Phyre^2

Email	l.a.kelley@imperial.ac.uk
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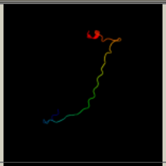
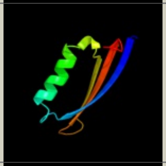
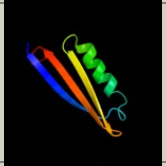
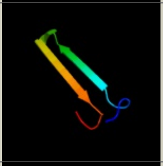
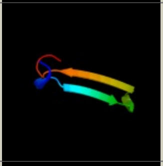
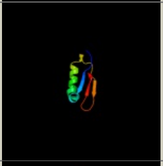
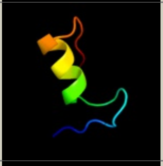
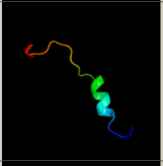
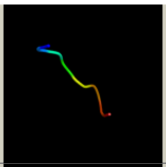
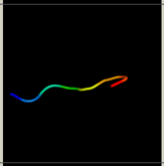
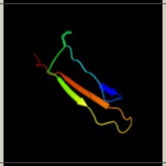
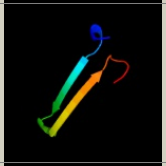
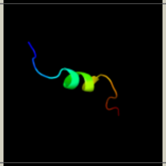
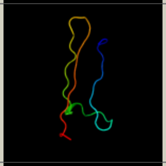
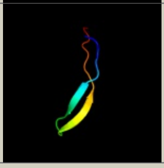
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n7xA_	Alignment		52.5	27	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** crystal structure of penaeus stylirostris densovirus capsid
2	d1q5ya_	Alignment		45.8	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Nickel responsive regulator NikR, C-terminal domain
3	c2y3yC_	Alignment		43.2	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** holo-ni(ii) hpnikr is a symmetric tetramer containing four2 canonic square-planar ni(ii) ions at physiological ph
4	d2bj7a2	Alignment		34.5	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Nickel responsive regulator NikR, C-terminal domain
5	d1e8oa_	Alignment		28.1	10	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
6	d1914a1	Alignment		22.7	11	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
7	c2ca9B_	Alignment		21.5	12	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
8	c2bj3D_	Alignment		20.9	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
9	d2b5ib1	Alignment		20.8	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
10	d3seba1	Alignment		20.1	27	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
11	c3l4qA_	Alignment		14.0	63	**PDB header:**viral protein/protein binding **Chain:** A: **PDB Molecule:**non-structural protein 1; **PDBTitle:** structural insights into phosphoinositide 3-kinase2 activation by the influenza a virus ns1 protein

12	c3d6rA_	Alignment		13.7	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 1; **PDBTitle:** structure of an avian influenza a virus ns1 protein2 effector domain
13	d2gx9a1	Alignment		13.6	63	**Fold:**Ns1 effector domain-like **Superfamily:**Ns1 effector domain-like **Family:**Ns1 effector domain-like
14	d1c5cl2	Alignment		12.7	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
15	c3f5tA_	Alignment		11.3	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nonstructural protein 1; **PDBTitle:** x-ray structure of h5n1 ns1
16	c1914A_	Alignment		10.6	11	**PDB header:**alu domain **Chain:** A: **PDB Molecule:**signal recognition particle 9/14 fusion protein; **PDBTitle:** signal recognition particle alu rna binding heterodimer, srp9/14
17	d1bxta1	Alignment		10.4	25	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
18	d1hyrc1	Alignment		10.0	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
19	d1je6a1	Alignment		8.5	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
20	c2e12B_	Alignment		8.2	24	**PDB header:**translation **Chain:** B: **PDB Molecule:**hypothetical protein xcc3642; **PDBTitle:** the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif
21	c2ns6A_	Alignment	not modelled	7.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mobilization protein a; **PDBTitle:** crystal structure of the minimal relaxase domain of moba2 from plasmid r1162
22	c3d33B_	Alignment	not modelled	7.2	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**domain of unknown function with an immunoglobulin-like **PDBTitle:** crystal structure of a duf3244 family protein with an immunoglobulin-2 like beta-sandwich fold (bvu_0276) from bacteroides vulgatus atcc3 8482 at 1.70 a resolution
23	c3mx7A_	Alignment	not modelled	6.9	12	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
24	d1tzoa_	Alignment	not modelled	6.7	16	**Fold:**Anthrax protective antigen **Superfamily:**Anthrax protective antigen **Family:**Anthrax protective antigen
25	d1irub_	Alignment	not modelled	6.4	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
26	c1cqtJ_	Alignment	not modelled	6.4	19	**PDB header:**gene regulation/dna **Chain:** J: **PDB Molecule:**pou domain, class 2, associating factor 1; **PDBTitle:** crystal structure of a ternary complex containing an oca-b2 peptide, the oct-1 pou domain, and an octamer element
27	c2p64B_	Alignment	not modelled	6.1	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**f-box/wd repeat protein 1a; **PDBTitle:** d domain of b-trcp
28	d2q86b2	Alignment	not modelled	6.1	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)

29	c3sqgF_	Alignment	not modelled	5.6	28	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methyl-coenzyme m reductase, gamma subunit; **PDBTitle:** crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
30	c3n1uA_	Alignment	not modelled	5.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, had superfamily, subfamily iii a; **PDBTitle:** structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila