Phyre2

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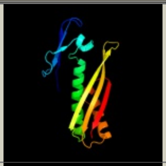
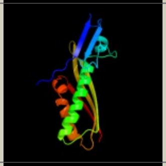
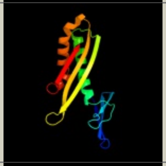
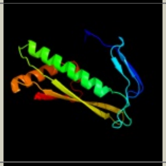
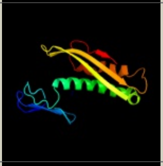
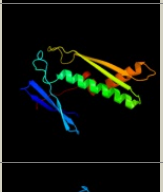
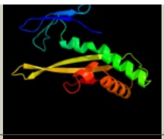
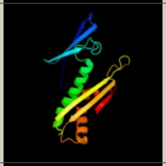
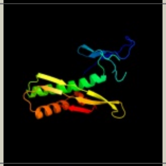
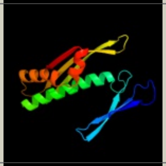
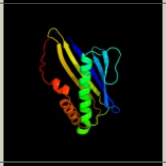
Description	P0C0L2
Date	Thu Jan 5 11:29:53 GMT 2012
Unique Job ID	36859079f33fab52

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qwia_	Alignment		100.0	98	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
2	d1nyed_	Alignment		100.0	100	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
3	d1ukka_	Alignment		100.0	39	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
4	c3eerA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**organic hydroperoxide resistance protein, putative; **PDBTitle:** high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961
5	c2bjoA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**organic hydroperoxide resistance protein ohrb; **PDBTitle:** crystal structure of the organic hydroperoxide resistance2 protein ohrb of bacillus subtilis
6	d2onfa1	Alignment		100.0	16	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
7	d1n2fa_	Alignment		100.0	22	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
8	d1uspa_	Alignment		100.0	25	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
9	d1vlaa_	Alignment		100.0	17	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**YhfA-like
10	d2pn2a1	Alignment		99.9	9	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
11	d2opla1	Alignment		99.9	13	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins

12	c1zb8B_	Alignment		99.9	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**organic hydroperoxide resistance protein; **PDBTitle:** crystal structure of xylella fastidiosa organic peroxide resistance2 protein
13	d1lqla_	Alignment		99.9	19	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
14	c1lqlE_	Alignment		99.9	19	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**osmotical inducible protein c like family; **PDBTitle:** crystal structure of osmc like protein from mycoplasma2 pneumoniae
15	d2d7va1	Alignment		99.9	15	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
16	c2ql8A_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative redox protein; **PDBTitle:** crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
17	d1ml8a_	Alignment		99.9	14	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**YhfA-like
18	c2egtA_	Alignment		99.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein aq_1549; **PDBTitle:** crystal structure of hypothetical protein (aq1549) from aquifex2 aeolicus
19	c3cjeA_	Alignment		99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**osmc-like protein; **PDBTitle:** crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
20	d3c7bb2	Alignment		21.1	8	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
21	d1gsma1	Alignment	not modelled	11.7	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
22	d1zbsa2	Alignment	not modelled	11.5	50	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
23	d1szpa1	Alignment	not modelled	10.7	22	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
24	c3m05A_	Alignment	not modelled	8.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480; **PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
25	d1zxoa1	Alignment	not modelled	8.6	40	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
26	d1szpb1	Alignment	not modelled	8.6	22	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
27	d1ozbg_	Alignment	not modelled	7.4	11	**Fold:**SecB-like **Superfamily:**SecB-like **Family:**Bacterial protein-export protein SecB
28	c3luyA_	Alignment	not modelled	7.3	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
29	d1b22a_	Alignment	not modelled	7.3	26	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain

30	c1b22A_	Alignment	not modelled	7.3	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
31	d1p42a1	Alignment	not modelled	7.2	29	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
32	c3mwbA_	Alignment	not modelled	7.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
33	d2fgca2	Alignment	not modelled	6.8	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
34	c2cx8B_	Alignment	not modelled	6.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)
35	d2v4jb2	Alignment	not modelled	6.1	8	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
36	d2pc6a2	Alignment	not modelled	5.8	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
37	d1v6za2	Alignment	not modelled	5.7	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
38	c2egwB_	Alignment	not modelled	5.5	16	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
39	c1vhyB_	Alignment	not modelled	5.5	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein hi0303; **PDBTitle:** crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558