Phyre^2

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Description	P0AFX0
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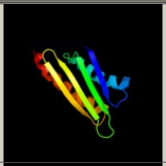
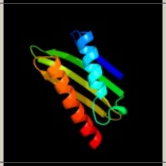
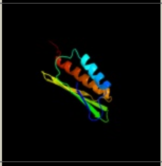
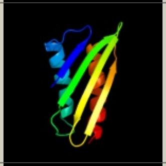
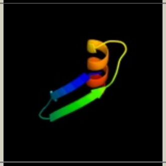
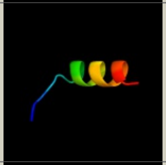
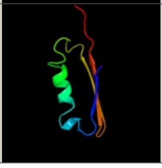
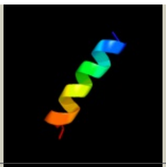
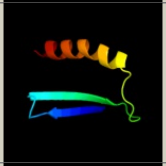
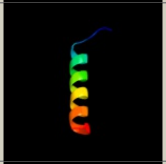
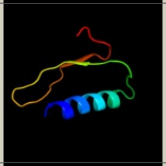
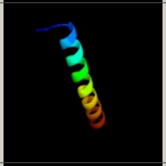
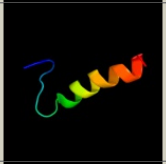
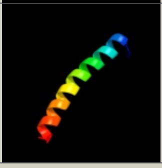
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rqlA_	Alignment		100.0	100	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable sigma-54 modulation protein; **PDBTitle:** solution structure of the e. coli ribosome hibernation2 promoting factor hpf
2	d1imua_	Alignment		100.0	34	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
3	c3tqmD_	Alignment		99.9	33	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** structure of an ribosomal subunit interface protein from coxiella2 burnetii
4	d1l4sa_	Alignment		99.9	38	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
5	d2ywqa1	Alignment		99.9	33	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
6	d1sr9a3	Alignment		24.2	22	**Fold:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Superfamily:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Family:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
7	c3f6hA_	Alignment		23.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-isopropylmalate synthase; **PDBTitle:** crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
8	d1uila_	Alignment		21.7	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
9	c3kxeD_	Alignment		19.9	18	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
10	c1i7nA_	Alignment		19.7	13	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin ii; **PDBTitle:** crystal structure analysis of the c domain of synapsin ii2 from rat brain
11	c2kxoA_	Alignment		19.2	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae

12	c1by0A_	Alignment		18.9	41	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
13	c1pk8D_	Alignment		18.0	9	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**rat synapsin i; **PDBTitle:** crystal structure of rat synapsin i c domain complexed to2 ca.atp
14	c2yh5A_	Alignment		17.6	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
15	d2clyc1	Alignment		16.6	17	**Fold:**Mitochondrial ATP synthase coupling factor 6 **Superfamily:**Mitochondrial ATP synthase coupling factor 6 **Family:**Mitochondrial ATP synthase coupling factor 6
16	d2r85a2	Alignment		12.3	8	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
17	d2hkja2	Alignment		12.2	23	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
18	d1vzsa_	Alignment		11.0	20	**Fold:**Mitochondrial ATP synthase coupling factor 6 **Superfamily:**Mitochondrial ATP synthase coupling factor 6 **Family:**Mitochondrial ATP synthase coupling factor 6
19	c3r9jD_	Alignment		11.0	9	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** D: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 4.3a resolution structure of a mind-mine(i24n) protein complex
20	c1mx0D_	Alignment		10.8	23	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
21	c2p0aA_	Alignment	not modelled	10.2	17	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin-3; **PDBTitle:** the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
22	d2e9xd1	Alignment	not modelled	9.8	20	**Fold:**GINS helical bundle-like **Superfamily:**GINS helical bundle-like **Family:**SLD5 N-terminal domain-like
23	c3r23B_	Alignment	not modelled	9.7	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
24	d1hk8a_	Alignment	not modelled	9.6	16	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
25	c1hk8A_	Alignment	not modelled	9.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
26	c3l2iB_	Alignment	not modelled	9.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
27	d1o6da_	Alignment	not modelled	8.9	10	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
28	c3ehuA	Alignment	not modelled	8.3	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fusion protein of crfr1 extracellular domain and mbp;

28	c3ehuA_	Alignment	not modelled	8.3	19	**PDBTitle:** crystal structure of the extracellular domain of human corticotropin2 releasing factor receptor type 1 (crfr1) in complex with crf
29	d1sfla_	Alignment	not modelled	8.2	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
30	d1gsoa3	Alignment	not modelled	8.2	5	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
31	d2i52a1	Alignment	not modelled	8.1	5	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
32	c3q2oB_	Alignment	not modelled	7.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
33	c3rd6A_	Alignment	not modelled	7.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mll3558 protein; **PDBTitle:** crystal structure of mll3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403
34	c1hf9B_	Alignment	not modelled	7.4	31	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
35	d1lr0a_	Alignment	not modelled	7.4	12	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
36	c2yr1B_	Alignment	not modelled	6.7	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
37	d2r7ka2	Alignment	not modelled	6.5	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
38	d1xppa_	Alignment	not modelled	6.1	13	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RBP11/RpoL
39	c1q0vA_	Alignment	not modelled	6.0	19	**PDB header:**transport binding **Chain:** A: **PDB Molecule:**hydrophilic protein; has cysteine rich putative **PDBTitle:** solution structure of tandem uims of vps27
40	d1ehia2	Alignment	not modelled	6.0	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
41	c3e5nA_	Alignment	not modelled	5.9	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
42	c2l5gB_	Alignment	not modelled	5.9	30	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative uncharacterized protein ncor2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
43	c1a92B_	Alignment	not modelled	5.9	35	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
44	c2l9pA_	Alignment	not modelled	5.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q5hli9 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147
45	c1g6uB_	Alignment	not modelled	5.7	23	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**domain swapped dimer; **PDBTitle:** crystal structure of a domain swapped dimer
46	c1ulzA_	Alignment	not modelled	5.7	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
47	d1ghha_	Alignment	not modelled	5.6	12	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
48	c3oqvA_	Alignment	not modelled	5.4	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**albc; **PDBTitle:** albc, a cyclodipeptide synthase from streptomyces noursei
49	c2q2eB_	Alignment	not modelled	5.3	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei