



(/#/)

HHpred

JobID: 2700928 Created: Aug 4, 2017 1:24 AM

ID	Date	Tool
2700928		HHPR
3119767		HHPR
6199860		HHPR
8817073		HHPR
3704600		HHPR
9605646		HHPR
7985539		HHPR
8544793		HHPR
9823795		HHPR
8928703		HHPR
1479409		HHPR
7015139		HHPR

Input Parameters Results (/api/job/result/2700928/hhpred/Results)

Raw Output (/api/job/result/2700928/hhpred/Raw Output)

Probability Plot (/api/job/result/2700928/hhpred/Probability Plot)

Query Template MSA (/api/job/result/2700928/hhpred/Query Template MSA)

Query MSA (/api/job/result/2700928/hhpred/Query MSA)



Vis Hits Aln | Select all Forward Forward Query A3M

Number of hits: 33

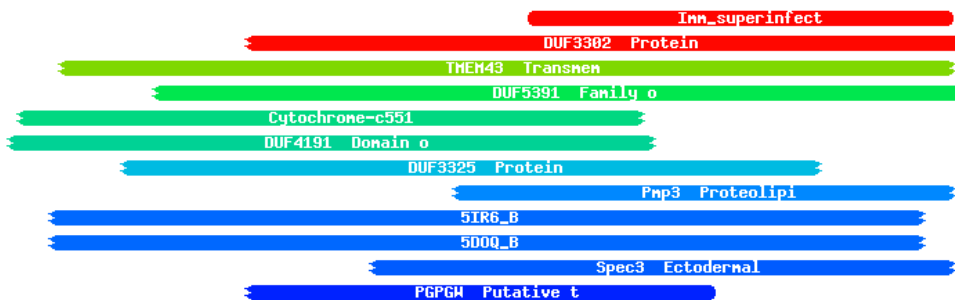
We have detected 3 transmembrane helices in your query protein!

Visualization

Resubmit section

62

103



Hitlist

Show 25 entries

Nr	Hit	Name	Probability	E
1	PF14373.5	; Imm_superinfect ; Superinfection immunity protein	99.64	1

Nr	Hit	Name	Probability	E
<input type="checkbox"/> <u>2</u>	PF11742.7 (http://pfam.xfam.org/family/PF11742.7#tabview=tab0)	; DUF3302 ; Protein of unknown function (DUF3302)	99.42	7
<input type="checkbox"/> <u>3</u>	PF07787.11 (http://pfam.xfam.org/family/PF07787.11#tabview=tab0)	; TMEM43 ; Transmembrane protein 43	77.53	5
<input type="checkbox"/> <u>4</u>	PF17369.1 (http://pfam.xfam.org/family/PF17369.1#tabview=tab0)	; DUF5391 ; Family of unknown function (DUF5391)	65.42	1
<input type="checkbox"/> <u>5</u>	PF10643.8 (http://pfam.xfam.org/family/PF10643.8#tabview=tab0)	; Cytochrome-c551 ; Photosystem P840 reaction-centre cytochrome c-551	62.41	1
<input type="checkbox"/> <u>6</u>	PF13829.5 (http://pfam.xfam.org/family/PF13829.5#tabview=tab0)	; DUF4191 ; Domain of unknown function (DUF4191)	61.23	1
<input type="checkbox"/> <u>7</u>	PF11804.7 (http://pfam.xfam.org/family/PF11804.7#tabview=tab0)	; DUF3325 ; Protein of unknown function (DUF3325)	56.72	1
<input type="checkbox"/> <u>8</u>	PF01679.16 (http://pfam.xfam.org/family/PF01679.16#tabview=tab0)	; Pmp3 ; Proteolipid membrane potential modulator	51.54	1
<input type="checkbox"/> <u>9</u>	5IR6 B (http://pdb.rcsb.org/pdb/explore.do?structureId=5IR6)	Bd-type quinol oxidase subunit I; bd oxidase, terminal oxidase, oxidoreductase; HET: HDD, HEB; 3.8A {Geobacillus stearothermophilus K1041}	48.83	4
<input type="checkbox"/> <u>10</u>	5DOQ B (http://pdb.rcsb.org/pdb/explore.do?structureId=5DOQ)	Bd-type quinol oxidase subunit I; bd oxidase, terminal oxidase, oxidoreductase; HET: HDD, HEB; 3.05A {Geobacillus thermodenitrificans (strain NG80-2)}	48.83	4
<input type="checkbox"/> <u>11</u>	PF15795.4 (http://pfam.xfam.org/family/PF15795.4#tabview=tab0)	; Spec3 ; Ectodermal ciliogenesis protein	47.74	2
<input type="checkbox"/> <u>12</u>	PF09656.9 (http://pfam.xfam.org/family/PF09656.9#tabview=tab0)	; PGPGW ; Putative transmembrane protein (PGPGW)	42.93	1
<input type="checkbox"/> <u>13</u>	PF13198.5 (http://pfam.xfam.org/family/PF13198.5#tabview=tab0)	; DUF4014 ; Protein of unknown function (DUF4014)	33.16	3

Nr	Hit	Name	Probability	E
<input type="checkbox"/> 14	PF05656.13 (http://pfam.xfam.org/family/PF05656.13#tabview=tab0)	; DUF805 ; Protein of unknown function (DUF805)	32.31	4
<input type="checkbox"/> 15	PF06305.10 (http://pfam.xfam.org/family/PF06305.10#tabview=tab0)	; LapA_dom ; Lipopolysaccharide assembly protein A domain	31.71	3
<input type="checkbox"/> 16	PF14256.5 (http://pfam.xfam.org/family/PF14256.5#tabview=tab0)	; YwiC ; YwiC-like protein	31.26	5
<input type="checkbox"/> 17	TIGR00947 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR00947)	2A73; putative bicarbonate transporter, IctB family. This family of proteins is suggested to transport inorganic carbon (HCO ₃ ⁻), based on the phenotype of a mutant of IctB in <i>Synechococcus</i> sp.	30.94	7
<input type="checkbox"/> 18	3HD7 F (http://pdb.rcsb.org/pdb/explore.do?structureId=3HD7)	Vesicle-associated membrane protein 2, Syntaxin-1A; MEMBRANE PROTEIN, COILED-COIL, 4-HELICAL BUNDLE; HET: SO4, GGG; 3.4A { <i>Rattus norvegicus</i> }	30.28	4
<input type="checkbox"/> 19	2M8R A (http://pdb.rcsb.org/pdb/explore.do?structureId=2M8R)	Syntaxin-1A; syntaxin, SNARE, Prefusion, membrane protein; NMR { <i>Rattus norvegicus</i> }	30.28	4
<input type="checkbox"/> 20	PF12273.7 (http://pfam.xfam.org/family/PF12273.7#tabview=tab0)	; RCR ; Chitin synthesis regulation, resistance to Congo red	30.19	1
<input type="checkbox"/> 21	PF04505.11 (http://pfam.xfam.org/family/PF04505.11#tabview=tab0)	; CD225 ; Interferon-induced transmembrane protein	28.34	1
<input type="checkbox"/> 22	PF05084.12 (http://pfam.xfam.org/family/PF05084.12#tabview=tab0)	; GRA6 ; Granule antigen protein (GRA6)	28.27	2

Nr	Hit	Name	Probability	
<input type="checkbox"/> 23	TIGR03750 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03750)	conj_TIGR03750; conjugative transfer region protein, TIGR03750 family. Members of this protein family are found occasionally on plasmids.	26.61	7
<input type="checkbox"/> 24	PF06789.11 (http://pfam.xfam.org/family/PF06789.11#tabview=tab0)	; UPF0258 ; Uncharacterised protein family (UPF0258)	26.29	4
<input type="checkbox"/> 25	PF12263.7 (http://pfam.xfam.org/family/PF12263.7#tabview=tab0)	; DUF3611 ; Protein of unknown function (DUF3611)	26.22	9

Showing 1 to 25 of 33 entries

Previous 1 2 [Next](#)



Alignments

1. [Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam14373\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam14373)
[PF14373.5 \(http://pfam.xfam.org/family/PF14373.5#tabview=tab0\)](http://pfam.xfam.org/family/PF14373.5#tabview=tab0) ; **Imm_superinfect** ; **Superinfection imm**
Probability: 99.64 E-value: 1.1E-18 Score: 108.42 Aligned Cols: 42 Identities: 36% Similarity: 0.

```

Q ss_pred          HHHHHHHHHHcCCCCHHHHHHHHHHHHHHHHHHHHHHHHH
Q Q_2700928      62  AYFVPTIVAYYRKASLKQPVAVINVFLGWTFIGWVVALAMAV 103 (104)
Q Consensus       62  YFFLPtIIA~R~h~I~1L1N1~1GWTvIGWv~ALIWA~    103 (104)
                  +|+|+++|..|+|+++..|+++|+++| |++| |++|++|+
T Consensus        1  Yf1P~iiA~r~h~I~1N1~1GWT~igW~aliwA~    42 (42)
T PF14373.5       1  FYFVPSLLAWTRKHSRSLPAIIALNILLGWTGLGWIGAFVWSL 42 (42)
T ss_pred          CCcHHHHHHHHcCCCCHHHHHHHHHHHHHHHHHHHHHHHH

```

2. [Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam11742\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam11742)
[PF11742.7 \(http://pfam.xfam.org/family/PF11742.7#tabview=tab0\)](http://pfam.xfam.org/family/PF11742.7#tabview=tab0) ; **DUF3302** ; **Protein of unknown function**
Probability: 99.42 E-value: 7.5E-15 Score: 100.47 Aligned Cols: 62 Identities: 16% Similarity: 0.

```

Q ss_pred          HHHHHHHHHHhccChhHHHHHHHHHHHHHHHHHHHHcCCCCHHHHHHHHHHHHH -HHHHHHHHH
Q Q_2700928      35  LALGAIVALIVLMSISPGHALLVVFGTAYFVPTIVAYYRKASLKQPVAVINVFLGWT-FIGWVVALAM
Q Consensus       35  ~L~i~p~g~L~v~i~l~YFFLPtIIA~R~h~I~1L1N1~1GWT-vIGWv~ALIWA
                  +++..+++..+++..          +..+..+|+|+++|..|+|+++..|+++|+++| | | ++| |++|++|
T Consensus        4  ~~~~~~-----~ly~lP~iA~r~h~aI~1n1l~gwt~igWv~AliW
T PF11742.7       4  FALGLLIFVALVI-----FYGIIVIHDIPEIAKERDHPHQDAIHVSGWVSLFTLHAIWPFLLIWA
T ss_pred          HHHHHHHHHHHH-----HHHHHHHHHHHHHHHHHHcCCCcHHHHHHHHHHHHHHHHHHHH

```



```

Q ss_pred          C
Q Q_2700928      104  K 104 (104)
Q Consensus       104  ~ 104 (104)
                  +
T Consensus        66  ~ 66 (77)

```



```
Q ss_pred          CCHHHHHHHHHHHHHHHHHHHHHHH
Q Q_2700928       76 SLKQPVAVINFLGWTFIGWVVALA 100 (104)
Q Consensus       76 ~~~~I~l1N1~lGWTvIGWv~ALI 100 (104)
                   +...-...-+...-.+.|+..+.
T Consensus      257 ~~~af~s~y 281 (342)
T 5IR6_B         257 RFGWAFIALLFQYAFAYGISHY 281 (342)
T ss_dssp         CTHHHHHHHHHHHHHHHHHHHHHHC
T ss_pred         cchHHHHHHHHHHHHHHHHHHHh
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5dog\)](#)

10. [5DOQ_B \(http://pdb.rcsb.org/pdb/explore.do?structureId=5DOQ\)](http://pdb.rcsb.org/pdb/explore.do?structureId=5DOQ) **Bd-type quinol oxidase subunit I; bd oxidase, oxidoreductase; HET: HDD, HEB; 3.05A {Geobacillus thermodenitrificans (strain NG80-2)}**
Probability: 48.83 E-value: 420.0 Score: 23.42 Aligned Cols: 83 Identities: 12% Similarity: 0.07

```
Q ss_pred          chhhhhhhhhhccHHHHHHHHHHHHhccC-----hHHHHHHHHHHHHHHHHHHc
Q Q_2700928       16 PQADAAARAARKGRIEGLALGAIVALIVLMSIS-----PGHALLVVFGTAYFVPTIVAYYR
Q Consensus       16 ~~~~~~l~i~-----pg~L~vi~l~lyfLptIIA~F
                   +..++.|.+++.....+...+..+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.|.+.+ ++.... +++...+.|
T Consensus      189 ~l~ra~a~n~l~-----~l~-----~
T 5DOQ_B         189 AGDEQARALLRRYALLWSGPTMLSALLIYQLRYHNPEHYDNLWNVAWML-VISFLF-FVITVWLLGR
T ss_dssp         SSCHHHHHHHHHHHHCCCCCHHHHHHHHHHTTSCHHHHHHHHSHHHH-HHHHHH-HHHHHHHHS
T ss_pred         cchHHHHHHHHHHHHHHHHHHHHhCCHHHhhhhhhHHHHH-HHHHHH-HHHHHHHHC
```

```
Q ss_pred          CCHHHHHHHHHHHHHHHHHHHHHHH
Q Q_2700928       76 SLKQPVAVINFLGWTFIGWVVALA 100 (104)
Q Consensus       76 ~~~~I~l1N1~lGWTvIGWv~ALI 100 (104)
                   +...-...-+...-.+.|+..+.
T Consensus      257 ~~~af~s~y 281 (342)
T 5DOQ_B         257 RFGWAFIALLFQYAFAYGISHY 281 (342)
T ss_dssp         CTHHHHHHHHHHHHHHHHHHHHHHC
T ss_pred         cchHHHHHHHHHHHHHHHHHHHh
```

[Template alignment](#) | [CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam15795\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam15795)

11. [PF15795.4 \(http://pfam.xfam.org/family/PF15795.4#tabview=tab0\)](http://pfam.xfam.org/family/PF15795.4#tabview=tab0); **Spec3; Ectodermal ciliogenesis protein**
Probability: 47.74 E-value: 260.0 Score: 21.05 Aligned Cols: 57 Identities: 16% Similarity: 0.125

```
Q ss_pred          hccChhhhhhhhhHHHHHHHHHHHH-----HcCCCCHHHHHHHH-----HHHHHHHH
Q Q_2700928       47 MSISPGHALLVVFGTAYFVPTIVAY-----YRKASLKQPVAVINV-----FLGWTFIGWV
Q Consensus       47 ~i~pg~L~vi~l~lyfLptIIA~-----~R~h~I~l1N1-----~lGWTvIGWv
                   +|..-...++=+++---+=|+++...+++++..+.+|+ ..+.++||+
T Consensus       6 1p~a~c~ilNi~PG~GTiisg~C~-----~vG~lQl~t~lVgWi
T PF15795.4      6 LPMWLAIICCIFNFIIPGSGTIISGLSLLCHEVKKKKDRFRKLKQCLINVSQVIQFACIVFCLIGWF
T ss_pred         cchHHHHHHHHHHHcchHHHHHHHHHHhcccCccccchHHHHHHHHHHHHHHHHHHHH
```

```
Q ss_pred          HHHHh
Q Q_2700928       99 LAMAV 103 (104)
Q Consensus       99 LIWA~ 103 (104)
                   .+|.+.
T Consensus      76 I~WGi 80 (86)
T PF15795.4     76 IIWGT 80 (86)
T ss_pred         HHHHH
```

[Template alignment](#) | [CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam09656\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam09656)

16. [Template alignment | CDD \(<http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam14256>\) PF14256.5 \(<http://pfam.xfam.org/family/PF14256.5#tabview=tab0>\)](#) ; **YwiC ; YwiC-like protein**
Probability: 31.26 E-value: 530.0 Score: 20.04 Aligned Cols: 60 Identities: 8% Similarity: 0.004

```
Q ss_pred           HHHHHHHHhccccHHHHHHHHHHHHHHHHHHHHcCchHHHHHHHHHHHHHHHHHHHHhCCCCCh
Q Q_2700928       20 AAARAAKRKGRIEGWLALGAIVALIVLMSISPGHALLVVFGTAYFVPTIVAYYRKASLKQ 79 (10)
Q Consensus       20 ~~~~~l~~~~~i~pg~L~vi~l~LYFLPtIIA~R~h~ 79 (10)
                    |.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus       50 k~~~~~Y~ia~~~~~l~~~~p~l~~~~~l~~~~~a~~~~r~eRsl~ 109 (1)
T PF14256.5       50 KTKRNDPYVPAARYGAIIVVGLVSLWQPALFYFGLAMTPFFLVNTYYSKKKNERAFW 109 (1)
T ss_pred         hcCCCCchHHHHHHHHHHHHHHHHHHHHhCCchHHHHHHHHHHHHHHHHHHHHhCCchHH
```

17. [Template alignment](#) TIGR00947 (<http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR00947>) **2A73; putative bicarbo IctB family. This family of proteins is suggested to transport inorganic carbon (HCO3-), based on the phenoc of IctB in Synechococcus sp.**
Probability: 30.94 E-value: 700.0 Score: 20.59 Aligned Cols: 74 Identities: 15% Similarity: 0.09

```
Q ss_pred           HHHHHhccccHHHHHHHHHHHHHHHHHHHHcCchHHHHHHHHHHHHHHHHHHHHhCCCCCh--HHHHHHHHH
Q Q_2700928       23 RAAKRKGRIEGWLALGAIVALIVLMSISPGHALLVVFGTAYFVPTIVAYYRKASLK--QPVAVINVFL
Q Consensus       23 ~~~~~l~~~~~i~pg~L~vi~l~LYFLPtIIA~R~h~-----I~l~l~l~l~l~
                    |..+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus       9  ~~~~~l~~~~~p~~~~~
T TIGR00947       9  RASSWLLQWLEPLAGGLALLLVLPAFVSTTGLGLVLAACGALWLLLTLDVDPQKRLTPIHLLVLLYk
T ss_pred         cccHHHHHHHHHHHHHHHHHHHHhcccCchHHHHHHHHHHHHHHHHHHhCCCCCHHHHHHHHHH

Q ss_pred           HHHHHH
Q Q_2700928       91 TFIGWV 96 (104)
Q Consensus       91 TvIGWv 96 (104)
                    .+.+.+
T Consensus       79 ~~is~ 84 (425)
T TIGR00947       79 AALATG 84 (425)
T ss_pred         HHHHHH
```

18. [Template alignment | Template 3D structure | PDBe \(<http://www.ebi.ac.uk/pdbe/entry/pdb/3hd7>\) 3HD7 F \(<http://pdb.rcsb.org/pdb/explore.do?structureId=3HD7>\) Vesicle-associated membrane protein 2, S1 MEMBRANE PROTEIN, COILED-COIL, 4-HELICAL BUNDLE; HET: SO4, GGG; 3.4A {Rattus norvegicus}](#)
Probability: 30.28 E-value: 430.0 Score: 17.99 Aligned Cols: 31 Identities: 10% Similarity: 0.187

```
Q ss_pred           hHHHHHHHHhccccHHHHHHHHHHHHHHHH
Q Q_2700928       17 QADAAARAARKGRIEGWLALGAIVALIVLM 47 (104)
Q Consensus       17 ~~~~~l~~~~~ 47 (104)
                    ..+++..+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus       71 ~l~a~ 101 (109)
T 3HD7_F         71 DTKKAVKYQSKARRKKIMIIICCVILGIIIA 101 (109)
T ss_dssp         HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
T ss_pred         HHHHHHHHHhHHHHHHHHHHHHHHHHHHHHH
```

19. [Template alignment | Template 3D structure | PDBe \(<http://www.ebi.ac.uk/pdbe/entry/pdb/2m8r>\) 2M8R A \(<http://pdb.rcsb.org/pdb/explore.do?structureId=2M8R>\) Syntaxin-1A; syntaxin, SNARE, Prefusion, NMR {Rattus norvegicus}](#)

Probability: 30.28 E-value: 430.0 Score: 17.99 Aligned Cols: 31 Identities: 10% Similarity: 0.187

```

Q ss_pred          hHHHHHHHHHHhcHHHHHHHHHHHHHHHH
Q Q_2700928      17  QADAAARAARKRGRIEGLALGAIIVALIVLM 47 (104)
Q Consensus       17  ~~~~~~l~~~~~ 47 (104)
                  . . + + . + . . + + . . - + . + + + + . + + + .
T Consensus       71  ~l~a~~~~~i~~~~~ 101 (109)
T 2M8R_A          71  DTKKAVKYQSKARRKIMIIICCVILGIIIA 101 (109)
T ss_dssp         HHTCSCCSSTHHHHHHHHHHHHHHHHHH
T ss_pred         HHHHHHHHHHHHHHHHHHHHHHHHHHHHH

```

20. [Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam12273\)](#)
PF12273.7 (http://pfam.xfam.org/family/PF12273.7#tabview=tab0); RCR; Chitin synthesis regulation, resis
 Probability: 30.19 E-value: 140.0 Score: 23.86 Aligned Cols: 29 Identities: 7% Similarity: -0.032

```

Q ss_pred          HHHHHHHHHHHHHHHHHHHcCCCHHH
Q Q_2700928      52  GHALLVVFGTAYFVPTIVAYYRKASLKQP 80 (104)
Q Consensus       52  g~L~vi~l~YFLPtIIA~R~h~~~~~ 80 (104)
                  . | + + . + + + + . + + + + . + + . + + + + . +
T Consensus        1  RWvL~viI~l~l~l~l~l~aRRRrrr 29 (133)
T PF12273.7       1  RWIVLGVLLLVLLVAFSCSCLARRRRR 29 (133)
T ss_pred         ChHHHHHHHHHHHHHHHHHHHHHHHHHH

```

21. [Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam04505\)](#)
PF04505.11 (http://pfam.xfam.org/family/PF04505.11#tabview=tab0); CD225; Interferon-induced transmem
 Probability: 28.34 E-value: 130.0 Score: 19.92 Aligned Cols: 37 Identities: 22% Similarity: -0.00

```

Q ss_pred          cCCCCCCCCchHHHHHHHHHHhcHHHHHHHHHH
Q Q_2700928      6   DQPAYQPGYYPQADAAARAARKRGRIEGLALGAIIVA 42 (104)
Q Consensus       6   ~~~~~~l~~~~~ 42 (104)
                  . + . | . + . + . + + + . + + | . - . - . + + + . + + .
T Consensus       31  ~~~~~g~~~~a~~~~a~~~~i~~~~i~~~~i~ 67 (68)
T PF04505.11     31  SRDRKMVGDVIGAQAFAFIKLNISALTIQLLVLA 67 (68)
T ss_pred         HHHHHHhCCHHHHHHHHHHHHHHHHHHHHHHH

```

22. [Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam05084\)](#)
PF05084.12 (http://pfam.xfam.org/family/PF05084.12#tabview=tab0); GRA6; Granule antigen protein (GRA
 Probability: 28.27 E-value: 240.0 Score: 24.79 Aligned Cols: 42 Identities: 21% Similarity: 0.381

```

Q ss_pred          cCCCCCCCCchHHHHHHHHHHhcHHHHHHHHHHHH
Q Q_2700928      6   DQPAYQPGYYPQADAAARAARKRGRIEGLALGAIIVALIVLM 47 (104)
Q Consensus       6   ~~~~~~l~~~~~ 47 (104)
                  | . | . + + . | | + . - . + . + . . | + . | - . | . + . + + + . .
T Consensus      128  ~~~rp~~Vqe~~kv~sKR~Q~RHRlIGa~VlAa~VA~L~ 169 (215)
T PF05084.12    128  TRRRYSVQEPQAKVPSKRTQKRHLIGAVVLAVSVAMLTAF 169 (215)
T ss_pred        cCCCCCCCCCCCCchHHHHHHHHHHHHHHHHHHHHHH

```

23. [Template alignment](#)
TIGR03750 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03750) conj_TIGR03750; conjuc
 region protein, TIGR03750 family. Members of this protein family are found occasionally on plasmids.
 Probability: 26.61 E-value: 700.0 Score: 19.2 Aligned Cols: 43 Identities: 23% Similarity: 0.258

```

Q ss_pred          HHHHHHHHHHHHH - ccChHHHHHHHHHHHHHHHHHHHHHHcCCC

```



References

If you use our HHpred server for your research, please cite:

The MPI bioinformatics Toolkit as an integrative platform for advanced protein sequence and structure analysis.

Alva V, Nam SZ, Söding J, Lupas AN. *Nucleic Acids Res.* 2016 Jul 8;44(W1):W410-5

([//academic.oup.com/nar/article-lookup/doi/10.1093/nar/gkw348](http://academic.oup.com/nar/article-lookup/doi/10.1093/nar/gkw348)).

And one or more of the following:

Protein homology detection by HMM-HMM comparison.

Söding J. *Bioinformatics.* 2005 Apr 1;21(7):951-60 ([//academic.oup.com/bioinformatics/article-lookup/doi/10.1093/bioinformatics/bti125](http://academic.oup.com/bioinformatics/article-lookup/doi/10.1093/bioinformatics/bti125)),

Fast and accurate automatic structure prediction with HHpred.

Hildebrand A, Remmert M, Biegert A, Söding J. *Proteins.* 2009;77 Suppl 9:128-32

([//onlinelibrary.wiley.com/doi/10.1002/prot.22499/abstract;jsessionid=6FF63B8F61E35391B79F4681BB12DB2C.f02t04](http://onlinelibrary.wiley.com/doi/10.1002/prot.22499/abstract;jsessionid=6FF63B8F61E35391B79F4681BB12DB2C.f02t04))

Automatic Prediction of Protein 3D Structures by Probabilistic Multi-template Homology Modeling.

Meier A, Söding J. *PLoS Comput Biol.* 2015 Oct 23;11(10):e1004343

([//journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004343](http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004343)).