MPI
Bioinformatics
Toolkit

HHpred

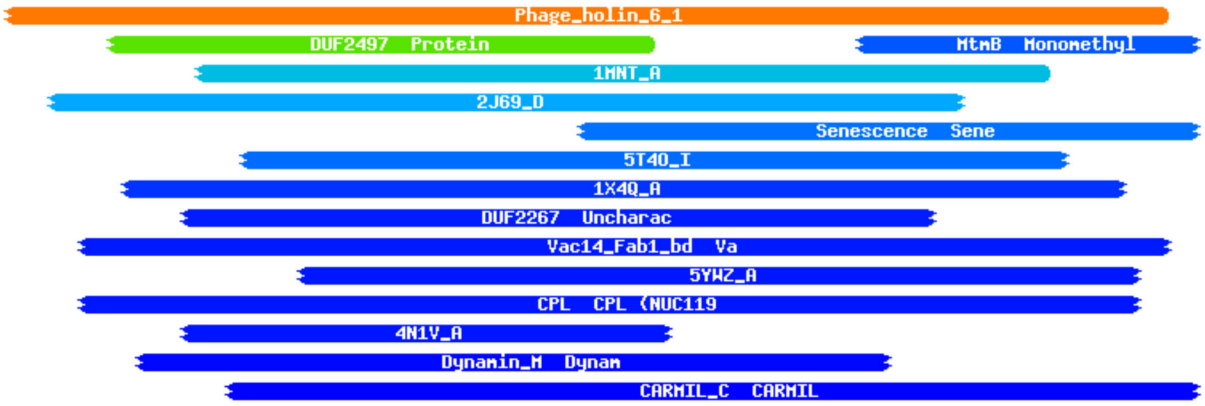
JobID: Zet_3980 Created: Nov 20, 2018 1:59 P

Results

Note: your query alignment consists of only 13 sequence(s). You could improve the sensitivity of your search vastly by building a larger query alignment either with HHblits over Uniclust30 or with PSI-BLAST over nre70. You could also consider increasing the number of MSA generation iterations and/or relaxing the inclusion threshold.

Number of hits:

Visualization



Hitlist

Show 25 entries Search:

Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
1	PF09682.10	; Phage_holin_6_1 ; Bacteriophage holin of superfamily 6 (Holin_LLH)	89.9	6.6	7.6	79	101
2	PF10691.9	; DUF2497 ; Protein of unknown function (DUF2497)	75.2	42	5.7	38	74
3	1MNT_A	MNT REPRESSOR MUTANT WITH C-TERMINAL; TRANSCRIPTION REGULATION; NMR {Enterobacteria phage P22} SCOP: a.43.1.1	56.67	30	2	59	76
4	2J69_D	BACTERIAL DYNAMIN-LIKE PROTEIN; DYNAMIN, FZO, FZL, GTPASE, HYDROLASE; 3.0A {NOSTOC PUNCTIFORME}	54.19	82	4.8	59	695
5	PF06911.12	; Senescence ; Senescence-associated protein	49.63	85	3.5	43	179
6	5T4O_I	ATP synthase subunit alpha (E.C.3.6.3.14); ATP synthase, ATPase, rotary motor; HET: ATP, ADP; 6.9A {Escherichia coli}	49.02	200	5.2	57	155
7	PF05369.12	; MtmB ; Monomethylamine methyltransferase MtmB	47.26	67	3	24	451
8	1X4Q_A	U4/U6 small nuclear ribonucleoprotein Prp3; PWI domain, Structural Genomics, NPPSFA; NMR {Homo sapiens}	44.27	210	5.5	66	92
9	PF10025.9	; DUF2267 ; Uncharacterized conserved protein (DUF2267)	42.38	230	4.4	49	118
10	PF12755.7	; Vac14_Fab1_bd ; Vacuolar 14 Fab1-binding region	42.24	170	4.7	74	95
11	5YWZ_A	SUN domain-containing protein 1; LINC complex SUN proteins; 2.2A {Mus musculus}	41.88	370	6.8	58	242
12	PF08144.11	; CPL ; CPL (NUC119) domain	41.86	310	5.6	73	138
13	4N1V_A	DNA-binding protein HU-beta; DNA Binding, DNA BINDING PROTEIN; 1.36A {Spiroplasma melliferum} SCOP: a.55.1.0, l.1.1.1	41.76	230	5.1	34	100
14	PF01031.20	; Dynamin_M ; Dynamin central region	40.56	320	6.2	52	274
15	PF16000.5	; CARMIL_C ; CARMIL C-terminus	40.23	130	3.6	67	293
16	5ED8_A	MKIAA0668 protein; SUN domain, nuclear membrane, TRANSPORT; 2.5A {Mus musculus}	38.95	450	7.1	58	268

Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
☐ 17	PF11301.8	; DUF3103 ; Protein of unknown function (DUF3103)	38.01	140	3.5	39	352
☐ 18	PF17157.4	; GAPES4 ; Gammaproteobacterial periplasmic sensor domain	35.96	110	2.1	31	96
☐ 19	PF10667.9	; DUF2486 ; Protein of unknown function (DUF2486)	35.8	540	6.4	51	255
☐ 20	PF17150.4	; CHASE6_C ; C-terminal domain of two-partite extracellular sensor domain	35.61	350	5.2	52	87
☐ 21	1IBR_B	RAN IMPORTIN BETA SUBUNIT; SMALL GTPASE NUCLEAR TRANSPORT; HET: GNP; 2.3A {Homo sapiens} SCOP: a.118.1.1	35.52	390	4.8	75	462
☐ 22	3E8T_A	Takeout-like protein 1; Takeout, Epiphyas postvittana, TRANSPORT PROTEIN; HET: UQ8; 1.3A {Epiphyas postvittana}	34.48	420	5.1	46	220
☐ 23	3UV1_B	Der f 7 allergen; Super-roll, ALLERGEN; HET: MSE; 2.0A {Dermatophagoides farinae}	34.42	360	4.5	34	196
☐ 24	cd08054	gp6; Head-Tail Connector Protein gp6 of Bacteriophage HK97 and similar proteins. The bacteriophage HK97 gp6 protein is critical in the assembly of the connector, a specialized structure that serves as an interface for head and tail attachment, as well as a point at which DNA exits the head during infection by the bacteriophage.	34.35	240	3.3	26	91
☐ 25	d3dnua_	d.144.1.7 (A:) Multidrug tolerance (MDT) protein HipA N-terminal domain {Escherichia coli K-12 [TaxId: 83333]}	33.93	480	5.7	52	436

Showing 1 to 25 of 69 entries

Previous 1 2 3 Next

Alignments

Template alignment | CDD

☐ **1.** **PF09682.10 ; Phage_holin_6_1 ; Bacteriophage holin of superfamily 6 (Holin_LLH)**

Probability: 89.9 E-value: 6.6 Score: 26.28 Aligned Cols: 79 Identities: 18% Similarity: 0.114

```
Q ss_pred              hHHHHHHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHcchhcchhHHhhcC----------CC
Q Zetzy_3980     2     LATIAKLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYI----------PG  61 (85)
Q Consensus      2     ~~~~~~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~I----------PG  61 (85)
                       +..++..+..++.|.+.....+-.+.+..+.+..|..+ |+..++-.+|.||...++          .=
T Consensus      13    l~~~~~~~~~~~~~~lk~~~~~~~~~~i~~~A~~aV~~a-Eq~~~~~~~G~~K~~~A~~~~~~~l~~~gi  81 (101)
T PF09682.10     13    VTIILGFLGMKIKNYYNVKISFEQQKQIANIAKAAVMFV-EQVAGEHLLSDDKLSMAKHRAKVTLNQVGI  81 (101)
T ss_pred              HHHHHHHHHHHHHHHHHHcCCHHHHHHHHHHHHHHHHHH-HHHHhcCCChHHHHHHHHHHHHHHHHHcCC

Q ss_pred              CcchhhhHHHHHHHHHHHHH
Q Zetzy_3980     62    KLDDQIIDPIVKRGLEIFRD  81 (85)
Q Consensus      62    ~lDD~IiDplV~Ra~~~fr~  81 (85)
```

```
                        +++|..++.++..|...|++
T Consensus     82      ~it~~~i~~~IE~Av~~~k~  101 (101)
T PF09682.10    82      DITDEELTMWIEAFVGGLNH  101 (101)
T ss_pred               CCCHHHHHHHHHHHHHhhcC
```

Template alignment | CDD

☐ 2. **PF10691.9 ; DUF2497 ; Protein of unknown function (DUF2497)**

Probability: 75.2 E-value: 42.0 Score: 23.14 Aligned Cols: 38 Identities: 11% Similarity: 0.182

```
Q ss_pred               HHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHc
Q Zetzy_3980    9       IAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAAT  46 (85)
Q Consensus     9       i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~  46 (85)
                        +-......+.-.+++++++++|.+.+.+|..=.|.+.+
T Consensus     37      lE~lv~e~lrP~L~~WLd~nLp~iVe~~V~~EI~ri~~  74 (74)
T PF10691.9     37      IEDIVRDMLQPLLRQWLDDNLPTMIERMVQKELEKLAQ  74 (74)
T ss_pred               HHHHHHHHHHHHHHHHHHHchHHHHHHHHHHHHHHHHhC
```

Template alignment | Template 3D structure | PDBe

☐ 3. **1MNT_A MNT REPRESSOR MUTANT WITH C-TERMINAL; TRANSCRIPTION REGULATION; NMR {Enterobacteria phage P22} SCOP: a.43.1.1; Related PDB entries: 1MNT_B**

Probability: 56.67 E-value: 30.0 Score: 21.84 Aligned Cols: 59 Identities: 12% Similarity: 0.174

```
Q ss_pred               HHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHcchhc-----chhHHHhcCCCCcchhhhHHHHH
Q Zetzy_3980    15      PIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAER-----GADKLTDYIPGKLDDQIIDPIVK  73 (85)
Q Consensus     15      p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~-----gaDkiTD~IPG~lDD~IiDplV~  73 (85)
                        |.+.+.+...-..+=-.+..-+..++.+.+.....     .++++.+.+|..+...+++.|++
T Consensus     13      ~~l~~~l~~~A~~~g~S~~~~i~~~l~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  76 (76)
T 1MNT_A        13      MEVREKLKFRAEANGRSMNSELLQIVQDALSKPSPVTGYRNDAERLADEQSELVKKMVFDTLKD  76 (76)
T ss_dssp               HHHHHHHHHTHHHHTSCTHHHHHHHHHHHHHCCCCSSSCCCSHHHHHHHHHHTC----------
T ss_pred               HHHHHHHHHHHHHhCCCHHHHHHHHHHHHHhcCCCCCCcchHHHHHHHHHHHHHHHHHHHHHcC
```

Template alignment | Template 3D structure | PDBe

☐ 4. **2J69_D BACTERIAL DYNAMIN-LIKE PROTEIN; DYNAMIN, FZO, FZL, GTPASE, HYDROLASE; 3.0A {NOSTOC PUNCTIFORME}; Related PDB entries: 2J69_A 2J69_C 2W6D_A 2J69_B 2J68_A 2W6D_B**

Probability: 54.19 E-value: 82.0 Score: 28.83 Aligned Cols: 59 Identities: 19% Similarity: 0.223

```
Q ss_pred               HHHHHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHcchhcchhHHHhcCCCCcchhh
Q Zetzy_3980    5       IAKLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQI  67 (85)
Q Consensus     5       ~~~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~I  67 (85)
                        ....-+......+.+++.+++.++.|.+.......+.+++.+     ..+++-+.+-..+|+.|
T Consensus     581     ~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~i~~~v~~----~~~~~~~~~~~~~i~~~i  639 (695)
T 2J69_D        581     VGFLQADQARRELVKTAKKELVKHLPQVAHEQSQVVYNAVKE----CFDSYEREVSKRINDDI  639 (695)
T ss_dssp               TTSSCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH----HHHHHHHHHHHHHHHH
T ss_pred               HHHHHHHHHHHHHHHHHHHHHHHHcHHhhHHHHHHHHHHHHH----HHHHHHHHHHHHHHHH
```

Template alignment | CDD

☐ 5. **PF06911.12 ; Senescence ; Senescence-associated protein**

Probability: 49.63 E-value: 85.0 Score: 23.08 Aligned Cols: 43 Identities: 12% Similarity: 0.168

```
Q ss_pred               HHHHHcchhcchhHHhhcCCCCcchhhhHHHHHHHHHHHHHHc
Q Zetzy_3980    41      TEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIFRDLT  83 (85)
Q Consensus     41      ~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~fr~~~  83 (85)
                        ++.++++...+.|++...+|..-+..-++|-+++.++..|..+
T Consensus     16      a~~~~~~i~~g~~~~~~~~~p~~~P~~vsp~~~~~~~~~~~~t  58 (179)
T PF06911.12    16      SDKVSSMLQSGATAITAKSKPASKPMTFKPATHERIRRINTFT  58 (179)
T ss_pred               HHHHHHHHHHHHHHHHHcCCCCCCCCcCCHHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

☐ **6.** **5T4O_I ATP synthase subunit alpha (E.C.3.6.3.14); ATP synthase, ATPase, rotary motor; HET: ATP, ADP; 6.9A {Escherichia coli}; Related PDB entries: 5T4Q_I 5T4Q_J 5T4P_I 5T4O_J 5T4P_J**

Probability: 49.02 E-value: 200.0 Score: 20.18 Aligned Cols: 57 Identities: 19% Similarity: 0.254

```
Q ss_pred              HHHHHHHHHHHhHHHHHHHHHHHHHHHHcchhcchhHH-hhcCCCCcchhhhHHHHHH
Q Zetzy_3980     18    AKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKL-TDYIPGKLDDQIIDPIVKR  74 (85)
Q Consensus      18    ~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDki-TD~IPG~lDD~IiDplV~R  74 (85)
                       .+.+.++..+.|..-.+.....+-..+...+.+-+.++ ...++.+.+.+++|.+++.
T Consensus      97    ~~~~~~~a~~~i~~~~~~~~~~l~~~i~~~a~~~~~k~l~~~~~~~~~~~li~~~l~~  154 (155)
T 5T4O_I         97    RTKIVAQAQAEIEAERKRAREELRKQVAILAVAGAEKIIERSVDEAANSDIVDKLVAE  154 (155)
T ss_dssp              HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCSCCCCCCCCCC
T ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHcCCHHHHHHHHHHHHh
```

Template alignment | CDD

☐ **7.** **PF05369.12 ; MtmB ; Monomethylamine methyltransferase MtmB**

Probability: 47.26 E-value: 67.0 Score: 26.88 Aligned Cols: 24 Identities: 25% Similarity: 0.411

```
Q ss_pred              CCCcchhhhHHHHHHHHHHHHHc
Q Zetzy_3980     60    PGKLDDQIIDPIVKRGLEIFRDLT  83 (85)
Q Consensus      60    PG~lDD~IiDplV~Ra~~~fr~~~  83 (85)
                       |=..||...|++..+++++|++.+
T Consensus      46    ~~~~d~~~~d~~~~~ale~l~~~G  69 (451)
T PF05369.12     46    FIPTDEDLIDRLFQAGLEMLVETG  69 (451)
T ss_pred              cCCCCHHHHHHHHHHHHHHHHcC
```

Template alignment | Template 3D structure | PDBe

☐ **8.** **1X4Q_A U4/U6 small nuclear ribonucleoprotein Prp3; PWI domain, Structural Genomics, NPPSFA; NMR {Homo sapiens}**

Probability: 44.27 E-value: 210.0 Score: 19.13 Aligned Cols: 66 Identities: 18% Similarity: 0.261

```
Q ss_pred              HHHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHcchhcchhHHHhcCCCCcchhhhHHHHHHHHHH
Q Zetzy_3980     10    AQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEI  78 (85)
Q Consensus      10    ~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~  78 (85)
                       ...|.|.|.+.|.+.+...-+.+.+.++..|.+  ......-.+++.+.+.++- .+.++.|-+.....
T Consensus      15    ~~~lk~wI~~~i~~~lg~~d~~l~~~i~~~l~~-~~~~~~~l~~~L~~~l~~~a-~~Fv~~Lw~~l~~~  80 (92)
T 1X4Q_A         15    LDELKPWIEKTVKRVLGFSEPTVVTAALNCVGK--GMDKKKAADHLKPFLDDST-LRFVDKLFEAVEEG  80 (92)
T ss_dssp              HHHHHHHHHHHHHHHHSSCCHHHHHHHHHHHHT--TCCHHHHHHHHTTTTGGGT-HHHHHHHHHHHHHH
T ss_pred              HHHHHHHHHHHHHHHcCCCHHHHHHHHHHHHHc--CCCHHHHHHHHHHHHcHhH-HHHHHHHHHHHHHH
```

Template alignment | CDD

☐ **9.** **PF10025.9 ; DUF2267 ; Uncharacterized conserved protein (DUF2267)**

Probability: 42.38 E-value: 230.0 Score: 19.3 Aligned Cols: 49 Identities: 16% Similarity: 0.237

```
Q ss_pred              HHHHHHHHHHHH---HHhhHHHHHHHHHHHHHHHHcchhcchhHHHhcCCCCcch
Q Zetzy_3980     14    LPIIAKQIAEEF---GKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDD  65 (85)
Q Consensus      14    ~p~I~~aVa~ei---~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD  65 (85)
                       ...+...|++..   .......+.++..+|.+.+..   .-++++..+.|.++.+
T Consensus      66    ~~~F~~~V~~~~~~~~~~a~~~~~aVl~~l~~~l~~---~e~~~~~~~LP~el~~  117 (118)
T PF10025.9      66    VQEFYRRLAHRTGTDEQTAALHTRALMSLLREAVTG---TAYAHVLAQLPQEYAD  117 (118)
T ss_pred              HHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHCCh---HHHHHHHHhCCHHHhc
```

Template alignment | CDD

☐ **10.** **PF12755.7 ; Vac14_Fab1_bd ; Vacuolar 14 Fab1-binding region**

Probability: 42.24 E-value: 170.0 Score: 17.48 Aligned Cols: 74 Identities: 11% Similarity: 0.07

```
Q ss_pred                HHHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHH---HHHcchhcchhHHhhcCCCCcchhhhHHHHH
Q Zetzy_3980    7      KLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTE---AAATGAERGADKLTDYIPGKLDDQIIDPIVK  73 (85)
Q Consensus     7      ~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~E---aa~~~a~~gaDkiTD~IPG~lDD~IiDplV~  73 (85)
                         +.-+-..+-.+.+...+.+.++++.+...+...+..   .+...+.+....+.+.++..++. ..+.++.
T Consensus     3      r~~al~~l~~i~~~~~~~~~~~~~~~~~~l~~l~~~l~d~~~~vr~~a~~~l~~l~~~~~~~~~~~~-~~~~~~~  71 (95)
T PF12755.7     3      CRGGVIALAAIVTGIGKEANQYMKDVIPVILRCFDDSDKETRFFACEAMYNIAKVIRDDILM-YLNDVFK  71 (95)
T ss_pred                HHHHHHHHHHHHHhccHHHHHHHHHHHHHHHHHHHhcCCCHHHHHHHHHHHHHHHHHHhHHHHHH-HHHHHHH


Q ss_pred                HHHHHHHH
Q Zetzy_3980    74     RGLEIFRD  81 (85)
Q Consensus     74     Ra~~~fr~  81 (85)
                         ..++.+.+
T Consensus     72     ~l~~~l~d  79 (95)
T PF12755.7     72     GLSKLIGD  79 (95)
T ss_pred                HHHHHhCC
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe](#)

☐ **11.** **5YWZ_A SUN domain-containing protein 1; LINC complex SUN proteins; 2.2A {Mus musculus}**

Probability: 41.88 E-value: 370.0 Score: 21.14 Aligned Cols: 58 Identities: 14% Similarity: 0.181

```
Q ss_pred                HHHHHHHhHHHHHHHHHHHHHHHHHHHHcc-----hhcchhHHhhcCCCCcchhhhHHHHHHHHHHHH
Q Zetzy_3980    22     AEEFGKHVEPLTKALVTAVTEAAATG-----AERGADKLTDYIPGKLDDQIIDPIVKRGLEIF  79 (85)
Q Consensus     22     a~ei~k~ipal~kavV~av~Eaa~~~-----a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~f  79 (85)
                         .+|+.+++..+-..+...+.+.+...      ..+.....+...+..+-+..+..+|+++++.|
T Consensus     2      ~~el~~~l~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~lv~~~l~~~  64 (242)
T 5YWZ_A        2      KDELQVLLHDLELKLLQNITHHITVTGQAPTSEAIVSAVNQAGISGITEAQAHIIVNNALKLY  64 (242)
T ss_dssp               HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHSSCCCHHHHHHHHHHHTTCCCCCHHHHHHHHHHHHHHHS
T ss_pred                hHHHHHHHHHHHHHHHHHHHHHHHHHHHhhccCCCChHHHHHHhhhhccCCCCCHHHHHHHHHHHHHHH
```

[Template alignment](#) | [CDD](#)

☐ **12.** **PF08144.11 ; CPL ; CPL (NUC119) domain**

Probability: 41.86 E-value: 310.0 Score: 20.27 Aligned Cols: 73 Identities: 16% Similarity: 0.283

```
Q ss_pred                HHHHHHHHHHHHHHHHHHHHHHhh-HHHHHHHHHHHHHHHHHcchhcchhHHhhcC---CCCcchhhhHHHH
Q Zetzy_3980    7      KLIAQALLPIIAKQIAEEFGKHV-EPLTKALVTAVTEAAATGAERGADKLTDYI---PGKLDDQIIDPIV  72 (85)
Q Consensus     7      ~~i~~~l~p~I~~aVa~ei~k~i-pal~kavV~av~Eaa~~~a~~gaDkiTD~I---PG~lDD~IiDplV  72 (85)
                         +.+.+.+.|.+.+.+.+.+....++ ....--++..+.+...+.-....+.|-+.+    |.+-.--+-+|.+
T Consensus     51     ~ELl~~isp~Ll~~~~~~~~~~~ll~~~~~~~~~v~~evL~~~~~~~~~~~~~~~aia~~~~~~~~~~~~~h~ie~~~~  120 (138)
T PF08144.11    51     EEINKGMSPLILEAIANNAYELMNDTLGSQFISEALLSCDGDKSEAIAALMEVLSADPAGDNHVIKQPNA  120 (138)
T ss_pred                HHHHHhhhHHHHHHHHHHHhHHHHHhcChHHHHHHHHHHHhcCCCChHHHHHHHHHHHHcCCCCCCCchhcCHHH


Q ss_pred                HHHHHHH
Q Zetzy_3980    73     KRGLEIF  79 (85)
Q Consensus     73     ~Ra~~~f  79 (85)
                         .|+++.+
T Consensus     121    ~r~LK~L  127 (138)
T PF08144.11    121    QRALRTL  127 (138)
T ss_pred                HHHHHHH
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe](#)

☐ **13.** **4N1V_A DNA-binding protein HU-beta; DNA Binding, DNA BINDING PROTEIN; 1.36A {Spiroplasma melliferum} SCOP: a.55.1.0, l.1.1.1; Related PDB entries: 5OGU_B 5L8Z_A 5OGU_A**

Probability: 41.76 E-value: 230.0 Score: 18.73 Aligned Cols: 34 Identities: 32% Similarity: 0.455

```
Q ss_pred                HHHHHHHHHHHH-----HHhhHHHHHHHHHHHHHHHHHcc
```

```
Q Zetzy_3980    14    LPIIAKQIAEEF-----GKHVEPLTKALVTAVTEAAATG  47 (85)
Q Consensus     14    ~p~I~~aVa~ei------~k~ipal~kavV~av~Eaa~~~  47 (85)
                      .+.+.+.|++++     .+.+..+.+++...+.|.+.+|
T Consensus     9     ~~~~~~~ia~~~~~~~s~~~v~~vl~~~~~~i~~~L~~G  47 (100)
T 4N1V_A        9     KKELAAQIAEKFTDVLSKTHAEEITNFVFDHIKKALVAG  47 (100)
T ss_dssp             HHHHHHHHHHHCTTTCCHHHHHHHHHHHHHHHHHHHHTT
T ss_pred             HHHHHHHHHHHhCCCCCHHHHHHHHHHHHHHHHHHHCC
```

Template alignment | CDD

☐ **14.** **PF01031.20 ; Dynamin_M ; Dynamin central region**

Probability: 40.56 E-value: 320.0 Score: 20.11 Aligned Cols: 52 Identities: 19% Similarity: 0.173

```
Q ss_pred             HHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHcchhcc-----------hhHHhhcCCCC
Q Zetzy_3980    11    QALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERG-----------ADKLTDYIPGK  62 (85)
Q Consensus     11    ~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~g-----------aDkiTD~IPG~  62 (85)
                      ..|...+.+-..+.|.+.+|.+.+.+...+.|.-.+...=|            .+.+.+.+.|+
T Consensus     58    ~~L~~~L~~ll~~~i~~~lP~i~~~i~~~l~~~~~~L~~lg~~~~~~~~~~f~~~~~~~~~g~  120 (274)
T PF01031.20    58    AYLRRSLSKLLVEHIRATLPDLTMKISLLRRQFQSQLANYGEPVKDFSGNEVKSSAIDIIDGA  120 (274)
T ss_pred             HHHHHHHHHHHHHHHHHHcHHHHHHHHHHHHHHHHHHHhCCCCCCCCcChhHHHHHHHhCCC
```

Template alignment | CDD

☐ **15.** **PF16000.5 ; CARMIL_C ; CARMIL C-terminus**

Probability: 40.23 E-value: 130.0 Score: 25.25 Aligned Cols: 67 Identities: 12% Similarity: 0.122

```
Q ss_pred             HHHHHHHHHHHHhHHHHHHHHHHHHHHHHcchhcchhHHhhcCCCCcchhhhHHHHHHHHHHHHHHc
Q Zetzy_3980    17    IAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIFRDLT  83 (85)
Q Consensus     17    I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~fr~~~  83 (85)
                      +.+++...+.+++.---..|-.+|.|++++-+.+-...+-=.+-..+=|+|+|.++.-.-...+.+.
T Consensus     14    ~~~~L~~~~~~k~~ip~~fv~~~lleqag~dI~nKlsE~~Lsva~~lsd~Ivdevl~~Ls~~~~~L~  80 (293)
T PF16000.5     14    IRQDLIETSTEKMFIPRTFVKNVLLEQSGIDIFNKVSEVKLTVASLLSDRVVDEILEALSASHHKLA  80 (293)
T ss_pred             HHHHHHHHHHcccCCHHHHHHHHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

☐ **16.** **5ED8_A MKIAA0668 protein; SUN domain, nuclear membrane, TRANSPORT; 2.5A {Mus musculus}**

Probability: 38.95 E-value: 450.0 Score: 21.27 Aligned Cols: 58 Identities: 19% Similarity: 0.287

```
Q ss_pred             HHHHHHhhHHHHHHHHHHHHHHHHcchhcchhHHh----hcCCCCcchhhhHHHHHHHHHHH
Q Zetzy_3980    22    AEEFGKHVEPLTKALVTAVTEAAATGAERGADKLT----DYIPGKLDDQIIDPIVKRGLEIF  79 (85)
Q Consensus     22    a~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiT----D~IPG~lDD~IiDplV~Ra~~~f  79 (85)
                      .+|+.+++..+-+.+...+.|...+.....+.+.    ..=|..+-..-+..+|..+++.+
T Consensus     29    ~~e~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~lv~~~l~~~  90 (268)
T 5ED8_A        29    RDEMHAQLQELENKILTKMAEMQGKSAREAAASLGQILQKEGIVGVTEEQVHRIVKQALQRY  90 (268)
T ss_dssp             SCSHHHHHHHHHHHHHHHHGGGTTSCHHHHHHHHHHHHTTTCCSCCCHHHHHHHHHHHTTSC
T ss_pred             HHHHHHHHHHHHHHHHHHHHHhhhccHHHHHHHHHHHHHHcCCCCCCHHHHHHHHHHHHHHH
```

Template alignment | CDD

☐ **17.** **PF11301.8 ; DUF3103 ; Protein of unknown function (DUF3103)**

Probability: 38.01 E-value: 140.0 Score: 25.88 Aligned Cols: 39 Identities: 23% Similarity: 0.45

```
Q ss_pred             HHHHHHHHHHHHHHHcchh----------cchhHHhhcCCCCc---chhhhH
Q Zetzy_3980    31    PLTKALVTAVTEAAATGAE----------RGADKLTDYIPGKL---DDQIID  69 (85)
Q Consensus     31    al~kavV~av~Eaa~~~a~----------~gaDkiTD~IPG~l---DD~IiD  69 (85)
                      .|.++++.++.+-+....-           .-+++|-+++|.++   ||..+|
T Consensus     268   ~la~~l~~~~~~~~~~i~~~~~~~~~ii~~i~~~ii~AmP~~w~tnddDyvD  319 (352)
T PF11301.8     268   QLAQTILKAASDFLATIPDKEAQTYLIIPQMTSAIIALLPDDLFVNDDDFVD  319 (352)
T ss_pred             HHHHHHHHHHHHHHHcCCChhHHhhcchHHHHHHHHHHcCcccccCChHHhc
```

Template alignment | CDD

☐ **18.** **PF17157.4 ; GAPES4 ; Gammaproteobacterial periplasmic sensor domain**

Probability: 35.96 E-value: 110.0 Score: 21.07 Aligned Cols: 31 Identities: 26% Similarity: 0.24

```
Q ss_pred              hHHHHHHHHHHHHHHHHHHHHHHHHHhhHHHHHHH
Q Zetzy_3980     2     LATIAKLIAQALLPIIAKQIAEEFGKHVEPLTKAL  36 (85)
Q Consensus      2     ~~~~~~~i~~~l~p~I~~aVa~ei~k~ipal~kav  36 (85)
                       +..++..|-++|...    =.+++..|+|.++++.
T Consensus      10    v~~v~~~iD~~l~~~----~~~~l~~WLP~ll~a~  40 (96)
T PF17157.4      10    LREVTASIDQALLVQ----SPENIQYWLPGMMKTA  40 (96)
T ss_pred              HHHHHHHHHHHHHcC----CHHHHHhhhHHhhccc
```

Template alignment | CDD

☐ **19.** **PF10667.9 ; DUF2486 ; Protein of unknown function (DUF2486)**

Probability: 35.8 E-value: 540.0 Score: 22.57 Aligned Cols: 51 Identities: 18% Similarity: 0.031

```
Q ss_pred              HHHHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHcchhcchhHH
Q Zetzy_3980     5     IAKLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKL  55 (85)
Q Consensus      5     ~~~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDki  55 (85)
                       +-+.+.++|...+..-|...++..+...+..+|..++-++..+-.....++
T Consensus      190   Lr~Rvl~~L~g~gr~vIE~RcRDaL~eh~~~lV~qitrEV~~~Le~el~~w  240 (255)
T PF10667.9      190   LRGRFATYLNGDGRNLIEARCRDAFQDHTTWLVNQITREVALALETEMLRW  240 (255)
T ss_pred              HHHHHHHHHchHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
```

Template alignment | CDD

☐ **20.** **PF17150.4 ; CHASE6_C ; C-terminal domain of two-partite extracellular sensor domain**

Probability: 35.61 E-value: 350.0 Score: 19.06 Aligned Cols: 52 Identities: 6% Similarity: -0.097

```
Q ss_pred              HHHHHHHHHHHHHHHHcchhcchhHHhhcC--------------CCCcchhhhHHHHHHHHHHHH
Q Zetzy_3980     30    EPLTKALVTAVTEAAATGAERGADKLTDYI--------------PGKLDDQIIDPIVKRGLEIFRD  81 (85)
Q Consensus      30    pal~kavV~av~Eaa~~~a~~gaDkiTD~I--------------PG~lDD~IiDplV~Ra~~~fr~  81 (85)
                       |.+...-...+.+.+..--.+-++++....              ++..|-.-.+++|+|+...+..
T Consensus      15    p~vv~~Aa~lll~~i~~y~PeLa~kl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~RlVtYLqa  80 (87)
T PF17150.4      15    RRVACSAADWLLGHIKNYRPELTEKLERAREFYNLNQNVSSKPFLLTSQSIDLGIFTQRLVTYLQA  80 (87)
T ss_pred              HHHHHHHHHHHHHHHHHHChHHHHHHHHHHHHHHccccccCCCccccCCcccchHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

☐ **21.** **1IBR_B RAN IMPORTIN BETA SUBUNIT; SMALL GTPASE NUCLEAR TRANSPORT; HET: GNP; 2.3A {Homo sapiens} SCOP: a.118.1.1; Related PDB entries: 1M5N_S 1IBR_D 1GCJ_A 1GCJ_B 1F59_A 1O6O_C 1O6O_B 1O6P_A 1O6O_A 1O6P_B 1F59_B**

Probability: 35.52 E-value: 390.0 Score: 19.53 Aligned Cols: 75 Identities: 12% Similarity: 0.152

```
Q ss_pred              HHHHHHHHHHHHHHHHH-HHHHhhHHHHHHHHHHH---HHHHHcchhcchhHHhhcCCCCc-chhhhHHH
Q Zetzy_3980     7     KLIAQALLPIIAKQIAE-EFGKHVEPLTKALVTAV---TEAAATGAERGADKLTDYIPGKL-DDQIIDPI  71 (85)
Q Consensus      7     ~~i~~~l~p~I~~aVa~-ei~k~ipal~kavV~av---~Eaa~~~a~~gaDkiTD~IPG~l-DD~IiDpl  71 (85)
                       +.-+-..+..+.+.... .+..+++.+...+...+   ...+...|....-++...+|+.. ....+.++
T Consensus      383   r~~al~~l~~~~~~~~~~~~~~~~~~~~~l~~~l~d~~~~vr~~a~~~l~~l~~~~~~~~~~~~~~~~l  452 (462)
T 1IBR_B         383   RDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVYLAPL  452 (462)
T ss_dssp              HHHHHHHHHHTSSSSCTTTTCTTTTTHHHHHHHGGGCSCHHHHHHHHHHHHHHHHHGGGGCCSTTTHHHH
T ss_pred              HHHHHHHHHHHHcCCCHHHHHHHHHHHHHHHHHHHcCCCCHHHHHHHHHHHHHHHHHhChHhhhccchHHHH

Q ss_pred              HHHHHHHHHH
Q Zetzy_3980     72    VKRGLEIFRD  81 (85)
Q Consensus      72    V~Ra~~~fr~  81 (85)
                       +...++.+.+
T Consensus      453   l~~l~~~l~~  462 (462)
```

```
T 1IBR_B        453   LQCLIEGLSA  462 (462)
T ss_dssp             HHHHHCC---
T ss_pred             HHHHHHhhcC
```

Template alignment | Template 3D structure | PDBe

☐ **22.** **3E8T_A Takeout-like protein 1; Takeout, Epiphyas postvittana, TRANSPORT PROTEIN; HET: UQ8; 1.3A {Epiphyas postvittana}; Related PDB entries: 4G0S_A 3E8W_A 4G0S_B**

Probability: 34.48 E-value: 420.0 Score: 19.58 Aligned Cols: 46 Identities: 13% Similarity: 0.189

```
Q ss_pred             HHHHHHHHHHHHHhhHHHHHHHHHHHHHHHcchhcchhHHhhcCC
Q Zetzy_3980    15    PIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIP  60 (85)
Q Consensus     15    p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IP  60 (85)
                      +.+.+.+.+.+.+..+.+.+.+...+.|.+.+....-+.++...+|
T Consensus     168   ~~l~~~~~~~ln~~~~~i~~~~~~~~~~~~~~~~~~~n~~l~~~p  213 (220)
T 3E8T_A        168   KELSDTMLTFLNQNWKQVSEEFGKPVMEAAAKKIFKNIKHFLAKVP  213 (220)
T ss_dssp             HHHHHHHHHHHHHTHHHHHHHHHHHHHHHHHHHHHHHHHHHHHSC
T ss_pred             HHHHHHHHHHHHHcHHHHHHHHcHHHHHHHHHHHHHHHHHHHHcCC
```

Template alignment | Template 3D structure | PDBe

☐ **23.** **3UV1_B Der f 7 allergen; Super-roll, ALLERGEN; HET: MSE; 2.0A {Dermatophagoides farinae}; Related PDB entries: 3UV1_A**

Probability: 34.42 E-value: 360.0 Score: 19.23 Aligned Cols: 34 Identities: 3% Similarity: 0.209

```
Q ss_pred             ChHHHHHHHHHHHHHHHHHHHHHHHHHHhhHHHHH
Q Zetzy_3980    1     MLATIAKLIAQALLPIIAKQIAEEFGKHVEPLTK  34 (85)
Q Consensus     1     ~~~~~~~~i~~~l~p~I~~aVa~ei~k~ipal~k  34 (85)
                      ++..+...+...+.+.|.+.+.+.+.+.+....+
T Consensus     161   ~~~~~~~~~~~~~~~~i~~~i~~~l~~~i~~~l~  194 (196)
T 3UV1_B        161   IFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELE  194 (196)
T ss_dssp             HHHHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHC
T ss_pred             HHHHHHHHHHHHhHHHHHHHHHHhHHHHHHHHHh
```

Template alignment

☐ **24.** **cd08054 gp6; Head-Tail Connector Protein gp6 of Bacteriophage HK97 and similar proteins. The bacteriophage HK97 gp6 protein is critical in the assembly of the connector, a specialized structure that serves as an interface for head and tail attachment, as well as a point at which DNA exits the head during infection by the bacteriophage.**

Probability: 34.35 E-value: 240.0 Score: 17.45 Aligned Cols: 26 Identities: 23% Similarity: 0.339

```
Q ss_pred             CCCCcchhhhHHHHHHHHHHHHHcC
Q Zetzy_3980    59    IPGKLDDQIIDPIVKRGLEIFRDLTR  84 (85)
Q Consensus     59    IPG~lDD~IiDplV~Ra~~~fr~~~~  84 (85)
                      |.++-||..+..++..|.+.+.+.+.
T Consensus     11    i~~~~~D~~i~~~i~~A~~~i~~~~~  36 (91)
T cd08054       11    IDHDDDDALIELLIDAAEEYIENYTG  36 (91)
T ss_pred             CCCCCchHHHHHHHHHHHHHHHHHC
```

Template alignment | Template 3D structure | PDB | NCBI

☐ **25.** **d3dnua_ d.144.1.7 (A:) Multidrug tolerance (MDT) protein HipA N-terminal domain {Escherichia coli K-12 [TaxId: 83333]}**

Probability: 33.93 E-value: 480.0 Score: 22.05 Aligned Cols: 52 Identities: 12% Similarity: 0.264

```
Q ss_pred             HHHHHHHHHHHHcchhcchhHHHhcCCCCcchhhhHHHHHHHHHHHHHcCC
Q Zetzy_3980    34    KALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIFRDLTRZ  85 (85)
Q Consensus     34    kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~fr~~~~~  85 (85)
                      ...+..+.+++...+....+++....|..+-+.+.+.|.++.....+++.+|
T Consensus     384   ~~~a~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~  435 (436)
T d3dnua_       384   EVQMHEILSDFARMIPAALDNVKTSLPTDFPENVVTAVESNVLRLHGRLSRE  435 (436)
T ss_dssp             HHHHHHHHHHHHHHHHHHHHHHHGGGSCTTSCHHHHHHHHHHHHHHHHHHTT
```

```
T ss_pred              HHHHHHHHHHHHHHHHHHHHHHHhCCCCCCHHHHHHHHHHHHHHHHHHhc
```

Template alignment | Template 3D structure | PDBe

☐ **26.** **3V53_C RNA-binding protein 25; PWI, RNA-binding domain, RNA BINDING; 2.9A {Homo sapiens}; Related PDB entries: 3V53_B 3V53_D 3V53_A 3V53_E**

Probability: 33.79 E-value: 420.0 Score: 19.36 Aligned Cols: 66 Identities: 18% Similarity: 0.294

```
Q ss_pred              HHHHHHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHHHcchhcchhHHhhcCCCCcchhhhHHHHHHHH
Q Zetzy_3980     7     KLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGL  76 (85)
Q Consensus      7     ~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~  76 (85)
                       ..+...|.|.|.+.|.+.+...=+.+.+.++.-|.+      ....+++.+.+=+-+|+ =-..+|.+..
T Consensus      41    ~~l~~~lrpwI~kkv~e~LG~ed~~lv~~i~~~L~~------~~~~~~l~~~L~~~Lde-~a~~FV~~LW  103 (119)
T 3V53_C         41    ILMERRIRPWINKKIIEYIGEEEATLVDFVCSKVMA------HSSPQSILDDVAMVLDE-EAEVFIVKMW  103 (119)
T ss_dssp              HHCCCCCHHHHHHHHHHHSSCCHHHHHHHHHHHH------TCCHHHHHHHHTTTCTT-THHHHHHHHH
T ss_pred              HHHHHhHHHHHHHHHHHHCCcHHHHHHHHHHHHHh------CCCHHHHHHHHHHhccH-HHHHHHHHHH

Q ss_pred              HHH
Q Zetzy_3980     77    EIF  79 (85)
Q Consensus      77    ~~f  79 (85)
                       +.+
T Consensus      104   ~~L  106 (119)
T 3V53_C         104   RLL  106 (119)
T ss_dssp              HHH
T ss_pred              HHH
```

Template alignment | CDD

☐ **27.** **PF05405.14 ; Mt_ATP-synt_B ; Mitochondrial ATP synthase B chain precursor (ATP-synt_B)**

Probability: 32.74 E-value: 370.0 Score: 18.46 Aligned Cols: 70 Identities: 11% Similarity: -0.036

```
Q ss_pred              HHHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHHcchhcchhHHhhcC-CCCcchhhhHHHHHH
Q Zetzy_3980     6     AKLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYI-PGKLDDQIIDPIVKR  74 (85)
Q Consensus      6     ~~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~I-PG~lDD~IiDplV~R  74 (85)
                       +............+.+...+.+....+......+..+--.+....+.+.+...+ +.+.+.++++..++.
T Consensus      92    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~a~~~~~k~l~~~~~~~~~i~~~i~~  161 (163)
T PF05405.14     92    SKATQKGAQSSLKQQIDFQIYKMYTHLYKLQQSFPQKLQKKIHDNVLLNIQQSLALSQKPINSIKNAKKK  161 (163)
T ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHchHHHHHHHHHHHHHHHHHHHHHHccCchhHHHHHHHh

Q ss_pred              H
Q Zetzy_3980     75    G  75 (85)
Q Consensus      75    a  75 (85)
                       .
T Consensus      162   l  162 (163)
T PF05405.14     162   L  162 (163)
T ss_pred              c
```

Template alignment | Template 3D structure | PDBe

☐ **28.** **3TPD_A Serine/threonine-protein kinase HipA (E.C.2.7.11.1); HipA, persistence, multidrug tolerance, HipB; 1.5A {Escherichia coli} SCOP: d.144.1.7; Related PDB entries: 5K98_D 5K98_A 2WIU_A 2WIU_C 3DNT_A 3TPT_A 3HZI_A 3TPT_B 3TPB_A 3DNT_B 3DNU_A 3DNV_A 3TPE_A 3TPV_B 3FBR_A 4YG7_K 4YG7_D**

Probability: 32.4 E-value: 490.0 Score: 22.09 Aligned Cols: 52 Identities: 12% Similarity: 0.264

```
Q ss_pred              HHHHHHHHHHHHcchhcchhHHhhcCCCCcchhhhHHHHHHHHHHHHHHcCC
Q Zetzy_3980     34    KALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIFRDLTRZ  85 (85)
Q Consensus      34    kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~fr~~~~~  85 (85)
                       ...+..+.+++........+.+-...|..+-+.+.+.+.++.....+.+++|
T Consensus      385   ~~~a~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~l~~~  436 (440)
```

```
T 3TPD_A        385   EVQMHEILSDFARMIPAALDNVKTSLPTDFPENVVTAVESNVLRLHGRLSRE  436 (440)
T ss_dssp             HHHHHHHHHHHHHHHHHHHHHHHTTSCTTCCHHHHHHHHHHHHHHHHHHHTT
T ss_pred             HHHHHHHHHHHHHHHHHHHHHHHhhCCCCcCHHHHHHHHHHHHHHHHHHHHh
```

Template alignment | CDD

☐ **29.** **PF12787.7 ; EcsC ; EcsC protein family**

Probability: 31.65 E-value: 490.0 Score: 19.53 Aligned Cols: 71 Identities: 11% Similarity: 0.134

```
Q ss_pred             HHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHcchhcchhHHHhcCCCCcchhhhHHHHHHHHHHHHHh
Q Zetzy_3980    13    LLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIFRDL  82 (85)
Q Consensus     13    l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~fr~~  82 (85)
                      +++.+.+.+.+.+.+.+|.-.........+.+.+.+.+.....+.-.-.++..-.|.+.++.....+..
T Consensus     20    ~~~~~~~~~~~~~~~iP~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~a~~~i~~~~~~  89 (232)
T PF12787.7     20    IIDRASKGIQSKFNTVLPQGYNDIMTSAIKTLTRAVLFGSKYITKPPVKNISLIEREKLVTEKTKFYRTT  89 (232)
T ss_pred             HHHHHHHHHHHHHHHhCCHHHHHHHHHHHHHHHHHHHHcCCccCCCCcCCCCHHHHHHHHHHHHHHHHHH

Q ss_pred             c
Q Zetzy_3980    83    T  83 (85)
Q Consensus     83    ~  83 (85)
                      +
T Consensus     90    a  90 (232)
T PF12787.7     90    A  90 (232)
T ss_pred             H
```

Template alignment | CDD

☐ **30.** **PF06078.11 ; DUF937 ; Bacterial protein of unknown function (DUF937)**

Probability: 31.45 E-value: 400.0 Score: 18.46 Aligned Cols: 69 Identities: 16% Similarity: 0.126

```
Q ss_pred             HHHHHHHHHHHHHHHHHHHHH---hhHHHHHHHHHHHHHHHHcch--hcchhHHhhcCC-CCcchhhhHH
Q Zetzy_3980    7     KLIAQALLPIIAKQIAEEFGK---HVEPLTKALVTAVTEAAATGA--ERGADKLTDYIP-GKLDDQIIDP  70 (85)
Q Consensus     7     ~~i~~~l~p~I~~aVa~ei~k---~ipal~kavV~av~Eaa~~~a--~~gaDkiTD~IP-G~lDD~IiDp  70 (85)
                      +.+...+-+...+.++..+..   .+...+.+++-++...+.+.+  ..+++.+-+.+- +..+...++.
T Consensus     1     ~~~~~~~~~~~~~~la~~~g~~~~~~~~a~~~~~p~~l~gl~~~~~~~~g~~~l~~~~~~~~~~~~~l~~  70 (135)
T PF06078.11    1     ELITRELSGENTGKIAALTGESNAGVIDSIGTASATIMGGLMNKAATPDGATEILTRITSSGYNGDFLNR  70 (135)
T ss_pred             ChhhhhcCHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHcCChhHHHHHHHHHHcCCCCCchhhh

Q ss_pred             HHHHH
Q Zetzy_3980    71    IVKRG  75 (85)
Q Consensus     71    lV~Ra  75 (85)
                      +.+..
T Consensus     71    ~~~~~  75 (135)
T PF06078.11    71    FGDML  75 (135)
T ss_pred             HHHHH
```

Template alignment | CDD

☐ **31.** **PF04843.12 ; Herpes_teg_N ; Herpesvirus tegument protein, N-terminal conserved region**

Probability: 30.87 E-value: 220.0 Score: 20.77 Aligned Cols: 23 Identities: 17% Similarity: -0.015

```
Q ss_pred             CCCCcchhhhHHHHHHHHHHHH
Q Zetzy_3980    59    IPGKLDDQIIDPIVKRGLEIFRD  81 (85)
Q Consensus     59    IPG~lDD~IiDplV~Ra~~~fr~  81 (85)
                      ||..|+-.++|.++...-+.++.
T Consensus     34    ~~~~Wt~~~iD~IL~~G~~ly~~  56 (175)
T PF04843.12    34    GVPLKDRTELDHVLNVGSKIDFV  56 (175)
T ss_pred             CCCCCCHHHHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

☐ **32.** **5JK9_B Izumo sperm-egg fusion protein 1; fertilization, IZUMO1, JUNO, CELL ADHESION; HET: NAG; 2.1A {Homo sapiens}; Related PDB entries: 5F4V_A 5JK9_F 5JKE_A 5JKD_A 5JK9_E 5JKC_A 5JK9_C 5JK9_A 5JK9_D 5JKE_C 5F4T_A 5F4E_A**

Probability: 30.59 E-value: 210.0 Score: 22.79 Aligned Cols: 26 Identities: 31% Similarity: 0.616

```
Q ss_pred              hhcCCCCcchhhhHHHHHHHHHHHHH
Q Zetzy_3980     56    TDYIPGKLDDQIIDPIVKRGLEIFRD  81 (85)
Q Consensus      56    TD~IPG~lDD~IiDplV~Ra~~~fr~  81 (85)
                       ++.|||.++.+....+.+|+-+.|++
T Consensus      21    ~~~~p~~~~~~~~~~~~~r~~~~~~~  46 (246)
T 5JK9_B         21    KDYLPGHLDAKHHKAMMERVENAVKD  46 (246)
T ss_dssp              CCCHHHHSCGGGHHHHHHHHHHHHSC
T ss_pred              HhhCCcCCCHHHHHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDB | NCBI

☐ **33.** **d1nh2d1 a.32.1.1 (D:5-54) Small chain TOA2, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae) [TaxId: 4932]}**

Probability: 28.78 E-value: 170.0 Score: 18.51 Aligned Cols: 23 Identities: 26% Similarity: 0.297

```
Q ss_pred              HHHHHHHHHHHHHHHHhhHHHHH
Q Zetzy_3980     12    ALLPIIAKQIAEEFGKHVEPLTK  34 (85)
Q Consensus      12    ~l~p~I~~aVa~ei~k~ipal~k  34 (85)
                       ++.|.++.+|..+|++.|....+
T Consensus      27    ~I~~~la~~il~~FD~~i~~~L~  49 (50)
T d1nh2d1        27    RIEASLAMRVLETFDKVVAETLK  49 (50)
T ss_dssp              SSCHHHHHHHHHHHHHHHHHHH
T ss_pred              CCCHHHHHHHHHHHHHHHHHhh
```

Template alignment | Template 3D structure | PDBe

☐ **34.** **5XAH_B Importin-4; Histone, Chromatin, Assembly, PROTEIN TRANSPORT; HET: MSE; 3.004A {Homo sapiens}; Related PDB entries: 5XBK_D 5XBK_A 5XBK_C 5XAH_D 5XAH_A 5XBK_B 5XAH_C**

Probability: 28.36 E-value: 510.0 Score: 18.63 Aligned Cols: 71 Identities: 11% Similarity: 0.044

```
Q ss_pred              HHHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHH----HHHHHcchhcchhHHhhcCCCCcchhhhHHHH
Q Zetzy_3980     7     KLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAV----TEAAATGAERGADKLTDYIPGKLDDQIIDPIV  72 (85)
Q Consensus      7     ~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av----~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV  72 (85)
                       +.-+-..+..+.....+.+..+++.+...+...+    ...+...+.....++....|...+   ++.++
T Consensus      251   r~~a~~~l~~l~~~~~~~~~~~~~~~~~~l~~~l~~~~~~~~~~~a~~~l~~l~~~~~~~~~---~~~~l  317 (416)
T 5XAH_B         251   RSNAIFGMGVLAEHGGHPAQEHFPKLLGLLFPLLARERHDRVRDNICGALARLLMASPTRKP---EPQVL  317 (416)
T ss_dssp              HHHHHHHHHHHHHHSHHHHHTTHHHHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHSCC--C---CHHHH
T ss_pred              HHHHHHHHHHHHHhCCchHHHHHHHHHHHHHHHHHcccCHHHHHHHHHHHHHHHHHhCCCCCC---HHHHH

Q ss_pred              HHHHHHHH
Q Zetzy_3980     73    KRGLEIFR  80 (85)
Q Consensus      73    ~Ra~~~fr  80 (85)
                       ...++.++
T Consensus      318   ~~l~~~l~  325 (416)
T 5XAH_B         318   AALLHALP  325 (416)
T ss_dssp              HHHHHTCS
T ss_pred              HHHHHhCC
```

Template alignment

☐ **35.** **cd10145 TFIIA_gamma_N; Gamma subunit of transcription initiation factor IIA, N-terminal helical domain.**

Probability: 27.66 E-value: 190.0 Score: 18.35 Aligned Cols: 23 Identities: 17% Similarity: 0.346

```
Q ss_pred              HHHHHHHHHHHHHHHHhhHHHHH
```

```
Q Zetzy_3980     12    ALLPIIAKQIAEEFGKHVEPLTK  34 (85)
Q Consensus      12    ~l~p~I~~aVa~ei~k~ipal~k  34 (85)
                       .+.|..+.+|-..|++.|+...+
T Consensus      26    ~I~p~la~~Il~~FD~~i~~~L~  48 (49)
T cd10145        26    QITPQLAMKVLLQFDKSINEALA  48 (49)
T ss_pred              CCCHHHHHHHHHHHHHHHHHHHh
```

Template alignment

☐ **36.** **cd08051 gp6_gp15_like; Head-Tail Connector Proteins gp6 and gp15, and similar proteins. Members of this family include the proteins gp6 and gp15 from bacteriophage HK97 and SPP1, respectively.**

Probability: 27.23 E-value: 370.0 Score: 16.96 Aligned Cols: 26 Identities: 4% Similarity: 0.098

```
Q ss_pred              CCCCcchhhhHHHHHHHHHHHHHHcC
Q Zetzy_3980     59    IPGKLDDQIIDPIVKRGLEIFRDLTR  84 (85)
Q Consensus      59    IPG~lDD~IiDplV~Ra~~~fr~~~~  84 (85)
                       |.++-||.++..++..|.+...+.+.
T Consensus      9     i~~~~dD~~l~~~i~~A~~~i~~~~~  34 (94)
T cd08051        9     FEEDDRDELLTLYAQAAFDYCXRWCD  34 (94)
T ss_pred              CCCCchhHHHHHHHHHHHHHHHHHcC
```

Template alignment | CDD

☐ **37.** **PF09261.11 ; Alpha-mann_mid ; Alpha mannosidase middle domain**

Probability: 26.8 E-value: 340.0 Score: 17.4 Aligned Cols: 26 Identities: 12% Similarity: 0.055

```
Q ss_pred              hcCCCCcchhhhHHHHHHHHHHHHHh
Q Zetzy_3980     57    DYIPGKLDDQIIDPIVKRGLEIFRDL  82 (85)
Q Consensus      57    D~IPG~lDD~IiDplV~Ra~~~fr~~  82 (85)
                       |.|||.--|...+....|........
T Consensus      62    D~i~Gt~~~~v~~d~~~~~~~~~~~~  87 (98)
T PF09261.11     62    DVVTGSCIQLVAEDAMNYYEDIRSHG  87 (98)
T ss_pred              hcCCCCCHHHHHHHHHHHHHHHHHHH
```

Template alignment | CDD

☐ **38.** **PF04837.12 ; MbeB_N ; MbeB-like, N-term conserved region**

Probability: 26.56 E-value: 480.0 Score: 17.66 Aligned Cols: 34 Identities: 18% Similarity: 0.163

```
Q ss_pred              HHHHHHhhHHHHHHHHHHHHHHHHcchhcchhHHhhcC
Q Zetzy_3980     22    AEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYI  59 (85)
Q Consensus      22    a~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~I  59 (85)
                       ++-+++.+..-.+.....|.+++..    +.-+|.|+|
T Consensus      19    a~~te~~lk~af~~hE~~v~~aL~~----Se~~I~~aI  52 (52)
T PF04837.12     19    AVSTENMLNSEFRKLEASVDRELKL----NGQKIRDAI  52 (52)
T ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHH----HHHHHHHhC
```

Template alignment | Template 3D structure | PDB | NCBI

☐ **39.** **d1nvpd1 a.32.1.1 (D:3-53) Small chain TOA2, N-terminal domain {Human (Homo sapiens) [TaxId: 9606]}**

Probability: 26.39 E-value: 220.0 Score: 18.1 Aligned Cols: 23 Identities: 22% Similarity: 0.356

```
Q ss_pred              HHHHHHHHHHHHHHHHhhHHHHH
Q Zetzy_3980     12    ALLPIIAKQIAEEFGKHVEPLTK  34 (85)
Q Consensus      12    ~l~p~I~~aVa~ei~k~ipal~k  34 (85)
                       .+.|.++..|-..|++.|+...+
T Consensus      25    ~I~~~la~~il~~FD~~i~~~L~  47 (51)
T d1nvpd1        25    QITPQLALQVLLQFDKAINAALA  47 (51)
T ss_dssp              SSCHHHHHHHHHHHHHHHHHHH
T ss_pred              CCCHHHHHHHHHHHHHHHHHHH
```

Template alignment | CDD

☐ **40.** **PF14005.6 ; YpjP ; YpjP-like protein**

Probability: 25.87 E-value: 720.0 Score: 19.53 Aligned Cols: 41 Identities: 20% Similarity: 0.222

```
Q ss_pred                HHHHHHHHHHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHH
Q Zetzy_3980     3       ATIAKLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEA  43 (85)
Q Consensus      3       ~~~~~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Ea  43 (85)
                         ..+.....+.+=|+|...|-++|.+.|-+=++.++..+++.
T Consensus      9       ~~~~~A~~qKfG~kI~~~I~def~~~IlPkie~~i~~~~~~  49 (127)
T PF14005.6      9       FALKEAVKKKMGKRIQRMAYDEFEERIESEIWAEVEALHEQ  49 (127)
T ss_pred                HHHHHHHHHhccCHHHHHHhHHHHHHhHHHHHHHHHHHHHHh
```

Template alignment | CDD

☐ **41.** **PF16507.5 ; BLM10_mid ; Proteasome-substrate-size regulator, mid region**

Probability: 25.75 E-value: 630.0 Score: 21.96 Aligned Cols: 68 Identities: 18% Similarity: 0.19

```
Q ss_pred                HHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHHcchhcchhHHhhcCCCCcchhhhHHHHHHHHHHHHH
Q Zetzy_3980     14      LPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIFRD  81 (85)
Q Consensus      14      ~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~fr~  81 (85)
                         ........-..+..|+-.+.+.+..-+......+.....-.....+-.++++++++.+++|..+.+.+
T Consensus      232     e~~~~~~~t~~~~d~~~~f~drif~l~~~~~e~~~~~~~~~~~~~l~~~~s~~l~~~~~~kv~~f~~~  299 (522)
T PF16507.5      232     LLTTFRASSSIFKDILKTYIDKVYSFVDIDLDPAVVNKINQTTLIILESMDDDMFDYFTKQFLKLFWD  299 (522)
T ss_pred                HHHHHHHHHHHHHHHHHHHHHHHHHHHHcCccHHHHHHHHHHHHHHHHcCCHHHHHHHHHHHHHHHc
```

Template alignment | CDD

☐ **42.** **PF18851.1 ; baeRF_family8 ; Bacterial archaeo-eukaryotic release factor family 8**

Probability: 25.55 E-value: 91.0 Score: 20.83 Aligned Cols: 75 Identities: 12% Similarity: 0.139

```
Q ss_pred                HHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHcchhcchhH---HhhcCCCCcchhhhHHHHHHHH
Q Zetzy_3980     10      AQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADK---LTDYIPGKLDDQIIDPIVKRGL  76 (85)
Q Consensus      10      ~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDk---iTD~IPG~lDD~IiDplV~Ra~  76 (85)
                         .......+++.|.+.+.+.... ..-||-+-.+..-+.--+..+.   +++.|+|+++..-.+.|.+++.
T Consensus      61      ~~~~~~~f~~~v~~~l~~~~~~-~~pLvl~a~~~~l~~~r~~~~~~~~~~~~i~~~~~~~~~~eL~~~~~  129 (140)
T PF18851.1      61      KKVRIRQFARQVDRALRPVLRG-DVPLILAATEPLQSIFRSVSGAPELAPVGLTGNPEESTDRELASAAR  129 (140)
T ss_pred                hHHHHHHHHHHHHHHHHHHhCC-CCCEEEEechhHHHHHHHHhCCccccccCccCChhhCCHHHHHHHHH

Q ss_pred                HHHHHhcCC
Q Zetzy_3980     77      EIFRDLTRZ  85 (85)
Q Consensus      77      ~~fr~~~~~  85 (85)
                         +.+.....+
T Consensus      130     ~~~~~~~~~  138 (140)
T PF18851.1      130     SVLDDLHAD  138 (140)
T ss_pred                HHHHHHHhh
```

Template alignment | Template 3D structure | PDBe

☐ **43.** **1W9C_B CRM1 PROTEIN; NUCLEAR PROTEIN, EXPORTIN 1, NUCLEAR; 2.3A {HOMO SAPIENS} SCOP: a.118.1.19; Related PDB entries: 1W9C_A**

Probability: 25.46 E-value: 850.0 Score: 20.21 Aligned Cols: 67 Identities: 15% Similarity: 0.335

```
Q ss_pred                HHHHHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHHcchhcchhHHhhcCCCCcchhhhHHHHHHHH
Q Zetzy_3980     7       KLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGL  76 (85)
Q Consensus      7       ~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~  76 (85)
                         ..+...+.|.+.+.|-.-..+..|....+-|=.+...+.+       |+.+.|++.+.+ |++.+...-+
T Consensus      64      ~~v~~~~ip~l~~~vl~DY~~~~p~~r~~evL~l~~~ii~-------k~~~~i~~~v~~-i~~~vf~~Tl  125 (321)
T 1W9C_B         64      QMVAENFVPPLLDAVLIDYQRNVPAAREPEVLSTMAIIVN-------KLGGHITAEIPQ-IFDAVFECTL  125 (321)
```

```
T ss_dssp              HHHHHHTHHHHHHHHHHHHHTSCGGGCCHHHHHHHHHHHH-------HHGGGGGGGHHH-HHHHHHHHHH
T ss_pred              HHHHHHcHHHHHHHHHHHHHHCChhhcCHHHHHHHHHHHH-------HHhhcchHhHHH-HHHHHHHHHH

Q ss_pred              HHHHH
Q Zetzy_3980     77    EIFRD  81 (85)
Q Consensus      77    ~~fr~  81 (85)
                       ++.+.
T Consensus      126   ~mI~~  130 (321)
T 1W9C_B         126   NMINK  130 (321)
T ss_dssp              HHHSS
T ss_pred              HHHhh
```

Template alignment | Template 3D structure | PDB | NCBI

☐ **44.** **d1w9ca_ a.118.1.19 (A:) Exportin-1 (Xpo1, Crm1) {Human (Homo sapiens) [TaxId: 9606]}**

Probability: 25.46 E-value: 850.0 Score: 20.21 Aligned Cols: 67 Identities: 15% Similarity: 0.335

```
Q ss_pred              HHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHHcchhcchhHHhhcCCCCcchhhhHHHHHHHH
Q Zetzy_3980     7     KLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGL  76 (85)
Q Consensus      7     ~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~  76 (85)
                       ..+...+.|.+.+.|-.-..+..|....+-|=.+...+.+       |+.+.|++.+.+ |++.+...-+
T Consensus      64    ~~v~~~~ip~l~~~vl~DY~~~~p~~r~~evL~l~~~ii~-------k~~~~i~~~v~~-i~~~vf~~Tl  125 (321)
T d1w9ca_        64    QMVAENFVPPLLDAVLIDYQRNVPAAREPEVLSTMAIIVN-------KLGGHITAEIPQ-IFDAVFECTL  125 (321)
T ss_dssp              HHHHHHTHHHHHHHHHHHHHTSCGGGCCTHHHHHHHHHHH-------HHGGGGGGGHHH-HHHHHHHHHH
T ss_pred              HHHHHHcHHHHHHHHHHHHHHCChhhcCHHHHHHHHHHHH-------HHhhcchHhHHH-HHHHHHHHHH

Q ss_pred              HHHHH
Q Zetzy_3980     77    EIFRD  81 (85)
Q Consensus      77    ~~fr~  81 (85)
                       ++.+.
T Consensus      126   ~mI~~  130 (321)
T d1w9ca_        126   NMINK  130 (321)
T ss_dssp              HHHSS
T ss_pred              HHHhh
```

Template alignment | Template 3D structure | PDBe

☐ **45.** **5B0O_E Flagellum-specific ATP synthase (E.C.3.6.3.14), Flagellar; Bacterial flagellum, type III secretion; HET: ADP; 3.0A {Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)}; Related PDB entries: 5B0O_L 5B0O_K 5B0O_J 5B0O_I 5B0O_F 5B0O_G 5B0O_H**

Probability: 25.36 E-value: 500.0 Score: 17.46 Aligned Cols: 55 Identities: 15% Similarity: 0.269

```
Q ss_pred              HHHHHHHHHHhhHHHHHHHHHHHHHHHcchhcchhHHhhcCCCCcchhhhHHHHHHHHH
Q Zetzy_3980     18    AKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLE  77 (85)
Q Consensus      18    ~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~  77 (85)
                       .....+++.+....+.+.+...+.+-+-.    .+.++....+.+-.+ .+-.++++++.
T Consensus      10    l~~~~~~~~~~~~~~~~~~~~l~~l~~~----~~~~il~~~~~~~~~-~l~~~i~~~l~  64 (140)
T 5B0O_E         10    MQQLVSEFQNTLDALDSVIASRLMQMALE----AARQVIGQTPAVDNS-ALIKQIQQLLQ  64 (140)
T ss_dssp              HHHHHHHHHHHHHHHHHHHHHHHHHHHH----HHHHHHHHCCCSCCH-HHHHHHHHHHT
T ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHHHHH----HHHHHHcccccCCHH-HHHHHHHHHHh
```

Template alignment | CDD

☐ **46.** **PF10691.9 ; DUF2497 ; Protein of unknown function (DUF2497)**

Probability: 25.17 E-value: 190.0 Score: 20.04 Aligned Cols: 38 Identities: 26% Similarity: 0.303

```
Q ss_pred              HHHHHHcchhcchhHHhhcCCCCcc-----hhhhHHHHHHHHH
Q Zetzy_3980     40    VTEAAATGAERGADKLTDYIPGKLD-----DQIIDPIVKRGLE  77 (85)
Q Consensus      40    v~Eaa~~~a~~gaDkiTD~IPG~lD-----D~IiDplV~Ra~~  77 (85)
                       +++..+..+.++.+++++.+..+-.     ...++.+|..++.
```

```
T Consensus      4     iS~~t~~a~~~af~~L~~~~~~~~~~~~~~~~tlE~lv~e~lr  46 (74)
T PF10691.9      4     LGEVAASATFAGFARLANNIAVDRRRQTGEGVTIEDIVRDMLQ  46 (74)
T ss_pred              ccHHHHHHHHHHHHHHHHHhHhhhhhhcCCCCCCHHHHHHHHHH
```

Template alignment | Template 3D structure | PDB | NCBI

☐ **47.** **d1mp1a1 a.188.1.1 (A:27-134) Ser/Arg-related nuclear matrix protein srm160 {Human (Homo sapiens) [TaxId: 9606]}**

Probability: 24.48 E-value: 530.0 Score: 18.19 Aligned Cols: 63 Identities: 11% Similarity: 0.2

```
Q ss_pred              HHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHH-HHcchhcchhHHHhcCCCCcchhhhHHHHHHHHHHH
Q Zetzy_3980     11    QALLPIIAKQIAEEFGKHVEPLTKALVTAVTEA-AATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIF  79 (85)
Q Consensus      11    ~~l~p~I~~aVa~ei~k~ipal~kavV~av~Ea-a~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~f  79 (85)
                       ..+.|.|.+.|.+.+...=+.+.+.++.-|.+. ...      .++.+.+-+-||+.---++|.+..+.+
T Consensus      20    ~~lr~wI~kkv~e~lG~ed~~lv~~v~~~L~~~~~~~------~~l~~~L~~~Ld~~~a~~Fv~~Lw~~l  83 (108)
T d1mp1a1        20    EVIKPWITKRVTEILGFEDDVVIEFIFNQLEVKNPDS------KMMQINLTGFLNGKNAREFMGELWPLL  83 (108)
T ss_dssp              GGGHHHHHHHHHHHHSSCCSHHHHHHHHHTTSSSCCH------HHHHHHHTTTSCSHHHHHHHHHHHHH
T ss_pred              HHHHHHHHHHHHHHcCCCcHHHHHHHHHHHHhccCCCH------HHHHHHHHHHcCchhHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

☐ **48.** **1N1C_B Crystal Structure Of The Dimeric; CHAPERONE, TORD, 3D-domain swapping; HET: DTT, MSE; 2.4A {Shewanella massilia} SCOP: a.184.1.1, l.1.1.1; Related PDB entries: 1N1C_A**

Probability: 24.41 E-value: 560.0 Score: 19.26 Aligned Cols: 39 Identities: 15% Similarity: 0.16

```
Q ss_pred              ChHHHHHHHHHHHHHHHHHHHHHHHHHHhHHHHHHHHHHH
Q Zetzy_3980     1     MLATIAKLIAQALLPIIAKQIAEEFGKHVEPLTKALVTA  39 (85)
Q Consensus      1     ~~~~~~~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~a  39 (85)
                       +|.-++-.+.........+.+.+.+..|+|.+.+++...
T Consensus      139   eL~fma~L~~~~~~~~~~~fl~~hl~~Wi~~f~~~l~~~  177 (217)
T 1N1C_B         139   MLAYMAHLCCHSENSVQLSFLQTCVNSWLAKFINHLTQC  177 (217)
T ss_dssp              HHHHHHHHHHHSCHHHHHHHCCCCCTTTHHHHHHHHTTT
T ss_pred              HHHHHHHHHhccChHHHHHHHHHHHHHhhHHHHHHHHHh
```

Template alignment | Template 3D structure | PDBe

☐ **49.** **3T38_A Arsenate Reductase (E.C.1.-.-.-); Low molecular weight tyrosine phosphatase; HET: MSE; 2.2A {Corynebacterium glutamicum}; Related PDB entries: 3T38_B**

Probability: 24.13 E-value: 490.0 Score: 19.73 Aligned Cols: 36 Identities: 14% Similarity: 0.131

```
Q ss_pred              HHHHcchhcchhHHHhcCCCCcchhhhHHHHHHHHHHH-HH
Q Zetzy_3980     42    EAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIF-RD  81 (85)
Q Consensus      42    Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~f-r~  81 (85)
                       +.+..    .++++....|+.+|-.-|+.+|..+...| ++
T Consensus      12    ~~~~~----i~~~L~~~~~~~~~~~~v~~~v~~~~~~~~~~  48 (213)
T 3T38_A         12    NILNR----IANELALTYQGVFSAETINRYIFESYVSLART  48 (213)
T ss_dssp              HHHHH----HHHHHHHHTTTTSCHHHHHHHHHHHHHHHHHH
T ss_pred              HHHHH----HHHHHHHHcCCCCCHHHHHHHHHHHHHHHHhh
```

Template alignment | Template 3D structure | PDBe

☐ **50.** **5A21_D PORTAL PROTEIN, 15 PROTEIN, HEAD; VIRAL PROTEIN, VIRAL INFECTION, TAILED; 7.2A {BACILLUS PHAGE SPP1}; Related PDB entries: 5A21_C 5A20_C 5A20_D 2KBZ_A**

Probability: 23.69 E-value: 440.0 Score: 16.72 Aligned Cols: 26 Identities: 19% Similarity: 0.243

```
Q ss_pred              CCCCcchhhhHHHHHHHHHHHHHcC
Q Zetzy_3980     59    IPGKLDDQIIDPIVKRGLEIFRDLTR  84 (85)
Q Consensus      59    IPG~lDD~IiDplV~Ra~~~fr~~~~  84 (85)
                       ++++-||.++..++..|-+...+...
T Consensus      12    ~~~~~~D~~l~~~i~~A~~~i~~~~~  37 (102)
T 5A21_D         12    ITNDKHDEYLTEMVPLLVEFAKDECH  37 (102)
```

```
T ss_dssp          SHHHHCHHHHHHHHHHHHHHSSSSC
T ss_pred          CCCccchHHHHHHHHHHHHHHHHHhC
```

Template alignment | CDD

☐ **51.** **PF16984.5 ; Grp7_allergen ; Group 7 allergen**

Probability: 23.45 E-value: 570.0 Score: 17.48 Aligned Cols: 31 Identities: 10% Similarity: 0.251

```
Q ss_pred          ChHHHHHHHHHHHHHHHHHHHHHHHHHhhHH
Q Zetzy_3980   1   MLATIAKLIAQALLPIIAKQIAEEFGKHVEP  31 (85)
Q Consensus    1   ~~~~~~~~i~~~l~p~I~~aVa~ei~k~ipa  31 (85)
                   ++..+...+...+.+.|.+.+..++.+.+..
T Consensus    152 ~~~~~~~~~~~~~~~~i~~~i~~~i~~~i~~  182 (184)
T PF16984.5    152 MANIFVNIITTVFRNTITNVVSNGIHDFIQA  182 (184)
T ss_pred          HHHHHHHHHHHHhHHHHHHHHHHHHHHHHHh
```

Template alignment | CDD

☐ **52.** **PF05589.11 ; DUF768 ; Protein of unknown function (DUF768)**

Probability: 23.44 E-value: 520.0 Score: 16.99 Aligned Cols: 55 Identities: 11% Similarity: 0.098

```
Q ss_pred          HHHHHHHHHHHHHHh-------HHHHHHHHHHHHHHHcchhcchhHHhhcCCCCcchhhhHHH
Q Zetzy_3980   15  PIIAKQIAEEFGKHV-------EPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPI  71 (85)
Q Consensus    15  p~I~~aVa~ei~k~i-------pal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDpl  71 (85)
                   .+..+++-++|.+|+       +.-...++..+...+.. +-=+.+.|.+.+ |++-..|.|.+
T Consensus    3   ~r~~~Fld~Wi~~~~~~~~~~d~~~v~~la~~l~adA~~-~GI~~~ei~ee~-gdl~~~i~~a~  64 (64)
T PF05589.11   3   TRGINFLDQWIANNIPETTKADVISVDELTHKLIADAKA-LGIKRGEIDEEV-DSLYRTILDAI  64 (64)
T ss_pred          HHHHHHHHHHHHHhCCCCCcCCccCHHHHHHHHHHHHHH-cCCCHHHHHHHH-hhHHHHHHHhC
```

Template alignment | CDD

☐ **53.** **PF02061.16 ; Lambda_CIII ; Lambda Phage CIII**

Probability: 23.31 E-value: 420.0 Score: 17.28 Aligned Cols: 22 Identities: 14% Similarity: 0.354

```
Q ss_pred          CCcchhhHHHHHHHHHHHHHh
Q Zetzy_3980   61  GKLDDQIIDPIVKRGLEIFRDL  82 (85)
Q Consensus    61  G~lDD~IiDplV~Ra~~~fr~~  82 (85)
                   |-.....+|+++.|....+|++
T Consensus    11  g~~~ES~Ldri~rrlr~~~r~l  32 (42)
T PF02061.16   11  GCPSESLLERITRKLRDGWKRL  32 (42)
T ss_pred          CCCCHHHHHHHHHHHHHHHHH
```

Template alignment | CDD

☐ **54.** **PF04344.13 ; CheZ ; Chemotaxis phosphatase, CheZ**

Probability: 22.93 E-value: 800.0 Score: 19.0 Aligned Cols: 56 Identities: 18% Similarity: 0.205

```
Q ss_pred          hHHHHHHHHHHHHHHHHH-HHHHHHHHHhHHHHHHH--HHHHHHHHHcchhcchhHHHh
Q Zetzy_3980   2   LATIAKLIAQALLPIIAK-QIAEEFGKHVEPLTKAL--VTAVTEAAATGAERGADKLTD  57 (85)
Q Consensus    2   ~~~~~~~i~~~l~p~I~~-aVa~ei~k~ipal~kav--V~av~Eaa~~~a~~gaDkiTD  57 (85)
                   +..+++.|...+...=.. ...+.-...+|...+.|  |...+|.+++.....+|.+-+
T Consensus    7   lg~l~r~l~~~~~~l~~~~~~~~~~~~~~ip~a~~~L~~V~~~TE~Aa~~ild~~E~i~~  65 (211)
T PF04344.13   7   VGKLTRQLHDSLNNFQIDERIANLMQDEIPDARSRLIYVIEETEKAANTTMDAVEKCMP  65 (211)
T ss_pred          HHHHHHHHHHHHHHccccHHHHHHHHHcChHHHHHHHHHHHHHHHHHHHHHHHHHHHH
```

Template alignment | CDD

☐ **55.** **PF06074.12 ; DUF935 ; Protein of unknown function (DUF935)**

Probability: 22.56 E-value: 1100.0 Score: 20.49 Aligned Cols: 63 Identities: 10% Similarity: 0.001

```
Q ss_pred              HHHHHHHHHHhHHHHHHHHHHHHHHHHcchhcchhHHHhcCCCCcchhhhHHHHHHHHHHHHHHcC
Q Zetzy_3980     19    KQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIFRDLTR  84 (85)
Q Consensus      19    ~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~fr~~~~  84 (85)
                       +.+-+.+++..+.+++.|..++.++  ++.++..++|....| ++|+.-+-..+.+++-..+-.++
T Consensus      475   ~~~d~~~~~~~~~~~~~i~~~~~~a-~~s~ee~~~~L~~~~~-~~~~~~l~~~l~~a~~~a~l~G~  537 (539)
T PF06074.12     475   ATVEALSRQVQEELVAPLLARLQAC--GSFEEALATVQTGFD-HAATEGLGHRLARAGFIANLYGQ  537 (539)
T ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHC--CCHHHHHHHHHHhhc-cCCHHHHHHHHHHHHHHHHHhhc
```

Template alignment | Template 3D structure | PDBe

☐ **56.** **1KMI_Z Chemotaxis protein cheY, Chemotaxis protein; four-helix bundle, SIGNALING PROTEIN; HET: BCN; 2.9A {Escherichia coli} SCOP: h.4.11.1**

Probability: 22.42 E-value: 890.0 Score: 19.29 Aligned Cols: 56 Identities: 16% Similarity: 0.211

```
Q ss_pred              hHHHHHHHHHHHHHHHHHHHHHHHHHHhhHHHHHHH--HHHHHHHHHcchhcchhHHHh
Q Zetzy_3980     2     LATIAKLIAQALLPIIAKQIAEEFGKHVEPLTKAL--VTAVTEAAATGAERGADKLTD  57 (85)
Q Consensus      2     ~~~~~~~i~~~l~p~I~~aVa~ei~k~ipal~kav--V~av~Eaa~~~a~~gaDkiTD  57 (85)
                       +..+++.|-..+...=.+.-..+....+|.....+  |...+|.+++.....+|++-+
T Consensus      21    ig~l~r~Lh~~l~~l~~d~~l~~~~~~lp~A~~~L~~V~~~TE~AA~~iLd~vE~~~~  78 (214)
T 1KMI_Z         21    IGSLTRMLRDSLRELGLDQAIAEAAEAIPDARDRLYYVVQMTAQAAERALNSVEASQP  78 (214)
T ss_dssp              HHHHHHHHHHHHHHHTHHHHHHHTTTTHHHHHHHTTTHHHHHHHTTTHHHHHHHHHHH
T ss_pred              HHHHHHHHHHHHHHcCccHHHHHHHHhhHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

☐ **57.** **1MP1_A Ser/Arg-related nuclear matrix protein; four helix bundle, RNA BINDING; NMR {Homo sapiens} SCOP: l.1.1.1, a.188.1.1**

Probability: 22.31 E-value: 630.0 Score: 17.97 Aligned Cols: 63 Identities: 11% Similarity: 0.2

```
Q ss_pred              HHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHH-HHcchhcchhHHHhcCCCCcchhhhHHHHHHHHHHH
Q Zetzy_3980     11    QALLPIIAKQIAEEFGKHVEPLTKALVTAVTEA-AATGAERGADKLTDYIPGKLDDQIIDPIVKRGLEIF  79 (85)
Q Consensus      11    ~~l~p~I~~aVa~ei~k~ipal~kavV~av~Ea-a~~~a~~gaDkiTD~IPG~lDD~IiDplV~Ra~~~f  79 (85)
                       ..+.|.|.+.|.+.+...=+.+.+.++.-|.+. ...      .++.+.+-+-+|+.---++|.+....+
T Consensus      23    ~~lrpwI~kki~e~lG~ed~~lv~~i~~~L~~~~~~~------~~l~~~L~~~Ld~~~a~~Fv~~Lw~~l  86 (111)
T 1MP1_A         23    EVIKPWITKRVTEILGFEDDVVIEFIFNQLEVKNPDS------KMMQINLTGFLNGKNAREFMGELWPLL  86 (111)
T ss_dssp              GGGHHHHHHHHHHHHSSCCSHHHHHHHHHTTSSSCCH------HHHHHHHTTTSCSHHHHHHHHHHHHH
T ss_pred              HHHHHHHHHHHHHHcCCCcHHHHHHHHHHHhccCCCh------HHHHHHHHHHcCchhHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

☐ **58.** **3F42_B protein HP0035; Helicobacter pylori Unknown-function, Structural Genomics; HET: EDO, MSE; 1.78A {Helicobacter pylori} SCOP: d.222.1.0; Related PDB entries: 3F42_A**

Probability: 22.23 E-value: 500.0 Score: 17.3 Aligned Cols: 32 Identities: 13% Similarity: 0.157

```
Q ss_pred              HHHHHHHHHHHHHHHHcchhcchhHHHhcCCC
Q Zetzy_3980     30    EPLTKALVTAVTEAAATGAERGADKLTDYIPG  61 (85)
Q Consensus      30    pal~kavV~av~Eaa~~~a~~gaDkiTD~IPG  61 (85)
                       ..|-+.|+.++.++..+..........+..||
T Consensus      64    ~~L~~~i~~a~~~A~~~a~~~~~~~~~~~~~~  95 (99)
T 3F42_B         64    EAMQIYLMSALNDGYKAVEENRKNLAFNMLGN  95 (99)
T ss_dssp              HHHHHHHHHHHHHHHHHHHHHHHHHHHHHC--
T ss_pred              HHHHHHHHHHHHHHHHHHHHHHHHHHHhhhcc
```

Template alignment | Template 3D structure | PDB | NCBI

☐ **59.** **d1jwya4 c.37.1.8 (A:786-1091) Dynamin G domain {Slime mold (Dictyostelium discoideum) [TaxId: 44689]}**

Probability: 21.8 E-value: 790.0 Score: 18.48 Aligned Cols: 31 Identities: 10% Similarity: 0.071

```
Q ss_pred              HHHHHHHHHHHHHHHHHHhHHHHHHHHHHH
Q Zetzy_3980     10    AQALLPIIAKQIAEEFGKHVEPLTKALVTAV  40 (85)
Q Consensus      10    ~~~l~p~I~~aVa~ei~k~ipal~kavV~av  40 (85)
```

```
                        ...|...+.+.+...+.+++|.+.+-+...|
T Consensus     275     ~~~l~~~l~~~l~~~~~~~lp~~~~~~~~~~  305 (306)
T d1jwya4       275     TAYLSKTLNKLLMFHIRDTLPDLKVKVSKML  305 (306)
T ss_dssp               HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHT
T ss_pred               HHHHHHHHHHHHHHHHHHHCHHHHHHHHHHc
```

Template alignment | Template 3D structure | PDB | NCBI

☐ **60.** **g1o7d.1 a.8.3.1 (B:385-422,C:431-487) Lysosomal alpha-mannosidase {Cow (Bos taurus) [TaxId: 9913]}**

Probability: 21.67 E-value: 470.0 Score: 17.03 Aligned Cols: 26 Identities: 15% Similarity: 0.239

```
Q ss_pred               hcCCCCcchhhhHHHHHHHHHHHHHh
Q Zetzy_3980    57      DYIPGKLDDQIIDPIVKRGLEIFRDL  82 (85)
Q Consensus     57      D~IPG~lDD~IiDplV~Ra~~~fr~~  82 (85)
                        |.|||.-=|...+...++..+..+..
T Consensus     56      D~i~Gt~~~~v~~~~~~~l~~~~~~~  81 (96)
T g1o7d.1       56      DAVSGTSRQHVANDYARQLSEGWRPC  81 (96)
T ss_dssp               TTTTCCSCHHHHHHHHHHHHHHHHHH
T ss_pred               cCCCCCCHHHHHHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

☐ **61.** **3ZVR_A DYNAMIN-1 (E.C.3.6.5.5); HYDROLASE, DRP1, DRP, ENDOCYTOSIS, MITOCHONDRIAL; HET: 1PE; 3.1A {RATTUS NORVEGICUS}; Related PDB entries: 5A3F_C 5A3F_D 5A3F_A 5A3F_B 6DLU_B 6DLV_f 6DLV_c 6DLV_b 6DLV_g 6DLU_P 3SNH_A**

Probability: 21.64 E-value: 1300.0 Score: 20.73 Aligned Cols: 67 Identities: 12% Similarity: 0.197

```
Q ss_pred               HHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHcchhcchhHHhhcCCCCcch--hhhHHHHHHHHHH
Q Zetzy_3980    11      QALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIPGKLDD--QIIDPIVKRGLEI  78 (85)
Q Consensus     11      ~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IPG~lDD--~IiDplV~Ra~~~  78 (85)
                        ..|...+.+.+.+.+.+.+|.+.+.+...+.+.-.+     .+++.+..|.+..+  ..+..++.+..+.
T Consensus     295     ~~l~~~L~~~l~~~i~~~Lp~l~~~l~~~l~~~~~~-----L~~l~~~~~~~~~~~~~~l~~~i~~f~~~  359 (772)
T 3ZVR_A        295     PYLQKVLNQQLTNHIRDTLPGLRNKLQSQLLSIEKE-----VDEYKNFRPDDPARKTKALLQMVQQFAVD  359 (772)
T ss_dssp               HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-----HHHHHHHCCCSSSCSHHHHHHHHHHHHH
T ss_pred               HHHHHHHHHHHHHHHHHhCHHHHHHHHHHHHHHHHH-----HHHccCCCCCCHHHHHHHHHHHHHHHHH

Q ss_pred               HHHHh
Q Zetzy_3980    79      FRDL  82 (85)
Q Consensus     79      fr~~  82 (85)
                        |+..
T Consensus     360     ~~~~  363 (772)
T 3ZVR_A        360     FEKR  363 (772)
T ss_dssp               HHHH
T ss_pred               HHHH
```

Template alignment | CDD

☐ **62.** **PF15005.6 ; IZUMO ; Izumo sperm-egg fusion, Ig domain-associated**

Probability: 21.44 E-value: 380.0 Score: 20.42 Aligned Cols: 28 Identities: 28% Similarity: 0.592

```
Q ss_pred               hhcCCCCcchhhhHHHHHHHHHHHHHhc
Q Zetzy_3980    56      TDYIPGKLDDQIIDPIVKRGLEIFRDLT  83 (85)
Q Consensus     56      TD~IPG~lDD~IiDplV~Ra~~~fr~~~  83 (85)
                        ++.+|+.+|-.-...+..|+-+.++++.
T Consensus     18      ~~~~P~~~~~~~~~~l~~r~~~~l~~~~  45 (145)
T PF15005.6     18      KDYLPSHLDEKHHQHLMKRVHDALKALQ  45 (145)
T ss_pred               HccCcccCCHHHHHHHHHHHHHHHHhcc
```

Template alignment | Template 3D structure | PDB | NCBI

☐ **63.** d1l2ra_ **c.1.25.1 (A:) Monomethylamine methyltransferase MtmB {Methanosarcina barkeri [TaxId: 2208]}**

Probability: 21.43 E-value: 340.0 Score: 23.34 Aligned Cols: 24 Identities: 17% Similarity: 0.322

```
Q ss_pred              CCCcchhhhHHHHHHHHHHHHHc
Q Zetzy_3980     60    PGKLDDQIIDPIVKRGLEIFRDLT  83 (85)
Q Consensus      60    PG~lDD~IiDplV~Ra~~~fr~~~  83 (85)
                       |=.-||+..|++-.+++++|++.+
T Consensus      50    ~v~~d~~~~d~~~~~alell~~~G  73 (457)
T d1l2ra_        50    FIPTDKDMMEKLFKAGFEMLLECG  73 (457)
T ss_dssp              SSCCCHHHHHHHHHHHHHHHHHC
T ss_pred              cCCCCHHHHHHHHHHHHHHHHcC
```

Template alignment | CDD

☐ **64.** PF16007.5 **; DUF4777 ; Domain of unknown function (DUF4777)**

Probability: 21.3 E-value: 440.0 Score: 15.36 Aligned Cols: 54 Identities: 17% Similarity: 0.143

```
Q ss_pred              ChHHHHHHHHHHHH--------HHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHcchhcchhH
Q Zetzy_3980     1     MLATIAKLIAQALL--------PIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADK  54 (85)
Q Consensus      1     ~~~~~~~~i~~~l~--------p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDk  54 (85)
                       |+-..+..|-..|-        +.|.+.+.+++....+.+.+.+...+.+-..++...-.+.
T Consensus      1     ~ln~~~~~i~~~l~~~~~~~t~~~i~~~~~~~~~~~~~~~~~v~~~l~~l~~~gli~~~~~  62 (66)
T PF16007.5      1     MPNFNGAIIVHTLQLLKIPATVRQIVNTISNHTDLPEEDIKKPVKQTLEMGTRLGFLQKMDG  62 (66)
T ss_pred              CCcchHHHHHHHHHCCCCCCHHHHHHHHHHhcCCCHHHhHHHHHHHHHHHHHHcccceEeeCC
```

Template alignment | Template 3D structure | PDBe

☐ **65.** 1NTH_A **Monomethylamine methyltransferase mtmB1 (E.C.2.1.1.-); TIM BARREL, TRANSFERASE; 1.55A {Methanosarcina barkeri} SCOP: c.1.25.1; Related PDB entries: 1TV4_A 1TV3_A 1L2Q_A 1TV2_A**

Probability: 21.12 E-value: 340.0 Score: 23.39 Aligned Cols: 24 Identities: 17% Similarity: 0.322

```
Q ss_pred              CCCcchhhhHHHHHHHHHHHHHc
Q Zetzy_3980     60    PGKLDDQIIDPIVKRGLEIFRDLT  83 (85)
Q Consensus      60    PG~lDD~IiDplV~Ra~~~fr~~~  83 (85)
                       |=.-||+..|++-..++++|++.+
T Consensus      51    ~~~~d~~~~d~~~~~al~ll~~~G  74 (458)
T 1NTH_A         51    FIPTDKDMMEKLFKAGFEMLLECG  74 (458)
T ss_dssp              SSCCCHHHHHHHHHHHHHHHHHC
T ss_pred              cCCCCHHHHHHHHHHHHHHHHcC
```

Template alignment | Template 3D structure | PDBe

☐ **66.** 1U9P_A **pArc; Arc, pArc, UNKNOWN FUNCTION; 1.9A {Escherichia coli} SCOP: a.43.1.0**

Probability: 20.89 E-value: 790.0 Score: 18.14 Aligned Cols: 70 Identities: 13% Similarity: 0.134

```
Q ss_pred              HHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHcch----------hcchhHHhhcCCCCcchhhhHHHHHH
Q Zetzy_3980     15    PIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGA----------ERGADKLTDYIPGKLDDQIIDPIVKR  74 (85)
Q Consensus      15    p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a----------~~gaDkiTD~IPG~lDD~IiDplV~R  74 (85)
                       |.+.+++...-.++=-.+-.-|+.+|.+.+....          .+..-.+....-|...+.+-+.+..+
T Consensus      27    ~el~~~L~~~A~~~grS~N~eIv~~L~~~l~~~~~~~~~~~~~~~~e~l~~~~~~a~~~~~~~~~eii~~  96 (120)
T 1U9P_A         27    REVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIGGTGGSGGGREVLDLVRKVAEENGRSVNSEIYQR  96 (120)
T ss_dssp              HHHHHHHHHHHHHHTCCHHHHHHHHHHHHHHHTTSCCC-----CSHHHHHHHHHHHHHHTCCHHHHHHHH
T ss_pred              HHHHHHHHHHHHHcCCCHHHHHHHHHHHHHHHHcCCcCCCCCCCCHHHHHHHHHHHHHHHcCCCcCHHHHHH

Q ss_pred              HHHHHHHHcC
Q Zetzy_3980     75    GLEIFRDLTR  84 (85)
Q Consensus      75    a~~~fr~~~~  84 (85)
                       ..+.+|+-.+
T Consensus      97    i~~~lk~~~~  106 (120)
T 1U9P_A         97    VMESFKKEGR  106 (120)
```

```
T ss_dssp              HHHHHHHTTC
T ss_pred              HHHHHhhcCc
```

Template alignment | CDD

67. **PF09052.10 ; SipA ; SipA N-terminal domain**

Probability: 20.87 E-value: 880.0 Score: 20.8 Aligned Cols: 53 Identities: 34% Similarity: 0.517

```
Q ss_pred              hHHHH-------------HHHHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHcchhcchhH
Q Zetzy_3980     2     LATIA-------------KLIAQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADK  54 (85)
Q Consensus      2     ~~~~~--------------~~i~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDk  54 (85)
                       |+.++              +++.....|-|.+-|...+....+..+-.=.+-|+.+++..|.++.+.
T Consensus      110   La~l~~~~~~gd~~~Lg~~fm~~EVmp~I~~~IE~qlG~~Ld~~t~~~i~gLVd~aA~~AfdaLr~  175 (214)
T PF09052.10     110   LLDIIKNNTGGELSKLSTNLVMQEVMPYIASCIEHNFGCTLDPLTRSNLTHLVDKAAAKAVEALDM  175 (214)
T ss_pred              HHHHHHHHccccHHHHHHHHHHHhHHHHHHHHHHHHHhCCCCCHHHHHHHHHHhhHHHHHHHHHHHH
```

Template alignment | CDD

68. **PF06585.11 ; JHBP ; Haemolymph juvenile hormone binding protein (JHBP)**

Probability: 20.86 E-value: 810.0 Score: 18.23 Aligned Cols: 46 Identities: 2% Similarity: -0.052

```
Q ss_pred              HHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHcchhcchhHHHhcCC
Q Zetzy_3980     15    PIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLTDYIP  60 (85)
Q Consensus      15    p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiTD~IP  60 (85)
                       +...+.+.+.+.+..+.+.+.+...+.+.+.+.......++-..+|
T Consensus      184   ~~l~~~~~~~ln~~~~~~~~~~~~~i~~~~~~~~~~~~n~~l~~~p  229 (235)
T PF06585.11     184   HWANDALNKLLNDNSRLLFNSFSQIAEKMVQDVFAEALKPMLLNYS  229 (235)
T ss_pred              HHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHHHHHHHHHHhcCC
```

Template alignment | Template 3D structure | PDBe

69. **1Z67_A hypothetical protein S4005; structural genomics, hypothetical protein, Shigella; 1.45A {Shigella flexneri 2a} SCOP: a.259.1.1**

Probability: 20.39 E-value: 880.0 Score: 18.48 Aligned Cols: 66 Identities: 9% Similarity: 0.143

```
Q ss_pred              HHHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHcchhcchhHHh--hcCCCCcchhhhHHHHHHHHH
Q Zetzy_3980     10    AQALLPIIAKQIAEEFGKHVEPLTKALVTAVTEAAATGAERGADKLT--DYIPGKLDDQIIDPIVKRGLE  77 (85)
Q Consensus      10    ~~~l~p~I~~aVa~ei~k~ipal~kavV~av~Eaa~~~a~~gaDkiT--D~IPG~lDD~IiDplV~Ra~~  77 (85)
                       ..++..-+-....+++.++.+.=.+++...+++-.-+    .+|++|  ..+|.+.+..+.+..++-+..
T Consensus      66    ~~qi~~~lg~~~i~~lA~~~Gl~~~~~~~~La~~LP~-----~vd~~tp~G~~~~~~~~~~~~~~~~~~~  131 (135)
T 1Z67_A         66    GEQLESALGTNAVSDLGQKLGVDTSTASSLLAEQLPK----IIDALSPQGEVSAQANNDLLSAGMELLKG  131 (135)
T ss_dssp              HHHHHHHHCHHHHHHHHHHHTCCHHHHHHHHHHHHHH----HHHHTCTTSCC--CTTTCHHHHHHHHHH
T ss_pred              HHHHHHHHCHHHHHHHHHHCCCHHHHHHHHHHHHHH----HHHHcCCCCCCCchhchHHHHHHHHHhh

Q ss_pred              HH
Q Zetzy_3980     78    IF  79 (85)
Q Consensus      78    ~f  79 (85)
                       .+
T Consensus      132   ~~  133 (135)
T 1Z67_A         132   KL  133 (135)
T ss_dssp              HH
T ss_pred              hh
```

References

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

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