Phyre2

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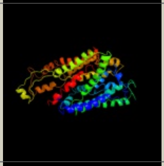
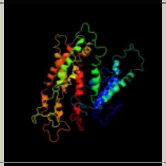
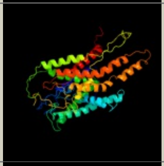
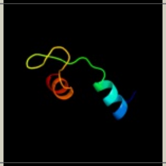
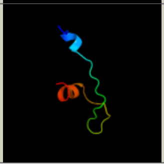
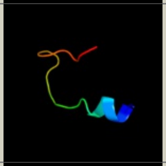
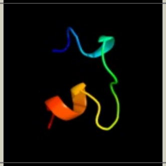
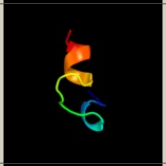
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j01A_	Alignment		100.0	100	**PDB header:**ribosome/ribosomal protein **Chain:** A: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
2	c3dinF_	Alignment		100.0	43	**PDB header:**membrane protein, protein transport **Chain:** F: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
3	c3dl8H_	Alignment		100.0	46	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
4	c2zqpY_	Alignment		100.0	41	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** crystal structure of secye translocon from thermus2 thermophilus
5	c2akiY_	Alignment		100.0	100	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
6	c2wwbA_	Alignment		100.0	22	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**protein transport protein sec61 subunit alpha isoform 1; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
7	d1rh5a_	Alignment		100.0	19	**Fold:**Preprotein translocase SecY subunit **Superfamily:**Preprotein translocase SecY subunit **Family:**Preprotein translocase SecY subunit
8	c2wwaA_	Alignment		100.0	19	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**sec sixty-one protein homolog; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
9	c3mp7A_	Alignment		100.0	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
10	c2nscA_	Alignment		70.2	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritima
11	d1p9ya_	Alignment		67.5	11	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain

12	d1t11a2	Alignment		56.4	16	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
13	d1w26a2	Alignment		52.3	17	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
14	c2d3o1_	Alignment		46.0	31	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**trigger factor; **PDBTitle:** structure of ribosome binding domain of the trigger factor2 on the 50s ribosomal subunit from d. radiodurans
15	c1w26B_	Alignment		38.5	25	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
16	c3kysC_	Alignment		28.0	38	**PDB header:**transcription/protein binding **Chain:** C: **PDB Molecule:**transcriptional enhancer factor tef-1; **PDBTitle:** crystal structure of human yap and tead complex
17	d1zl8a1	Alignment		27.1	18	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
18	c1t11A_	Alignment		25.8	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
19	c3l15A_	Alignment		25.4	45	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional enhancer factor tef-4; **PDBTitle:** human tead2 transcriptional factor
20	d1y74a1	Alignment		23.5	23	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
21	d1wpga4	Alignment	not modelled	22.0	10	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
22	d1wmxb_	Alignment	not modelled	16.6	33	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
23	c2bbjB_	Alignment	not modelled	8.4	15	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
24	d1ebfa2	Alignment	not modelled	7.9	29	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Homoserine dehydrogenase-like
25	d1zq1c1	Alignment	not modelled	7.7	21	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
26	c3kpaB_	Alignment	not modelled	7.5	36	**PDB header:**ligase **Chain:** B: **PDB Molecule:**probable ubiquitin fold modifier conjugating enzyme; **PDBTitle:** ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable)
27	d1to9a_	Alignment	not modelled	7.4	25	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
28	c1to9A_	Alignment	not modelled	7.4	25	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thi-4 protein; **PDBTitle:** crystal structure of thi-4 protein from bacillus subtilis

29	d1jjcb1	Alignment	not modelled	7.0	19	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
30	d2bs2c1	Alignment	not modelled	7.0	11	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Fumarate reductase respiratory complex cytochrome b subunit, FrdC
31	c3qxlB_	Alignment	not modelled	6.2	27	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ras-specific guanine nucleotide-releasing factor ralgps1; **PDBTitle:** crystal structure of the cdc25 domain from ral-specific guanine-2 nucleotide exchange factor ralgps1a
32	d1xo1a1	Alignment	not modelled	6.2	16	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
33	c2voyK_	Alignment	not modelled	6.0	11	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
34	d2gycf1	Alignment	not modelled	5.6	28	**Fold:**Ribosomal protein L9 C-domain **Superfamily:**Ribosomal protein L9 C-domain **Family:**Ribosomal protein L9 C-domain
35	c1mhsA_	Alignment	not modelled	5.6	13	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
36	c1ysmA_	Alignment	not modelled	5.5	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** nmr structure of n-terminal domain (residues 1-77) of siah-2 interacting protein.
37	d1ysma1	Alignment	not modelled	5.5	30	**Fold:**Long alpha-hairpin **Superfamily:**Calcyclin-binding protein-like **Family:**Siah interacting protein N terminal domain-like
38	d1uv7a_	Alignment	not modelled	5.5	14	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
39	c1uv7A_	Alignment	not modelled	5.5	14	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
40	d2huec1	Alignment	not modelled	5.5	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
41	c2k72A_	Alignment	not modelled	5.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-23; **PDBTitle:** solution nmr structure of toxin-like potassium channel2 blocking domain in mmp23
42	d1nexa2	Alignment	not modelled	5.3	35	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
43	d1qd1a2	Alignment	not modelled	5.3	16	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
44	c8tfvA_	Alignment	not modelled	5.1	18	**PDB header:**antimicrobial **Chain:** A: **PDB Molecule:**protein (thanatin); **PDBTitle:** insect defense peptide