Phyre^2

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Description	P64540
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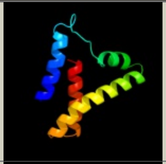
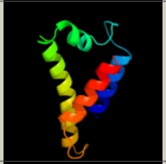
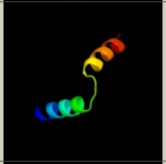
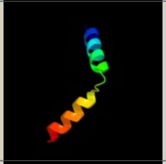
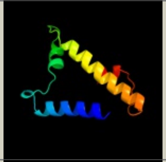
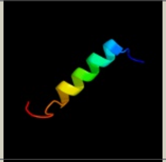
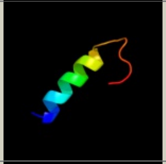
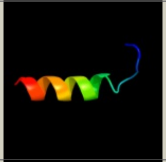
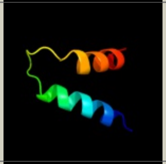
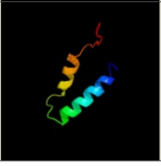
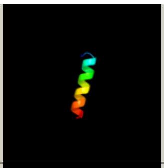
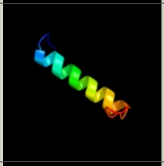
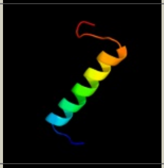
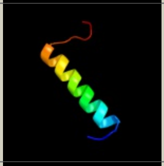
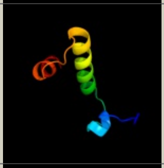
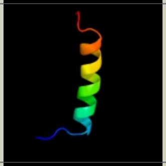
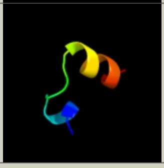
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sgma2	Alignment		60.0	10	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
2	d2hyja2	Alignment		47.5	14	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
3	c3dfgA_	Alignment		36.8	20	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris
4	c3c1dA_	Alignment		35.6	16	**PDB header:**recombination, dna binding protein **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** x-ray crystal structure of recx
5	d2g7sa2	Alignment		26.3	15	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
6	d1uw0a_	Alignment		25.4	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**PARP-type zinc finger
7	d1ug8a_	Alignment		25.2	14	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
8	c3fgrA_	Alignment		23.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phospholipase b-like 2 28 kda form; **PDBTitle:** two chain form of the 66.3 kda protein at 1.8 angstroem
9	c2k0mA_	Alignment		20.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
10	d1pzra_	Alignment		18.8	100	**Fold:**HLH-like **Superfamily:**Docking domain B of the erythromycin polyketide synthase (DEBS) **Family:**Docking domain B of the erythromycin polyketide synthase (DEBS)
11	d2i76a1	Alignment		17.4	12	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like

12	d1hlba_	Alignment		15.9	24	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
13	d1xhoa_	Alignment		14.0	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
14	c1xhoB_	Alignment		14.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**chorismate mutase; **PDBTitle:** chorismate mutase from clostridium thermocellum cth-682
15	c2vxdA_	Alignment		13.5	26	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** the structure of the c-terminal domain of nucleophosmin
16	d1fnja_	Alignment		13.1	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
17	d2v4jc1	Alignment		12.8	13	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
18	c2dmjA_	Alignment		12.7	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase family, member 1; **PDBTitle:** solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
19	d2lhba_	Alignment		12.6	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
20	c3hugJ_	Alignment		12.3	28	**PDB header:**transcription/membrane protein **Chain:** J: **PDB Molecule:**probable conserved membrane protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
21	c3s1sA_	Alignment	not modelled	11.8	24	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**restriction endonuclease bpusi; **PDBTitle:** characterization and crystal structure of the type iig restriction2 endonuclease bpusi
22	d2ea9a1	Alignment	not modelled	11.7	19	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
23	d1it2a_	Alignment	not modelled	11.4	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
24	c3e3vA_	Alignment	not modelled	10.1	27	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx from lactobacillus salivarius
25	c3k66A_	Alignment	not modelled	10.1	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**beta-amyloid-like protein; **PDBTitle:** x-ray crystal structure of the e2 domain of c. elegans apl-1
26	d1dbfa_	Alignment	not modelled	9.9	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
27	d2h28a1	Alignment	not modelled	9.3	24	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
28	d2ox6a1	Alignment	not modelled	9.1	33	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**YdiL-like
29	c2xycA	Alignment	not modelled	9.0	33	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**escrt-iii;

29	c2xvcA_	Alignment	not modelled	9.0	33	**PDBTitle:** molecular and structural basis of escrt-iii recruitment to2 membranes during archaeal cell division
30	d2inwa1	Alignment	not modelled	8.9	24	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
31	d1uc3a_	Alignment	not modelled	8.5	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
32	d3sdha_	Alignment	not modelled	8.3	25	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
33	c1o06A_	Alignment	not modelled	7.1	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein vps27; **PDBTitle:** crystal structure of the vps27p ubiquitin interacting motif (uim)
34	c1q15A_	Alignment	not modelled	7.1	56	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
35	c1g2cN_	Alignment	not modelled	7.1	37	**PDB header:**viral protein **Chain:** N: **PDB Molecule:**fusion protein (f); **PDBTitle:** human respiratory syncytial virus fusion protein core
36	c3mjhD_	Alignment	not modelled	6.5	63	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**early endosome antigen 1; **PDBTitle:** crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
37	c3b5nE_	Alignment	not modelled	6.3	15	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**synaptobrevin homolog 1; **PDBTitle:** structure of the yeast plasma membrane snare complex
38	c3iz5t_	Alignment	not modelled	6.2	33	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein l19 (l19e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
39	d1hlma_	Alignment	not modelled	6.1	33	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
40	d2fq4a2	Alignment	not modelled	6.0	36	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
41	c2vsgB_	Alignment	not modelled	6.0	20	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**variant surface glycoprotein iltat 1.24; **PDBTitle:** a structural motif in the variant surface glycoproteins of2 trypanosoma brucei
42	c1o1nA_	Alignment	not modelled	5.9	19	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin alpha chain; **PDBTitle:** deoxy hemoglobin (a-glyglygly-c:v1m,l29w; b,d:v1m)
43	c1yx3A_	Alignment	not modelled	5.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
44	d1gdta1	Alignment	not modelled	5.9	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
45	c2lbfA_	Alignment	not modelled	5.8	42	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p1; **PDBTitle:** solution structure of the dimerization domain of human ribosomal2 protein p1/p2 heterodimer
46	c3izct_	Alignment	not modelled	5.5	25	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein rpl19 (l19e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
47	c2v3sB_	Alignment	not modelled	5.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase osr1; **PDBTitle:** structural insights into the recognition of substrates and2 activators by the osr1 kinase
48	c3hq2A_	Alignment	not modelled	5.2	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillus subtilis m32 carboxypeptidase; **PDBTitle:** bsucp crystal structure