Phyre^2

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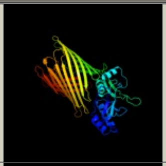
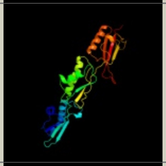
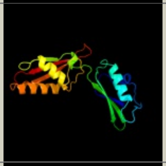
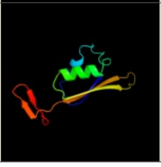
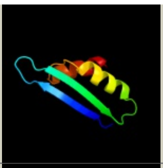
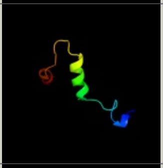
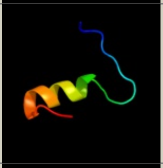
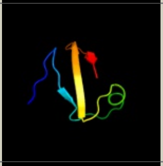
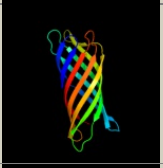
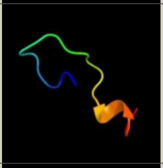
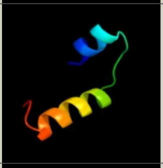
Description	P0ADE4
Date	Thu Jan 5 11:20:47 GMT 2012
Unique Job ID	9f91a680a0ac1d64

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qdzA_	Alignment		100.0	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**tpsb transporter fhac; **PDBTitle:** structure of the membrane protein fhac: a member of the2 omp85/tpsb transporter family
2	c3efcA_	Alignment		100.0	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor yaet; **PDBTitle:** crystal structure of yaet periplasmic domain
3	c2x8xX_	Alignment		100.0	18	**PDB header:**chaperone **Chain:** X: **PDB Molecule:**tlr1789 protein; **PDBTitle:** structure of the n-terminal domain of omp85 from the2 thermophilic cyanobacterium thermosynechococcus elongatus
4	c3mc8A_	Alignment		100.0	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**alr2269 protein; **PDBTitle:** potra1-3 of the periplasmic domain of omp85 from anabaena
5	c2qczA_	Alignment		100.0	16	**PDB header:**membrane protein, protein transport **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor yaet; **PDBTitle:** structure of n-terminal domain of e. coli yaet
6	c3og5A_	Alignment		99.9	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane protein assembly complex, yaet protein; **PDBTitle:** crystal structure of bama potra45 tandem
7	c2v9hA_	Alignment		99.4	14	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor yaet; **PDBTitle:** solution structure of an escherichia coli yaet tandem potra2 domain
8	c2vh2A_	Alignment		90.6	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsq; **PDBTitle:** crystal structure of cell divison protein ftsq from2 yersinia enterecolitica
9	d1vqza1	Alignment		89.2	14	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
10	c1vqzA_	Alignment		87.4	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
11	c2vh1A_	Alignment		78.6	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsq; **PDBTitle:** crystal structure of bacterial cell division protein ftsq2 from e.coli

12	d1x2ga1	Alignment		72.6	15	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
13	c1x2gB_	Alignment		42.2	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lipoate-protein ligase a; **PDBTitle:** crystal structure of lipate-protein ligase a from2 escherichia coli
14	c2k4vA_	Alignment		29.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1076; **PDBTitle:** solution structure of uncharacterized protein pa1076 from2 pseudomonas aeruginosa. northeast structural genomics3 consortium (nesg) target pat3, ontario center for4 structural proteomics target pa1076 .
15	d2h7aa1	Alignment		17.8	17	**Fold:**YcgL-like **Superfamily:**YcgL-like **Family:**YcgL-like
16	c3e19D_	Alignment		14.6	10	**PDB header:**transcription regulator, metal binding p **Chain:** D: **PDB Molecule:**feoa; **PDBTitle:** crystal structure of iron uptake regulatory protein (feoa) solved by2 sulfur sad in a monoclinic space group
17	d1p4ta_	Alignment		13.6	6	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
18	d1m6ya1	Alignment		13.3	25	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
19	d2fnaa1	Alignment		9.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
20	d1nija2	Alignment		9.1	14	**Fold:**Hypothetical protein YjiA, C-terminal domain **Superfamily:**Hypothetical protein YjiA, C-terminal domain **Family:**Hypothetical protein YjiA, C-terminal domain
21	d2gcxa1	Alignment	not modelled	9.1	8	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
22	c2y50A_	Alignment	not modelled	8.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**collagenase; **PDBTitle:** crystal structure of collagenase g from clostridium2 histolyticum at 2.80 angstrom resolution
23	d2fsqa1	Alignment	not modelled	8.4	22	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**Atu0111-like
24	d1vqqa1	Alignment	not modelled	7.8	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
25	c2k0lA_	Alignment	not modelled	7.7	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
26	c3hrlA_	Alignment	not modelled	7.4	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endonuclease-like protein; **PDBTitle:** crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
27	d1ssna_	Alignment	not modelled	7.4	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
28	d1wg8a1	Alignment	not modelled	7.4	32	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
						PDB header:peptide binding protein

29	c3bd0D_	Alignment	not modelled	7.3	17	**Chain:** D: **PDB Molecule:**protein memo1; **PDBTitle:** crystal structure of memo, form ii
30	c1bmlD_	Alignment	not modelled	7.3	14	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**streptokinase; **PDBTitle:** complex of the catalytic domain of human plasmin and streptokinase
31	d1g90a_	Alignment	not modelled	6.0	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
32	d1seia_	Alignment	not modelled	6.0	23	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
33	c3kvnA_	Alignment	not modelled	5.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
34	c3fpnB_	Alignment	not modelled	5.6	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**geobacillus stearothermophilus uvrb interaction **PDBTitle:** crystal structure of uvra-uvrb interaction domains
35	c1nijA_	Alignment	not modelled	5.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yjia; **PDBTitle:** yjia protein