Phyre^2

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Description	P0AB35
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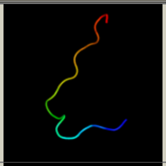
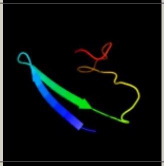
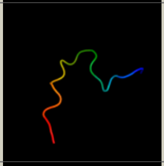
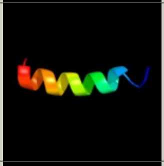
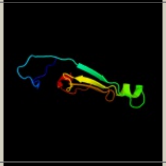
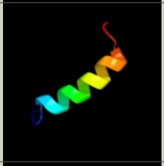
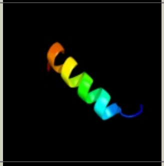
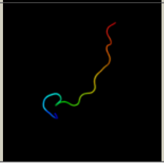
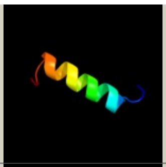
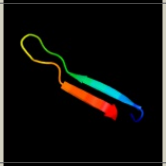
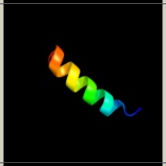
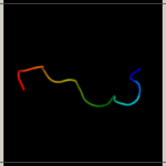
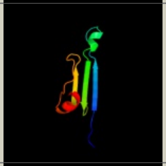
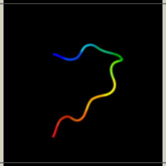
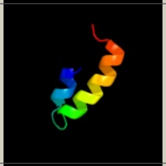
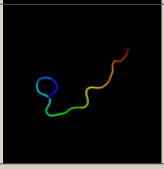
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i4ma_	Alignment		39.7	28	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
2	c2lbgA_	Alignment		23.2	37	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major prion protein; **PDBTitle:** structure of the chr of the prion protein in dpc micelles
3	c1v7wA_	Alignment		22.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
4	c2cqtA_	Alignment		22.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
5	d1u5la_	Alignment		21.8	39	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
6	c3hfwA_	Alignment		21.2	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
7	d1ktdb2	Alignment		20.7	18	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
8	d1i3rb2	Alignment		17.4	18	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
9	c2qtyB_	Alignment		16.0	41	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(adp-ribose) glycohydrolase arh3; **PDBTitle:** crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
10	d1t5ja_	Alignment		16.0	36	**Fold:**ADP-ribosylglycohydrolase **Superfamily:**ADP-ribosylglycohydrolase **Family:**ADP-ribosylglycohydrolase
11	d1u3ma_	Alignment		15.9	39	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like

12	c3g9dB_	Alignment		13.6	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dinitrogenase reductase activacting **PDBTitle:** crystal structure glycohydrolase
13	c1i7oC_	Alignment		11.5	30	**PDB header:**isomerase, lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate degradation bifunctional **PDBTitle:** crystal structure of hpce
14	c2wocA_	Alignment		11.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosyl-[dinitrogen reductase] glycohydrolase; **PDBTitle:** crystal structure of the dinitrogenase reductase-activating2 glycohydrolase (drag) from rhodospirillum rubrum
15	d1xyka_	Alignment		10.3	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
16	d1bx2b2	Alignment		9.8	12	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
17	d2vv5a1	Alignment		9.4	18	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
18	c1amlA_	Alignment		9.2	31	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**amyloid a4; **PDBTitle:** the alzheimer`s disease amyloid a4 peptide (residues 1-40)
19	c2yzwA_	Alignment		8.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosylglycohydrolase; **PDBTitle:** adp-ribosylglycohydrolase-related protein complex
20	d1xyxa_	Alignment		8.9	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
21	d1xyqa_	Alignment	not modelled	8.9	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
22	d1nppa2	Alignment	not modelled	8.8	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
23	d1d5mb2	Alignment	not modelled	7.6	13	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
24	d1xyua_	Alignment	not modelled	7.5	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
25	d2gu3a1	Alignment	not modelled	7.4	24	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**PepSY-like
26	d1v7wa1	Alignment	not modelled	6.6	21	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
27	d1q5xa_	Alignment	not modelled	6.2	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
28	d2ifra1	Alignment	not modelled	5.8	18	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Peptidase A4
29	c3ge2A_	Alignment	not modelled	5.5	27	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**lipoprotein, putative; **PDBTitle:** crystal structure of putative lipoprotein sp_0198 from

						streptococcus2 pneumoniae
30	d1fngb2	Alignment	not modelled	5.4	15	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
31	c1iclA_	Alignment	not modelled	5.4	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**th1ox; **PDBTitle:** solution structure of designed beta-sheet mini-protein th1ox
32	d1nfia2	Alignment	not modelled	5.4	13	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**Rel/Dorsal transcription factors, DNA-binding domain
33	d1mj4a_	Alignment	not modelled	5.3	42	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
34	c2jcbA_	Alignment	not modelled	5.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formyltetrahydrofolate cyclo-ligase family protein; **PDBTitle:** the crystal structure of 5-formyl-tetrahydrofolate2 cycloligase from bacillus anthracis (ba4489)
35	c2rfuA_	Alignment	not modelled	5.1	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**influenza b hemagglutinin (ha); **PDBTitle:** crystal structure of influenza b virus hemagglutinin in complex with2 lstc receptor analog
36	c3c8oB_	Alignment	not modelled	5.1	25	**PDB header:**hydrolase regulator **Chain:** B: **PDB Molecule:**regulator of ribonuclease activity a; **PDBTitle:** the crystal structure of rraa from pao1