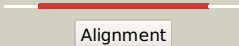



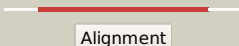

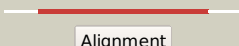

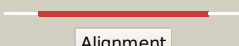
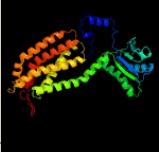
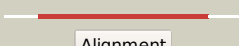

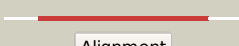




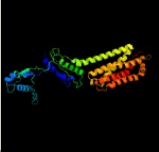








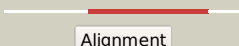
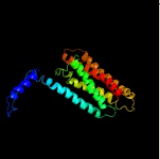
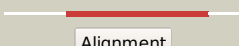
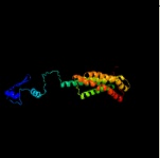
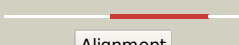
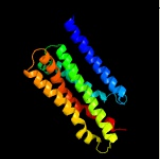
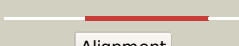


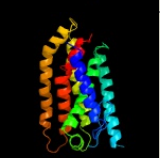

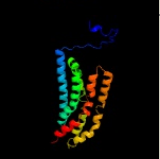



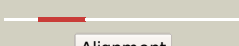
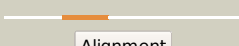
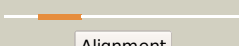

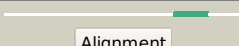



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1557_(mmpL6)_1761750_1762943
Date	Fri Aug 2 13:30:14 BST 2019
Unique Job ID	de7f7fed963c70dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5lq3F_	 Alignment		100.0	16	PDB header: transport protein Chain: F: PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
2	c3k07A_	 Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
3	c4k0eA_	 Alignment		100.0	12	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
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	c6ajjA_	 Alignment		100.0	22	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
6	c2v50A_	 Alignment		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	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
8	c1oy8A_	 Alignment		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 acrB multidrug efflux pump
9	c6csxA_	 Alignment		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
10	c4k0eC_	 Alignment		100.0	11	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
11	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

12	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
13	c3aaqB_	 Alignment		100.0	13	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	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
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	c5mg3D_	 Alignment		100.0	20	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	d1iwga7	 Alignment		99.9	13	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
19	c5mg3F_	 Alignment		99.9	11	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
20	c5ensA_	 Alignment		99.4	12	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	99.0	8	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	95.8	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
23	d1iwga2	 Alignment	not modelled	82.7	12	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	d1iwga5	 Alignment	not modelled	80.1	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
25	c5n9yB_	 Alignment	not modelled	42.9	18	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
26	c4ev6E_	 Alignment	not modelled	40.7	16	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
27	c2yvxD_	 Alignment	not modelled	24.9	16	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte;

						PDBTitle: crystal structure of magnesium transporter mgte
28	c2k2pA_	Alignment	not modelled	11.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
29	c6gctA_	Alignment	not modelled	10.0	17	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
30	c4y2iA_	Alignment	not modelled	8.9	15	PDB header: metal transport Chain: A: PDB Molecule: putative metal-binding transport protein; PDBTitle: gold ion bound to golb
31	c4ky0B_	Alignment	not modelled	8.6	13	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
32	c5oonA_	Alignment	not modelled	8.0	15	PDB header: membrane protein Chain: A: PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, baca
33	c2aj1A_	Alignment	not modelled	7.9	17	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
34	d1qupa2	Alignment	not modelled	7.4	10	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
35	c2mk9B_	Alignment	not modelled	6.9	16	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
36	c2mk9A_	Alignment	not modelled	6.9	16	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
37	c2mkaC_	Alignment	not modelled	6.9	16	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	c2mkaB_	Alignment	not modelled	6.9	16	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	c2mkaA_	Alignment	not modelled	6.9	16	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
40	c6g68D_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: D: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
41	c6g68J_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: J: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
42	c6g68Q_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: Q: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
43	c6g68M_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: M: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
44	c6g68L_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: L: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
45	c6g68I_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: I: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
46	c6g68R_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: R: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
47	c6g68C_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: C: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
48	c6g68O_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: O: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
49	c6g68B_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: B: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
50	c6g68K_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: K: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
51	c6g68F_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: F: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
52	c6g68A_	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: A: PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg

53	c6g68E	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: E; PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
54	c6g68H	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: H; PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
55	c6g68P	Alignment	not modelled	6.9	15	PDB header: de novo protein Chain: P; PDB Molecule: cc-type2-il-sg; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-il-sg
56	c5gasN	Alignment	not modelled	6.7	16	PDB header: hydrolase Chain: N; PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
57	c2bbjB	Alignment	not modelled	6.3	11	PDB header: metal transport/membrane protein Chain: B; PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
58	c6g69N	Alignment	not modelled	5.8	15	PDB header: de novo protein Chain: N; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
59	d1cpza	Alignment	not modelled	5.6	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
60	c2rogA	Alignment	not modelled	5.5	13	PDB header: metal binding protein Chain: A; PDB Molecule: heavy metal binding protein; PDBTitle: solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
61	c6eznH	Alignment	not modelled	5.5	11	PDB header: membrane protein Chain: H; PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
62	c4p6vE	Alignment	not modelled	5.4	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
63	c4pnbA	Alignment	not modelled	5.4	15	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
64	c4pnbD	Alignment	not modelled	5.4	15	PDB header: de novo protein Chain: D; PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
65	c4pnbB	Alignment	not modelled	5.4	15	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
66	c4hkrB	Alignment	not modelled	5.4	11	PDB header: transport protein Chain: B; PDB Molecule: calcium release-activated calcium channel protein 1; PDBTitle: calcium release-activated calcium (crac) channel orai
67	c6g69H	Alignment	not modelled	5.1	15	PDB header: de novo protein Chain: H; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
68	c2vpzG	Alignment	not modelled	5.1	25	PDB header: oxidoreductase Chain: G; PDB Molecule: hypothetical membrane spanning protein; PDBTitle: polysulfide reductase native structure
69	c6g69D	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: D; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
70	c6g69C	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: C; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
71	c6g69L	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: L; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
72	c6g69J	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: J; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
73	c6g69I	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: I; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
74	c6g69K	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: K; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
75	c6g69F	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: F; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
76	c6g69A	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: A; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
77	c6g69B	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: B; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
78	c6g69M	Alignment	not modelled	5.0	15	PDB header: de novo protein Chain: M; PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e

79 [c6g69E](#)

Alignment

not modelled

5.0

15

PDB header: de novo protein
Chain: E: **PDB Molecule:** cc-type2-il-sg-l17e;
PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e