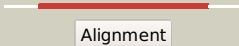


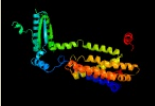
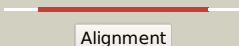

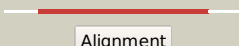

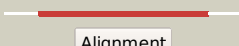

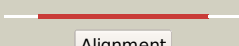

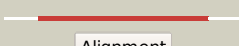











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1146_(mmpL13b)_1273360_1274772
Date	Wed Jul 31 22:05:23 BST 2019
Unique Job ID	e000192fa0e67bdb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ajjA_</a>	 Alignment		100.0	31	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmpL3 from mycobacterium2 smegmatis complexed with ica38
2	<a href="#">c5khnB_</a>	 Alignment		100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> rnd transporter; <b>PDBTitle:</b> crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
3	<a href="#">c6dmoA_</a>	 Alignment		100.0	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein patched homolog 1; <b>PDBTitle:</b> cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
4	<a href="#">c5lq3F_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> cmeb; <b>PDBTitle:</b> structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
5	<a href="#">c3aaqB_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable secdf protein-export membrane protein; <b>PDBTitle:</b> crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
6	<a href="#">c6owsB_</a>	 Alignment		100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> efflux pump membrane transporter; <b>PDBTitle:</b> cryo-em structure of an acinetobacter baumannii multidrug efflux pump
7	<a href="#">c3jd8A_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> niemann-pick c1 protein; <b>PDBTitle:</b> cryo-em structure of the full-length human npc1 at 4.4 angstrom
8	<a href="#">c3k07A_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa; <b>PDBTitle:</b> crystal structure of cusa
9	<a href="#">c4mt1A_</a>	 Alignment		100.0	20	<b>PDB header:</b> membrane protein, tranport protein <b>Chain:</b> A: <b>PDB Molecule:</b> drug efflux protein; <b>PDBTitle:</b> crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
10	<a href="#">c5xamA_</a>	 Alignment		100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit secd; <b>PDBTitle:</b> crystal structure of secdf in i form at 4 a resolution
11	<a href="#">c2v50A_</a>	 Alignment		100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein mexb; <b>PDBTitle:</b> the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb

12	<a href="#">c1oy8A_</a>	Alignment		100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
13	<a href="#">c4k0eA_</a>	Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii
14	<a href="#">c6csxA_</a>	Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug efflux pump subunit acrb; <b>PDBTitle:</b> single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
15	<a href="#">c4k0eC_</a>	Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii
16	<a href="#">c5mg3F_</a>	Alignment		99.9	17	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> protein translocase subunit secf; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
17	<a href="#">d1iwga8</a>	Alignment		99.9	16	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
18	<a href="#">d1iwga7</a>	Alignment		99.9	18	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
19	<a href="#">c5mg3D_</a>	Alignment		99.9	13	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein translocase subunit secd; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
20	<a href="#">d1t4za_</a>	Alignment		48.5	38	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> KaiB-like
21	<a href="#">c5m87A_</a>	Alignment	not modelled	35.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> crystal structure of eremococcus coleocola manganese transporter
22	<a href="#">c5t42A_</a>	Alignment	not modelled	34.6	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> structure of the ebola virus envelope protein mper/tm domain and its2 interaction with the fusion loop explains their fusion activity
23	<a href="#">c5t6oA_</a>	Alignment	not modelled	34.1	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> poly-beta-hydroxybuterate polymerase; <b>PDBTitle:</b> structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
24	<a href="#">c5xavB_</a>	Alignment	not modelled	33.9	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> intracellular polyhydroxyalkanoate synthase; <b>PDBTitle:</b> structure of phac from chromobacterium sp. usm2
25	<a href="#">c2na9A_</a>	Alignment	not modelled	33.6	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
26	<a href="#">c2na8A_</a>	Alignment	not modelled	33.2	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the cytokine receptor common subunit beta
27	<a href="#">c6gctA_</a>	Alignment	not modelled	30.2	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutral amino acid transporter b(0); <b>PDBTitle:</b> cryo-em structure of the human neutral amino acid transporter asct2
28	<a href="#">c3lrcC_</a>	Alignment	not modelled	25.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)

29	<a href="#">c5oonA</a>	Alignment	not modelled	13.1	6	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> undecaprenyl-diphosphatase; <b>PDBTitle:</b> structure of undecaprenyl-pyrophosphate phosphatase, baca
30	<a href="#">c3ut7A</a>	Alignment	not modelled	13.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structural view of a non pfam singleton and crystal packing analysis
31	<a href="#">c6b2zf</a>	Alignment	not modelled	12.6	41	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> atp synthase subunit c, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
32	<a href="#">c4ev6E</a>	Alignment	not modelled	12.5	15	<b>PDB header:</b> metal transport <b>Chain:</b> E: <b>PDB Molecule:</b> magnesium transport protein cora; <b>PDBTitle:</b> the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
33	<a href="#">d2hkua2</a>	Alignment	not modelled	12.2	17	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
34	<a href="#">c6b8ht</a>	Alignment	not modelled	12.0	41	<b>PDB header:</b> membrane protein <b>Chain:</b> T: <b>PDB Molecule:</b> atp synthase subunit 9, mitochondrial; <b>PDBTitle:</b> mosaic model of yeast mitochondrial atp synthase monomer
35	<a href="#">c6hwhb</a>	Alignment	not modelled	11.2	17	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
36	<a href="#">c5b16C</a>	Alignment	not modelled	10.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> microprocessor complex subunit dgcr8; <b>PDBTitle:</b> x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
37	<a href="#">c5b16B</a>	Alignment	not modelled	9.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> microprocessor complex subunit dgcr8; <b>PDBTitle:</b> x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
38	<a href="#">c5xu1M</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> M: <b>PDB Molecule:</b> abc transporter permease; <b>PDBTitle:</b> structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
39	<a href="#">c4n8oA</a>	Alignment	not modelled	9.5	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsx; <b>PDBTitle:</b> crystal structure of mycobacterial ftsx extracellular domain, bromide2 derivative
40	<a href="#">c6iu3A</a>	Alignment	not modelled	9.3	16	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vit1; <b>PDBTitle:</b> crystal structure of iron transporter vit1 with zinc ions
41	<a href="#">c5gasN</a>	Alignment	not modelled	9.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
42	<a href="#">c3j20P</a>	Alignment	not modelled	9.1	9	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 30s ribosomal protein s14p type z; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
43	<a href="#">c6mk7A</a>	Alignment	not modelled	8.8	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsx; <b>PDBTitle:</b> solution structure of the large extracellular loop of ftsx in2 streptococcus pneumoniae
44	<a href="#">c6m97A</a>	Alignment	not modelled	8.8	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of high affinity copper uptake protein 1 <b>PDBTitle:</b> crystal structure of the high-affinity copper transporter ctr1
45	<a href="#">c5n9yB</a>	Alignment	not modelled	8.7	7	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the full-length structure of zntb
46	<a href="#">c5vwxB</a>	Alignment	not modelled	8.2	15	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bak core latch dimer in complex with bim-h0-h3glt
47	<a href="#">c5vwxD</a>	Alignment	not modelled	8.2	15	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bak core latch dimer in complex with bim-h0-h3glt
48	<a href="#">c5lm4A</a>	Alignment	not modelled	8.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> excitatory amino acid transporter 1,neutral amino acid <b>PDBTitle:</b> structure of the thermostabilized eaat1 cryst-ii mutant in complex2 with l-asp and the allosteric inhibitor ucph101
49	<a href="#">c1p58E</a>	Alignment	not modelled	8.0	13	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
50	<a href="#">c1p58F</a>	Alignment	not modelled	8.0	13	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
51	<a href="#">c2n7rA</a>	Alignment	not modelled	7.7	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> nicastrin; <b>PDBTitle:</b> structure of the transmembrane domain of human nicastrin in dpc2 micelles
52	<a href="#">c1yewF</a>	Alignment	not modelled	7.3	16	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> particulate methane monooxygenase, a subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
53	<a href="#">c3c4rC</a>	Alignment	not modelled	7.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein encoded by2 cryptic prophage

54	<a href="#">c2yvxD_</a>	Alignment	not modelled	7.1	14	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
55	<a href="#">c3ilaG_</a>	Alignment	not modelled	6.9	30	<b>PDB header:</b> signaling protein <b>Chain:</b> G: <b>PDB Molecule:</b> ryanodine receptor 1; <b>PDBTitle:</b> crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
56	<a href="#">c5y9vA_</a>	Alignment	not modelled	6.7	33	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ryanodine receptor 1; <b>PDBTitle:</b> crystal structure of diamondback moth ryanodine receptor n-terminal2 domain
57	<a href="#">c4gnOD_</a>	Alignment	not modelled	6.6	15	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> hamp domain of af1503; <b>PDBTitle:</b> de novo phasing of a hamp-complex using an improved arcimboldo method
58	<a href="#">c3j2pD_</a>	Alignment	not modelled	6.5	8	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> cryoem structure of dengue virus envelope protein heterotetramer
59	<a href="#">c1wyoA_</a>	Alignment	not modelled	6.4	7	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> microtubule-associated protein rp/eb family <b>PDBTitle:</b> solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
60	<a href="#">c4hkrA_</a>	Alignment	not modelled	6.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium release-activated calcium channel protein 1; <b>PDBTitle:</b> calcium release-activated calcium (crac) channel orai
61	<a href="#">c1agqB_</a>	Alignment	not modelled	6.0	0	<b>PDB header:</b> growth factor <b>Chain:</b> B: <b>PDB Molecule:</b> glial cell-derived neurotrophic factor; <b>PDBTitle:</b> glial cell-derived neurotrophic factor from rat
62	<a href="#">c5j8vD_</a>	Alignment	not modelled	6.0	27	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> ryanodine receptor 1; <b>PDBTitle:</b> structure of rabbit ryanodine receptor ryr1 open state activated by2 calcium ion
63	<a href="#">c5n2sA_</a>	Alignment	not modelled	5.9	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562,adenosine receptor a1; <b>PDBTitle:</b> crystal structure of stabilized a1 receptor in complex with psb36 at2 3.3a resolution
64	<a href="#">c4hkrB_</a>	Alignment	not modelled	5.9	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> calcium release-activated calcium channel protein 1; <b>PDBTitle:</b> calcium release-activated calcium (crac) channel orai
65	<a href="#">c5wsnD_</a>	Alignment	not modelled	5.9	8	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> structure of japanese encephalitis virus
66	<a href="#">c5o5oD_</a>	Alignment	not modelled	5.9	11	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> rnase adapter protein rapz; <b>PDBTitle:</b> x-ray crystal structure of rapz from escherichia coli (p32 space2 group)
67	<a href="#">c4i4iA_</a>	Alignment	not modelled	5.8	29	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ryanodine receptor 2; <b>PDBTitle:</b> crystal structure of mouse ryanodine receptor isoform 2 (ryr2) 1-5472 disease mutant r420q
68	<a href="#">c6mq2D_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
69	<a href="#">c6mctG_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> G: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
70	<a href="#">c6mctL_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> L: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
71	<a href="#">c6mctE_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
72	<a href="#">c6mctJ_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> J: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
73	<a href="#">c6mpwA_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
74	<a href="#">c6mctB_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
75	<a href="#">c6mctI_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
76	<a href="#">c6mctA_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
77	<a href="#">c6mctK_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> K: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
78	<a href="#">c6mctH_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> H: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
79	<a href="#">c6mctF_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> mini-evgl membrane protein;

79	<a href="#">c6mctI_</a>	Alignment	not modelled	5.8	27	<b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction <b>PDB header:</b> de novo protein
80	<a href="#">c6mctN_</a>	Alignment	not modelled	5.8	27	<b>Chain:</b> N: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
81	<a href="#">c6mctD_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
82	<a href="#">c6mctM_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> M: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
83	<a href="#">c6mctC_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
84	<a href="#">c6mctO_</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> O: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
85	<a href="#">c5v2sA_</a>	Alignment	not modelled	5.8	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type i
86	<a href="#">c2oceA_</a>	Alignment	not modelled	5.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa5201; <b>PDBTitle:</b> crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
87	<a href="#">c6mq2B_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
88	<a href="#">c6mpwC_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
89	<a href="#">c6mpwD_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
90	<a href="#">c6mq2E_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
91	<a href="#">c6mq2A_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
92	<a href="#">c6mq2C_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
93	<a href="#">c6mpwB_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
94	<a href="#">c6mpwE_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
95	<a href="#">c3chxF_</a>	Alignment	not modelled	5.6	19	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> pmoa; <b>PDBTitle:</b> crystal structure of methylosinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)
96	<a href="#">c6bm8A_</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type i
97	<a href="#">c5ireD_</a>	Alignment	not modelled	5.5	8	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> the cryo-em structure of zika virus
98	<a href="#">d3bzka3</a>	Alignment	not modelled	5.5	23	<b>Fold:</b> Tex N-terminal region-like <b>Superfamily:</b> Tex N-terminal region-like <b>Family:</b> Tex N-terminal region-like
99	<a href="#">d1jb0m_</a>	Alignment	not modelled	5.3	25	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit XII of photosystem I reaction centre, PsaM <b>Family:</b> Subunit XII of photosystem I reaction centre, PsaM