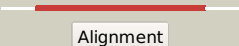



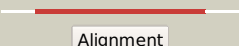





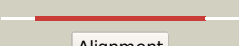

















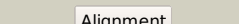

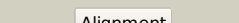

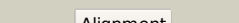

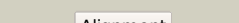





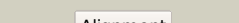
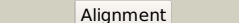

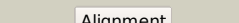
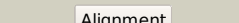

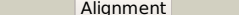


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2339_(mmpL9)_2614703_2617591
Date	Mon Aug 5 13:25:49 BST 2019
Unique Job ID	f6a38ad0bd679116

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ajjA_</a>	 Alignment		100.0	18	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
2	<a href="#">c5lq3F_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> cmeb; <b>PDBTitle:</b> structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
3	<a href="#">c3k07A_</a>	 Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa; <b>PDBTitle:</b> crystal structure of cusa
4	<a href="#">c6owsB_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> efflux pump membrane transporter; <b>PDBTitle:</b> cryo-em structure of an acinetobacter baumannii multidrug efflux pump
5	<a href="#">c4mt1A_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> drug efflux protein; <b>PDBTitle:</b> crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
6	<a href="#">c2v50A_</a>	 Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein mexb; <b>PDBTitle:</b> the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
7	<a href="#">c4k0eA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii
8	<a href="#">c1oy8A_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
9	<a href="#">c5khnB_</a>	 Alignment		100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> rnd transporter; <b>PDBTitle:</b> crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
10	<a href="#">c6dmoA_</a>	 Alignment		100.0	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein patched homolog 1; <b>PDBTitle:</b> cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
11	<a href="#">c4k0eC_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii

12	<a href="#">c6csxA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug efflux pump subunit acrb; <b>PDBTitle:</b> single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
13	<a href="#">c3jd8A_</a>	 Alignment		100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> niemann-pick c1 protein; <b>PDBTitle:</b> cryo-em structure of the full-length human npc1 at 4.4 angstrom
14	<a href="#">c3aqpB_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable secdf protein-export membrane protein; <b>PDBTitle:</b> crystal structure of secdf, a translocon-associated membrane protein,2 from thermus throphilus
15	<a href="#">c5xamA_</a>	 Alignment		100.0	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit secd; <b>PDBTitle:</b> crystal structure of secdf in i form at 4 a resolution
16	<a href="#">c5mg3D_</a>	 Alignment		100.0	15	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein translocase subunit secd; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
17	<a href="#">d1iwga8</a>	 Alignment		100.0	15	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
18	<a href="#">c5mg3F_</a>	 Alignment		100.0	13	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> protein translocase subunit secf; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
19	<a href="#">d1iwga7</a>	 Alignment		100.0	15	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
20	<a href="#">c5ensaA_</a>	 Alignment		99.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug efflux pump subunit acrb,multidrug efflux pump <b>PDBTitle:</b> rhodamine bound structure of bacterial efflux pump.
21	<a href="#">c4r86B_</a>	 Alignment	not modelled	99.0	12	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> rnd family aminoglycoside/multidrug efflux pump; <b>PDBTitle:</b> crystal structure of aminoglycoside/multidrug efflux system acrd from2 salmonella typhimurium
22	<a href="#">d1iwga3</a>	 Alignment	not modelled	94.8	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
23	<a href="#">c2yvxD_</a>	 Alignment	not modelled	89.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
24	<a href="#">d1iwga6</a>	 Alignment	not modelled	74.7	15	<b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
25	<a href="#">d1iwga4</a>	 Alignment	not modelled	73.1	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
26	<a href="#">d1iwga2</a>	 Alignment	not modelled	58.0	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
27	<a href="#">c2bbjB_</a>	 Alignment	not modelled	23.3	16	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein;

					<b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
28	<a href="#">c5vc8B_</a>	Alignment	not modelled	16.5	21 <b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> histone-lysine n-methyltransferase nsd2; <b>PDBTitle:</b> crystal structure of the whsc1 pwwp1 domain
29	<a href="#">d2yvxa3</a>	Alignment	not modelled	15.5	11 <b>Fold:</b> MgtE membrane domain-like <b>Superfamily:</b> MgtE membrane domain-like <b>Family:</b> MgtE membrane domain-like
30	<a href="#">c6n52B_</a>	Alignment	not modelled	14.6	12 <b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> metabotropic glutamate receptor 5; <b>PDBTitle:</b> metabotropic glutamate receptor 5 apo form
31	<a href="#">c6eznH_</a>	Alignment	not modelled	11.2	14 <b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
32	<a href="#">d1a87a_</a>	Alignment	not modelled	10.9	17 <b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
33	<a href="#">c1a87A_</a>	Alignment	not modelled	10.9	17 <b>PDB header:</b> bacteriocin <b>Chain:</b> A: <b>PDB Molecule:</b> colicin n; <b>PDBTitle:</b> colicin n
34	<a href="#">c4a01B_</a>	Alignment	not modelled	10.7	15 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proton pyrophosphatase; <b>PDBTitle:</b> crystal structure of the h-translocating pyrophosphatase
35	<a href="#">c6bqiA_</a>	Alignment	not modelled	10.7	22 <b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> protein impact homolog; <b>PDBTitle:</b> structure of two-domain translational regulator yih1 reveals a2 possible mechanism of action
36	<a href="#">c1ciiA_</a>	Alignment	not modelled	10.5	16 <b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
37	<a href="#">c2mk9A_</a>	Alignment	not modelled	9.7	22 <b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> toll-like receptor 3; <b>PDBTitle:</b> spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3
38	<a href="#">c2mkaB_</a>	Alignment	not modelled	9.7	22 <b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> toll-like receptor 3; <b>PDBTitle:</b> spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
39	<a href="#">c2mkaA_</a>	Alignment	not modelled	9.7	22 <b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> toll-like receptor 3; <b>PDBTitle:</b> spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
40	<a href="#">c2mk9B_</a>	Alignment	not modelled	9.7	22 <b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> toll-like receptor 3; <b>PDBTitle:</b> spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3
41	<a href="#">c2mkaC_</a>	Alignment	not modelled	9.7	22 <b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> toll-like receptor 3; <b>PDBTitle:</b> spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
42	<a href="#">d1h3za_</a>	Alignment	not modelled	9.7	17 <b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Tudor/PWWP/MBT <b>Family:</b> PWWP domain
43	<a href="#">c2kseA_</a>	Alignment	not modelled	9.4	33 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein qsec; <b>PDBTitle:</b> backbone structure of the membrane domain of e. coli histidine kinase2 receptor qsec, center for structures of membrane proteins (csm)3 target 4311c
44	<a href="#">c2jo1A_</a>	Alignment	not modelled	9.4	17 <b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
45	<a href="#">c4y0lA_</a>	Alignment	not modelled	9.0	10 <b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein mmp111; <b>PDBTitle:</b> mycobacterial membrane protein mmp11d2
46	<a href="#">c3tijA_</a>	Alignment	not modelled	8.6	13 <b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> snpc family protein; <b>PDBTitle:</b> crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
47	<a href="#">c5n9yB_</a>	Alignment	not modelled	8.3	8 <b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the full-length structure of zntb
48	<a href="#">c2l89A_</a>	Alignment	not modelled	8.2	14 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pwwp domain-containing protein 1; <b>PDBTitle:</b> solution structure of pdp1 pwwp domain reveals its unique binding2 sites for methylated h4k20 and dna
49	<a href="#">d1khca_</a>	Alignment	not modelled	7.2	32 <b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Tudor/PWWP/MBT <b>Family:</b> PWWP domain
50	<a href="#">d1kf6d_</a>	Alignment	not modelled	7.1	9 <b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
51	<a href="#">c5l2bC_</a>	Alignment	not modelled	6.9	14 <b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> nucleoside permease; <b>PDBTitle:</b> structure of cntnw n149s, e332a in an outward-facing state
52	<a href="#">c2ww9B_</a>	Alignment	not modelled	6.7	10 <b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> protein transport protein sss1; <b>PDBTitle:</b> cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
53	<a href="#">c5zlgA_</a>	Alignment	not modelled	6.7	6 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b reductase 1; <b>PDBTitle:</b> human duodenal cytochrome b (dcytb) in zinc ion and

						ascorbate bound2 form
54	<a href="#">c6o7ua_</a>	Alignment	not modelled	6.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
55	<a href="#">c6ahrB_</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleases p/mrp protein subunit pop1; <b>PDBTitle:</b> cryo-em structure of human ribonuclease p
56	<a href="#">c4gn0D_</a>	Alignment	not modelled	6.4	10	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> hamp domain of af1503; <b>PDBTitle:</b> de novo phasing of a hamp-complex using an improved arcimboldo method
57	<a href="#">c6m97A_</a>	Alignment	not modelled	6.4	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of high affinity copper uptake protein 1 <b>PDBTitle:</b> crystal structure of the high-affinity copper transporter ctr1
58	<a href="#">c6g25A_</a>	Alignment	not modelled	6.4	24	<b>PDB header:</b> oncoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase nsd3; <b>PDBTitle:</b> x-ray structure of nsd3-pwpp1 in complex with compound 4
59	<a href="#">d1iwga1</a>	Alignment	not modelled	6.3	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
60	<a href="#">c4ev6E_</a>	Alignment	not modelled	6.2	21	<b>PDB header:</b> metal transport <b>Chain:</b> E: <b>PDB Molecule:</b> magnesium transport protein cora; <b>PDBTitle:</b> the complete structure of cora magnesium transporter from 2 methanocaldococcus jannaschii
61	<a href="#">c2m1hA_</a>	Alignment	not modelled	6.1	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor s-ii; <b>PDBTitle:</b> solution structure of a pwpp domain from trypanosoma brucei
62	<a href="#">c6elhA_</a>	Alignment	not modelled	6.0	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide reductase; <b>PDBTitle:</b> low resolution structure of neisseria meningitidis qnor
63	<a href="#">c4fu6A_</a>	Alignment	not modelled	5.9	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pc4 and sfrs1-interacting protein; <b>PDBTitle:</b> crystal structure of the psip1 pwpp domain
64	<a href="#">d3bzka3</a>	Alignment	not modelled	5.7	17	<b>Fold:</b> Tex N-terminal region-like <b>Superfamily:</b> Tex N-terminal region-like <b>Family:</b> Tex N-terminal region-like
65	<a href="#">c2m67A_</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
66	<a href="#">c3llrA_</a>	Alignment	not modelled	5.5	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 3a; <b>PDBTitle:</b> crystal structure of the pwpp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
67	<a href="#">c3l2uA_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitegravir)
68	<a href="#">c3w66A_</a>	Alignment	not modelled	5.2	6	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> magnetosome protein mamm; <b>PDBTitle:</b> mamm-ctd d249a and h285a
69	<a href="#">c2k1kB_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
70	<a href="#">c2k1lA_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
71	<a href="#">c2k1lB_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
72	<a href="#">c2k1kA_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
73	<a href="#">c4hkrB_</a>	Alignment	not modelled	5.1	8	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> calcium release-activated calcium channel protein 1; <b>PDBTitle:</b> calcium release-activated calcium (crac) channel orai
74	<a href="#">c4or2A_</a>	Alignment	not modelled	5.1	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562, metabotropic glutamate receptor 1; <b>PDBTitle:</b> human class c g protein-coupled metabotropic glutamate receptor 1 in2 complex with a negative allosteric modulator