Phyre^2

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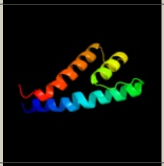
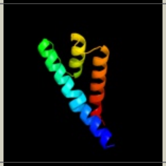
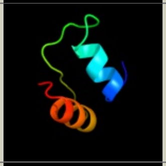
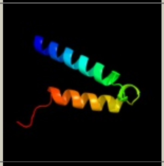
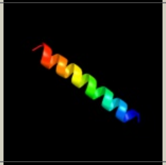
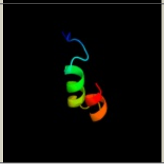
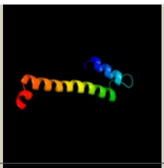
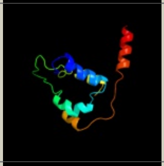
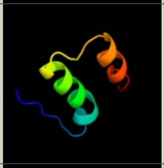
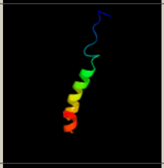
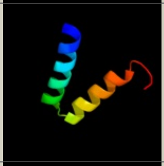
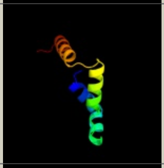
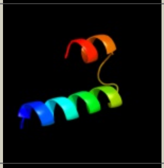
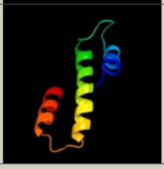
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3brja1	Alignment		100.0	24	**Fold:**MtlR-like **Superfamily:**MtlR-like **Family:**MtlR-like
2	d3c8ga1	Alignment		100.0	91	**Fold:**MtlR-like **Superfamily:**MtlR-like **Family:**MtlR-like
3	c1ylmA_	Alignment		62.7	11	**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
4	c1wwpA_	Alignment		31.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha0636; **PDBTitle:** crystal structure of ttk003001694 from thermus thermophilus2 hb8
5	d2nn4a1	Alignment		21.7	17	**Fold:**YqgQ-like **Superfamily:**YqgQ-like **Family:**YqgQ-like
6	d1wtya_	Alignment		21.3	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
7	d1vkfa_	Alignment		18.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**GlpP-like **Family:**GlpP-like
8	c3pr6A_	Alignment		13.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**trapp-associated protein tca17; **PDBTitle:** crystal structure analysis of yeast trapp associate protein tca17
9	c2a45J_	Alignment		12.2	12	**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
10	d1twfc2	Alignment		10.5	22	**Fold:**Insert subdomain of RNA polymerase alpha subunit **Superfamily:**Insert subdomain of RNA polymerase alpha subunit **Family:**Insert subdomain of RNA polymerase alpha subunit
11	c1gxsC_	Alignment		10.2	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

12	c3ulwA_	Alignment		9.9	7	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s15; **PDBTitle:** 30s ribosomal protein s15 from campylobacter jejuni
13	d1vmda_	Alignment		9.7	29	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
14	d2fexa1	Alignment		9.1	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
15	c2rkhA_	Alignment		8.5	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative apha-like transcription factor; **PDBTitle:** crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution
16	c3o2rD_	Alignment		7.3	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**ribonuclease iii; **PDBTitle:** structural flexibility in region involved in dimer formation of2 nuclease domain of ribonuclase iii (rnc) from campylobacter jejuni
17	c3dfgA_	Alignment		7.0	9	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris
18	d2gsca1	Alignment		6.8	19	**Fold:**Bromodomain-like **Superfamily:**IVS-encoded protein-like **Family:**IVS-encoded protein-like
19	d1i27a_	Alignment		6.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
20	d1g1xb_	Alignment		6.3	8	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
21	d1zata2	Alignment	not modelled	6.3	7	**Fold:**L,D-transpeptidase pre-catalytic domain-like **Superfamily:**L,D-transpeptidase pre-catalytic domain-like **Family:**L,D-transpeptidase pre-catalytic domain-like
22	d1k8ke_	Alignment	not modelled	6.1	21	**Fold:**Arp2/3 complex 21 kDa subunit ARPC3 **Superfamily:**Arp2/3 complex 21 kDa subunit ARPC3 **Family:**Arp2/3 complex 21 kDa subunit ARPC3
23	d1irqa_	Alignment	not modelled	5.8	27	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Omega transcriptional repressor
24	c1irqB_	Alignment	not modelled	5.7	27	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**omega transcriptional repressor; **PDBTitle:** crystal structure of omega transcriptional repressor at2 1.5a resolution
25	d2rlda1	Alignment	not modelled	5.6	15	**Fold:**Bromodomain-like **Superfamily:**IVS-encoded protein-like **Family:**IVS-encoded protein-like
26	d1s5qb_	Alignment	not modelled	5.5	9	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
27	c2keyA_	Alignment	not modelled	5.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
28	d1qkia1	Alignment	not modelled	5.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						PDB header:ribosome

29	c1p0oA_	Alignment	not modelled	5.0	25	**Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles