Phyre^2

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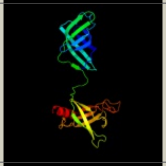
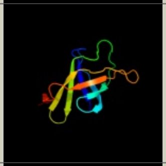
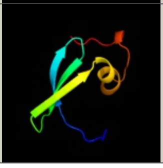
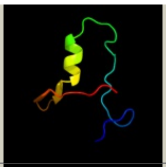
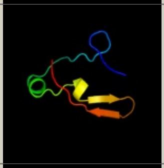
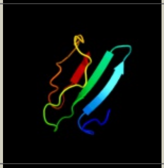
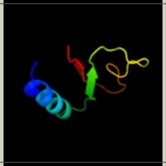
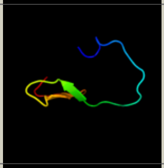
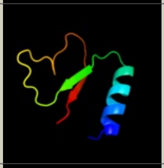
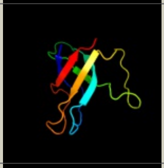
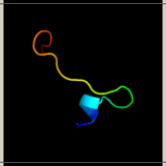
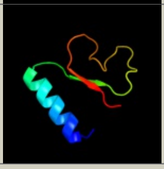
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gjgA_	Alignment		100.0	21	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**hypothetical protein pp4397; **PDBTitle:** crystal structure of a pilz-containing protein (pp4397) from2 pseudomonas putida kt2440 at 2.25 a resolution
2	c3kygB_	Alignment		99.9	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein vca0042; **PDBTitle:** crystal structure of vca0042 (l135r) complexed with c-di-gmp
3	c2rdeB_	Alignment		99.9	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vca0042; **PDBTitle:** crystal structure of vca0042 complexed with c-di-gmp
4	d1ywua1	Alignment		99.1	20	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
5	c1ywuA_	Alignment		99.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa4608; **PDBTitle:** solution nmr structure of pseudomonas aeruginosa protein pa4608.2 northeast structural genomics target pat7
6	c3ph1C_	Alignment		98.8	17	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of a pathogenic protein from the xanthomonas2 campestris reveals a new tetrameric pilz domain self-assembled via a3 unusual helical bundle
7	d2rdea1	Alignment		98.7	12	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
8	c3cnrA_	Alignment		98.2	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**type iv fimbriae assembly protein; **PDBTitle:** crystal structure of pilz (xac1133) from xanthomonas2 axonopodis pv citri
9	d2rdea2	Alignment		97.4	20	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain-associated domain
10	c2l1tA_	Alignment		88.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of the n-terminal domain of np_954075.1
11	d2ix0a3	Alignment		81.2	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

12	d1x9la_	Alignment		33.1	18	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
13	c2k6zA_	Alignment		20.5	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943; **PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
14	d1kwga1	Alignment		16.1	8	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
15	c3fwaA_	Alignment		14.4	13	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
16	c3cw4A_	Alignment		13.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** large c-terminal domain of influenza a virus rna-dependent polymerase2 pb2
17	c3d2hA_	Alignment		13.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme; **PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
18	d2ftsa1	Alignment		12.3	14	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
19	d1gtra1	Alignment		11.0	14	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain
20	c1zr6A_	Alignment		9.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
21	c2oxgD_	Alignment	not modelled	9.6	24	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**soxy protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
22	c2k8iA_	Alignment	not modelled	7.5	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
23	c2kfwA_	Alignment	not modelled	7.3	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
24	c2vs1A_	Alignment	not modelled	7.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized rna methyltransferase pyrab10780; **PDBTitle:** the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine
25	d2d9ra1	Alignment	not modelled	6.8	10	**Fold:**Double-split beta-barrel **Superfamily:**AF2212/PG0164-like **Family:**PG0164-like
26	d2fg9a1	Alignment	not modelled	6.6	11	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
27	d2z1ea2	Alignment	not modelled	6.6	22	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
28	c2ipiD_	Alignment	not modelled	6.2	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox); **PDBTitle:** crystal structure of aclacinomycin oxidoreductase

29	d1vk3a3	Alignment	not modelled	6.1	44	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
30	d1kq1a_	Alignment	not modelled	6.1	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
31	c3uc0B_	Alignment	not modelled	6.0	19	**PDB header:**viral protein/immune system **Chain:** B: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
32	d1ib8a1	Alignment	not modelled	5.9	3	**Fold:**Sm-like fold **Superfamily:**YhbC-like, C-terminal domain **Family:**YhbC-like, C-terminal domain
33	d1hl9a1	Alignment	not modelled	5.9	11	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**Putative alpha-L-fucosidase C-terminal domain
34	c1kq1W_	Alignment	not modelled	5.7	13	**PDB header:**translation **Chain:** W: **PDB Molecule:**host factor for q beta; **PDBTitle:** 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq
35	d1hk9a_	Alignment	not modelled	5.5	19	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
36	c3qhsD_	Alignment	not modelled	5.4	19	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of full-length hfq from escherichia coli
37	d1t3ta6	Alignment	not modelled	5.3	33	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like