Phyre2

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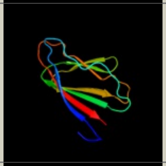
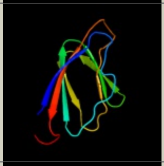
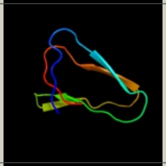
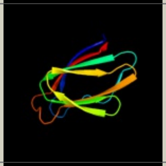
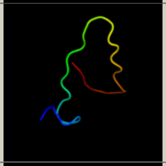
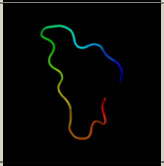
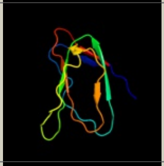
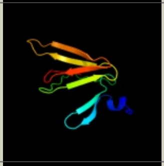
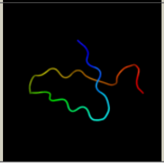
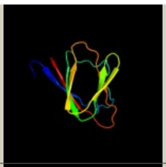
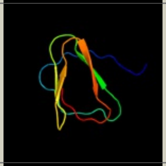
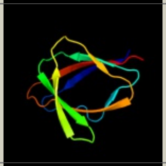
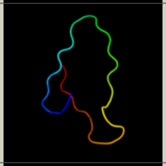
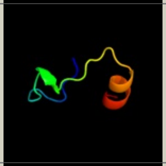
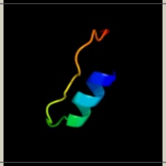
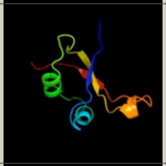
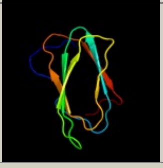
Description	P37673
Date	Thu Jan 5 11:56:46 GMT 2012
Unique Job ID	c40fba6e3aaeca56

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s4ca1	Alignment		100.0	30	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YhcH-like
2	d1yfua1	Alignment		82.5	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
3	d1v70a_	Alignment		70.9	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
4	c3cewA_	Alignment		56.5	20	**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	c2i45C_	Alignment		47.5	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
6	d1o4ta_	Alignment		42.0	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
7	c2xueB_	Alignment		30.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of jmjd3
8	c2xxzA_	Alignment		29.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of the human jmjd3 jumonji domain
9	c2oa2A_	Alignment		27.4	9	**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
10	d1zvfa1	Alignment		25.3	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
11	d2arca_	Alignment		23.8	21	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC

12	d1vj2a_	Alignment		23.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
13	c3d82A_	Alignment		20.7	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
14	c2fqpD_	Alignment		19.1	10	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hypothetical protein bp2299; **PDBTitle:** crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
15	d1a6qa1	Alignment		17.5	21	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
16	c3ebrA_	Alignment		15.9	16	**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
17	c2hdlA_	Alignment		15.7	12	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**small inducible cytokine b14; **PDBTitle:** solution structure of brak/cxcl14
18	c2pyhB_	Alignment		15.4	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4; **PDBTitle:** azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
19	c2kkuA_	Alignment		15.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein af2351 from archaeoglobus2 fulgidus. northeast structural genomics consortium target3 att9/ontario center for structural proteomics target af2351
20	d2pa7a1	Alignment		14.8	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
21	c3kgzA_	Alignment	not modelled	14.3	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
22	c2oziA_	Alignment	not modelled	14.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa4178; **PDBTitle:** structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
23	c2w2iC_	Alignment	not modelled	13.8	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate oxygenase; **PDBTitle:** crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
24	d3dl3a1	Alignment	not modelled	12.7	31	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
25	c3bn8A_	Alignment	not modelled	12.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative sterol carrier protein 2; **PDBTitle:** crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
26	c2q8eB_	Alignment	not modelled	12.2	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** specificity and mechanism of jmjd2a, a trimethyllysine-2 specific histone demethylase
27	c2os2A_	Alignment	not modelled	12.1	25	**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
						Fold: Double-stranded beta-helix

28	d3bb6a1	Alignment	not modelled	11.8	28	**Superfamily:**Clavaminate synthase-like **Family:**TehB-like
29	d1y9qa2	Alignment	not modelled	11.5	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
30	d1j3pa_	Alignment	not modelled	11.3	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
31	d2es7a1	Alignment	not modelled	11.3	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
32	c2r32A_	Alignment	not modelled	10.7	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
33	c2ozjB_	Alignment	not modelled	10.3	13	**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
34	c2bx6A_	Alignment	not modelled	10.2	12	**PDB header:**transduction protein **Chain:** A: **PDB Molecule:**xrp2 protein; **PDBTitle:** crystal structure of the human retinitis pigmentosa2 protein 2 (rp2)
35	c2yrvA_	Alignment	not modelled	9.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**at-rich interactive domain-containing protein 4a; **PDBTitle:** solution structure of the rbb1nt domain of human2 rb(retinoblastoma)-binding protein 1
36	c2kpsA_	Alignment	not modelled	9.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of domain iv from the ybbr family protein of2 desulfitobacterium hafniense
37	c3opwA_	Alignment	not modelled	8.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dna damage-responsive transcriptional repressor rph1; **PDBTitle:** crystal structure of the rph1 catalytic core
38	c2rq7A_	Alignment	not modelled	8.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase epsilon chain; **PDBTitle:** solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
39	d1xsqa_	Alignment	not modelled	7.9	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
40	c3fjsC_	Alignment	not modelled	7.9	9	**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
41	c2e5yA_	Alignment	not modelled	7.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase epsilon chain; **PDBTitle:** epsilon subunit and atp complex of f1f0-atp synthase from2 the thermophilic bacillus ps3
42	d1tvfa1	Alignment	not modelled	7.7	19	**Fold:**Penicillin-binding protein associated domain **Superfamily:**Penicillin-binding protein associated domain **Family:**Pencillin binding protein 4 (PbpD), C-terminal domain
43	c3h8uA_	Alignment	not modelled	7.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
44	c2zklA_	Alignment	not modelled	7.5	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
45	c3ibmB_	Alignment	not modelled	7.2	9	**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
46	c2nnzA_	Alignment	not modelled	7.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
47	c3jurA_	Alignment	not modelled	7.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-poly-alpha-d-galacturonosidase; **PDBTitle:** the crystal structure of a hyperthermoactive exopolygalacturonase from2 thermotoga maritima
48	d1zx8a1	Alignment	not modelled	7.0	15	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**TM1367-like
49	d1lg4a_	Alignment	not modelled	6.8	30	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
50	c2qe7H_	Alignment	not modelled	6.4	10	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**atp synthase subunit epsilon; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
51	c1fs0E_	Alignment	not modelled	6.4	16	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**atp synthase epsilon subunit; **PDBTitle:** complex of gamma/epsilon atp synthase from e.coli

52	d1aqta2_	Alignment	not modelled	6.2	15	**Fold:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Superfamily:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Family:**Epsilon subunit of F1F0-ATP synthase N-terminal domain
53	c2ca9B_	Alignment	not modelled	6.1	10	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
54	c2pfwB_	Alignment	not modelled	6.1	15	**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
55	c3tekA_	Alignment	not modelled	5.8	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism