

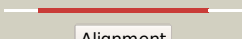

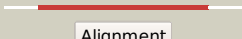



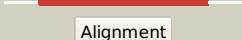



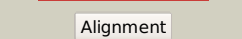
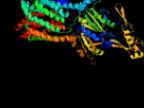
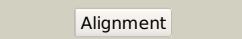

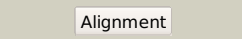

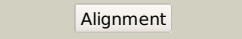

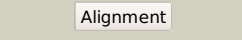




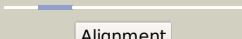
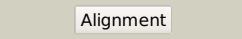
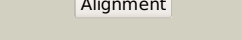
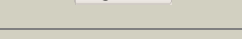

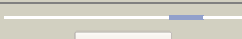
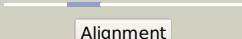
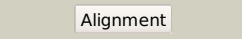
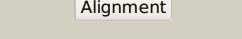
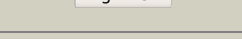
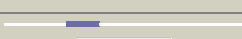
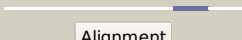
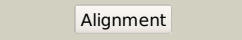
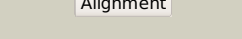
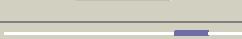
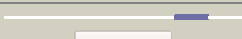

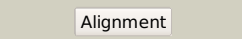
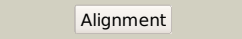
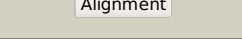


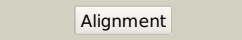


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3823c_(mmpL8)_4288438_4291707
Date	Fri Aug 9 18:20:53 BST 2019
Unique Job ID	101488b9319a0c5f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ajjA_	 Alignment		100.0	23	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_	 Alignment		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_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
4	c4mt1A_	 Alignment		100.0	16	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	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_	 Alignment		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_	 Alignment		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	c5khnB_	 Alignment		100.0	18	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
10	c6dmoA_	 Alignment		100.0	13	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	c4k0eC_	 Alignment		100.0	15	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	14	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	18	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	18	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	17	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	16	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
17	d1iwga8	Alignment		99.9	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		99.9	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	16	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
20	c5ensA_	Alignment		99.2	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	98.1	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	81.3	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
23	c2yvxD_	Alignment	not modelled	73.7	14	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
24	d1iwga6	Alignment	not modelled	62.7	6	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	d1iwga2	Alignment	not modelled	48.9	16	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	47.6	20	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	c5sxpG_	Alignment	not modelled	46.3	47	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
28	c4av3A_	 Alignment	not modelled	46.2	23	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
29	c4b03D_	 Alignment	not modelled	27.8	20	PDB header: virus Chain: D: PDB Molecule: dengue virus 1 prm protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
30	c6n52B_	 Alignment	not modelled	26.3	14	PDB header: membrane protein Chain: B: PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
31	c2mk9A_	 Alignment	not modelled	25.9	4	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
32	c2mkaB_	 Alignment	not modelled	25.9	4	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
33	c2mkaA_	 Alignment	not modelled	25.9	4	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
34	c2mkaC_	 Alignment	not modelled	25.9	4	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
35	c2mk9B_	 Alignment	not modelled	25.9	4	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	c4a2nB_	 Alignment	not modelled	22.8	7	PDB header: transferase Chain: B: PDB Molecule: isoprenylcysteine carboxyl methyltransferase; PDBTitle: crystal structure of ma-icmt
37	c5sxpF_	 Alignment	not modelled	22.7	50	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
38	c1p58E_	 Alignment	not modelled	19.1	24	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
39	c1p58F_	 Alignment	not modelled	19.1	24	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
40	c1a87A_	 Alignment	not modelled	18.6	20	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
41	d1a87a_	 Alignment	not modelled	18.6	20	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
42	c5zlgA_	 Alignment	not modelled	16.9	9	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
43	c2bbjB_	 Alignment	not modelled	15.5	8	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
44	c2m67A_	 Alignment	not modelled	14.6	14	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
45	d2yvxa3	 Alignment	not modelled	14.5	14	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
46	c1ciiA_	 Alignment	not modelled	13.8	16	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
47	c3chxF_	 Alignment	not modelled	13.5	21	PDB header: membrane protein Chain: F: PDB Molecule: pmoa; PDBTitle: crystal structure of methylosinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)
48	c1rijA_	 Alignment	not modelled	13.3	55	PDB header: de novo protein Chain: A: PDB Molecule: e6apn1 peptide; PDBTitle: e6-bind trp-cage (e6apn1)
49	c4or2A_	 Alignment	not modelled	12.3	13	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
50	c1qu7A_	 Alignment	not modelled	11.4	12	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
51	c4kppA_	 Alignment	not modelled	11.3	7	PDB header: membrane protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
52	c6o7ua_	 Alignment	not modelled	11.2	13	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
53	c2li2A_	 Alignment	not modelled	11.2	12	PDB header: membrane protein Chain: A: PDB Molecule: merf;

53	c2j2A	Alignment	not modelled	11.2	12	PDBTitle: integral membrane core domain of the mercury transporter merf in lipid2 bilayer membranes PDB header: oxidoreductase, membrane protein Chain: F; PDB Molecule: particulate methane monooxygenase, a subunit; PDBTitle: crystal structure of particulate methane monooxygenase
54	c1yewF	Alignment	not modelled	11.1	13	Chain: F; PDB Molecule: particulate methane monooxygenase, a subunit; PDB header: crystal structure of particulate methane monooxygenase
55	c2kseA	Alignment	not modelled	11.1	20	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
56	d1jb0i	Alignment	not modelled	10.9	16	Fold: Single transmembrane helix Superfamily: Subunit VIII of photosystem I reaction centre, PsaI Family: Subunit VIII of photosystem I reaction centre, PsaI
57	c4fe1l	Alignment	not modelled	10.9	16	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
58	c3ex7l	Alignment	not modelled	10.9	55	PDB header: hydrolase/rna binding protein/rna Chain: I; PDB Molecule: protein casc3; PDBTitle: the crystal structure of ejc in its transition state
59	c5lnka	Alignment	not modelled	10.8	25	PDB header: oxidoreductase Chain: A; PDB Molecule: mitochondrial complex i, nd3 subunit; PDBTitle: entire ovine respiratory complex i
60	c3j2pD	Alignment	not modelled	10.4	23	PDB header: viral protein Chain: D; PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer
61	d1sd4a	Alignment	not modelled	10.0	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
62	c2ch7A	Alignment	not modelled	9.9	14	PDB header: chemotaxis Chain: A; PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
63	c3n4dF	Alignment	not modelled	9.8	8	PDB header: hydrolase Chain: F; PDB Molecule: putative tautomerase; PDBTitle: crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
64	c2k1aA	Alignment	not modelled	9.7	23	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iib; PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment
65	c3javD	Alignment	not modelled	9.5	16	PDB header: transport protein Chain: D; PDB Molecule: inositol 1,4,5-trisphosphate receptor type 1; PDBTitle: structure of full-length ip3r1 channel in the apo-state determined by2 single particle cryo-em
66	c5lpcA	Alignment	not modelled	9.4	20	PDB header: oxidoreductase Chain: A; PDB Molecule: vanadium-dependent bromoperoxidase; PDBTitle: crystal structure of vanadium-dependent haloperoxidase from a. marina
67	c4p6vE	Alignment	not modelled	9.4	10	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
68	c3j20P	Alignment	not modelled	9.2	9	PDB header: ribosome Chain: P; PDB Molecule: 30s ribosomal protein s14p type z; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
69	c2lugA	Alignment	not modelled	9.2	56	PDB header: lipid binding protein Chain: A; PDB Molecule: myelin basic protein; PDBTitle: solution nmr structure of a s72-s107 peptide of 18.5kda murine myelin2 basic protein (mbp) in association with dodecylphosphocholine3 micelles
70	c5ws4A	Alignment	not modelled	9.1	12	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
71	c5n9yB	Alignment	not modelled	9.0	13	PDB header: membrane protein Chain: B; PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
72	c1fv1C	Alignment	not modelled	8.8	63	PDB header: immune system Chain: C; PDB Molecule: myelin basic protein; PDBTitle: structural basis for the binding of an immunodominant peptide from2 myelin basic protein in different registers by two hla-dr2 alleles
73	c6f0kA	Alignment	not modelled	8.7	28	PDB header: membrane protein Chain: A; PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
74	c2kncA	Alignment	not modelled	8.7	21	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
75	c6bqiA	Alignment	not modelled	8.4	10	PDB header: translation Chain: A; PDB Molecule: protein impact homolog; PDBTitle: structure of two-domain translational regulator yih1 reveals a2 possible mechanism of action
76	c4gn0D	Alignment	not modelled	8.3	13	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
77	d1kf6d	Alignment	not modelled	8.3	8	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase

						transmembrane subunits (SdhC/FrdC and SdhD/FrdD) PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
78	c6hu9u_	Alignment	not modelled	8.1	20	
79	c3vepC_	Alignment	not modelled	7.9	50	PDB header: membrane protein/transcription Chain: C: PDB Molecule: uncharacterized protein rv3413c/mt3522; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
80	c5ireD_	Alignment	not modelled	7.8	24	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus
81	c6mctE_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: E: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
82	c6mctA_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: A: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
83	c6mctN_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: N: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
84	c6mctB_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: B: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
85	c6mctG_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: G: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
86	c6mctH_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: H: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
87	c6mctJ_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: J: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
88	c6mctM_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: M: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
89	c6mctC_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: C: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
90	c6mctL_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: L: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
91	c6mctO_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: O: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
92	c6mpwA_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: A: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
93	c6mctF_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: F: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
94	c6mctD_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
95	c6mq2D_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
96	c6mctI_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: I: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
97	c6mctK_	Alignment	not modelled	7.8	33	PDB header: de novo protein Chain: K: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
98	c6adqP_	Alignment	not modelled	7.8	23	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
99	c3w66A_	Alignment	not modelled	7.7	11	PDB header: metal transport Chain: A: PDB Molecule: magnetosome protein mamm; PDBTitle: mamm-ctd d249a and h285a