Phyre^2

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Description	Q47702
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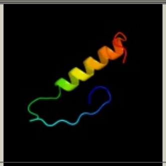
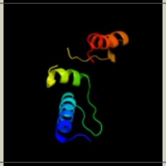
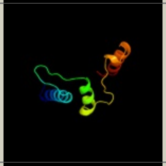
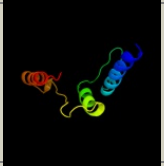
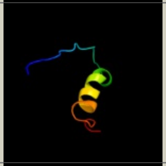
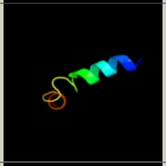
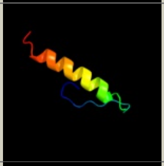
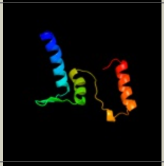
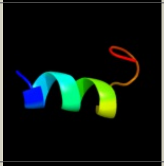
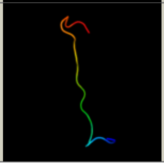
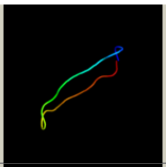
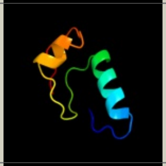
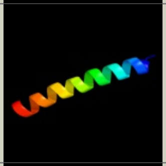
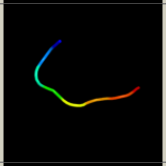
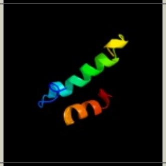
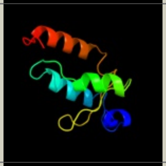
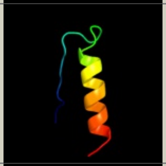
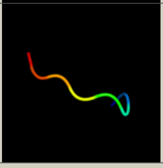
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t3ua_	Alignment		81.3	21	**Fold:**Cell division protein ZapA-like **Superfamily:**Cell division protein ZapA-like **Family:**Cell division protein ZapA-like
2	c2jtcA_	Alignment		66.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**streptopain; **PDBTitle:** 3d structure and backbone dynamics of spe b
3	d1dkia_	Alignment		63.8	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
4	d1pvja_	Alignment		55.5	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
5	d1v61a_	Alignment		44.3	21	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
6	d1iyjb5	Alignment		37.9	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
7	d1miua5	Alignment		28.7	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
8	c3hnwB_	Alignment		15.9	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
9	c3bb7A_	Alignment		15.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interpain a; **PDBTitle:** structure of prevotella intermedia prointerpain a fragment 39-3592 (mutant c154a)
10	d1o5ha_	Alignment		14.9	29	**Fold:**Methenyltetrahydrofolate cyclohydrolase-like **Superfamily:**Methenyltetrahydrofolate cyclohydrolase-like **Family:**Methenyltetrahydrofolate cyclohydrolase-like
11	c2eelA_	Alignment		14.9	30	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**cell death activator cide-a; **PDBTitle:** solution structure of the cide-n domain of human cell death2 activator cide-a

12	d1xaua_	Alignment		11.6	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
13	c3ln3A_	Alignment		11.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of putative reductase (np_038806.2) from2 mus musculus at 1.18 a resolution
14	c2p4vA_	Alignment		10.6	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
15	d2ae8a2	Alignment		10.1	50	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
16	d1rhya2	Alignment		10.1	38	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
17	d1mhqa_	Alignment		10.0	18	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
18	c3zyqA_	Alignment		9.6	15	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
19	c3cxbB_	Alignment		9.4	7	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**pleckstrin homology domain-containing family m **PDBTitle:** crystal structure of sifa and skip
20	d2f1da2	Alignment		9.2	38	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
21	c2hj3A_	Alignment	not modelled	9.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfhydryl oxidase erv1p; **PDBTitle:** structure of the arabidopsis thaliana erv1 thiol oxidase
22	d1eg3a2	Alignment	not modelled	8.8	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
23	d1mjda_	Alignment	not modelled	8.7	50	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
24	d2p6va1	Alignment	not modelled	8.7	27	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
25	d1f45b_	Alignment	not modelled	8.6	18	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
26	d1rxwa1	Alignment	not modelled	8.5	26	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
27	c2dnfA_	Alignment	not modelled	8.4	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**doublecortin domain-containing protein 2; **PDBTitle:** solution structure of rsgi ruh-062, a dcx domain from human
28	c3s6n2_	Alignment	not modelled	8.0	33	**PDB header:**splicing **Chain:** 2: **PDB Molecule:**survival of motor neuron protein-interacting protein 1; **PDB Fragment:**gemin2-binding domain; **PDBTitle:** crystal structure of the gemin2-binding domain of smn, gemin2 in2

						complex with smd1/d2/f/e/g from human
29	d1dj0a_	Alignment	not modelled	8.0	25	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase I TruA
30	d1mg4a_	Alignment	not modelled	7.8	50	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
31	d2aw2a1	Alignment	not modelled	7.6	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
32	d1huna_	Alignment	not modelled	7.5	0	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
33	c3bbaB_	Alignment	not modelled	7.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interpain a; **PDBTitle:** structure of active wild-type prevotella intermedia interpain a2 cysteine protease
34	d1jr8a_	Alignment	not modelled	7.3	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**FAD-dependent thiol oxidase **Family:**FAD-dependent thiol oxidase
35	c2ae8C_	Alignment	not modelled	7.3	50	**PDB header:**lyase **Chain:** C: **PDB Molecule:**imidazoleglycerol-phosphate dehydratase; **PDBTitle:** crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
36	d2cmda2	Alignment	not modelled	7.1	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
37	c1rhyB_	Alignment	not modelled	7.1	38	**PDB header:**lyase **Chain:** B: **PDB Molecule:**imidazole glycerol phosphate dehydratase; **PDBTitle:** crystal structure of imidazole glycerol phosphate dehydratase
38	d1dvpa1	Alignment	not modelled	7.0	17	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
39	c1tg6G_	Alignment	not modelled	7.0	14	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**putative atp-dependent clp protease proteolytic subunit; **PDBTitle:** crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
40	d1gvpa_	Alignment	not modelled	6.9	50	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
41	d1uf0a_	Alignment	not modelled	6.8	45	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
42	d1f5qb2	Alignment	not modelled	6.8	38	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
43	d2raxa1	Alignment	not modelled	6.6	15	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
44	c2f1dP_	Alignment	not modelled	6.6	38	**PDB header:**lyase **Chain:** P: **PDB Molecule:**imidazoleglycerol-phosphate dehydratase 1; **PDBTitle:** x-ray structure of imidazoleglycerol-phosphate dehydratase
45	d1v89a_	Alignment	not modelled	6.6	15	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
46	d1a77a1	Alignment	not modelled	6.5	18	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
47	c3rruA_	Alignment	not modelled	6.5	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tom1l1 protein; **PDBTitle:** x-ray crystal structure of the vhs domain of human tom1-like protein,2 northeast structural genomics consortium target hr3050e
48	c3nqwB_	Alignment	not modelled	6.5	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
49	d1grja1	Alignment	not modelled	6.2	14	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
50	c1miuA_	Alignment	not modelled	6.1	23	**PDB header:**gene regulation/antitumor protein **Chain:** A: **PDB Molecule:**breast cancer type 2 susceptibility protein; **PDBTitle:** structure of a brca2-dss1 complex
51	c2uxsA_	Alignment	not modelled	6.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** 2.7a crystal structure of inorganic pyrophosphatase (rv3628)2 from mycobacterium tuberculosis at ph 7.5
52	c1jfiA_	Alignment	not modelled	5.8	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcription regulator nc2 alpha chain; **PDBTitle:** crystal structure of the nc2-tbp-dna ternary complex
53	d1jfia_	Alignment	not modelled	5.8	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
						Fold: Histone-fold

54	d1h3ob_	Alignment	not modelled	5.7	33	**Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
55	c3m1eA_	Alignment	not modelled	5.7	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of benm_dbd
56	c2jobA_	Alignment	not modelled	5.7	31	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
57	d2pp4a1	Alignment	not modelled	5.6	23	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
58	d1v5ua_	Alignment	not modelled	5.6	18	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
59	c2jveA_	Alignment	not modelled	5.5	83	**PDB header:**toxin **Chain:** A: **PDB Molecule:**prod1; **PDBTitle:** solution structure of the extracellular domain of prod1, a2 protein implicated in proximodistal identity during3 amphibian limb regeneration
60	c2k9iB_	Alignment	not modelled	5.3	21	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
61	c1tt9B_	Alignment	not modelled	5.3	24	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**formimidoyltransferase-cyclodeaminase **PDBTitle:** structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
62	c1vs3B_	Alignment	not modelled	5.2	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trna pseudouridine synthase a; **PDBTitle:** crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8