Phyre2

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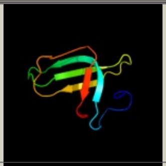
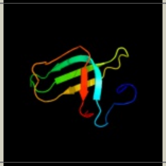
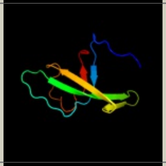
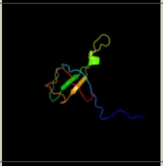
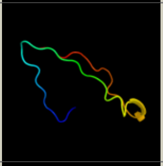
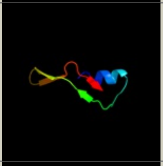
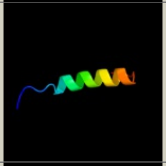
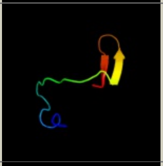
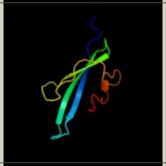
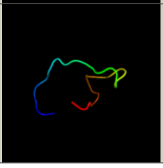
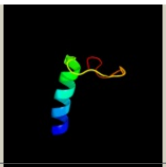
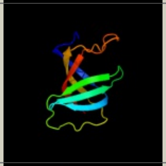
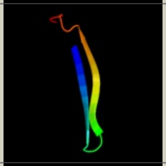
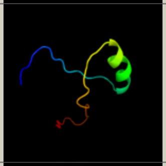
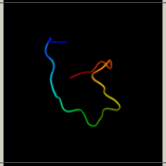
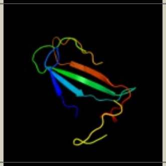
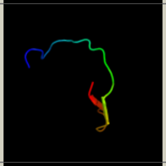
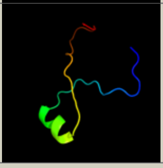
Description	P0AA91
Date	Thu Jan 5 11:12:14 GMT 2012
Unique Job ID	3fd7b3d2821c53fe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1j6qA_	Alignment		82.1	24	**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		82.1	24	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
3	d1sr3a_	Alignment		45.5	30	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
4	c2kctA_	Alignment		45.1	22	**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		39.1	31	**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	c2wkdA_	Alignment		38.6	31	**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
7	c2dzlA_	Alignment		27.6	16	**PDB header:**structural genomics unknown function **Chain:** A: **PDB Molecule:**protein fam100b; **PDBTitle:** solution structure of the uba domain in human protein2 fam100b
8	d1n9wa1	Alignment		27.4	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
9	c2wp8J_	Alignment		25.4	23	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
10	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
11	c3h43F_	Alignment		22.1	23	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii

12	d2ijra1	Alignment		21.1	21	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
13	c1wydB_	Alignment		20.6	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
14	d2vnud1	Alignment		20.3	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
15	d1t3ta6	Alignment		19.5	21	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
16	d2pi2e1	Alignment		19.4	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
17	c2wg6L_	Alignment		19.3	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
18	c2jwyA_	Alignment		18.6	15	**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
19	d1l0wa1	Alignment		16.5	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
20	c2zauB_	Alignment		13.2	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
21	c1yrlD_	Alignment	not modelled	12.2	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** escherichia coli ketol-acid reductoisomerase
22	c2p39A_	Alignment	not modelled	11.5	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fibroblast growth factor 23; **PDBTitle:** crystal structure of human fgf23
23	c1pwaA_	Alignment	not modelled	11.4	24	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**fibroblast growth factor-19; **PDBTitle:** crystal structure of fibroblast growth factor 19
24	d1pwaa_	Alignment	not modelled	11.4	24	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
25	c2jn4A_	Alignment	not modelled	11.2	39	**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.
26	d2jn4a1	Alignment	not modelled	11.2	39	**Fold:**NifT/FixU barrel-like **Superfamily:**NifT/FixU-like **Family:**NifT/FixU
27	c2zodB_	Alignment	not modelled	11.1	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
28	c2pqaB_	Alignment	not modelled	10.9	10	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer

29	d1so0a_	Alignment	not modelled	10.6	23	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
30	c1b8aB_	Alignment	not modelled	10.4	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
31	c1vqwB_	Alignment	not modelled	8.7	16	**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
32	d1ps9a2	Alignment	not modelled	8.5	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
33	c2pi2A_	Alignment	not modelled	7.1	11	**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
34	d2zoda2	Alignment	not modelled	6.9	5	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
35	d1c0aa1	Alignment	not modelled	6.2	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
36	d1b33n_	Alignment	not modelled	6.1	63	**Fold:**Allophycocyanin linker chain (domain) **Superfamily:**Allophycocyanin linker chain (domain) **Family:**Allophycocyanin linker chain (domain)
37	d2z1ea2	Alignment	not modelled	6.1	17	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
38	c3ls1A_	Alignment	not modelled	6.0	16	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
39	d1yloa1	Alignment	not modelled	5.7	13	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
40	d1krta_	Alignment	not modelled	5.6	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
41	d1geha2	Alignment	not modelled	5.6	8	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
42	d2gycb1	Alignment	not modelled	5.4	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
43	c2esyA_	Alignment	not modelled	5.2	36	**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
44	c3m9bK_	Alignment	not modelled	5.1	20	**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
45	c2pxgA_	Alignment	not modelled	5.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein; **PDBTitle:** nmr solution structure of omla
46	d1lura_	Alignment	not modelled	5.0	18	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)