


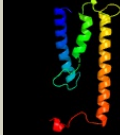








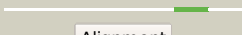


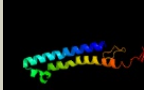

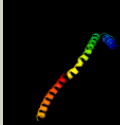
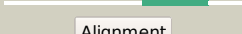

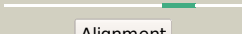
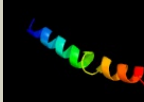


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0007 (-) _9914_10828
Date	Tue Jul 23 14:50:03 BST 2019
Unique Job ID	61c82ce27ecd319

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4gx2B_	 Alignment		87.4	16	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: gsuk channel bound to nad
2	c6eu6A_	 Alignment		73.9	11	PDB header: membrane protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: sensor amt protein
3	c6o7xa_	 Alignment		73.6	14	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
4	c1ciiA_	 Alignment		59.3	16	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
5	c5yyiC_	 Alignment		53.6	20	PDB header: signaling protein Chain: C: PDB Molecule: apisimin; PDBTitle: structure of major royal jelly protein 1 oligomer
6	c4gx5D_	 Alignment		53.4	14	PDB header: transport protein Chain: D: PDB Molecule: trka domain protein; PDBTitle: gsuk channel
7	c5yyiD_	 Alignment		51.9	20	PDB header: signaling protein Chain: D: PDB Molecule: apisimin; PDBTitle: structure of major royal jelly protein 1 oligomer
8	c3aygA_	 Alignment		51.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno
9	c5voxb_	 Alignment		48.3	14	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
10	c6mizC_	 Alignment		42.4	12	PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: human trpm2 ion channel in an adpr-bound state
11	c6fkip_	 Alignment		41.0	17	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3

12	c5ws4A_	Alignment		40.7	18	PDB header: membrane protein Chain: A; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
13	c5vkqC_	Alignment		38.7	18	PDB header: membrane protein Chain: C; PDB Molecule: no mechanoreceptor potential c isoform l; PDBTitle: structure of a mechanotransduction ion channel drosophila nomp c in2 nanodisc
14	c6o7ua_	Alignment		37.2	10	PDB header: membrane protein Chain: A; PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
15	c6iu3A_	Alignment		35.9	14	PDB header: metal transport Chain: A; PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
16	c6d79A_	Alignment		35.6	23	PDB header: transport protein Chain: A; PDB Molecule: sulfate transporter cysz; PDBTitle: structure of cysz, a sulfate permease from pseudomonas fragi
17	c4j7cK_	Alignment		35.1	14	PDB header: transport protein Chain: K; PDB Molecule: ktr system potassium uptake protein b; PDBTitle: ktrab potassium transporter from bacillus subtilis
18	c4mndA_	Alignment		33.8	9	PDB header: transferase Chain: A; PDB Molecule: ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l- PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
19	c5tj5A_	Alignment		33.0	16	PDB header: motor protein Chain: A; PDB Molecule: v-type proton atpase subunit a; PDBTitle: atomic model for the membrane-embedded motor of a eukaryotic v-atpase
20	d3bnea1	Alignment		33.0	24	Fold: Lipoxigenase Superfamily: Lipoxigenase Family: Plant lipoxigenases
21	c3e8gB_	Alignment	not modelled	32.9	16	PDB header: membrane protein Chain: B; PDB Molecule: potassium channel protein; PDBTitle: crystal structure of the the open nak channel-na+/ca2+ complex
22	c3rlbB_	Alignment	not modelled	32.6	20	PDB header: thiamine-binding protein Chain: B; PDB Molecule: thit; PDBTitle: crystal structure at 2.0 a of the s-component for thiamin from an ecf-2 type abc transporter
23	c3b9yA_	Alignment	not modelled	31.9	23	PDB header: transport protein Chain: A; PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
24	c5tfpA_	Alignment	not modelled	31.4	16	PDB header: transferase Chain: A; PDB Molecule: histone-lysine n-methyltransferase setdb2; PDBTitle: crystal structure of the setdb2 amino terminal domain
25	c5t4oJ_	Alignment	not modelled	31.4	17	PDB header: hydrolase Chain: J; PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
26	c2voyG_	Alignment	not modelled	31.2	33	PDB header: hydrolase Chain: G; PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
27	c5aezA_	Alignment	not modelled	31.1	10	PDB header: membrane protein Chain: A; PDB Molecule: mep2; PDBTitle: crystal structure of candida albicans mep2
28	c2qksA_	Alignment	not modelled	31.0	16	PDB header: metal transport Chain: A; PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera
						PDB header: transport protein

29	c3pjzA_	Alignment	not modelled	30.7	16	Chain: A: PDB Molecule: potassium uptake protein trkh; PDBTitle: crystal structure of the potassium transporter trkh from vibrio2 parahaemolyticus
30	c4o6mA_	Alignment	not modelled	29.3	15	PDB header: transferase Chain: A: PDB Molecule: af2299, a cdp-alcohol phosphotransferase; PDBTitle: structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
31	c1ijjA_	Alignment	not modelled	29.3	26	PDB header: signaling protein Chain: A: PDB Molecule: erbb-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbb-2 membrane spanning2 segment
32	c2b2hA_	Alignment	not modelled	28.7	14	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: ammonium transporter amt-1 from a. fulgidus (as)
33	c3s0xB_	Alignment	not modelled	28.1	12	PDB header: hydrolase Chain: B: PDB Molecule: peptidase a24b, flak domain protein; PDBTitle: the crystal structure of gxgd membrane protease flak
34	c5d92B_	Alignment	not modelled	28.0	15	PDB header: membrane protein Chain: B: PDB Molecule: af2299 protein,phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
35	c3j1zP_	Alignment	not modelled	27.6	18	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
36	c3hd7A_	Alignment	not modelled	27.1	16	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
37	d1r11a3	Alignment	not modelled	26.7	20	Fold: MutS N-terminal domain-like Superfamily: tRNA-intron endonuclease N-terminal domain-like Family: tRNA-intron endonuclease N-terminal domain-like
38	d1r3jc_	Alignment	not modelled	25.9	16	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
39	c3vvpA_	Alignment	not modelled	25.5	12	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
40	c6n52B_	Alignment	not modelled	24.9	11	PDB header: membrane protein Chain: B: PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
41	d1rrha1	Alignment	not modelled	24.3	24	Fold: Lipoxygenase Superfamily: Lipoxygenase Family: Plant lipoxygenases
42	c5uowB_	Alignment	not modelled	24.2	18	PDB header: membrane protein Chain: B: PDB Molecule: n-methyl-d-aspartate receptor subunit nr2a; PDBTitle: triheteromeric nmda receptor glun1/glun2a/glun2b in complex with2 glycine, glutamate, mk-801 and a glun2b-specific fab, at ph 6.5
43	c3pjzB_	Alignment	not modelled	24.2	16	PDB header: transport protein Chain: B: PDB Molecule: potassium uptake protein trkh; PDBTitle: crystal structure of the potassium transporter trkh from vibrio2 parahaemolyticus
44	c1no3A_	Alignment	not modelled	24.1	24	PDB header: oxidoreductase Chain: A: PDB Molecule: lipoxygenase-3; PDBTitle: refined structure of soybean lipoxygenase-3 with 4-nitrocatechol at2 2.15 angstrom resolution
45	c4dveA_	Alignment	not modelled	23.3	14	PDB header: transport protein Chain: A: PDB Molecule: biotin transporter bioy; PDBTitle: crystal structure at 2.1 a of the s-component for biotin from an ecf-2 type abc transporter
46	c5nikK_	Alignment	not modelled	23.2	16	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
47	c5lj7B_	Alignment	not modelled	22.9	15	PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
48	c2vv5D_	Alignment	not modelled	21.1	13	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of msccs
49	c6n3qB_	Alignment	not modelled	20.9	25	PDB header: transport protein Chain: B: PDB Molecule: protein transport protein sbh1; PDBTitle: cryo-em structure of the yeast sec complex
50	d2a9ha1	Alignment	not modelled	20.5	13	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
51	c6r7tB_	Alignment	not modelled	19.9	17	PDB header: immune system Chain: B: PDB Molecule: melanoma-associated antigen b1; PDBTitle: crystal structure of human melanoma-associated antigen b1 (mageb1) in2 complex with nanobody
52	c2yvxD_	Alignment	not modelled	18.6	12	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
53	c3jycA_	Alignment	not modelled	17.6	14	PDB header: metal transport Chain: A: PDB Molecule: inward-rectifier k+ channel kir2.2; PDBTitle: crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
54	c2nuwF_	Alignment	not modelled	17.2	10	PDB header: transport protein/signaling protein Chain: F: PDB Molecule: ammonia channel;

54	c2100r_	Alignment	not modelled	17.2	19	PDBTitle: regulating the escherichia coli ammonia channel: the crystal structure2 of the amtB-glnK complex
55	c5meeB_	Alignment	not modelled	16.7	29	PDB header: oxidoreductase Chain: B: PDB Molecule: arachidonate 15-lipoxygenase; PDBTitle: cyanothece lipoxygenase 2 (csplox2) variant - I304v
56	d2axtz1	Alignment	not modelled	16.1	22	Fold: Transmembrane helix hairpin Superfamily: PsbZ-like Family: PsbZ-like
57	c3rfuC_	Alignment	not modelled	15.5	13	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
58	d1rzhh2	Alignment	not modelled	15.4	25	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
59	c3hd6A_	Alignment	not modelled	14.4	14	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
60	d1l9bh2	Alignment	not modelled	14.2	25	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
61	c2h3oA_	Alignment	not modelled	14.0	31	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merft, a membrane protein with two trans-2 membrane helices
62	c4hg6B_	Alignment	not modelled	13.8	24	PDB header: transferase Chain: B: PDB Molecule: cellulose synthase subunit b; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
63	c4gn0D_	Alignment	not modelled	13.6	13	PDB header: signaling protein Chain: D: PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
64	c2n28A_	Alignment	not modelled	13.6	10	PDB header: viral protein Chain: A: PDB Molecule: protein vpu; PDBTitle: solid-state nmr structure of vpu
65	c4tqv_	Alignment	not modelled	13.5	17	PDB header: transport protein Chain: J: PDB Molecule: algm2; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
66	c5aexB_	Alignment	not modelled	12.9	12	PDB header: membrane protein Chain: B: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
67	c2ks1A_	Alignment	not modelled	12.9	8	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: heterodimeric association of transmembrane domains of erbB1 and erbB2 receptors enabling kinase activation
68	c2jwaA_	Alignment	not modelled	12.9	8	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: erbB2 transmembrane segment dimer spatial structure
69	c1zzaA_	Alignment	not modelled	12.9	29	PDB header: membrane protein Chain: A: PDB Molecule: stannin; PDBTitle: solution nmr structure of the membrane protein stannin
70	c3vouB_	Alignment	not modelled	12.7	15	PDB header: transport protein Chain: B: PDB Molecule: ion transport 2 domain protein, voltage-gated sodium PDBTitle: the crystal structure of nak-navsulp chimera channel
71	c2k9yA_	Alignment	not modelled	12.2	41	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
72	c2k9yB_	Alignment	not modelled	12.2	41	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
73	c4zwc_	Alignment	not modelled	12.1	14	PDB header: signaling protein Chain: C: PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
74	c6a69B_	Alignment	not modelled	11.7	14	PDB header: structural protein Chain: B: PDB Molecule: neuroplastin; PDBTitle: cryo-em structure of a p-type atpase
75	c2rmzA_	Alignment	not modelled	11.5	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
76	c3rfrK_	Alignment	not modelled	11.5	19	PDB header: oxidoreductase Chain: K: PDB Molecule: pmoc; PDBTitle: crystal structure of particulate methane monoxygenase (pmmo) from2 methylocystis sp. strain m
77	c2m67A_	Alignment	not modelled	11.4	31	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
78	c3k07A_	Alignment	not modelled	11.4	21	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
79	c2onkC_	Alignment	not modelled	11.2	10	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda

80	c2onkc1	Alignment	not modelled	11.2	10	Fold: Metl-like Superfamily: Metl-like Family: Metl-like
81	c5awwG	Alignment	not modelled	11.2	26	PDB header: protein transport/immune system Chain: G: PDB Molecule: putative preprotein translocase, secg subunit; PDBTitle: precise resting state of thermus thermophilus secyeg
82	c3rlbA	Alignment	not modelled	10.9	20	PDB header: thiamine-binding protein Chain: A: PDB Molecule: thit; PDBTitle: crystal structure at 2.0 a of the s-component for thiamin from an ecf-2 type abc transporter
83	c2kogA	Alignment	not modelled	10.7	23	PDB header: membrane protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: lipid-bound synaptobrevin solution nmr structure
84	c1lnqC	Alignment	not modelled	10.6	12	PDB header: metal transport Chain: C: PDB Molecule: potassium channel related protein; PDBTitle: crystal structure of mthk at 3.3 a
85	c5aexJ	Alignment	not modelled	10.5	19	PDB header: membrane protein Chain: J: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
86	c2wa0A	Alignment	not modelled	10.3	32	PDB header: immune system Chain: A: PDB Molecule: melanoma-associated antigen 4; PDBTitle: crystal structure of the human magea4
87	c1lj2B	Alignment	not modelled	9.6	26	PDB header: viral protein/ translation Chain: B: PDB Molecule: nonstructural rna-binding protein 34; PDBTitle: recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
88	c4f35C	Alignment	not modelled	9.4	17	PDB header: transport protein Chain: C: PDB Molecule: transporter, nadc family; PDBTitle: crystal structure of a bacterial dicarboxylate/sodium symporter
89	c4h33A	Alignment	not modelled	9.4	12	PDB header: membrane protein Chain: A: PDB Molecule: lmo2059 protein; PDBTitle: crystal structure of a voltage-gated k+ channel pore module in a2 closed state in lipid membranes, tetragonal crystal form
90	d1f6ga	Alignment	not modelled	9.1	9	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
91	c2m59A	Alignment	not modelled	9.1	20	PDB header: transferase Chain: A: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
92	c2m59B	Alignment	not modelled	9.1	20	PDB header: transferase Chain: B: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
93	c5zovA	Alignment	not modelled	8.9	13	PDB header: transport protein Chain: A: PDB Molecule: pts ascorbate-specific subunit iibc; PDBTitle: inward-facing conformation of l-ascorbate transporter ulaa
94	c4zwwA	Alignment	not modelled	8.9	14	PDB header: signaling protein Chain: A: PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
95	c3ifxB	Alignment	not modelled	8.9	12	PDB header: membrane protein Chain: B: PDB Molecule: voltage-gated potassium channel; PDBTitle: crystal structure of the spin-labeled kcsc mutant v48r1
96	c6d73B	Alignment	not modelled	8.8	15	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+m2
97	c4witB	Alignment	not modelled	8.8	18	PDB header: lipid transport Chain: B: PDB Molecule: predicted protein; PDBTitle: tmem16 lipid scramblase in crystal form 2
98	c5v96A	Alignment	not modelled	8.8	24	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
99	c2kixD	Alignment	not modelled	8.8	40	PDB header: transport protein Chain: D: PDB Molecule: bm2 protein; PDBTitle: channel domain of bm2 protein from influenza b virus