Phyre^2

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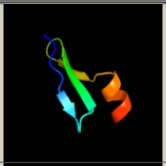
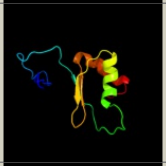
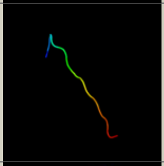
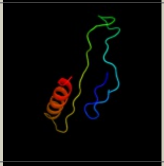
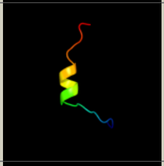
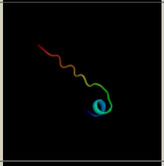
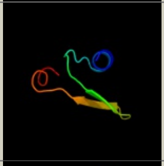
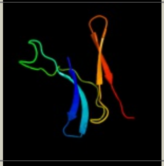
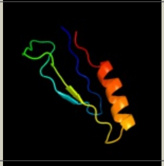
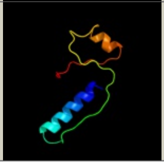
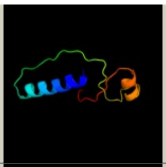
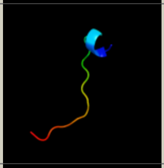
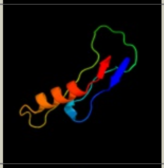
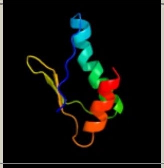
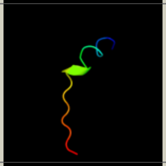
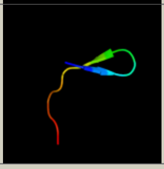
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cx1a2	Alignment		85.5	31	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Hypothetical protein APE0525, N-terminal domain
2	c1zhvA_	Alignment		69.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0741; **PDBTitle:** x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
3	d1zhva2	Alignment		57.5	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
4	d1ev7a_	Alignment		33.9	33	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease NaeI
5	d1w96a1	Alignment		33.2	7	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
6	d1e32a3	Alignment		29.7	59	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
7	c3zquA_	Alignment		25.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
8	c3qocD_	Alignment		24.2	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative metallopeptidase; **PDBTitle:** crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metallopeptidase from corynebacterium diphtheriae
9	d1n1ta2	Alignment		24.0	19	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
10	d2j9ga1	Alignment		23.9	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
11	c2qhsA_	Alignment		23.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoyltransferase; **PDBTitle:** structural basis of octanoic acid recognition by lipoate-protein2 ligase b

12	c2qhvA_	Alignment		23.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoyltransferase; **PDBTitle:** structural basis of octanoic acid recognition by lipoate-protein2 ligase b
13	d1p9oa_	Alignment		22.4	15	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
14	c2ejbA_	Alignment		21.2	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
15	c1n1vA_	Alignment		19.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sialidase; **PDBTitle:** trypanosoma rangeli sialidase in complex with dana
16	d1ulza1	Alignment		19.6	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
17	d1zvpa2	Alignment		19.5	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
18	d1sbza_	Alignment		18.4	29	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
19	d1w96c1	Alignment		18.3	11	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
20	c3a5zF_	Alignment		18.0	20	**PDB header:**ligase **Chain:** F: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of escherichia coli genx in complex with elongation2 factor p
21	c2k7mA_	Alignment	not modelled	16.9	71	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**gap junction alpha-5 protein; **PDBTitle:** structure of the connexin40 carboxyl terminal domain
22	c2g7rA_	Alignment	not modelled	16.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** x-ray structure of the death domain of the human mucosa associated2 lymphoid tissue lymphoma translocation protein 1
23	c2eifA_	Alignment	not modelled	16.3	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (eukaryotic translation initiation factor 5a); **PDBTitle:** eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
24	c3hksB_	Alignment	not modelled	14.3	19	**PDB header:**translation, rna binding protein **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of eukaryotic translation initiation2 factor eif-5a2 from arabidopsis thaliana
25	d2ah2a2	Alignment	not modelled	14.2	13	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
26	c3oooA_	Alignment	not modelled	13.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proline dipeptidase; **PDBTitle:** the structure of a proline dipeptidase from streptococcus agalactiae2 2603v
27	d1ueba1	Alignment	not modelled	12.3	20	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
						PDB header:cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-

28	c3b64A_	Alignment	not modelled	11.5	10	like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
29	d1fima_	Alignment	not modelled	11.5	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
30	d2g2xa1	Alignment	not modelled	11.2	18	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
31	d1vk6a3	Alignment	not modelled	11.1	35	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
32	c3kdpD_	Alignment	not modelled	11.0	47	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sodium/potassium-transporting atpase subunit beta-1; **PDBTitle:** crystal structure of the sodium-potassium pump
33	c2h31A_	Alignment	not modelled	10.3	21	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
34	d1pv8a_	Alignment	not modelled	9.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
35	c3fwtA_	Alignment	not modelled	8.4	11	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
36	c2zxeB_	Alignment	not modelled	8.0	44	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**na+,k+-atpase beta subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
37	c2wk1A_	Alignment	not modelled	7.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**novp; **PDBTitle:** structure of the o-methyltransferase novp
38	c3krnB_	Alignment	not modelled	7.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein c14a4.5, confirmed by transcript evidence; **PDBTitle:** crystal structure of c. elegans cell-death-related nuclease 5(crn-5)
39	d2gbsa1	Alignment	not modelled	7.2	22	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
40	d2gdta1	Alignment	not modelled	7.1	33	**Fold:**SARS Nsp1-like **Superfamily:**SARS Nsp1-like **Family:**SARS Nsp1-like
41	c3i7mA_	Alignment	not modelled	7.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** n-terminal domain of xaa-pro dipeptidase from lactobacillus brevis.
42	d1gd0a_	Alignment	not modelled	7.1	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
43	c3er0A_	Alignment	not modelled	6.9	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of the full length eif5a from2 saccharomyces cerevisiae
44	c2gk4A_	Alignment	not modelled	6.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
45	d1riea_	Alignment	not modelled	6.7	15	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
46	d2prva1	Alignment	not modelled	6.5	40	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
47	d1u7za_	Alignment	not modelled	6.4	11	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
48	d1laue_	Alignment	not modelled	6.4	11	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
49	c3o5vA_	Alignment	not modelled	6.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**x-pro dipeptidase; **PDBTitle:** the crystal structure of the creatinase/prolidase n-terminal domain of2 an x-pro dipeptidase from streptococcus pyogenes to 1.85a
50	c3c9pA_	Alignment	not modelled	6.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
51	c2f06B_	Alignment	not modelled	6.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
52	d2evea1	Alignment	not modelled	6.0	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
53	c3gacD_	Alignment	not modelled	5.7	20	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
						Fold: Tautomerase/MIF

54	d1hfoa_	Alignment	not modelled	5.7	15	**Superfamily:**Tautomerase/MIF **Family:**MIF-related
55	d2gdga1	Alignment	not modelled	5.7	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
56	c3ic8D_	Alignment	not modelled	5.6	24	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized gst-like proteinprotein; **PDBTitle:** the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
57	c3treA_	Alignment	not modelled	5.6	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of a translation elongation factor p (efp) from coxiella2 burnetii
58	d1u11a_	Alignment	not modelled	5.4	20	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
59	c2fw9A_	Alignment	not modelled	5.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
60	c4a1eF_	Alignment	not modelled	5.4	24	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl7a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
61	c2kllA_	Alignment	not modelled	5.3	27	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**interleukin-33; **PDBTitle:** solution structure of human interleukin-33
62	d1xgsa1	Alignment	not modelled	5.3	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Methionine aminopeptidase, insert domain
63	d1zcea1	Alignment	not modelled	5.2	18	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
64	d1okba_	Alignment	not modelled	5.2	17	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
65	c3lodA_	Alignment	not modelled	5.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyl-coa n-acyltransferase; **PDBTitle:** the crystal structure of the putative acyl-coa n-acyltransferase from2 klebsiella pneumoniae subsp.pneumoniae mgh 78578
66	d2icga1	Alignment	not modelled	5.1	20	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like