCCCCHHHHHHHHHHHHHCCCCCC
      988888877777777777777764456666546788887757899988888875788777

  61  VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
      CCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCC
      787765566665556778887654678888888888888876556677888744567888 7

 121  PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS 180
      CCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHCCCCCC
      778886445654788887665677766667788777777788888764678987688888

 181  SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV 240
      CCCCCCCCCCCCCCCCHHHHCCCCCCCCCCCCCCCEEEECCCCCCCCCCCCCCCEEEEEE
      775444666655666567775777563345788865775577888898888764556555

 241  SIFPVEEQQEVPPDT 255
      EEHHHCCCCCCCCCC
      543344578888878
```

JURY-OF-EXPERTS PREDICTION

```
   1  MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA 60
      CCECHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCHHHHHHHHHHHHCCCCCCC
      844357889999999998888888887654676778888776469999999875688777 7

  61  VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
      CCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHCCCCHHHHCCCCCCCC
      767777666655567888867999999999999999999988648874555556788777

 121  PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS 180
      CCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHCCCCCCCC
      777654345655687655468876556676654545665667877455555545678877

 181  SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV 240
      CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEECCCCCCCCCCCCHHHHHHHC
      776666666678865566666778877777888758888746777777887646789976 5

 241  SIFPVEEQQEVPPDT 255
      CCCCCCCCCCCCCCC
      666776677777788
```

PSI-BLAST ALIGNMENTS - 15 SEQUENCES USED BY JNET, TRANSSEC, and PSIPRED (below):

```
Blast e-value: 1.0E-94
1   >gi|12746448|ref|NP_075553.1| aspartyl beta-hydroxylase; cals
match: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGVYDADGDGDFDVDDAKVLL--------------
GLKERSPSERTFPPE--AETHAELEEQAPEGADIQNVEDEVKEQIQSLLQESVHTDHD-----
LEADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTNEQENSDPSEAVTDAGVLLPHAEEVRHQ
DYDE-PVYEPSEHEGVEIS-------DNTIDDSSIISEEINVASVEEQQDT~~~~
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET
```

```
Blast e-value: 3.0E-94
2   >gi|26326277|dbj|BAC26882.1| unnamed protein product [Mus mus
match: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGVYDADGDGDFDVDDAKVLL--------------
GLKERSPSERTFPPEEEAETHAELEEQAPEGADIQNVEDEVKEQIQSLLQESVHTDHD-----
LEADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTNEQENSDPSEAVTDAGVLLPHAEEVRHQ
DYDE-PVYEPSEHEGVAIS-------DNTIDDSSIISEEINVASVEEQQDT~~~~
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 6.0E-91
3   >gi|11692645|gb|AAG39913.1| aspartly beta-hydroxylase [Mus mu
match: ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~GKLGVYDADGDGDFDVDDAKVLL--------------
GLKERSPSERTFPPE--AETHAELEEQAPEGADIQNVEDEVKEQIQSLLQESVHTDHD-----
LEADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTNEQENSDPSEAVTDAGVLLPHAEEVRHQ
DYDE-PVYEPSEHEGVEIS-------DNTIDDSSIISEEINVASVEEQQDT~~~~
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 1.0E-80
4   >gi|14589860|ref|NP_115855.1| aspartate beta-hydroxylase isof
match: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPDT
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 4.0E-76
5   >gi|14589864|ref|NP_115857.1| aspartate beta-hydroxylase isof
match: ~~~~~~~~~~~~~~~~~~~~DYEEVLAKAKDFRYNLSEVLQGKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPDT
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 4.0E-71
6   >gi|11878114|gb|AAG40810.1| aspartyl beta-hydroxylase 2.8 kb
match: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGVYDADGDGDFDVDDAKVLL--------------
GLKERSPSERTFPPE--AETHAELEEQAPEGADIQNVEDEVKEQIQSLLQESVHTDHD-----
LEADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTNEQENSDPSEAVTDAGVLLPHAEEVRHQ
DYDE-PVYEPSEHEGVEIS-------DNTIDDSSIISEEINVASVEEQQDTPPDT
```

```
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 6.0E-70
7   >gi|34189305|gb|AAH15518.1| ASPH protein [Homo sapiens]
match: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEET-------------------
DSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPE~
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 7.0E-66
8   >gi|11692646|gb|AAG39914.1| aspartyl beta-hydroxylase Humbug
match: ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~GKLGVYDADGDGDFDVDDAKVLL--------------
GLKERSPSERTFPPE--AETHAELEEQAPEGADIQNVEDEVKEQIQSLLQESVHTDHD-----
LEADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTNEQENSDPSEAVTDAGVLLPHAEEVRHQ
DYDE-PVYEPSEHEGVEIS-------DNTIDDSSIISEEINVASVEEQQDTPPDT
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 4.0E-62
9   >gi|15929716|gb|AAH15281.1| Asph protein [Mus musculus]
match: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGVYDADGDGDFDVDDAKVLL--------------
GLKERSPSERTFPPE--AETHAELEEQAPEGADIQNVEDEVKEQIQSLLQESVHTDHD-----
LEADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTNEQENS----------------
EEVRHQDYDE-PVYEPSEHEGVEIS-------DNTIDDSSIISEEINVASVEEQQDTPPDT
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 9.0E-61
10  >gi|19263911|gb|AAH25236.1| ASPH protein [Homo sapiens]
match: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEH--------------------------------
-----------
ETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIV
EEVSIFPVEEQQEVPPDT
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 4.0E-44
11  >gi|15824394|gb|AAL09321.1| cardiac junctate 3 [Mus musculus]
```

```
match:
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~LEADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHE
EIEDTYHVEDTASQNHPNDMEEMTNEQENSDPSEAVTDAGVLLPHAEEVRHQDYDE-PVYEPSEHEGVEIS-------
DNTIDDSSIISEEINVASVEEQQDTPPDT
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 7.0E-19
12  >gi|34866142|ref|XP_342802.1| similar to aspartyl beta-hydrox
match:
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
~~~~~~~~~~~~~~~~~~~~~~~MSEQESSDHGEAVTDDGLQQH-AEEVRHEDYDE-PVYEPSENERIEIS-------
DNAIDDSNIISEEINVASVEEQQDTPP~~
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET


Blast e-value: 7.0E-17
13  >gi|11878122|gb|AAG40814.1| aspartyl beta-hydroxylase cardiac
match: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------
GKLGVYDADGDGDFDVDDAKVLLEGPGGLAKRKTKAKGLKERSPSERTFPPEA-EAHAELEEQA-
PEGADIQNVEDEVKEQIQSLLQESVHTDH~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
~
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET

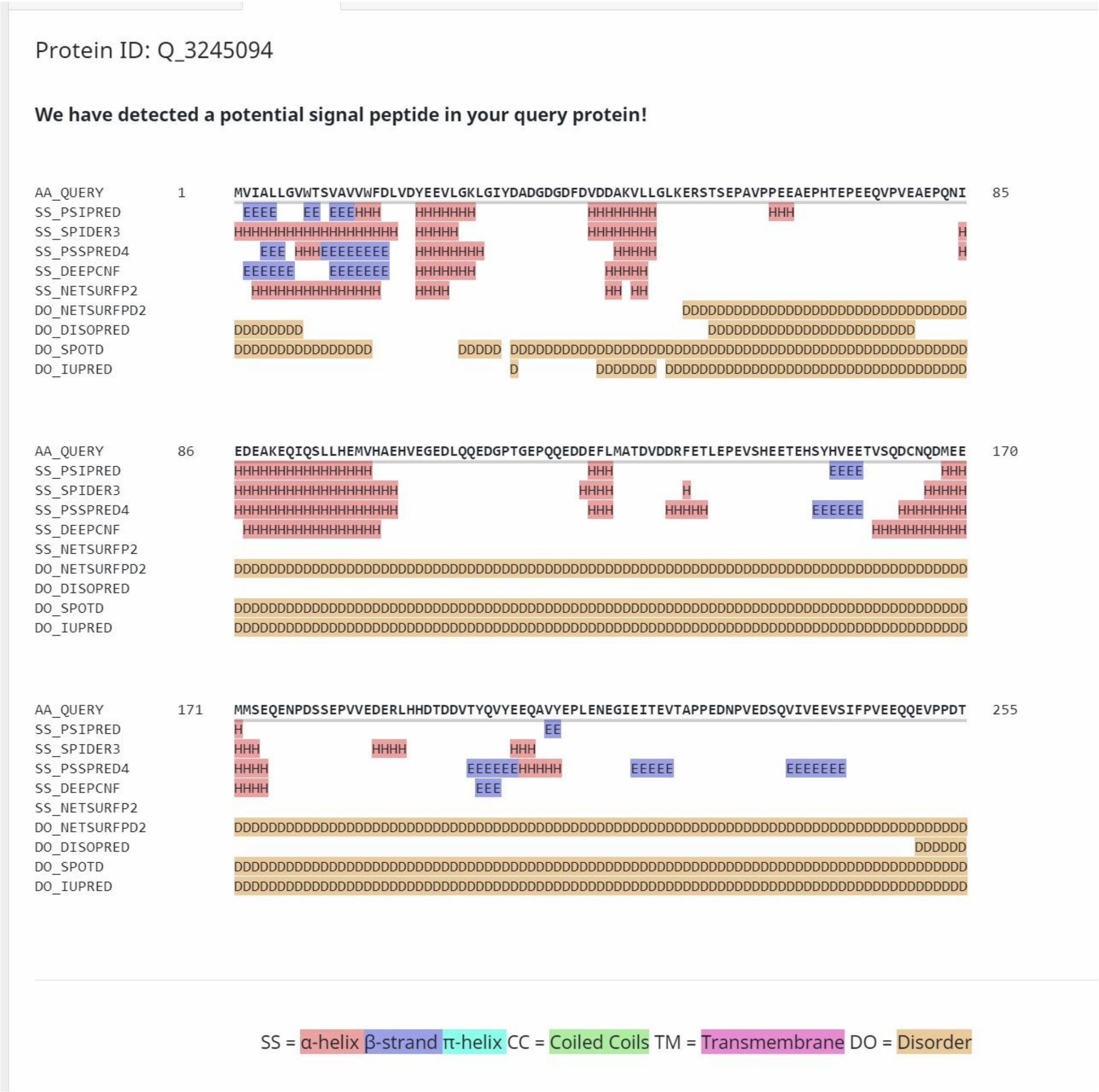

Blast e-value: 3.0E-11
14  >gi|7141075|gb|AAF37204.1| cardiac junctin [Oryctolagus cunic
match: ~~~~LLGVWTSVAVVWFELVDYEEVL---------------GKLGVYDADGDGDFDVDDAKALLEEPG----------
GVAKRKT~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
query: ~~~~~~~~~~~~~~~~~~~~DYEEVL---------------GKLGIYDADGDGDFDVDDAKVLL--------------
GLKERSTSEPAVPPEE-
AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSY
HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIF
PVEEQQEVPPET
```

Protein ID: Q_3245094

Quick2D

**Welcome to the Bioinformatics Toolkit
of the Max Planck Institute for Developmental Biology, Tübingen, Germany**

We have detected a potential signal peptide in your query protein!



Protein ID: Q_3245094

We have detected a potential signal peptide in your query protein!

```
AA_QUERY        1       MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNI   85
SS_PSIPRED               EEEE   EE EEEHHH    HHHHHHH             HHHHHHHH             HHH
SS_SPIDER3              HHHHHHHHHHHHHHHHHHH  HHHHH               HHHHHHHH                                   H
SS_PSSPRED4                EEE HHHEEEEEEEE   HHHHHHHH               HHHHH                                   H
SS_DEEPCNF               EEEEEE    EEEEEEE   HHHHHHH               HHHHH
SS_NETSURFP2              HHHHHHHHHHHHHHH    HHHH                  HH HH
DO_NETSURFPD2                                                               DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DO_DISOPRED             DDDDDDDD                                               DDDDDDDDDDDDDDDDDDDDDDDD
DO_SPOTD                DDDDDDDDDDDDDDDD          DDDDD DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DO_IUPRED                                               D         DDDDDDD DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

AA_QUERY        86      EDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEE   170
SS_PSIPRED              HHHHHHHHHHHHHHHH                         HHH                         EEEE         HHH
SS_SPIDER3              HHHHHHHHHHHHHHHHHHH                     HHHH        H                           HHHHH
SS_PSSPRED4             HHHHHHHHHHHHHHHHHHH                      HHH      HHHHH            EEEEEE    HHHHHHHH
SS_DEEPCNF               HHHHHHHHHHHHHHHH                                                         HHHHHHHHHHH
SS_NETSURFP2
DO_NETSURFPD2           DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DO_DISOPRED
DO_SPOTD                DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DO_IUPRED               DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

AA_QUERY        171     MMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPDT   255
SS_PSIPRED              H                                   EE
SS_SPIDER3              HHH             HHHH            HHH
SS_PSSPRED4             HHHH                       EEEEEEHHHHH        EEEEE             EEEEEEE
SS_DEEPCNF              HHHH                        EEE
SS_NETSURFP2
DO_NETSURFPD2           DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DO_DISOPRED                                                                                            DDDDDD
DO_SPOTD                DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DO_IUPRED               DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```

SS = α-helix β-strand π-helix CC = Coiled Coils TM = Transmembrane DO = Disorder

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If you use **Quick2D** on our Toolkit for your research, please cite as appropriate:
A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core.
Zimmermann L, Stephens A, Nam SZ, Rau D, Kübler J, Lozajic M, Gabler F, Söding J, Lupas AN, Alva V. J Mol Biol. 2018 Jul 20. S0022-2836(17)30587-9.

Protein Sequence Analysis Using the MPI Bioinformatics Toolkit.

Gabler F, Nam SZ, Till S, Mirdita M, Steinegger M, Söding J, Lupas AN, Alva V. Curr Protoc Bioinformatics. 2020 Dec;72(1):e108. doi: 10.1002/cpbi.108.

PSIPRED: Protein secondary structure prediction based on position-specific scoring matrices.
Jones DT. J Mol Biol. 1999 Sep 17;292(2):195-202.

SPIDER3: Capturing non-local interactions by long short-term memory bidirectional recurrent neural networks for improving prediction of protein secondary structure, backbone angles, contact numbers and solvent accessibility.
Heffernan R, Yang Y, Paliwal K, Zhou Y. Bioinformatics. 2017 Sep 15;33(18):2842-2849.

PSSPred: A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction.
Yan R, Xu D, Yang J, Walker S, Zhang Y. Sci Rep. 2013;3:2619.

DeepCNF-SS: Protein Secondary Structure Prediction Using Deep Convolutional Neural Fields.
Wang S, Peng J, Ma J, Xu J. Sci Rep. 2016 Jan 11;6:18962.

NetSurfP2: NetSurfP-2.0: Improved prediction of protein structural features by integrated deep learning.
Klausen et al. Proteins. 2019 Jun;87(6):520-527.

COILS: Predicting coiled coils from protein sequences.
Lupas A, Van Dyke M, Stock J. Science. 1991 May 24;252(5009):1162-4.

PCOILS: Comparative analysis of coiled-coil prediction methods.
Gruber M, Söding J, Lupas AN. J Struct Biol. 2006 Aug;155(2):140-5.

MARCOIL: An HMM model for coiled-coil domains and a comparison with PSSM-based predictions.
Delorenzi M, Speed T. Bioinformatics. 2002 Apr;18(4):617-25.

TMHMM: Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes.
Krogh A, Larsson B, von Heijne G, Sonnhammer EL. J Mol Biol. 2001 Jan 19;305(3):567-80.

Phobius: A combined transmembrane topology and signal peptide prediction method.
Käll L, Krogh A, Sonnhammer EL. J Mol Biol. 2004 May 14;338(5):1027-36.

PolyPhobius: An HMM posterior decoder for sequence feature prediction that includes homology information.
Käll L, Krogh A, Sonnhammer EL. Bioinformatics. 2005 Jun;21.

DISOPRED3: precise disordered region predictions with annotated protein-binding activity.
Jones DT, Cozzetto D. Bioinformatics. 2015 Mar 15;31(6):857-63.

SPOT-Disorder: Improving protein disorder prediction by deep bidirectional long short-term memory recurrent neural networks.
Hanson J, Yang Y, Paliwal K, Zhou Y. Bioinformatics. 2017 Mar 1;33(5):685-692.

IUPred: The pairwise energy content estimated from amino acid composition discriminates between folded and intrinsically unstructured proteins.
Dosztányi Z, Csizmók V, Tompa P, Simon I. J Mol Biol. 2005 Apr 8;347(4):827-39.

SignalP: SignalP 5.0 improves signal peptide predictions using deep neural networks.
Almagro Armenteros et al. Nat Biotechnol. 2019 Apr;37(4):420-423.

McIlhinney R.A.J. (1998) Membrane Targeting via Protein N-Myristoylation. In: Clegg R.A. (eds) Protein Targeting Protocols. Methods in Molecular Biology™, vol 88. Humana Press. https://doi.org/10.1385/0-89603-487-9:211

https://www.sciencedirect.com/science/article/pii/S007668790027287X

Targeting proteins to plasma membrane and membrane microdomains by N-terminal myristoylation and palmitoylation
Author links open overlay panel WouterVan't HofMarilyn D.Resh
Methods in Enzymology
Volume 327, 2000, Pages 317-330

Labyrinthin

found: 9 hits in 1 sequence

USERSEQ1 (255 aa)

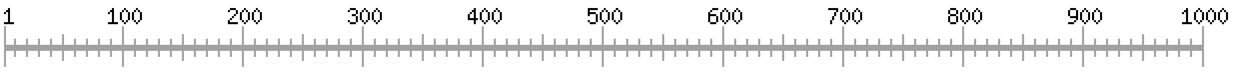
```
MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVPPEEA
EPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMAT
DVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVT
YQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPDT
```

Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function.
For more information about how these graphical representations are constructed, go to https://prosite.expasy.org/mydomains/.

hits by profiles with a high probability of occurrence: [1 hit (by 1 profile) on 1 sequence]

Upper case represents match positions, lower case insert positions, and the '-' symbol represents deletions relative to the matching profile.

ruler:



USERSEQ1

(255 aa)

[PS50313](https://prosite.expasy.org/PS50313) GLU_RICH Glutamic acid-rich region profile :

53 - 250: **score** = 12.256

```
Erstsepavppeeaephtepeeqvpveaepqniedeakeqiqsllhemvhaehvegedlq
qedgptgepqqeddeflmatdvddrfetlepevsheetehsyhveetvsqdcnqdmeemm
seqenpdssepvvederlhhdtddvtyqvyeeqavyeplenegieitevtappednpved
sqviveevsifpveeqqE
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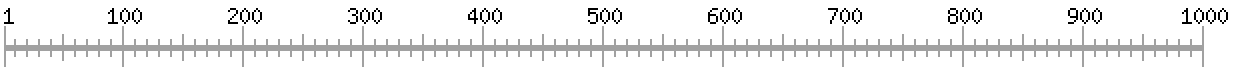
hits by patterns with a high probability of occurrence or by user-defined patterns: [8 hits (by 2 distinct patterns) on 1 sequence]

ruler:



USERSEQ1 (255 aa)

PS00008 MYRISTYL N-myristoylation site :
7 - 12: GVwtSV
30 - 35: GIydAD
215 - 220: GIeiTE
PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site :
55 - 58: StsE

Predicted feature:

MOD_RES 55 Phosphoserine [condition: S]
70 - 73: TepE

Predicted feature:

MOD_RES 70 Phosphothreonine [condition: T]
132 - 135: TdvD

Predicted feature:

MOD_RES 132 Phosphothreonine [condition: T]
146 - 149: SheE

Predicted feature:

MOD_RES 146 Phosphoserine [condition: S]
173 - 176: SeqE

Predicted feature:

MOD_RES 173 Phosphoserine [condition: S]