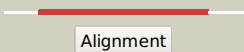

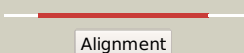
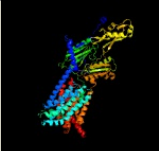
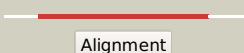

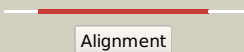

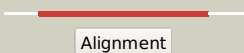
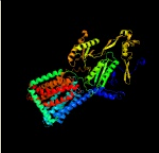
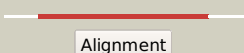

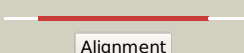





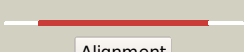

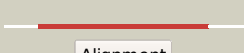


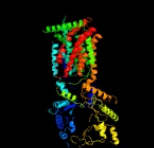
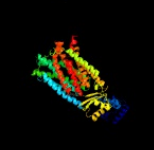








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1183_(mmpL10)_1321526_1324534
Date	Wed Jul 31 22:05:27 BST 2019
Unique Job ID	2daeb567671c229b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ajjA_	 Alignment		100.0	21	PDB header: membrane protein, hydrolase Chain: A; PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
2	c5lq3F_	 Alignment		100.0	15	PDB header: transport protein Chain: F; PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
3	c6owsB_	 Alignment		100.0	15	PDB header: membrane protein Chain: B; PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
4	c3k07A_	 Alignment		100.0	13	PDB header: transport protein Chain: A; PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
5	c4mt1A_	 Alignment		100.0	14	PDB header: membrane protein, transport protein Chain: A; PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
6	c2v50A_	 Alignment		100.0	14	PDB header: membrane protein Chain: A; PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
7	c1oy8A_	 Alignment		100.0	15	PDB header: membrane protein Chain: A; PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
8	c4k0eA_	 Alignment		100.0	12	PDB header: transport protein Chain: A; PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
9	c6dmoA_	 Alignment		100.0	13	PDB header: protein binding Chain: A; PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
10	c5khnB_	 Alignment		100.0	18	PDB header: membrane protein Chain: B; PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
11	c6csxA_	 Alignment		100.0	15	PDB header: transport protein Chain: A; PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom

12	c4k0eC	Alignment		100.0	13	PDB header: transport protein Chain: C: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
13	c3jd8A	Alignment		100.0	11	PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom
14	c3aqpB	Alignment		100.0	16	PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus throphilus
15	c5xamA	Alignment		100.0	18	PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secd; PDBTitle: crystal structure of secdf in i form at 4 a resolution
16	c5mg3D	Alignment		100.0	18	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
17	d1iwga8	Alignment		100.0	17	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
18	c5mg3F	Alignment		99.9	11	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
19	d1iwga7	Alignment		99.9	14	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
20	c5ensA	Alignment		99.4	13	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb,multidrug efflux pump PDBTitle: rhodamine bound structure of bacterial efflux pump.
21	c4r86B	Alignment	not modelled	98.8	8	PDB header: protein transport Chain: B: PDB Molecule: rnd family aminoglycoside/multidrug efflux pump; PDBTitle: crystal structure of aminoglycoside/multidrug efflux system acrd from2 salmonella typhimurium
22	d1iwga6	Alignment	not modelled	91.2	15	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
23	d1iwga4	Alignment	not modelled	83.5	10	Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
24	c6o7xa	Alignment	not modelled	82.3	9	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
25	c6o7ua	Alignment	not modelled	81.9	10	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
26	d1iwga2	Alignment	not modelled	74.8	11	Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
27	c2yvxD	Alignment	not modelled	49.1	8	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
						Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1,

28	d1iwga3	Alignment	not modelled	42.3	15	PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
29	d2nwwa1	Alignment	not modelled	42.0	9	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
30	c4av3A	Alignment	not modelled	41.7	17	PDB header: hydrolase Chain: A: PDB Molecule: k(+)-stimulated pyrophosphate-energized sodium pump; PDBTitle: crystal structure of thermotoga maritima sodium pumping membrane2 integral pyrophosphatase with metal ions in active site
31	c1ciiA	Alignment	not modelled	37.5	25	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
32	c5gasN	Alignment	not modelled	33.0	11	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
33	c5a96A	Alignment	not modelled	29.0	40	PDB header: viral protein Chain: A: PDB Molecule: polyhedrin; PDBTitle: crystal structure of lymantria dispar cpv14 polyhedra
34	c5zlgA	Alignment	not modelled	28.0	9	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
35	c3jcuZ	Alignment	not modelled	14.8	15	PDB header: membrane protein Chain: Z: PDB Molecule: photosystem ii reaction center protein z; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
36	c2mk9A	Alignment	not modelled	14.3	4	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3
37	c2mkaB	Alignment	not modelled	14.3	4	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
38	c2mkaC	Alignment	not modelled	14.3	4	PDB header: immune system Chain: C: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
39	c2mk9B	Alignment	not modelled	14.3	4	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3
40	c2mkaA	Alignment	not modelled	14.3	4	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
41	d1a87a	Alignment	not modelled	12.2	20	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
42	c1a87A	Alignment	not modelled	12.2	20	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
43	c2kncB	Alignment	not modelled	11.6	12	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIb-beta3 transmembrane-cytoplasmic2 heterocomplex
44	d1iwga5	Alignment	not modelled	11.5	16	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
45	d2d81a1	Alignment	not modelled	11.4	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PHB depolymerase-like
46	c3j20P	Alignment	not modelled	11.4	13	PDB header: ribosome Chain: P: PDB Molecule: 30s ribosomal protein s14p type z; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
47	c6n52B	Alignment	not modelled	9.4	15	PDB header: membrane protein Chain: B: PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
48	d1kf6d	Alignment	not modelled	9.3	8	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
49	c4cdiC	Alignment	not modelled	8.9	10	PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; PDBTitle: crystal structure of acrb-acrz complex
50	c3wo6A	Alignment	not modelled	8.8	18	PDB header: membrane protein Chain: A: PDB Molecule: membrane protein insertase yidc 2; PDBTitle: crystal structure of yidc from bacillus halodurans (form i)
51	c6b2zf	Alignment	not modelled	8.7	10	PDB header: membrane protein Chain: F: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
52	c6eznH	Alignment	not modelled	8.6	8	PDB header: membrane protein Chain: H: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex

53	c6b8ht	Alignment	not modelled	8.5	10	PDB header: membrane protein Chain: T: PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
54	c2qg8A	Alignment	not modelled	8.2	22	PDB header: transferase Chain: A: PDB Molecule: acyl carrier protein synthase py06285; PDBTitle: plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
55	d1jb0i	Alignment	not modelled	8.1	6	Fold: Single transmembrane helix Superfamily: Subunit VIII of photosystem I reaction centre, Psa Family: Subunit VIII of photosystem I reaction centre, Psa
56	c4fe1l	Alignment	not modelled	8.1	6	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: improving the accuracy of macromolecular structure refinement at 7 a2 resolution
57	c4gn0D	Alignment	not modelled	8.0	9	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
58	c2ww9B	Alignment	not modelled	8.0	7	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sss1; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
59	c4rfsS	Alignment	not modelled	7.8	16	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: substrate binding prtein s; PDBTitle: structure of a pantothenate energy coupling factor transporter
60	c2bbjB	Alignment	not modelled	7.8	6	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
61	c5n9yB	Alignment	not modelled	7.7	11	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
62	c2k1B	Alignment	not modelled	7.4	21	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
63	c2k1kA	Alignment	not modelled	7.4	21	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
64	c2k1IA	Alignment	not modelled	7.4	21	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
65	c2k1kB	Alignment	not modelled	7.4	21	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
66	c6ahrB	Alignment	not modelled	7.4	19	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonucleases p/mrp protein subunit pop1; PDBTitle: cryo-em structure of human ribonuclease p
67	c3v7oA	Alignment	not modelled	7.3	21	PDB header: transcription Chain: A: PDB Molecule: minor nucleoprotein vp30; PDBTitle: crystal structure of the c-terminal domain of ebola virus vp30 (strain2 reston-89)
68	c3wvfA	Alignment	not modelled	7.3	23	PDB header: chaperone Chain: A: PDB Molecule: membrane protein insertase yidc; PDBTitle: crystal structure of yidc from escherichia coli
69	c2bvtB	Alignment	not modelled	6.6	30	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,4-mannanase; PDBTitle: the structure of a modular endo-beta-1,4-mannanase from cellulomonas2 fimi explains the product specificity of glycoside hydrolase family3 26 mannanases.
70	c2kseA	Alignment	not modelled	6.5	37	PDB header: transferase Chain: A: PDB Molecule: sensor protein qsec; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor qsec, center for structures of membrane proteins (csm)3 target 4311c
71	c6dkuA	Alignment	not modelled	6.5	7	PDB header: unknown function Chain: A: PDB Molecule: vp35; PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
72	c3tjA	Alignment	not modelled	6.3	10	PDB header: membrane protein Chain: A: PDB Molecule: nupc family protein; PDBTitle: crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
73	c3eamB	Alignment	not modelled	6.2	12	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: glr4197 protein; PDBTitle: an open-pore structure of a bacterial pentameric ligand-2 gated ion channel
74	d2axtz1	Alignment	not modelled	6.1	27	Fold: Transmembrane helix hairpin Superfamily: PsbZ-like Family: PsbZ-like
75	d2yvxa3	Alignment	not modelled	6.0	7	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
76	c5ir6B	Alignment	not modelled	6.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
77	c3zm8A	Alignment	not modelled	5.9	33	PDB header: hydrolase Chain: A: PDB Molecule: gh26 endo-beta-1,4-mannanase; PDBTitle: crystal structure of podospira anserina gh26-cbm352 beta-(1,4)-mannanase
78	c4xtrG	Alignment	not modelled	5.8	19	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: pep12p; PDBTitle: structure of get3 bound to the transmembrane domain of

					pep12	
79	d2cwqa1	Alignment	not modelled	5.7	6	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
80	c5cmoB_	Alignment	not modelled	5.6	28	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of holo-[acyl-carrier-protein] synthase (acps) from2 neisseria meningitidis
81	c2i8bB_	Alignment	not modelled	5.5	19	PDB header: viral protein Chain: B: PDB Molecule: minor nucleoprotein vp30; PDBTitle: crystal structure of the c-terminal domain of ebola virus vp30
82	d1sd4a_	Alignment	not modelled	5.5	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
83	c6mctK_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: K: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
84	c6mctI_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: I: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
85	c6mq2D_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
86	c6mctA_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: A: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
87	c6mctE_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: E: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
88	c6mctO_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: O: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
89	c6mpwA_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: A: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
90	c6mctG_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: G: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
91	c6mctD_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
92	c6mctN_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: N: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
93	c6mctJ_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: J: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
94	c6mctC_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: C: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
95	c6mctB_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: B: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
96	c6mctM_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: M: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
97	c6mctH_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: H: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
98	c6mctL_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: L: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
99	c6mctF_	Alignment	not modelled	5.5	24	PDB header: de novo protein Chain: F: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction