Phyre^2

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Description	P0AF10
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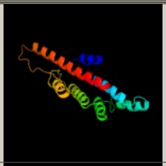
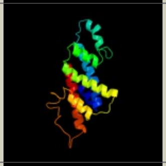
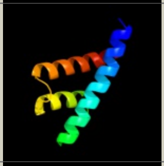
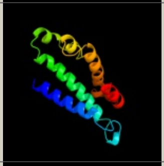
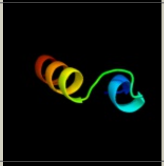
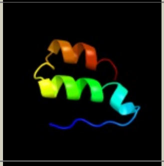
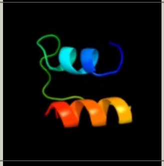
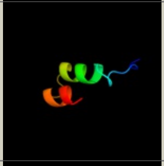
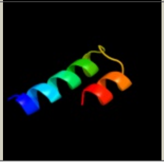
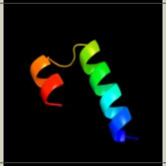
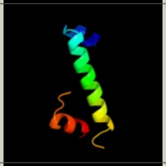
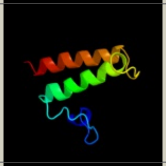
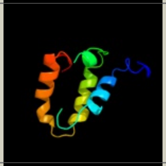
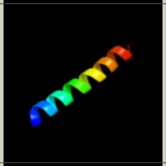
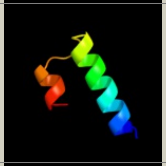
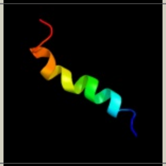
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3brja1	Alignment		100.0	40	**Fold:**MtlR-like **Superfamily:**MtlR-like **Family:**MtlR-like
2	d3c8ga1	Alignment		100.0	27	**Fold:**MtlR-like **Superfamily:**MtlR-like **Family:**MtlR-like
3	c1wwpA_	Alignment		59.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha0636; **PDBTitle:** crystal structure of ttk003001694 from thermus thermophilus2 hb8
4	d1wtya_	Alignment		39.7	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
5	c1ylmA_	Alignment		21.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu32300; **PDBTitle:** structure of cytosolic protein of unknown function yute2 from bacillus subtilis
6	d2nn4a1	Alignment		20.1	22	**Fold:**YqgQ-like **Superfamily:**YqgQ-like **Family:**YqgQ-like
7	d2fexa1	Alignment		14.9	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
8	d1twfc2	Alignment		10.7	33	**Fold:**Insert subdomain of RNA polymerase alpha subunit **Superfamily:**Insert subdomain of RNA polymerase alpha subunit **Family:**Insert subdomain of RNA polymerase alpha subunit
9	d1vkfa_	Alignment		10.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**GlpP-like **Family:**GlpP-like
10	c1gxsC_	Alignment		10.0	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**p-(s)-hydroxymandelonitrile lyase chain a; **PDBTitle:** crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
11	c1bcrA_	Alignment		9.7	11	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine carboxypeptidase ii; **PDBTitle:** complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature

12	d1qkia1	Alignment		7.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
13	d2gsca1	Alignment		7.3	19	**Fold:**Bromodomain-like **Superfamily:**IVS-encoded protein-like **Family:**IVS-encoded protein-like
14	d1a9xa1	Alignment		7.2	23	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
15	c2zttA_	Alignment		7.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase catalytic subunit; **PDBTitle:** crystal structure of rna polymerase pb1-pb2 subunits from2 influenza a virus
16	c2fulE_	Alignment		6.5	19	**PDB header:**translation **Chain:** E: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** crystal structure of the c-terminal domain of s. cerevisiae eif5
17	c2a45J_	Alignment		6.4	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** J: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
18	d2rlda1	Alignment		6.0	22	**Fold:**Bromodomain-like **Superfamily:**IVS-encoded protein-like **Family:**IVS-encoded protein-like
19	c2bcwC_	Alignment		5.6	9	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**elongation factor g; **PDBTitle:** coordinates of the n-terminal domain of ribosomal protein2 l11,c-terminal domain of ribosomal protein l7/l12 and a3 portion of the g' domain of elongation factor g, as fitted4 into cryo-em map of an escherichia coli 70s*ef-5 g*gdp*fusidic acid complex
20	c2wpyA_	Alignment		5.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with one vxxnxxx motif2 coordinating chloride
21	c2ll0A_	Alignment	not modelled	5.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the putative atpase regulatory protein yp_916642.12 from paracoccus denitrificans