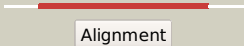

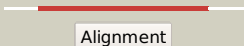

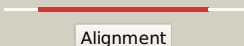




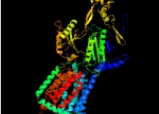


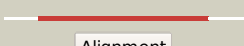











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2942_(mmpL7)_3285080_3287842
 Date Thu Aug 8 16:20:10 BST 2019
 Unique Job ID 4c1243b0a1812732

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ajjA_			100.0	15	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmpL3 from mycobacterium2 smegmatis complexed with ica38
2	c5lq3F_			100.0	11	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	12	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
4	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
5	c4mt1A_			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_			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	c1oy8A_			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
8	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
9	c5khnB_			100.0	16	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
10	c6csxA_			100.0	12	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
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	c6dmoA_	Alignment		100.0	12	PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations I282q/t500f/p504l
13	c3aaqB_	Alignment		100.0	14	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
14	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
15	c5xamA_	Alignment		100.0	12	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	d1iwga8	Alignment		99.9	10	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
17	c5mg3D_	Alignment		99.9	8	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
18	c5mg3F_	Alignment		99.8	13	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
19	d1iwga7	Alignment		99.8	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		99.3	13	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	98.4	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	d1iwga3	Alignment	not modelled	90.5	13	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	d1iwga2	Alignment	not modelled	82.1	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	d1iwga6	Alignment	not modelled	74.4	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
25	c4y0IA_	Alignment	not modelled	33.7	22	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein mmp111; PDBTitle: mycobacterial membrane protein mmp11d2
26	d1iwga4	Alignment	not modelled	28.2	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
27	c5v6xB_	Alignment	not modelled	24.8	20	PDB header: ligase/rna Chain: B: PDB Molecule: pyrrolysine--trna ligase; PDBTitle: crystal structure of the trna binding domain of pyrrolysyl-

						trna2 synthetase mutant (32a ntd) bound to trna(pyl) PDB header: hydrolase Chain: F; PDB Molecule: putative tautomerase; PDBTitle: crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
28	c3n4dF_	Alignment	not modelled	22.6	12	
29	c1ciiA_	Alignment	not modelled	18.5	15	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
30	c4ev6E_	Alignment	not modelled	18.2	4	PDB header: metal transport Chain: E; PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
31	c6adqP_	Alignment	not modelled	16.7	20	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
32	c6b2zf_	Alignment	not modelled	15.8	10	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
33	c3jlzP_	Alignment	not modelled	15.6	12	PDB header: metal transport Chain: P; PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
34	c6b8ht_	Alignment	not modelled	15.1	10	PDB header: membrane protein Chain: T; PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
35	c2m67A_	Alignment	not modelled	14.7	10	PDB header: transport protein Chain: A; PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
36	c2flzC_	Alignment	not modelled	14.5	10	PDB header: hydrolase Chain: C; PDB Molecule: cis-3-chloroacrylic acid dehalogenase; PDBTitle: the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site
37	c5gk9B_	Alignment	not modelled	14.2	100	PDB header: transferase/metal binding protein Chain: B; PDB Molecule: brd1 protein; PDBTitle: crystal structure of human hbo1 in complex with brpf2
38	d1pzra_	Alignment	not modelled	12.9	19	Fold: HLH-like Superfamily: Docking domain B of the erythromycin polyketide synthase (DEBS) Family: Docking domain B of the erythromycin polyketide synthase (DEBS)
39	d1a87a_	Alignment	not modelled	12.5	11	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
40	c1a87A_	Alignment	not modelled	12.5	11	PDB header: bacteriocin Chain: A; PDB Molecule: colicin n; PDBTitle: colicin n
41	c4rhoA_	Alignment	not modelled	12.1	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein (bps12088) from2 burkholderia pseudomallei k96243 at 2.25 a resolution
42	c4kppA_	Alignment	not modelled	12.1	12	PDB header: membrane protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
43	c6f0kA_	Alignment	not modelled	11.7	18	PDB header: membrane protein Chain: A; PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
44	c3tijA_	Alignment	not modelled	11.2	15	PDB header: membrane protein Chain: A; PDB Molecule: nupc family protein; PDBTitle: crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
45	c2lj2A_	Alignment	not modelled	11.1	11	PDB header: membrane protein Chain: A; PDB Molecule: merf; PDBTitle: integral membrane core domain of the mercury transporter merf in lipid2 bilayer membranes
46	c2yvxD_	Alignment	not modelled	10.9	14	PDB header: transport protein Chain: D; PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
47	c3tufA_	Alignment	not modelled	10.6	8	PDB header: signaling protein Chain: A; PDB Molecule: stage iii sporulation protein ah; PDBTitle: structure of the spoiiq-spoiiiah pore forming complex.
48	c2mkaB_	Alignment	not modelled	10.0	11	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
49	c2mkaC_	Alignment	not modelled	10.0	11	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
50	c2mk9B_	Alignment	not modelled	10.0	11	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
51	c2mkaA_	Alignment	not modelled	10.0	11	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
52	c2mk9A_	Alignment	not modelled	10.0	11	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
53	c125A_	Alignment	not modelled	9.9	16	PDB header: protein binding Chain: A; PDB Molecule: dap12-nkg2c tm;

53	c2192A_	Alignment	not modelled	9.9	10	PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer PDB header: hydrolase
54	c5xkrA_	Alignment	not modelled	9.7	17	Chain: A; PDB Molecule: cmp/dcmp deaminase, zinc-binding protein; PDBTitle: crystal structure of msmeg3575 in complex with benzoguanamine
55	d1gtra2	Alignment	not modelled	9.3	63	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
56	d1sd4a_	Alignment	not modelled	9.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
57	c5lj7B_	Alignment	not modelled	9.1	16	PDB header: transport protein Chain: B; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
58	c3bb5B_	Alignment	not modelled	9.0	7	PDB header: unknown function Chain: B; PDB Molecule: stress responsive alpha-beta protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
59	c6fkip_	Alignment	not modelled	8.3	24	PDB header: membrane protein Chain: P; PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
60	c5aj3m_	Alignment	not modelled	8.3	44	PDB header: ribosome Chain: M; PDB Molecule: PDBTitle: structure of the small subunit of the mammalian mitoribosome
61	c3w66A_	Alignment	not modelled	8.1	10	PDB header: metal transport Chain: A; PDB Molecule: magnetosome protein mamm; PDBTitle: mamm-ctd d249a and h285a
62	d1nzza_	Alignment	not modelled	7.9	75	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
63	d2cupa2	Alignment	not modelled	7.8	15	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
64	c4p6vE_	Alignment	not modelled	7.8	15	PDB header: oxidoreductase Chain: E; PDB Molecule: na(+)-translocating nadh-quinone reductase subunit e; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
65	d1kkga_	Alignment	not modelled	7.8	16	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
66	d1q4ra_	Alignment	not modelled	7.3	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
67	c6nbxG_	Alignment	not modelled	7.3	16	PDB header: oxidoreductase Chain: G; PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
68	c5lj3P_	Alignment	not modelled	7.2	15	PDB header: splicing Chain: P; PDB Molecule: cwc15; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
69	c3lw5H_	Alignment	not modelled	7.2	10	PDB header: photosynthesis Chain: H; PDB Molecule: putative uncharacterized protein; PDBTitle: improved model of plant photosystem i
70	c6f46A_	Alignment	not modelled	7.1	22	PDB header: apoptosis Chain: A; PDB Molecule: bcl-2-like protein 1; PDBTitle: structure of the transmembrane helix of bclxl in phospholipid2 nanodiscs
71	c3al0C_	Alignment	not modelled	6.9	75	PDB header: ligase/rna Chain: C; PDB Molecule: glutamyl-trna(gln) amidotransferase subunit c,linker, PDBTitle: crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
72	c2o5rA_	Alignment	not modelled	6.9	75	PDB header: ligase Chain: A; PDB Molecule: glutamyl-trna synthetase 1; PDBTitle: crystal structure of glutamyl-trna synthetase 1 (ec 6.1.1.17)2 (glutamate-trna ligase 1) (glurs 1) (tm1351) from thermotoga maritima3 at 2.5 a resolution
73	c3c6vB_	Alignment	not modelled	6.8	11	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: probable tautomerase/dehalogenase au4130; PDBTitle: crystal structure of au4130/apc7354, a probable enzyme from the2 thermophilic fungus aspergillus fumigatus
74	d1ulza1	Alignment	not modelled	6.7	19	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
75	d1nwba_	Alignment	not modelled	6.6	13	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
76	c4pf8A_	Alignment	not modelled	6.6	11	PDB header: transport protein Chain: A; PDB Molecule: trap-t family transporter, dctp (periplasmic binding) PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 sulfitebacter sp. nas-14.1 (target efi-510299) with bound beta-d-3 galacturonate
77	d1josa_	Alignment	not modelled	6.6	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA

78	c3afhA_	Alignment	not modelled	6.6	75	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase 2; PDBTitle: crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
79	c2wsfH_	Alignment	not modelled	6.6	9	PDB header: photosynthesis Chain: H: PDB Molecule: photosystem i reaction center subunit vi, chloroplastic; PDBTitle: improved model of plant photosystem i
80	c3cwcB_	Alignment	not modelled	6.6	21	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
81	d1aopa2	Alignment	not modelled	6.5	12	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
82	d1j09a2	Alignment	not modelled	6.5	63	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
83	c3uz0A_	Alignment	not modelled	6.5	8	PDB header: transport protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: crystal structure of spoiiiah and spoiiq complex
84	c5un4C_	Alignment	not modelled	6.4	11	PDB header: hydrolase Chain: C: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of native fused 4-ot
85	c2k1aA_	Alignment	not modelled	6.3	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment
86	c5u1dX_	Alignment	not modelled	6.2	10	PDB header: transport protein Chain: X: PDB Molecule: tap transporter inhibitor icp47; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
87	d1fnda2	Alignment	not modelled	6.2	5	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
88	c5jrlC_	Alignment	not modelled	6.2	21	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like PDBTitle: crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
89	c2qycA_	Alignment	not modelled	6.1	8	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
90	c3pg6D_	Alignment	not modelled	6.1	25	PDB header: ligase Chain: D: PDB Molecule: e3 ubiquitin-protein ligase dtx3l; PDBTitle: the carboxyl terminal domain of human deltex 3-like
91	c4g6zA_	Alignment	not modelled	6.1	63	PDB header: ligase Chain: A: PDB Molecule: glutamate-trna ligase; PDBTitle: crystal structure of a glutamyl-trna synthetase glurs from2 burkholderia thailandensis bound to l-glutamate
92	d1gawa2	Alignment	not modelled	6.1	7	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
93	c2cfoA_	Alignment	not modelled	6.1	75	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
94	c4ovqA_	Alignment	not modelled	6.0	11	PDB header: solute-binding protein Chain: A: PDB Molecule: trap dicarboxylate abc transporter, substrate-binding PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 roseobacter denitrificans, target efi-510230, with bound beta-d-3 glucuronate
95	d1iwga1	Alignment	not modelled	6.0	5	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
96	c1g59A_	Alignment	not modelled	6.0	63	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: glutamyl-trna synthetase complexed with trna(glu).
97	c5tcxA_	Alignment	not modelled	6.0	8	PDB header: cell invasion Chain: A: PDB Molecule: cd81 antigen; PDBTitle: crystal structure of human tetraspanin cd81
98	c6ithA_	Alignment	not modelled	5.9	20	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
99	c2qfiB_	Alignment	not modelled	5.9	12	PDB header: transport protein Chain: B: PDB Molecule: ferrous-iron efflux pump fief; PDBTitle: structure of the zinc transporter yiiip