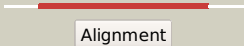

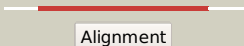
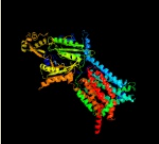
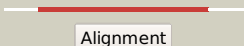







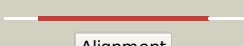











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0507_(mmpL2)_597202_600108
 Date Fri Jul 26 01:50:05 BST 2019
 Unique Job ID 61fd7b28a5cbeed5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ajjA_	 Alignment		100.0	19	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	12	PDB header: transport protein Chain: F; PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
3	c3k07A_	 Alignment		100.0	15	PDB header: transport protein Chain: A; PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
4	c4mt1A_	 Alignment		100.0	13	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
5	c6owsB_	 Alignment		100.0	11	PDB header: membrane protein Chain: B; PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
6	c2v50A_	 Alignment		100.0	12	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	c4k0eA_	 Alignment		100.0	15	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
8	c6dmoA_	 Alignment		100.0	15	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
9	c1oy8A_	 Alignment		100.0	12	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
10	c5khnB_	 Alignment		100.0	17	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	11	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	15	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	15	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	c3aaqB	Alignment		100.0	15	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 thrmophilus
15	c5xamA	Alignment		100.0	13	PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secdf; PDBTitle: crystal structure of secdf in i form at 4 a resolution
16	c5mg3D	Alignment		100.0	14	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secdf; PDBTitle: em fitted model of bacterial holo-translocon
17	c5mg3F	Alignment		99.9	11	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secdf; PDBTitle: em fitted model of bacterial holo-translocon
18	d1iwga8	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
19	d1iwga7	Alignment		99.9	15	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
20	c5ensA	Alignment		99.5	9	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	5	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	d1iwga3	Alignment	not modelled	95.2	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
23	d1iwga6	Alignment	not modelled	88.2	9	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
24	c2yvxD	Alignment	not modelled	86.1	10	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
25	d1iwga4	Alignment	not modelled	82.5	14	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
26	c4av3A	Alignment	not modelled	74.6	10	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
27	c5f1bC	Alignment	not modelled	66.6	22	PDB header: viral protein/transport protein Chain: C: PDB Molecule: niemann-pick c1 protein; PDBTitle: structural basis of ebola virus entry: viral glycoprotein

						bound to its2 endosomal receptor niemann-pick c1
28	d1iwga2	Alignment	not modelled	66.0	9	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
29	c5zlgA_	Alignment	not modelled	39.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
30	d2yvxa3	Alignment	not modelled	27.7	9	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
31	d1iwga5	Alignment	not modelled	27.6	1	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
32	c2mkaC_	Alignment	not modelled	23.5	17	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
33	c2mkaA_	Alignment	not modelled	23.5	17	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
34	c2mk9A_	Alignment	not modelled	23.5	17	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
35	c2mkaB_	Alignment	not modelled	23.5	17	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
36	c2mk9B_	Alignment	not modelled	23.5	17	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
37	c1ciiA_	Alignment	not modelled	20.1	11	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
38	c2bbjB_	Alignment	not modelled	16.7	12	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
39	d1iwga1	Alignment	not modelled	16.5	8	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
40	c6n52B_	Alignment	not modelled	15.0	14	PDB header: membrane protein Chain: B: PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
41	c1a87A_	Alignment	not modelled	14.9	12	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
42	d1a87a_	Alignment	not modelled	14.9	12	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
43	c2jo1A_	Alignment	not modelled	14.4	18	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
44	c2kseA_	Alignment	not modelled	13.1	33	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
45	c5n9yB_	Alignment	not modelled	12.3	13	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
46	c1p58F_	Alignment	not modelled	12.3	17	PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
47	c1vw4b_	Alignment	not modelled	12.1	29	PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
48	c6fkip_	Alignment	not modelled	11.8	6	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
49	d1jb0i_	Alignment	not modelled	11.7	19	Fold: Single transmembrane helix Superfamily: Subunit VIII of photosystem I reaction centre, PsaI Family: Subunit VIII of photosystem I reaction centre, PsaI
50	c4fe1l_	Alignment	not modelled	11.7	19	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
51	c5ws4A_	Alignment	not modelled	11.7	14	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
52	c3eamB_	Alignment	not modelled	11.3	10	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
53	c2m1hA_	Alignment	not modelled	11.2	60	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor s-ii; PDBTitle: solution structure of a pwwp domain from trypanosoma brucei
54	c1gk7A_	Alignment	not modelled	11.0	17	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
55	d1gmnbl	Alignment	not modelled	10.8	36	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain
56	c6dkuA_	Alignment	not modelled	10.5	7	PDB header: unknown function Chain: A: PDB Molecule: vp35; PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
57	c2n1pA_	Alignment	not modelled	10.3	17	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
58	c2lonA_	Alignment	not modelled	10.3	15	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b
59	d1qmgal	Alignment	not modelled	10.3	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Acetohydroxy acid isomeroeductase (ketol-acid reductoisomerase, KARI)
60	c5ho5D_	Alignment	not modelled	10.1	18	PDB header: metal transport Chain: D: PDB Molecule: magnetosome protein mamb; PDBTitle: mamb
61	c2lqxA_	Alignment	not modelled	10.0	22	PDB header: cell adhesion Chain: A: PDB Molecule: fermitin family homolog 2; PDBTitle: nmr structure for kindle-2 n-terminus
62	c5wvma_	Alignment	not modelled	9.8	18	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,two-component system PDBTitle: crystal structure of baes cocrystallized with 2 mm indole
63	c6fkib_	Alignment	not modelled	9.5	11	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
64	c2kncB_	Alignment	not modelled	9.5	13	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
65	c2k1IA_	Alignment	not modelled	9.4	16	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
66	c2k1IB_	Alignment	not modelled	9.4	16	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
67	c2k1kA_	Alignment	not modelled	9.4	16	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
68	c2k1kB_	Alignment	not modelled	9.4	16	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
69	d2hkua2	Alignment	not modelled	9.4	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
70	c6b2zf_	Alignment	not modelled	9.3	14	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
71	c2mkvA_	Alignment	not modelled	9.3	22	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
72	c2f1fA_	Alignment	not modelled	9.1	12	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli
73	c3zm8A_	Alignment	not modelled	9.1	56	PDB header: hydrolase Chain: A: PDB Molecule: gh26 endo-beta-1,4-mannanase; PDBTitle: crystal structure of podospora anserina gh26-cbm352 beta-(1,4)-mannanase
74	c2ww9B_	Alignment	not modelled	9.1	3	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
75	d1khca_	Alignment	not modelled	9.1	27	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
76	c2lowA_	Alignment	not modelled	8.9	33	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfp
77	c2bvtB_	Alignment	not modelled	8.7	50	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. PDB header: chaperone

78	c3ofgA_	Alignment	not modelled	8.7	11	Chain: A: PDB Molecule: boca/mesd chaperone for ywtd beta-propeller-egf protein 1; PDBTitle: structured domain of caenorhabditis elegans bmy-1
79	c6c08F_	Alignment	not modelled	8.7	20	PDB header: membrane protein Chain: F: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state
80	c6b8ht_	Alignment	not modelled	8.7	14	PDB header: membrane protein Chain: T: PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
81	c5oonA_	Alignment	not modelled	8.7	14	PDB header: membrane protein Chain: A: PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, boca
82	c3l2uA_	Alignment	not modelled	8.5	21	PDB header: recombination/dna Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitagravir)
83	c3v7oA_	Alignment	not modelled	8.4	17	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)
84	c4gn0D_	Alignment	not modelled	8.3	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
85	c6mctC_	Alignment	not modelled	8.1	14	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
86	c6mctJ_	Alignment	not modelled	8.1	14	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
87	c6mctN_	Alignment	not modelled	8.1	14	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
88	c6mctM_	Alignment	not modelled	8.1	14	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
89	c6mctI_	Alignment	not modelled	8.1	14	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
90	c6mctO_	Alignment	not modelled	8.1	14	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
91	c6mctK_	Alignment	not modelled	8.1	14	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
92	c6mctE_	Alignment	not modelled	8.1	14	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
93	c6mctH_	Alignment	not modelled	8.1	14	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
94	c6mctB_	Alignment	not modelled	8.1	14	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
95	c6mctL_	Alignment	not modelled	8.1	14	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
96	c6mctG_	Alignment	not modelled	8.1	14	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
97	c6mctD_	Alignment	not modelled	8.1	14	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
98	c6mpwA_	Alignment	not modelled	8.1	14	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
99	c6mq2D_	Alignment	not modelled	8.1	14	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