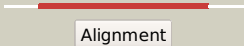

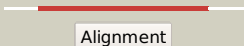
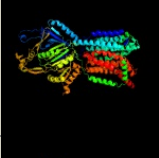
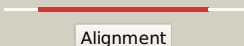
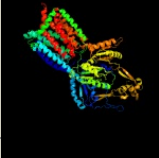






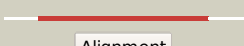




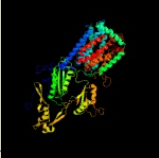



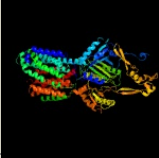


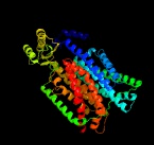

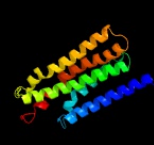






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1522c_(mmpL12)_1714178_1717618
Date	Fri Aug 2 13:30:11 BST 2019
Unique Job ID	38ba1a2b19b6e72a

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	17	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	13	PDB header: transport protein Chain: A; PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
4	c4mt1A_	 Alignment		100.0	17	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	14	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	15	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	c5khnB_	 Alignment		100.0	21	PDB header: membrane protein Chain: B; PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
8	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
9	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
10	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
11	c6csxA_	 Alignment		100.0	17	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	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
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	21	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	15	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	d1iwga8	Alignment		100.0	16	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	12	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
19	d1iwga7	Alignment		99.9	18	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
20	c5ensA	Alignment		99.0	10	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	98.5	10	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	c2yvxD	Alignment	not modelled	87.0	13	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
23	d1iwga2	Alignment	not modelled	80.2	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
24	d1iwga6	Alignment	not modelled	75.1	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
25	d1iwga3	Alignment	not modelled	53.3	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
26	d1iwga4	Alignment	not modelled	35.3	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
27	c6hwhb	Alignment	not modelled	33.9	22	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory

						supercomplex from2 mycobacterium smegmatis
28	c3j2wS_	Alignment	not modelled	29.9	23	PDB header: virus Chain: S: PDB Molecule: glycoprotein e2; PDBTitle: electron cryo-microscopy of chikungunya virus
29	c1ciiA_	Alignment	not modelled	26.6	15	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
30	c4fc2C_	Alignment	not modelled	24.3	26	PDB header: hydrolase Chain: C: PDB Molecule: poly(adp-ribose) glycohydrolase; PDBTitle: crystal structure of mouse poly(adp-ribose) glycohydrolase (parg)2 catalytic domain
31	c2vg2C_	Alignment	not modelled	21.6	25	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
32	c2mkaA_	Alignment	not modelled	20.1	13	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
33	c2mkaC_	Alignment	not modelled	20.1	13	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
34	c2mkaB_	Alignment	not modelled	20.1	13	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
35	c2mk9A_	Alignment	not modelled	20.1	13	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
36	c2mk9B_	Alignment	not modelled	20.1	13	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	c3flhC_	Alignment	not modelled	19.4	27	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein lp_1913; PDBTitle: crystal structure of lp_1913 protein from lactobacillus plantarum,2 northeast structural genomics consortium target lpr140b
38	c2kseA_	Alignment	not modelled	19.0	13	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
39	c6o7ua_	Alignment	not modelled	18.1	12	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
40	c5t6oA_	Alignment	not modelled	15.6	39	PDB header: biosynthetic protein Chain: A: PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
41	d1mska_	Alignment	not modelled	15.6	39	Fold: Methionine synthase activation domain-like Superfamily: Methionine synthase activation domain-like Family: Methionine synthase SAM-binding domain
42	c1k98A_	Alignment	not modelled	15.1	36	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
43	c6n52B_	Alignment	not modelled	14.2	13	PDB header: membrane protein Chain: B: PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
44	c2bbjB_	Alignment	not modelled	14.2	8	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
45	c2o2kA_	Alignment	not modelled	13.9	42	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n
46	c1p58F_	Alignment	not modelled	13.7	29	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	d1a87a_	Alignment	not modelled	13.1	11	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
48	c1a87A_	Alignment	not modelled	13.1	11	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
49	c3rq9B_	Alignment	not modelled	12.9	77	PDB header: tse2-binding protein Chain: B: PDB Molecule: type vi secretion immunity protein; PDBTitle: structure of tsi2, a tse2-immunity protein from pseudomonas aeruginosa
50	c1p58E_	Alignment	not modelled	12.9	27	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
51	c3dntB_	Alignment	not modelled	12.8	28	PDB header: transferase Chain: B: PDB Molecule: protein hipa; PDBTitle: structures of mdt proteins
52	c5ietA_	Alignment	not modelled	12.3	33	PDB header: gene regulation Chain: A: PDB Molecule: bacterial proteasome activator; PDBTitle: crystal structure of mycobacterium tuberculosis atp-independent2 proteasome activator
53	c2q6mA_	Alignment	not modelled	11.7	38	PDB header: toxin Chain: A: PDB Molecule: cholix toxin; PDBTitle: catalytic fragment of cholix toxin from vibrio cholerae in

						complex2 with the pj34 inhibitor PDB header: unknown function Chain: A: PDB Molecule: cerato-platanin 1; PDBTitle: crystal structure of cerato-platanin 1 from m. perniciosa (mpcp1)
54	c3sujA_	Alignment	not modelled	11.6	24	
55	c5xavB_	Alignment	not modelled	11.3	26	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
56	d2f20a1	Alignment	not modelled	10.5	58	Fold: BB1717-like Superfamily: BB1717-like Family: BB1717-like
57	c4b03A_	Alignment	not modelled	10.5	10	PDB header: virus Chain: A: PDB Molecule: dengue virus 1 e protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
58	d1vlba2	Alignment	not modelled	10.4	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
59	c5zlgA_	Alignment	not modelled	10.3	10	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
60	c5frtC_	Alignment	not modelled	10.1	15	PDB header: oxidoreductase Chain: C: PDB Molecule: dimeric (2fe-2s) protein; PDBTitle: structure of the fesii (shethna) protein of azotobacter vinelandii
61	c2k8oA_	Alignment	not modelled	10.0	58	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-I; PDBTitle: solution structure of integrin alpha I
62	c5xspF_	Alignment	not modelled	9.9	25	PDB header: signaling protein/ligase Chain: F: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
63	d1n62a2	Alignment	not modelled	9.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
64	d2yvxa3	Alignment	not modelled	9.4	13	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
65	c5knkB_	Alignment	not modelled	9.4	19	PDB header: transferase Chain: B: PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
66	c4gn0D_	Alignment	not modelled	9.4	8	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
67	c1ffuA_	Alignment	not modelled	9.3	39	PDB header: hydrolase Chain: A: PDB Molecule: cuts, iron-sulfur protein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
68	d1ffva2	Alignment	not modelled	9.1	39	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
69	c4gf5S_	Alignment	not modelled	9.0	30	PDB header: transferase Chain: S: PDB Molecule: cals11; PDBTitle: crystal structure of calicheamicin methyltransferase, cals11
70	c3j2pD_	Alignment	not modelled	8.9	27	PDB header: viral protein Chain: D: PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer
71	c5sxpG_	Alignment	not modelled	8.9	25	PDB header: signaling protein/ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
72	c5u0pF_	Alignment	not modelled	8.7	17	PDB header: transcription Chain: F: PDB Molecule: mediator complex subunit 6; PDBTitle: cryo-em structure of the transcriptional mediator
73	d1dgja2	Alignment	not modelled	8.7	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
74	c3tufA_	Alignment	not modelled	8.6	9	PDB header: signaling protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: structure of the spoiiq-spoiiiah pore forming complex.
75	c6b2zf_	Alignment	not modelled	8.5	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
76	c6b8ht_	Alignment	not modelled	8.4	14	PDB header: membrane protein Chain: T: PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
77	c4fe1l_	Alignment	not modelled	8.4	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
78	d1jb0i_	Alignment	not modelled	8.4	19	Fold: Single transmembrane helix Superfamily: Subunit VIII of photosystem I reaction centre, PsaI Family: Subunit VIII of photosystem I reaction centre, PsaI
79	c2jpkA_	Alignment	not modelled	8.3	29	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin lactococcin-g subunit beta; PDBTitle: lactococcin g-b in dpc

80	c6m97A_	Alignment	not modelled	8.0	6	PDB header: transport protein Chain: A; PDB Molecule: chimera protein of high affinity copper uptake protein 1 PDBTitle: crystal structure of the high-affinity copper transporter ctr1
81	c6adqP_	Alignment	not modelled	7.9	20	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
82	c4cbfB_	Alignment	not modelled	7.9	17	PDB header: virus Chain: B; PDB Molecule: m protein; PDBTitle: near-atomic resolution cryo-em structure of dengue serotype 4 virus
83	d2qlia2	Alignment	not modelled	7.8	56	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
84	c2jpmA_	Alignment	not modelled	7.8	36	PDB header: antimicrobial protein Chain: A; PDB Molecule: bacteriocin lactococcin-g subunit beta; PDBTitle: lactococcin g-b in tfe
85	d1iwga5	Alignment	not modelled	7.7	9	Fold: Multidrug efflux transporter AcrB ToIC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB ToIC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB ToIC docking domain; DN and DC subdomains
86	d1rm6c2	Alignment	not modelled	7.4	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
87	c6h4kA_	Alignment	not modelled	7.3	43	PDB header: immune system Chain: A; PDB Molecule: ubiquitin carboxyl-terminal hydrolase 25; PDBTitle: structure of the usp25 c-terminal domain
88	c2k1A_	Alignment	not modelled	7.3	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
89	c2k1B_	Alignment	not modelled	7.3	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
90	c2k1kB_	Alignment	not modelled	7.3	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
91	c2k1kA_	Alignment	not modelled	7.3	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
92	c5n9yB_	Alignment	not modelled	7.1	14	PDB header: membrane protein Chain: B; PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
93	c1wa7B_	Alignment	not modelled	7.0	29	PDB header: sh3 domain Chain: B; PDB Molecule: hypothetical 28.7 kda protein in dhfr 3'region PDBTitle: sh3 domain of human lyn tyrosine kinase in complex with a2 herpesviral ligand
94	c5xu1M_	Alignment	not modelled	7.0	14	PDB header: transport protein Chain: M; PDB Molecule: abc transporter permease; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
95	c4p6vD_	Alignment	not modelled	7.0	8	PDB header: oxidoreductase Chain: D; PDB Molecule: na(+)-translocating nadh-quinone reductase subunit d; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
96	c2x1A_	Alignment	not modelled	7.0	67	PDB header: translation Chain: A; PDB Molecule: arginine attenuator peptide; PDBTitle: structural basis of translational stalling by human cytomegalovirus2 (hcmv) and fungal arginine attenuator peptide (aap)
97	c6nbxG_	Alignment	not modelled	6.9	22	PDB header: oxidoreductase Chain: G; PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
98	c1p58C_	Alignment	not modelled	6.9	14	PDB header: virus Chain: C; PDB Molecule: major envelope protein e; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
99	c6mu1C_	Alignment	not modelled	6.9	11	PDB header: membrane protein Chain: C; PDB Molecule: inositol 1,4,5-trisphosphate receptor type 1; PDBTitle: structure of full-length ip3r1 channel bound with adenophostin a