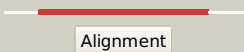

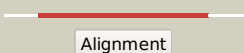
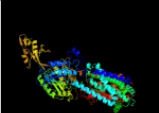
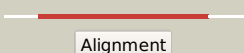

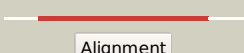





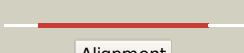

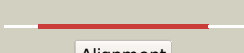











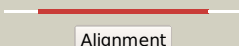

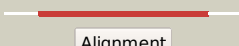

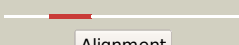

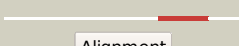




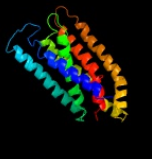

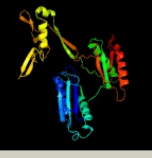

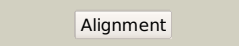



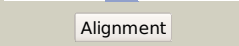



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0402c_(mmpL1)_480358_483234
Date	Tue Jul 23 14:50:47 BST 2019
Unique Job ID	6106bfb25e2b4443

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ajjA_			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_			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_			100.0	16	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
4	c4mt1A_			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_			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
6	c2v50A_			100.0	13	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_			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_			100.0	14	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_			100.0	14	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_			100.0	18	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
11	c4k0eC_			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	14	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	22	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	17	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
17	d1iwga8	 Alignment		100.0	13	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
18	c5mg3F_	 Alignment		100.0	14	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		99.6	11	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	99.1	11	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	92.6	10	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	c2yvxD_	 Alignment	not modelled	84.4	10	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
24	d1iwga2	 Alignment	not modelled	72.3	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
25	d1wija_	 Alignment	not modelled	30.5	17	Fold: LEM/SAP HeH motif Superfamily: DNA-binding domain of EIN3-like Family: DNA-binding domain of EIN3-like
26	d1iwga3	 Alignment	not modelled	26.6	7	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	c4av3A_	 Alignment	not modelled	22.9	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
28	c2kseA_	Alignment	not modelled	17.1	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
29	c1ciiA_	Alignment	not modelled	14.9	11	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
30	c5zlgA_	Alignment	not modelled	14.0	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	c6gctA_	Alignment	not modelled	13.7	14	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
32	d1iwga4	Alignment	not modelled	13.2	6	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
33	c6bqiA_	Alignment	not modelled	12.5	15	PDB header: translation Chain: A; PDB Molecule: protein impact homolog; PDBTitle: structure of two-domain translational regulator yih1 reveals a2 possible mechanism of action
34	c4a01B_	Alignment	not modelled	12.0	12	PDB header: hydrolase Chain: B; PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase
35	c2ww9B_	Alignment	not modelled	11.1	0	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
36	c1a87A_	Alignment	not modelled	10.9	11	PDB header: bacteriocin Chain: A; PDB Molecule: colicin n; PDBTitle: colicin n
37	d1a87a_	Alignment	not modelled	10.9	11	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
38	c2mkaC_	Alignment	not modelled	10.8	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
39	c2mkaB_	Alignment	not modelled	10.8	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
40	c2mk9B_	Alignment	not modelled	10.8	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
41	c2mkaA_	Alignment	not modelled	10.8	29	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
42	c2mk9A_	Alignment	not modelled	10.8	29	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
43	c4djiA_	Alignment	not modelled	10.2	10	PDB header: transport protein Chain: A; PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
44	c4fe1I_	Alignment	not modelled	9.5	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
45	d1jb0i_	Alignment	not modelled	9.5	19	Fold: Single transmembrane helix Superfamily: Subunit VIII of photosystem I reaction centre, PsaI Family: Subunit VIII of photosystem I reaction centre, PsaI
46	d2yvxa3	Alignment	not modelled	9.3	8	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
47	c2n1pA_	Alignment	not modelled	8.8	9	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
48	c2k9pA_	Alignment	not modelled	8.8	21	PDB header: membrane protein Chain: A; PDB Molecule: pheromone alpha factor receptor; PDBTitle: structure of tm1_tm2 in lppg micelles
49	d1iwga5	Alignment	not modelled	8.5	8	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
50	c3tijA_	Alignment	not modelled	8.2	12	PDB header: membrane protein Chain: A; PDB Molecule: npuc family protein; PDBTitle: crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
51	c3j2pD_	Alignment	not modelled	8.0	21	PDB header: viral protein Chain: D; PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer
52	c6b2zf_	Alignment	not modelled	7.9	18	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 PDB header: signaling protein
53	c2k1kA_	Alignment	not modelled	7.6	16	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
54	c2k1kB_	Alignment	not modelled	7.6	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
55	c2k1LA_	Alignment	not modelled	7.6	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
56	c2k1LB_	Alignment	not modelled	7.6	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
57	d3bzka3	Alignment	not modelled	7.5	21	Fold: Tex N-terminal region-like Superfamily: Tex N-terminal region-like Family: Tex N-terminal region-like
58	c6b8ht_	Alignment	not modelled	7.5	18	PDB header: membrane protein Chain: T: PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
59	c2bbjB_	Alignment	not modelled	7.4	13	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
60	c2m1hA_	Alignment	not modelled	7.4	26	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor s-ii; PDBTitle: solution structure of a pwwp domain from trypanosoma brucei
61	c5ireD_	Alignment	not modelled	7.2	18	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus
62	c4cbfB_	Alignment	not modelled	7.0	16	PDB header: virus Chain: B: PDB Molecule: m protein; PDBTitle: near-atomic resolution cryo-em structure of dengue serotype 4 virus
63	c3v7oA_	Alignment	not modelled	6.7	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)
64	c4ev6E_	Alignment	not modelled	6.6	21	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
65	c5wsnD_	Alignment	not modelled	6.5	16	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: structure of japanese encephalitis virus
66	c2qg8A_	Alignment	not modelled	6.4	26	PDB header: transferase Chain: A: PDB Molecule: acyl carrier protein synthase py06285; PDBTitle: plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
67	c4b03D_	Alignment	not modelled	6.3	16	PDB header: virus Chain: D: PDB Molecule: dengue virus 1 prm protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
68	c4or2A_	Alignment	not modelled	5.9	14	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
69	c3zf7e_	Alignment	not modelled	5.8	25	PDB header: ribosome Chain: E: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
70	c3l2uA_	Alignment	not modelled	5.7	29	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 (elvitegravir)
71	c2lqxA_	Alignment	not modelled	5.7	40	PDB header: cell adhesion Chain: A: PDB Molecule: fermitin family homolog 2; PDBTitle: nmr structure for kindle-2 n-terminus
72	c2lonA_	Alignment	not modelled	5.7	11	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b
73	c5gasN_	Alignment	not modelled	5.6	11	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
74	c5l2bC_	Alignment	not modelled	5.5	11	PDB header: transport protein Chain: C: PDB Molecule: nucleoside permease; PDBTitle: structure of cntnw n149s, e332a in an outward-facing state
75	c1p58E_	Alignment	not modelled	5.5	12	PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
76	c5ws4A_	Alignment	not modelled	5.4	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
77	c5ohdB_	Alignment	not modelled	5.2	20	PDB header: membrane protein Chain: B: PDB Molecule: growth hormone receptor; PDBTitle: putative inactive (dormant) dimeric state of ghr transmembrane domain
						PDB header: membrane protein

78	c5n9yB_	Alignment	not modelled	5.2	10	Chain: B; PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
79	c2kmcA_	Alignment	not modelled	5.1	40	PDB header: cell adhesion Chain: A; PDB Molecule: fermitin family homolog 1; PDBTitle: solution structure of the n-terminal domain of kindlin-1
80	c6dkuA_	Alignment	not modelled	5.0	11	PDB header: unknown function Chain: A; PDB Molecule: vp35; PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory2 domain