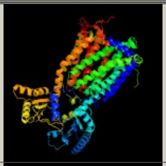
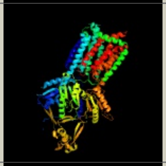
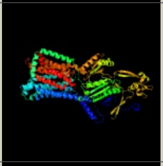
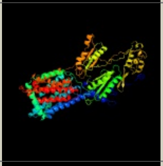
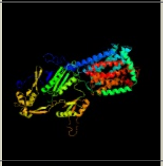
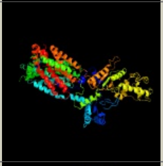
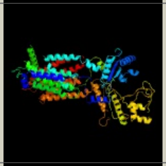
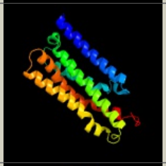
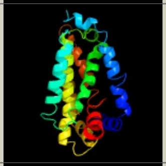
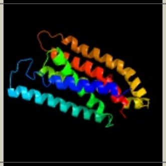
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0676c_(mmpL5)_775589_778483
Date	Fri Jul 26 01:50:24 BST 2019
Unique Job ID	f18b73e738f68313

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ajjA_	Alignment		100.0	18	**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	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
4	c4mt1A_	Alignment		100.0	14	**PDB header:**membrane protein, tranport 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	12	**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	c4k0eA_	Alignment		100.0	13	**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	13	**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	16	**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	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	c6csxA_	Alignment		100.0	13	**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	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	16	**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	16	**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	15	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**protein translocase subunit secd; **PDBTitle:** em fitted model of bacterial holo-translocon
17	d1iwga8	Alignment		100.0	14	**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	11	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**protein translocase subunit secf; **PDBTitle:** em fitted model of bacterial holo-translocon
19	d1iwga7	Alignment		99.9	17	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
20	c5ensA_	Alignment		99.5	9	**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	7	**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	90.6	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	c2yvxD_	Alignment	not modelled	82.6	10	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
24	d1iwga6	Alignment	not modelled	80.8	11	**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	64.7	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
26	d1iwga4	Alignment	not modelled	51.3	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
						PDB header:membrane protein **Chain:** A: **PDB Molecule:**soluble cytochrome b562 and glucagon

27	c4l6rA_	Alignment	not modelled	21.8	11	receptor chimera; **PDBTitle:** structure of the class b human glucagon g protein coupled receptor
28	c5zlgA_	Alignment	not modelled	17.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome b reductase 1; **PDBTitle:** human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
29	c3j6vR_	Alignment	not modelled	15.2	22	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**28s ribosomal protein s18a, mitochondrial; **PDBTitle:** cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
30	c6bqiA_	Alignment	not modelled	14.8	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein impact homolog; **PDBTitle:** structure of two-domain translational regulator yih1 reveals a2 possible mechanism of action
31	c2mk9A_	Alignment	not modelled	14.3	33	**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	c2mkaC_	Alignment	not modelled	14.3	33	**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
33	c2mk9B_	Alignment	not modelled	14.3	33	**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
34	c2mkaA_	Alignment	not modelled	14.3	33	**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
35	c2mkaB_	Alignment	not modelled	14.3	33	**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
36	c1a87A_	Alignment	not modelled	13.1	15	**PDB header:**bacteriocin **Chain:** A: **PDB Molecule:**colicin n; **PDBTitle:** colicin n
37	d1a87a_	Alignment	not modelled	13.1	15	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
38	d1iwga1	Alignment	not modelled	12.9	7	**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
39	c1ciiA_	Alignment	not modelled	12.0	13	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
40	c2k1kA_	Alignment	not modelled	10.0	16	**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
41	c2k1kB_	Alignment	not modelled	10.0	16	**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
42	c2k1lA_	Alignment	not modelled	10.0	16	**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
43	c2k1lB_	Alignment	not modelled	10.0	16	**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
44	d1iwga5	Alignment	not modelled	9.6	9	**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
45	c2nasA_	Alignment	not modelled	9.5	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of a pwwp doamin from trypanosoma brucei
46	c2qg8A_	Alignment	not modelled	9.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein synthase py06285; **PDBTitle:** plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
47	c6b2zf_	Alignment	not modelled	9.4	24	**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
48	c3w66A_	Alignment	not modelled	9.1	7	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**magnetosome protein mamm; **PDBTitle:** mamm-ctd d249a and h285a
49	c6b8ht_	Alignment	not modelled	8.9	24	**PDB header:**membrane protein **Chain:** T: **PDB Molecule:**atp synthase subunit 9, mitochondrial; **PDBTitle:** mosaic model of yeast mitochondrial atp synthase monomer
50	c1v1cA_	Alignment	not modelled	8.8	31	**PDB header:**sh3-domain **Chain:** A: **PDB Molecule:**obscurin; **PDBTitle:** solution structure of the sh3 domain of obscurin
51	c2n1pA_	Alignment	not modelled	8.6	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 5b, ns5b; **PDBTitle:** structure of the c-terminal membrane domain of hcv ns5b protein
52	c2bbjB_	Alignment	not modelled	8.6	17	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein;

						PDBTitle: crystal structure of the cora mg2+ transporter
53	c5ws4A_	Alignment	not modelled	8.5	15	**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
54	c6fkib_	Alignment	not modelled	8.5	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**atp synthase subunit beta, chloroplastic; **PDBTitle:** chloroplast f1fo conformation 3
55	c6eznH_	Alignment	not modelled	8.4	17	**PDB header:**membrane protein **Chain:** H: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
56	c2ww9B_	Alignment	not modelled	8.4	17	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
57	c2k9pA_	Alignment	not modelled	8.3	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pheromone alpha factor receptor; **PDBTitle:** structure of tm1_tm2 in lppg micelles
58	c2kncB_	Alignment	not modelled	8.2	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
59	c2kseA_	Alignment	not modelled	8.0	27	**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 (csmp)3 target 4311c
60	c6fkip_	Alignment	not modelled	7.8	8	**PDB header:**membrane protein **Chain:** P: **PDB Molecule:**atp synthase subunit c, chloroplastic; **PDBTitle:** chloroplast f1fo conformation 3
61	c2m1hA_	Alignment	not modelled	7.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** solution structure of a pwwp domain from trypanosoma brucei
62	c6mctF_	Alignment	not modelled	7.4	9	**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
63	c6mctG_	Alignment	not modelled	7.4	9	**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
64	c6mctA_	Alignment	not modelled	7.4	9	**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
65	c6mctK_	Alignment	not modelled	7.4	9	**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
66	c6mctB_	Alignment	not modelled	7.4	9	**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
67	c6mctM_	Alignment	not modelled	7.4	9	**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
68	c6mctO_	Alignment	not modelled	7.4	9	**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
69	c6mpwA_	Alignment	not modelled	7.4	9	**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
70	c6mctD_	Alignment	not modelled	7.4	9	**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
71	c6mctC_	Alignment	not modelled	7.4	9	**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
72	c6mctH_	Alignment	not modelled	7.4	9	**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
73	c6mq2D_	Alignment	not modelled	7.4	9	**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
74	c6mctE_	Alignment	not modelled	7.4	9	**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
75	c6mctI_	Alignment	not modelled	7.4	9	**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
76	c6mctL_	Alignment	not modelled	7.4	9	**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
77	c6mctN_	Alignment	not modelled	7.4	9	**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

78	c6mctJ_	Alignment	not modelled	7.4	9	**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
79	d2yvxa3	Alignment	not modelled	7.4	8	**Fold:**MgtE membrane domain-like **Superfamily:**MgtE membrane domain-like **Family:**MgtE membrane domain-like
80	c2n90A_	Alignment	not modelled	7.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**high affinity nerve growth factor receptor; **PDBTitle:** trka transmembrane domain nmr structure in dpc micelles
81	c2n90B_	Alignment	not modelled	7.4	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**high affinity nerve growth factor receptor; **PDBTitle:** trka transmembrane domain nmr structure in dpc micelles
82	c6dkuA_	Alignment	not modelled	7.3	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**vp35; **PDBTitle:** crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
83	c6mq2E_	Alignment	not modelled	7.2	9	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**mini-evgl membrane protein; **PDBTitle:** de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
84	c6mpwB_	Alignment	not modelled	7.2	9	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**mini-evgl membrane protein; **PDBTitle:** de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
85	c6mpwE_	Alignment	not modelled	7.2	9	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**mini-evgl membrane protein; **PDBTitle:** de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
86	c6mq2C_	Alignment	not modelled	7.2	9	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**mini-evgl membrane protein; **PDBTitle:** de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
87	c6mq2B_	Alignment	not modelled	7.2	9	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**mini-evgl membrane protein; **PDBTitle:** de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
88	c6mpwD_	Alignment	not modelled	7.2	9	**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-1
89	c6mpwC_	Alignment	not modelled	7.2	9	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**mini-evgl membrane protein; **PDBTitle:** de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
90	c6mq2A_	Alignment	not modelled	7.2	9	**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-2
91	c4fe1I_	Alignment	not modelled	7.0	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
92	d1jb0i_	Alignment	not modelled	7.0	16	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
93	c3tijA_	Alignment	not modelled	7.0	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**nupc family protein; **PDBTitle:** crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
94	c6nbxG_	Alignment	not modelled	7.0	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** t.elongatus ndh (data-set 2)
95	d1qmga1	Alignment	not modelled	6.9	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
96	c2jbzA_	Alignment	not modelled	6.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** crystal structure of the streptomyces coelicolor holo-2 [acyl-carrier-protein] synthase (acps) in complex with3 coenzyme a at 1.6 a
97	c3hqjA_	Alignment	not modelled	6.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
98	c4ev6E_	Alignment	not modelled	6.6	14	**PDB header:**metal transport **Chain:** E: **PDB Molecule:**magnesium transport protein cora; **PDBTitle:** the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
99	d1f7la_	Alignment	not modelled	6.6	15	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**Holo-(acyl carrier protein) synthase ACPS