Phyre2

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Description	P0A940
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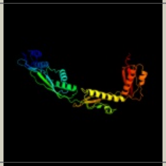
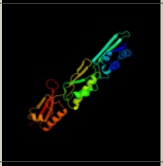
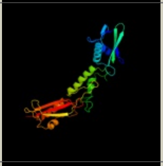
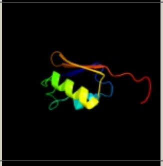
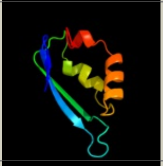
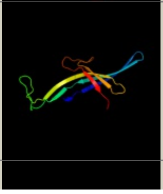
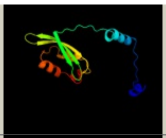
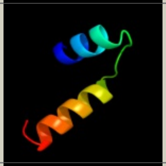
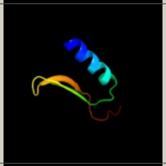
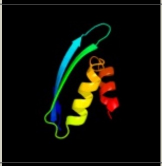
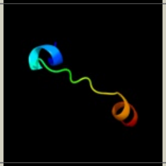
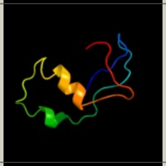
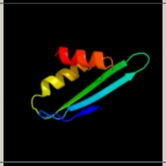
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qdzA_	Alignment		100.0	14	**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	100	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor yaet; **PDBTitle:** crystal structure of yaet periplasmic domain
3	c2qczA_	Alignment		100.0	97	**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
4	c2x8xX_	Alignment		100.0	21	**PDB header:**chaperone **Chain:** X: **PDB Molecule:**tlr1789 protein; **PDBTitle:** structure of the n-terminal domain of omp85 from the2 thermophilic cyanobacterium thermosynechococcus elongatus
5	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
6	c3og5A_	Alignment		100.0	97	**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		99.9	100	**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		95.6	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsq; **PDBTitle:** crystal structure of cell divison protein ftsq from2 yersinia enterecolitica
9	c2vh1A_	Alignment		94.0	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsq; **PDBTitle:** crystal structure of bacterial cell division protein ftsq2 from e.coli
10	d1vqza1	Alignment		61.4	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
11	c2k0lA_	Alignment		42.0	6	**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.

12	c1vqzA_	Alignment		40.5	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
13	c3t9aA_	Alignment		31.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inositol pyrophosphate kinase; **PDBTitle:** crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
14	d2fnaa1	Alignment		29.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
15	c3pjvD_	Alignment		25.4	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd periplasmic domain
16	d1x2ga1	Alignment		25.1	17	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
17	c2k4vA_	Alignment		24.3	10	**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 .
18	d1ssna_	Alignment		19.1	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
19	c1x2gB_	Alignment		13.1	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lipoate-protein ligase a; **PDBTitle:** crystal structure of lipate-protein ligase a from2 escherichia coli
20	c2f1tB_	Alignment		12.1	9	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
21	c1khdD_	Alignment	not modelled	10.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
22	c3bryB_	Alignment	not modelled	10.5	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
23	d1iooa_	Alignment	not modelled	8.7	15	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
24	d1bola_	Alignment	not modelled	8.3	21	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
25	c1vquB_	Alignment	not modelled	7.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
26	d1g90a_	Alignment	not modelled	7.7	6	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
27	c2x4gA_	Alignment	not modelled	7.6	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
28	c3e19D_	Alignment	not modelled	7.5	7	**PDB header:**transcription regulator, metal binding p **Chain:** D: **PDB Molecule:**feoa; **PDBTitle:** crystal structure of iron uptake regulatory protein (feoa)

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29	d1t16a_	Alignment	not modelled	7.4	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
30	d2saka_	Alignment	not modelled	6.8	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
31	c3h0dB_	Alignment	not modelled	6.7	9	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**ctsr; **PDBTitle:** crystal structure of ctsr in complex with a 26bp dna duplex
32	d1udxa3	Alignment	not modelled	6.4	48	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
33	d1vqqa1	Alignment	not modelled	6.2	17	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
34	d1hdoa_	Alignment	not modelled	5.4	63	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
35	c2nn2A_	Alignment	not modelled	5.3	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 7a; **PDBTitle:** crystal structure of the btb domain from the lrf/zbtb72 transcriptional regulator
36	c2yy9A_	Alignment	not modelled	5.3	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 48; **PDBTitle:** crystal structure of btb domain from mouse hkr3
37	c2glwA_	Alignment	not modelled	5.2	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii