Phyre2

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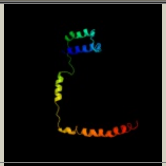
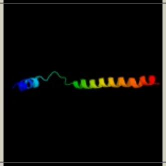
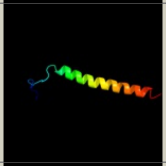
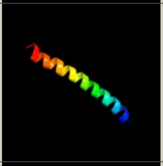
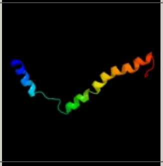
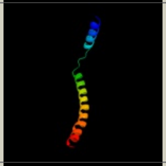
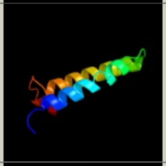
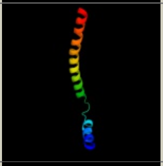
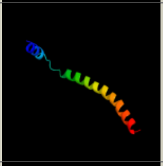
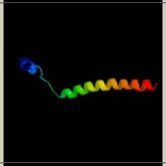
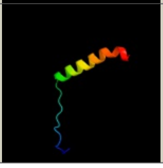
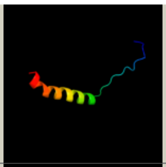
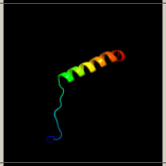
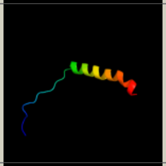
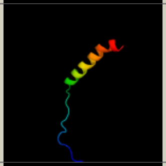
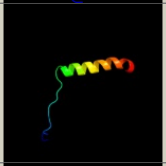
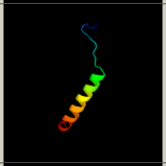
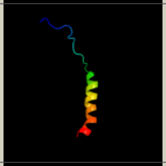
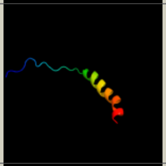
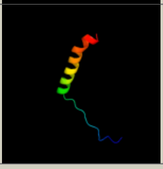
Description	P0AG96
Date	Thu Jan 5 11:28:31 GMT 2012
Unique Job ID	c6bcf1b1399ef897

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2akhZ_	Alignment		100.0	100	**PDB header:**protein transport **Chain:** Z: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a non-2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
2	c3dinD_	Alignment		99.7	35	**PDB header:**membrane protein, protein transport **Chain:** D: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
3	c2zjsE_	Alignment		98.9	30	**PDB header:**protein transport/immune system **Chain:** E: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** crystal structure of secye translocon from thermus thermophilus with a2 fab fragment
4	c3dl8D_	Alignment		97.2	31	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
5	c2wwbB_	Alignment		84.5	21	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
6	d1rhzb_	Alignment		83.0	16	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
7	d2r6gf1	Alignment		81.3	20	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
8	c2ww9B_	Alignment		75.6	20	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
9	d1rh5b_	Alignment		45.5	17	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
10	c3mp7B_	Alignment		38.9	17	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
11	c1s5lL_	Alignment		34.4	17	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center

12	c1s5lL_	Alignment		34.4	17	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
13	c2axtl_	Alignment		34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
14	c2axtL_	Alignment		34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
15	c3a0hl_	Alignment		34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
16	c3a0hL_	Alignment		34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
17	d2axtl1	Alignment		34.4	17	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
18	c3a0bL_	Alignment		34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
19	c3a0bl_	Alignment		34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
20	c3arcL_	Alignment		34.4	17	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
21	c3bz1L_	Alignment	not modelled	34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
22	c3prrL_	Alignment	not modelled	34.4	17	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
23	c3kziL_	Alignment	not modelled	34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
24	c3prqL_	Alignment	not modelled	34.4	17	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
25	c3bz2L_	Alignment	not modelled	34.4	17	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
26	c3arcl_	Alignment	not modelled	26.0	17	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
27	c1yq3C_	Alignment	not modelled	24.1	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate dehydrogenase cytochrome b, large subunit; **PDBTitle:** avian respiratory complex ii with oxaloacetate and ubiquinone
						PDB header:signalling protein/transferase

28	c2ehbD_	Alignment	not modelled	11.7	18	**Chain:** D: **PDB Molecule:**cbl-interacting serine/threonine-protein kinase 24; **PDBTitle:** the structure of the c-terminal domain of the protein kinase atsos22 bound to the calcium sensor atsos3
29	d1jy1a2	Alignment	not modelled	11.1	15	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
30	c3fwbB_	Alignment	not modelled	9.9	9	**PDB header:**cell cycle, transcription **Chain:** B: **PDB Molecule:**nuclear mrna export protein sac3; **PDBTitle:** sac3:sus1:cdc31 complex
31	c2okqB_	Alignment	not modelled	7.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ybaa; **PDBTitle:** crystal structure of unknown conserved ybaa protein from2 shigella flexneri
32	c3sq3C_	Alignment	not modelled	7.3	38	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna phosphodiesterase2 h182a mutant
33	c2qvoA_	Alignment	not modelled	6.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_1382; **PDBTitle:** crystal structure of af1382 from archaeoglobus fulgidus
34	d1q32a2	Alignment	not modelled	6.5	42	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
35	d2okqa1	Alignment	not modelled	6.0	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YbaA-like
36	c1usdA_	Alignment	not modelled	5.8	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
37	c2wmhA_	Alignment	not modelled	5.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fucolectin-related protein; **PDBTitle:** crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae tigr4 in3 complex with the h-disaccharide blood group antigen.
38	d3buxb2	Alignment	not modelled	5.8	19	**Fold:**N-cbl like **Superfamily:**N-terminal domain of cbl (N-cbl) **Family:**N-terminal domain of cbl (N-cbl)
39	c1nopB_	Alignment	not modelled	5.7	17	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure of human tyrosyl-dna phosphodiesterase2 (tdp1) in complex with vanadate, dna and a human3 topoisomerase i-derived peptide