Phyre2

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Description	P37194
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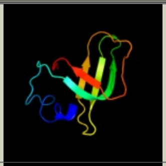
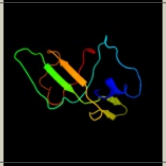
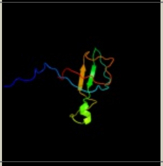
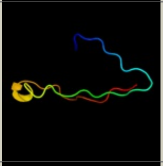
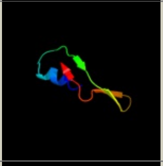
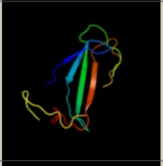
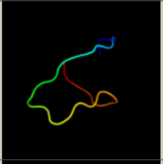
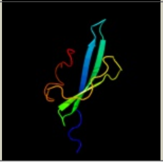
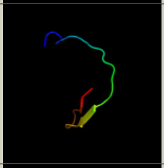
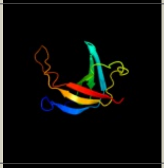
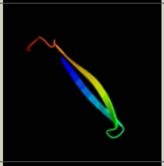
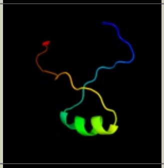
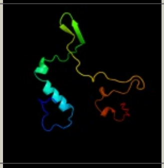
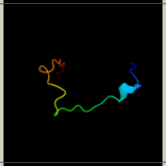
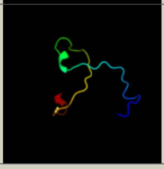
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1j6qA_	Alignment		82.3	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c maturation protein e; **PDBTitle:** solution structure and characterization of the heme2 chaperone ccme
2	d1j6qa_	Alignment		82.3	17	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
3	d1sr3a_	Alignment		66.0	21	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
4	c2kctA_	Alignment		49.5	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccme; **PDBTitle:** solution nmr structure of the ob-fold domain of heme2 chaperone ccme from desulfovibrio vulgaris. northeast3 structural genomics target dvr115g.
5	c2r9qD_	Alignment		40.9	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**2'-deoxycytidine 5'-triphosphate deaminase; **PDBTitle:** crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
6	c3h43F_	Alignment		27.8	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
7	c2wkdA_	Alignment		27.7	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf34p2; **PDBTitle:** crystal structure of a double ile-to-met mutant of protein2 orf34 from lactococcus phage p2
8	d1n9wa1	Alignment		26.4	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
9	c2jwyA_	Alignment		25.2	13	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yaji; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein yaji from2 escherichia coli. northeast structural genomics target er540
10	c2wg6L_	Alignment		24.9	8	**PDB header:**transcription,hydrolase **Chain:** L: **PDB Molecule:**general control protein gcn4, **PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
11	c2z14A_	Alignment		24.6	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ef-hand domain-containing family member c2; **PDBTitle:** crystal structure of the n-terminal duf1126 in human ef-2 hand domain containing 2 protein

12	c2wp8J_	Alignment		23.5	28	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
13	d2pi2e1	Alignment		20.2	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
14	d1l0wa1	Alignment		18.1	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
15	c1wydB_	Alignment		17.9	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
16	d2vnud1	Alignment		17.9	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
17	d1t3ta6	Alignment		16.8	18	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
18	c1vqwB_	Alignment		14.4	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein with similarity to flavin-containing **PDBTitle:** crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
19	c1yrlD_	Alignment		11.9	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** escherichia coli ketol-acid reductoisomerase
20	c3i7fA_	Alignment		11.5	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
21	c2zauB_	Alignment	not modelled	11.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
22	d1ps9a2	Alignment	not modelled	10.8	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
23	d2jn4a1	Alignment	not modelled	10.3	35	**Fold:**NifT/FixU barrel-like **Superfamily:**NifT/FixU-like **Family:**NifT/FixU
24	c2jn4A_	Alignment	not modelled	10.3	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein fixu, nift; **PDBTitle:** solution nmr structure of protein rp4601 from2 rhodopseudomonas palustris. northeast structural genomics3 consortium target rpt2; ontario center for structural4 proteomics target rp4601.
25	d1so0a_	Alignment	not modelled	9.7	19	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
26	c2p39A_	Alignment	not modelled	9.4	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fibroblast growth factor 23; **PDBTitle:** crystal structure of human fgf23
27	c1pwaA_	Alignment	not modelled	9.4	27	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**fibroblast growth factor-19; **PDBTitle:** crystal structure of fibroblast growth factor 19
28	d1pwaa_	Alignment	not modelled	9.4	27	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)

29	c2pqaB_	Alignment	not modelled	9.2	13	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
30	c2zodB_	Alignment	not modelled	9.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
31	c2pi2A_	Alignment	not modelled	7.1	17	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
32	d1geha2	Alignment	not modelled	7.1	8	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
33	d1krta_	Alignment	not modelled	7.0	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
34	d1yloa1	Alignment	not modelled	6.9	13	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
35	d2z1ea2	Alignment	not modelled	6.8	13	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
36	d1c0aa1	Alignment	not modelled	6.6	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
37	c3m9bK_	Alignment	not modelled	6.6	12	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
38	d2gycb1	Alignment	not modelled	6.6	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
39	d2ijra1	Alignment	not modelled	6.6	28	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
40	c1b8aB_	Alignment	not modelled	6.4	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
41	c3stbC_	Alignment	not modelled	6.2	9	**PDB header:**rna binding protein/immune system **Chain:** C: **PDB Molecule:**rna-editing complex protein mp42; **PDBTitle:** a complex of two editosome proteins and two nanobodies
42	d1b33n_	Alignment	not modelled	6.1	50	**Fold:**Allophycocyanin linker chain (domain) **Superfamily:**Allophycocyanin linker chain (domain) **Family:**Allophycocyanin linker chain (domain)
43	d2ns0a1	Alignment	not modelled	6.0	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
44	d2zoda2	Alignment	not modelled	5.7	15	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
45	c3gwdA_	Alignment	not modelled	5.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase; **PDBTitle:** closed crystal structure of cyclohexanone monooxygenase
46	d2d69a2	Alignment	not modelled	5.6	20	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
47	d2j01e1	Alignment	not modelled	5.4	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
48	c2esyA_	Alignment	not modelled	5.4	45	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**lung surfactant protein c; **PDBTitle:** structure and influence on stability and activity of the n-2 terminal propetide part of lung surfactant protein c
49	d2gv8a2	Alignment	not modelled	5.2	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains