Phyre2

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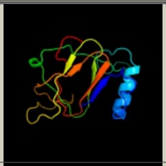
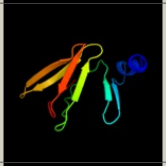
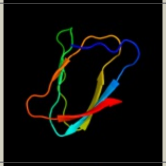
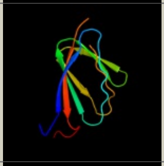
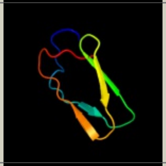
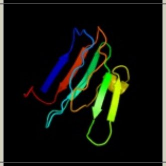
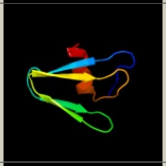
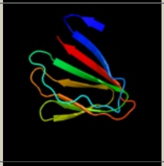
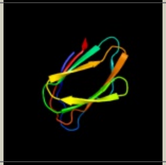
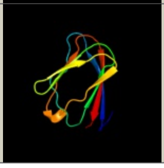
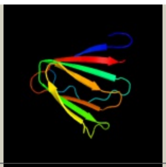
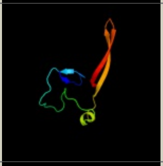
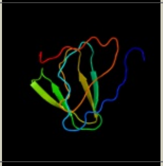
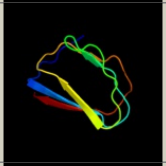
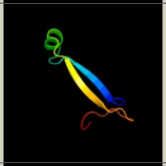
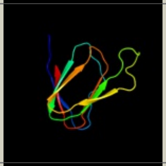
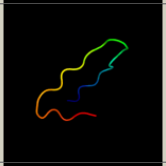
Description	P0AC73
Date	Thu Jan 5 11:17:27 GMT 2012
Unique Job ID	e686e4a3cbeb252b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s4ca1	Alignment		100.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YhcH-like
2	d1yfua1	Alignment		90.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
3	c2i45C_	Alignment		83.1	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
4	c3cewA_	Alignment		75.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cupin protein; **PDBTitle:** crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
5	d2arca_	Alignment		70.5	23	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
6	d2pa7a1	Alignment		58.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
7	c3d82A_	Alignment		52.5	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
8	d1v70a_	Alignment		46.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
9	d1o4ta_	Alignment		46.0	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
10	c2opkC_	Alignment		32.8	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
11	c2ozjB_	Alignment		30.0	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel; **PDBTitle:** crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution

12	c2oa2A_	Alignment		29.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2720 protein; **PDBTitle:** crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution
13	d1j0sa_	Alignment		25.5	23	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
14	c3ht2A_	Alignment		24.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
15	c2o8qA_	Alignment		24.0	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein with a cupin-like fold and unknown2 function (bxe_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
16	c2xp1A_	Alignment		21.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**spt6; **PDBTitle:** structure of the tandem sh2 domains from antonospora locustae2 transcription elongation factor spt6
17	d1lr5a_	Alignment		21.9	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
18	c3bcwB_	Alignment		21.4	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
19	c2xxzA_	Alignment		21.1	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of the human jmjd3 jumonji domain
20	d1zvfa1	Alignment		20.7	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
21	c2q30C_	Alignment	not modelled	20.5	13	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
22	d1vj2a_	Alignment	not modelled	20.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
23	d1x82a_	Alignment	not modelled	17.1	28	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
24	c3kgzA_	Alignment	not modelled	16.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
25	c2xueB_	Alignment	not modelled	15.1	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of jmjd3
26	c2pfwB_	Alignment	not modelled	14.9	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
27	d1j3pa_	Alignment	not modelled	13.7	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
28	d3dl3a1	Alignment	not modelled	12.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like

29	d1o5ua_	Alignment	not modelled	11.7	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
30	d3bb6a1	Alignment	not modelled	11.3	8	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
31	d1yhfa1	Alignment	not modelled	10.8	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
32	c3fjsC_	Alignment	not modelled	10.8	18	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like cupin fold; **PDBTitle:** crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
33	c3l2hD_	Alignment	not modelled	10.5	26	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative sugar phosphate isomerase; **PDBTitle:** crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
34	c2vqaC_	Alignment	not modelled	10.0	15	**PDB header:**metal-binding protein **Chain:** C: **PDB Molecule:**sll1358 protein; **PDBTitle:** protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
35	c3ibmB_	Alignment	not modelled	9.8	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
36	c3ebrA_	Alignment	not modelled	9.2	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
37	c3jzvA_	Alignment	not modelled	7.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rru_a2000; **PDBTitle:** crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
38	c2w2iC_	Alignment	not modelled	7.2	5	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate oxygenase; **PDBTitle:** crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
39	d1dgwa_	Alignment	not modelled	7.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
40	c2odbB_	Alignment	not modelled	6.7	13	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
41	c2ca9B_	Alignment	not modelled	6.3	9	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
42	c2os2A_	Alignment	not modelled	6.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 3a; **PDBTitle:** crystal structure of jmjd2a complexed with histone h3 peptide2 trimethylated at lys36
43	c2q8eB_	Alignment	not modelled	6.1	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** specificity and mechanism of jmjd2a, a trimethyllysine-2 specific histone demethylase
44	d1y9qa2	Alignment	not modelled	5.8	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
45	c3opwA_	Alignment	not modelled	5.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dna damage-responsive transcriptional repressor rph1; **PDBTitle:** crystal structure of the rph1 catalytic core
46	d1sfna_	Alignment	not modelled	5.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
47	d1rc6a_	Alignment	not modelled	5.6	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
48	d2es7a1	Alignment	not modelled	5.4	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like