










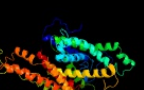

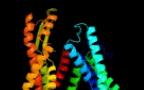

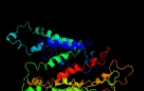











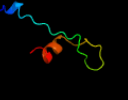
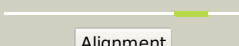

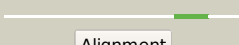

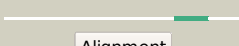
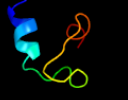
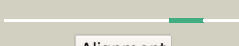




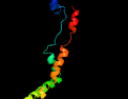


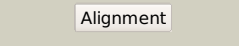


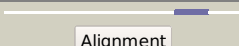
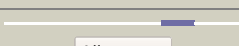



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0732_(secY)_824803_826128
Date	Fri Jul 26 01:50:30 BST 2019
Unique Job ID	e95dcc77b95c7a9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j01A_	 Alignment		100.0	41	PDB header: ribosome/ribosomal protein Chain: A; PDB Molecule: preprotein translocase secy subunit; PDBTitle: structure of the ribosome-secy 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	43	PDB header: protein transport Chain: H; PDB Molecule: preprotein translocase subunit secy; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
4	c2zqpY_	 Alignment		100.0	41	PDB header: protein transport Chain: Y; PDB Molecule: preprotein translocase secy subunit; PDBTitle: crystal structure of secy translocon from thermus2 thermophilus
5	c5eulY_	 Alignment		100.0	45	PDB header: protein transport Chain: Y; PDB Molecule: protein translocase subunit secy; PDBTitle: structure of the seca-secy complex with a translocating polypeptide2 substrate
6	c2wwbA_	 Alignment		100.0	21	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 the actively2 translating wheat germ 80s ribosome
7	c6n3qA_	 Alignment		100.0	23	PDB header: transport protein Chain: A; PDB Molecule: protein transport protein sec61; PDBTitle: cryo-em structure of the yeast sec complex
8	c2akiY_	 Alignment		100.0	44	PDB header: protein transport Chain: Y; PDB Molecule: preprotein translocase secy subunit; PDBTitle: normal mode-based flexible fitted coordinates of a translocating2 secyeg protein-conducting channel into the cryo-em map of a secyeg-3 nascent chain-70s ribosome complex from e. coli
9	c2wwaA_	 Alignment		100.0	20	PDB header: ribosome Chain: A; PDB Molecule: sec sixty-one protein homolog; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the yeast 80s2 ribosome
10	d1rh5a_	 Alignment		100.0	23	Fold: Preprotein translocase SecY subunit Superfamily: Preprotein translocase SecY subunit Family: Preprotein translocase SecY subunit
11	c1vx11_	 Alignment		100.0	23	PDB header: ribosome Chain: 1; PDB Molecule: sec61 alpha subunit; PDBTitle: structure of the translating mammalian ribosome-sec61 complex. this2 entry contains the large subunit ribosomal proteins.

12	c3mp7A_	 Alignment		100.0	24	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
13	c2nscA_	 Alignment		74.3	33	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: structures of and interactions between domains of trigger factor from2 themotoga maritima
14	d1p9ya_	 Alignment		70.8	21	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
15	d1t11a2	 Alignment		61.3	9	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
16	d1w26a2	 Alignment		55.1	17	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
17	c2d3o1_	 Alignment		49.2	21	PDB header: ribosome Chain: 1: PDB Molecule: trigger factor; PDBTitle: structure of ribosome binding domain of the trigger factor on the 50s2 ribosomal subunit from d. radiodurans
18	c1w26B_	 Alignment		44.7	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
19	c1t11A_	 Alignment		29.9	12	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: trigger factor
20	d1wpga4	 Alignment		27.9	12	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
21	d1wmxb_	 Alignment	not modelled	26.7	39	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 30 carbohydrate binding module, CBM30 (PKD repeat)
22	c2xzbB_	 Alignment	not modelled	23.5	30	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h,k-atpase with bound bef and sch28080
23	d1zl8a1	 Alignment	not modelled	22.7	23	Fold: L27 domain Superfamily: L27 domain Family: L27 domain
24	d1y74a1	 Alignment	not modelled	21.2	27	Fold: L27 domain Superfamily: L27 domain Family: L27 domain
25	c5ua4B_	 Alignment	not modelled	18.9	35	PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist; PDBTitle: crystal structure of a179l:bid bh3 complex
26	c5g3gA_	 Alignment	not modelled	14.0	24	PDB header: transferase Chain: A: PDB Molecule: wnk1; PDBTitle: crystal structure of a hypothetical domain in wnk1
27	c3kdpD_	 Alignment	not modelled	13.5	25	PDB header: hydrolase Chain: D: PDB Molecule: sodium/potassium-transporting atpase subunit beta-1; PDBTitle: crystal structure of the sodium-potassium pump
28	c2zxeB_	 Alignment	not modelled	11.6	30	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: na+ ,k+-atpase beta subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
						PDB header: structural genomics, unknown function

29	c5aweA	Alignment	not modelled	11.4	18	Chain: A: PDB Molecule: putative acetoin utilization protein, acetoin PDBTitle: crystal structure of a hypothetical protein, ttha0829 from thermus2 thermophilus hb8, composed of cystathionine-beta-synthase (cbs) and3 aspartate-kinase chorismate-mutase tyra (act) domains
30	d1ebfa2	Alignment	not modelled	10.4	29	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
31	d1jcb1	Alignment	not modelled	9.3	16	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
32	c2yn9B	Alignment	not modelled	8.3	30	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: cryo-em structure of gastric h+,k+-atpase with bound rubidium
33	c2voyK	Alignment	not modelled	8.3	6	PDB header: hydrolase Chain: K: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
34	c6a69A	Alignment	not modelled	8.0	13	PDB header: structural protein Chain: A: PDB Molecule: plasma membrane calcium-transporting atpase 1; PDBTitle: cryo-em structure of a p-type atpase
35	c3b8eB	Alignment	not modelled	8.0	26	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
36	c3ixzB	Alignment	not modelled	7.3	30	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
37	d2fiqa1	Alignment	not modelled	7.0	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
38	c5m1hA	Alignment	not modelled	6.6	25	PDB header: viral protein Chain: A: PDB Molecule: gag protein; PDBTitle: structure of a spumaretrovirus gag central domain reveals an ancient2 retroviral capsid
39	d1nexa2	Alignment	not modelled	6.5	29	Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain
40	c6alyA	Alignment	not modelled	6.2	11	PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription subunit 15; PDBTitle: solution structure of yeast med15 abd2 residues 277-368
41	d1fs1b2	Alignment	not modelled	6.1	29	Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain
42	d2gycf1	Alignment	not modelled	6.0	16	Fold: Ribosomal protein L9 C-domain Superfamily: Ribosomal protein L9 C-domain Family: Ribosomal protein L9 C-domain
43	c1to9A	Alignment	not modelled	5.9	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: thi-4 protein; PDBTitle: crystal structure of thi-4 protein from bacillus subtilis
44	d1to9a	Alignment	not modelled	5.9	21	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4
45	c6mbdC	Alignment	not modelled	5.6	36	PDB header: apoptosis Chain: C: PDB Molecule: dm1; PDBTitle: human mcl-1 in complex with the designed peptide dm1
46	c6mbdD	Alignment	not modelled	5.6	36	PDB header: apoptosis Chain: D: PDB Molecule: dm1; PDBTitle: human mcl-1 in complex with the designed peptide dm1
47	c6epgD	Alignment	not modelled	5.5	31	PDB header: toxin Chain: D: PDB Molecule: zeta_1 toxin; PDBTitle: structure of the epsilon_1 / zeta_1 antitoxin / toxin system from2 heisseria gonorrhoeae.
48	d1iqoa	Alignment	not modelled	5.5	32	Fold: Hypothetical protein MTH1880 Superfamily: Hypothetical protein MTH1880 Family: Hypothetical protein MTH1880
49	d1uv7a	Alignment	not modelled	5.5	36	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM
50	c1uv7A	Alignment	not modelled	5.5	36	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
51	c3hlsE	Alignment	not modelled	5.3	33	PDB header: signaling protein Chain: E: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: crystal structure of the signaling helix coiled-coil doimain2 of the beta-1 subunit of the soluble guanylyl cyclase
52	d1qd1a2	Alignment	not modelled	5.2	16	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
53	c4iu8A	Alignment	not modelled	5.2	8	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
						Fold: Histone-fold

54	d2huec1	Alignment	not modelled	5.2	19	Superfamily: Histone-fold Family: Nucleosome core histones
55	dlxo1a1	Alignment	not modelled	5.2	19	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
56	dluara1	Alignment	not modelled	5.2	7	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
57	c5onsB	Alignment	not modelled	5.1	50	PDB header: translation Chain: B: PDB Molecule: density-regulated protein; PDBTitle: crystal structure of the minimal denr-mcts1 complex
58	dlzq1c1	Alignment	not modelled	5.1	42	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like