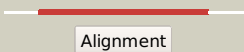

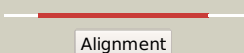

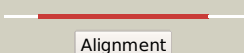

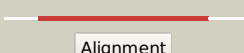





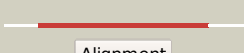

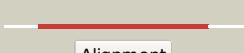












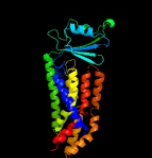





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0450c_(mmpL4)_538591_541494
Date	Tue Jul 23 14:50:52 BST 2019
Unique Job ID	48df5759b807b22c

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	14	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	14	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
4	c6owsB_	 Alignment		100.0	12	PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
5	c4mt1A_	 Alignment		100.0	12	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	c4k0eA_	 Alignment		100.0	14	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	c1oy8A_	 Alignment		100.0	13	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
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	17	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
11	c4k0eC_	 Alignment		100.0	14	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

12	c6csxA_	Alignment		100.0	13	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
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	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	14	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	14	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
17	c5mg3F_	Alignment		99.9	12	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
18	d1iwga8	Alignment		99.9	12	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	17	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
20	c5ensA_	Alignment		99.6	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	9	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	92.3	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
23	d1iwga3	Alignment	not modelled	90.6	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
24	c2yvxD_	Alignment	not modelled	78.5	10	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
25	d1iwga2	Alignment	not modelled	67.2	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	67.1	16	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
						Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1,

27	d1iwga4	Alignment	not modelled	62.3	6	PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains 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
28	c2mkvA	Alignment	not modelled	42.3	28	PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
29	c1p58E	Alignment	not modelled	39.9	14	PDB header: transport protein, membrane protein Chain: B: PDB Molecule: proton/glutamate symporter, sdf family; PDBTitle: crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
30	c4ky0B	Alignment	not modelled	25.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
31	c5zlgA	Alignment	not modelled	24.8	13	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
32	c1ciiA	Alignment	not modelled	20.4	14	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor s-ii; PDBTitle: solution structure of a pwwp domain from trypanosoma brucei
33	c2m1hA	Alignment	not modelled	20.0	17	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
34	d1iwga5	Alignment	not modelled	19.7	7	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	c2mk9A	Alignment	not modelled	19.3	29	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the dimeric transmembrane domain in2 the trimeric state
36	c2mkaA	Alignment	not modelled	19.3	29	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	c2mk9B	Alignment	not modelled	19.3	29	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
38	c2mkaC	Alignment	not modelled	19.3	29	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
39	c2mkaB	Alignment	not modelled	19.3	29	PDB header: translation Chain: A: PDB Molecule: protein impact homolog; PDBTitle: structure of two-domain translational regulator yih1 reveals a2 possible mechanism of action
40	c6bqiA	Alignment	not modelled	18.0	15	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
41	c2kseA	Alignment	not modelled	17.6	29	PDB header: transferase Chain: A: PDB Molecule: acyl carrier protein synthase py06285; PDBTitle: plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
42	c2qg8A	Alignment	not modelled	15.8	22	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
43	c6o7ua	Alignment	not modelled	15.2	15	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
44	c1a87A	Alignment	not modelled	14.4	13	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
45	d1a87a	Alignment	not modelled	14.4	13	PDB header: membrane protein Chain: A: PDB Molecule: neutral amino acid transporter b(0); PDBTitle: cryo-em structure of the human neutral amino acid transporter asct2
46	c6gctA	Alignment	not modelled	13.7	12	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
47	c6b2zf	Alignment	not modelled	13.4	18	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
48	c2bbjB	Alignment	not modelled	13.3	18	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
49	c2k1kA	Alignment	not modelled	13.3	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
50	c2k1A	Alignment	not modelled	13.3	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
51	c2k1kB	Alignment	not modelled	13.3	16	PDB header: signaling protein

52	c2k1B_	Alignment	not modelled	13.3	16	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
53	d1kf6d_	Alignment	not modelled	13.1	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)
54	c6b8ht_	Alignment	not modelled	12.7	18	PDB header: membrane protein Chain: T; PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
55	c6fkip_	Alignment	not modelled	12.7	10	PDB header: membrane protein Chain: P; PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
56	c2kncB_	Alignment	not modelled	11.5	14	PDB header: cell adhesion Chain: B; PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
57	c5kk2E_	Alignment	not modelled	11.1	17	PDB header: membrane protein, transport protein, sig Chain: E; PDB Molecule: voltage-dependent calcium channel gamma-2 subunit; PDBTitle: architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
58	c2lqxA_	Alignment	not modelled	11.0	29	PDB header: cell adhesion Chain: A; PDB Molecule: fermitin family homolog 2; PDBTitle: nmr structure for kindle-2 n-terminus
59	c1p58F_	Alignment	not modelled	10.9	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
60	c3w66A_	Alignment	not modelled	10.6	7	PDB header: metal transport Chain: A; PDB Molecule: magnetosome protein mamm; PDBTitle: mamm-ctd d249a and h285a
61	d2nwwa1	Alignment	not modelled	10.3	7	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
62	c3hqjA_	Alignment	not modelled	10.2	12	PDB header: transferase Chain: A; PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
63	c2ww9B_	Alignment	not modelled	10.2	12	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
64	c4cbfB_	Alignment	not modelled	10.0	14	PDB header: virus Chain: B; PDB Molecule: m protein; PDBTitle: near-atomic resolution cryo-em structure of dengue serotype 4 virus
65	c2kmcA_	Alignment	not modelled	9.9	29	PDB header: cell adhesion Chain: A; PDB Molecule: fermitin family homolog 1; PDBTitle: solution structure of the n-terminal domain of kindlin-1
66	d1f7la_	Alignment	not modelled	9.7	15	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: Holo-(acyl carrier protein) synthase ACPS
67	c6fkib_	Alignment	not modelled	9.7	13	PDB header: membrane protein Chain: B; PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
68	c2jp3A_	Alignment	not modelled	9.5	18	PDB header: transcription Chain: A; PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
69	c4y0lA_	Alignment	not modelled	9.5	14	PDB header: membrane protein Chain: A; PDB Molecule: putative membrane protein mmp11; PDBTitle: mycobacterial membrane protein mmp11d2
70	c2jzbA_	Alignment	not modelled	9.5	19	PDB header: transferase Chain: A; PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of the streptomyces coelicolor holo-2 [acyl-carrier-protein] synthase (acps) in complex with3 coenzyme a at 1.6 a
71	c4cdiC_	Alignment	not modelled	9.1	26	PDB header: membrane protein Chain: C; PDB Molecule: predicted protein; PDBTitle: crystal structure of acrb-acrz complex
72	c4fe1l_	Alignment	not modelled	9.0	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
73	d1jb0i_	Alignment	not modelled	9.0	19	Fold: Single transmembrane helix Superfamily: Subunit VIII of photosystem I reaction centre, PsaI Family: Subunit VIII of photosystem I reaction centre, PsaI
74	c4gn0D_	Alignment	not modelled	8.9	10	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
75	c4a2nB_	Alignment	not modelled	8.8	9	PDB header: transferase Chain: B; PDB Molecule: isoprenylcysteine carboxyl methyltransferase; PDBTitle: crystal structure of ma-icmt
76	c4or2A_	Alignment	not modelled	8.8	13	PDB header: signaling protein Chain: A; PDB Molecule: soluble cytochrome b562, metabotropic glutamate receptor 1; PDBTitle: human class c g protein-coupled metabotropic glutamate receptor 1 in2 complex with a negative allosteric modulator
77	c6dkuA_	Alignment	not modelled	8.6	11	PDB header: unknown function Chain: A; PDB Molecule: vp35;

77	c0ukvA_	Alignment	not modelled	8.0	11	PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
78	c5n9yB_	Alignment	not modelled	8.5	15	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
79	c4a01B_	Alignment	not modelled	8.2	11	PDB header: hydrolase Chain: B: PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase
80	c3v7oA_	Alignment	not modelled	8.2	19	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)
81	c2qfiB_	Alignment	not modelled	7.7	12	PDB header: transport protein Chain: B: PDB Molecule: ferrous-iron efflux pump fief; PDBTitle: structure of the zinc transporter yliip
82	d2qfia1	Alignment	not modelled	7.6	12	Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like
83	d2yvxa3	Alignment	not modelled	7.5	8	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
84	c4dh4A_	Alignment	not modelled	7.4	10	PDB header: isomerase Chain: A: PDB Molecule: mif; PDBTitle: macrophage migration inhibitory factor toxoplasma gondii
85	c5cmoB_	Alignment	not modelled	7.4	24	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
86	c5ho5D_	Alignment	not modelled	7.4	20	PDB header: metal transport Chain: D: PDB Molecule: magnetosome protein mamb; PDBTitle: mamb
87	c5gasN_	Alignment	not modelled	7.3	7	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
88	d1j3wa_	Alignment	not modelled	7.3	12	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
89	c3tufA_	Alignment	not modelled	7.0	8	PDB header: signaling protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: structure of the spoiii-spoiiiah pore forming complex.
90	d1hfoa_	Alignment	not modelled	6.9	10	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
91	c2xczA_	Alignment	not modelled	6.8	16	PDB header: immune system Chain: A: PDB Molecule: possible atls1-like light-inducible protein; PDBTitle: crystal structure of macrophage migration inhibitory factor homologue2 from prochlorococcus marinus
92	c2lowA_	Alignment	not modelled	6.8	33	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip
93	c5f1bC_	Alignment	not modelled	6.8	11	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
94	d1qmga1	Alignment	not modelled	6.8	19	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Acetohydroxy acid isomeroeductase (ketol-acid reductoisomerase, KARI)
95	d1sd4a_	Alignment	not modelled	6.8	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
96	d3bzka3	Alignment	not modelled	6.7	14	Fold: Tex N-terminal region-like Superfamily: Tex N-terminal region-like Family: Tex N-terminal region-like
97	d1kkga_	Alignment	not modelled	6.6	16	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
98	d2cwqa1	Alignment	not modelled	6.6	14	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
99	c3h88A_	Alignment	not modelled	6.6	37	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of 4'-phosphopantetheinyl transferase acps from2 vibrio cholerae o1 biovar eltor