Phyre^2

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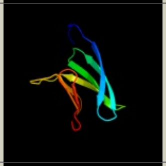
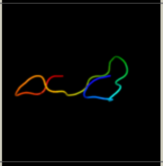
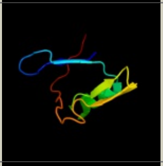
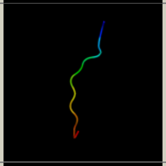
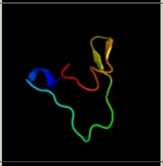
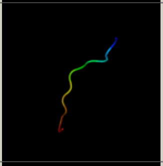
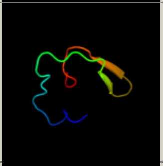
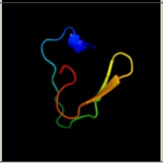
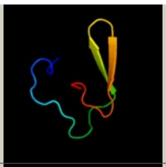
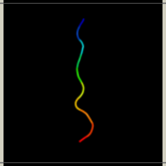
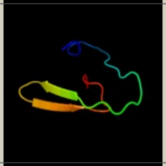
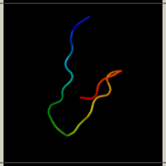
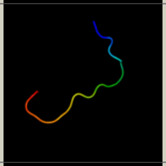
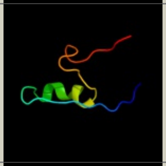
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2f09a1	Alignment		99.9	100	**Fold:**Streptavidin-like **Superfamily:**YdhA-like **Family:**YdhA-like
2	c3f6zB_	Alignment		99.8	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pseudomonas aeruginosa mlic in complex2 with hen egg white lysozyme
3	c3oe3B_	Alignment		99.8	22	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**putative periplasmic protein; **PDBTitle:** crystal structure of plic-st, periplasmic lysozyme inhibitor of c-type2 lysozyme from salmonella typhimurium
4	d1e88a3	Alignment		54.1	21	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
5	d1zpsa1	Alignment		31.2	15	**Fold:**HisI-like **Superfamily:**HisI-like **Family:**HisI-like
6	d1c01a_	Alignment		21.3	36	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Plant antimicrobial protein MIAMP1
7	d1wmxb_	Alignment		19.6	38	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
8	c3r7tA_	Alignment		17.2	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni
9	d1wmxa_	Alignment		16.2	38	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
10	d1qf5a_	Alignment		15.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
11	d1p9ba_	Alignment		14.0	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like

12	c1iweB_	Alignment		12.8	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** imp complex of the recombinant mouse-muscle2 adenylosuccinate synthetase
13	d2psmc1	Alignment		12.1	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
14	d1iwea_	Alignment		11.0	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
15	c2jgwA_	Alignment		10.9	10	**PDB header:**immune response **Chain:** A: **PDB Molecule:**complement factor h; **PDBTitle:** structure of ccp module 7 of complement factor h - the amd2 at risk varient (402h)
16	c2j42A_	Alignment		10.1	18	**PDB header:**toxin **Chain:** A: **PDB Molecule:**c2 toxin component-ii; **PDBTitle:** low quality crystal structure of the transport component c2-2 ii of the c2-toxin from clostridium botulinum
17	d2bosa_	Alignment		9.7	8	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
18	d1w44a_	Alignment		9.2	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
19	c3c0uA_	Alignment		9.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yaeq; **PDBTitle:** crystal structure of e.coli yaeq protein
20	d1hcca_	Alignment		9.0	30	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
21	c1hccA_	Alignment	not modelled	9.0	30	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**16th complement control protein; **PDBTitle:** three-dimensional structure of a complement control protein2 module in solution
22	c2z3rF_	Alignment	not modelled	8.9	20	**PDB header:**cytokine/cytokine receptor **Chain:** F: **PDB Molecule:**interleukin-15 receptor alpha chain; **PDBTitle:** crystal structure of the il-15/il-15ra complex
23	d2z3qb1	Alignment	not modelled	8.6	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
24	c1x3xA_	Alignment	not modelled	8.2	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome b5; **PDBTitle:** crystal structure of cytochrome b5 from ascaris suum
25	d1c4qa_	Alignment	not modelled	7.6	12	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
26	d2o39c1	Alignment	not modelled	7.3	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
27	c2jraB_	Alignment	not modelled	7.1	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein rpa2121; **PDBTitle:** a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
28	c2jgxA_	Alignment	not modelled	7.0	10	**PDB header:**immune response **Chain:** A: **PDB Molecule:**complement factor h; **PDBTitle:** structure of ccp module 7 of complement factor h - the amd2 not at risk varient (402y)

29	d1zjka2	Alignment	not modelled	7.0	10	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
30	d1gpza2	Alignment	not modelled	7.0	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
31	d1r4pb_	Alignment	not modelled	6.8	12	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
32	d1ly2a2	Alignment	not modelled	6.8	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
33	d1gkna1	Alignment	not modelled	6.8	30	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
34	c2qzfA_	Alignment	not modelled	6.6	30	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement decay-accelerating factor; **PDBTitle:** scr1 of daf from 1ojv fitted into cryoem density
35	d1edqa1	Alignment	not modelled	6.6	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
36	d1ok3a2	Alignment	not modelled	6.5	30	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
37	d1gkga2	Alignment	not modelled	6.2	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
38	c2d7uA_	Alignment	not modelled	6.2	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of hypothetical adenylosuccinate synthetase, ph04382 from pyrococcus horikoshii ot3
39	c3f0nB_	Alignment	not modelled	6.1	37	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mevalonate pyrophosphate decarboxylase; **PDBTitle:** mus musculus mevalonate pyrophosphate decarboxylase
40	d1ok3a1	Alignment	not modelled	6.0	30	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
41	d1dj2a_	Alignment	not modelled	5.8	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
42	d1quba1	Alignment	not modelled	5.8	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
43	d1dj3a_	Alignment	not modelled	5.6	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
44	d1h03p2	Alignment	not modelled	5.5	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
45	d1g40a2	Alignment	not modelled	5.5	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
46	c2fipA_	Alignment	not modelled	5.5	67	**PDB header:**transcription **Chain:** A: **PDB Molecule:**late genes activator; **PDBTitle:** phage phi29 transcription regulator p4
47	c2hkeB_	Alignment	not modelled	5.4	44	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diphosphomevalonate decarboxylase, putative; **PDBTitle:** mevalonate diphosphate decarboxylase from trypanosoma brucei
48	c1sy6A_	Alignment	not modelled	5.3	12	**PDB header:**signaling protein/antibiotic **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd3 gamma/epsilon **PDBTitle:** crystal structure of cd3gammaepsilon heterodimer in complex2 with okt3 fab fragment
49	d2o39c2	Alignment	not modelled	5.2	20	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain