Phyre2

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Description	P0A0I4
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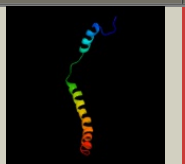
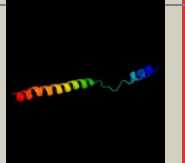
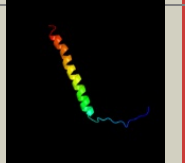
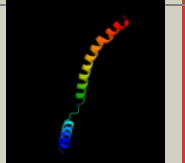
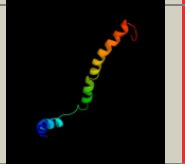
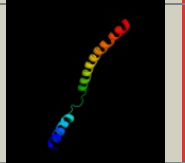
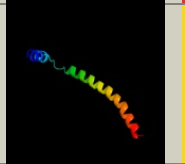
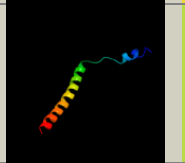
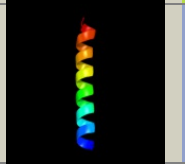
Unique Job ID	d62902ff64f127ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2akhZ_	Alignment		99.8	24	**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		99.8	27	**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	22	**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		96.9	24	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
5	d1rhzb_	Alignment		94.4	16	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
6	c2wwbB_	Alignment		93.9	13	**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
7	c2ww9B_	Alignment		93.4	17	**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
8	d1rh5b_	Alignment		70.9	17	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
9	c3mp7B_	Alignment		61.4	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
10	c1yq3C_	Alignment		28.6	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate dehydrogenase cytochrome b, large subunit; **PDBTitle:** avian respiratory complex ii with oxaloacetate and ubiquinone
11	c2ehbD_	Alignment		15.6	31	**PDB header:**signalling protein/transferase **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

12	d1v0da_	Alignment		14.3	11	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Caspase-activated DNase, CAD (DffB, DFF40)
13	c1v0dA_	Alignment		14.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna fragmentation factor 40 kda subunit; **PDBTitle:** crystal structure of caspase-activated dnase (cad)
14	c3fwbB_	Alignment		12.4	13	**PDB header:**cell cycle, transcription **Chain:** B: **PDB Molecule:**nuclear mrna export protein sac3; **PDBTitle:** sac3:sus1:cdc31 complex
15	d1qopa_	Alignment		11.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
16	d1jy1a2	Alignment		11.2	15	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
17	c2ekcA_	Alignment		8.9	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
18	d1xcfa_	Alignment		8.3	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
19	c3sq3C_	Alignment		8.0	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna phosphodiesterase2 h182a mutant
20	c2yskA_	Alignment		7.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1432; **PDBTitle:** crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
21	d1k8ke_	Alignment	not modelled	7.5	6	**Fold:**Arp2/3 complex 21 kDa subunit ARPC3 **Superfamily:**Arp2/3 complex 21 kDa subunit ARPC3 **Family:**Arp2/3 complex 21 kDa subunit ARPC3
22	d1q32a2	Alignment	not modelled	7.4	23	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
23	c3vrbG_	Alignment	not modelled	6.8	4	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** G: **PDB Molecule:**cytochrome b-large subunit; **PDBTitle:** mitochondrial rhodoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
24	d2okqa1	Alignment	not modelled	6.7	38	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YbaA-like
25	c2wmhA_	Alignment	not modelled	6.7	43	**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.
26	c1nopB_	Alignment	not modelled	6.4	15	**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