





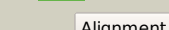









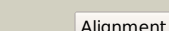




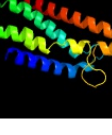
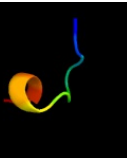
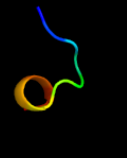


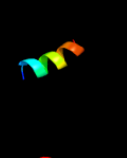
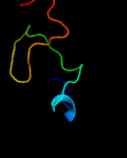





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3848 (-) _4322504_4323412
Date	Sat Aug 10 22:05:02 BST 2019
Unique Job ID	bab1f9baaab2e7c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5kvvA_</a>	 Alignment		95.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccda; <b>PDBTitle:</b> solution nmr structure of the membrane electron transporter ccda
2	<a href="#">c6mjpF_</a>	 Alignment		63.8	11	<b>PDB header:</b> lipid transport <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
3	<a href="#">c5x5yG_</a>	 Alignment		56.6	17	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
4	<a href="#">c5x5yF_</a>	 Alignment		53.0	10	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
5	<a href="#">c5I75G_</a>	 Alignment		44.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> fig000906: predicted permease; <b>PDBTitle:</b> a protein structure
6	<a href="#">c3hd6A_</a>	 Alignment		44.2	20	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter rh type c; <b>PDBTitle:</b> crystal structure of the human rhesus glycoprotein rhcg
7	<a href="#">c6mjpG_</a>	 Alignment		44.0	16	<b>PDB header:</b> lipid transport <b>Chain:</b> G: <b>PDB Molecule:</b> lps export abc transporter permease lptg; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
8	<a href="#">c5ze3B_</a>	 Alignment		36.2	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl oxidase homolog 2; <b>PDBTitle:</b> crystal structure of human lysyl oxidase-like 2 (hloxl2) in a2 precursor state
9	<a href="#">c5I75F_</a>	 Alignment		35.9	6	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> a protein structure
10	<a href="#">c5aezA_</a>	 Alignment		31.1	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mep2; <b>PDBTitle:</b> crystal structure of candida albicans mep2
11	<a href="#">c5a43B_</a>	 Alignment		30.3	9	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative fluoride ion transporter crcb; <b>PDBTitle:</b> crystal structure of a dual topology fluoride ion channel.

12	<a href="#">d1mxaa1</a>	Alignment		30.0	55	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
13	<a href="#">d2p02a1</a>	Alignment		28.5	55	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
14	<a href="#">d1qm4a1</a>	Alignment		28.3	55	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
15	<a href="#">d1ei5a2</a>	Alignment		28.1	62	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> D-aminopeptidase, middle and C-terminal domains <b>Family:</b> D-aminopeptidase, middle and C-terminal domains
16	<a href="#">d2e74f1</a>	Alignment		27.9	57	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetM subunit of the cytochrome b6f complex <b>Family:</b> PetM subunit of the cytochrome b6f complex
17	<a href="#">c4mbyB_</a>	Alignment		23.5	24	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> major capsid protein vp1; <b>PDBTitle:</b> structure of b-lymphotropic polyomavirus vp1 in complex with 3'-2 sialyllactose
18	<a href="#">c5aexj_</a>	Alignment		21.3	13	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> ammonium transporter mep2; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mep2
19	<a href="#">c5vn4A_</a>	Alignment		19.5	42	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> adenine phosphoribosyltransferase, putative; <b>PDBTitle:</b> crystal structure of adenine phosphoribosyl transferase from2 trypanosoma brucei in complex with amp, pyrophosphate, and ribose-5-3 phosphate
20	<a href="#">c3c1iA_</a>	Alignment		18.1	25	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> ammonia channel; <b>PDBTitle:</b> substrate binding, deprotonation and selectivity at the periplasmic2 entrance of the e. coli ammonia channel ambt
21	<a href="#">c2kr6A_</a>	Alignment	not modelled	16.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> presenilin-1; <b>PDBTitle:</b> solution structure of presenilin-1 ctf subunit
22	<a href="#">c2obvA_</a>	Alignment	not modelled	15.7	55	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> s-adenosylmethionine synthetase isoform type-1; <b>PDBTitle:</b> crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
23	<a href="#">c3im1B_</a>	Alignment	not modelled	15.6	45	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
24	<a href="#">c3rv2B_</a>	Alignment	not modelled	15.5	55	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
25	<a href="#">c5h9uC_</a>	Alignment	not modelled	15.5	45	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> crystal structure of a thermostable methionine adenosyltransferase
26	<a href="#">c1rg9D_</a>	Alignment	not modelled	15.5	55	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> s-adenosylmethionine synthetase complexed with sam and ppnp
27	<a href="#">c4odjA_</a>	Alignment	not modelled	15.0	45	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> crystal structure of a putative s-adenosylmethionine synthetase from2 cryptosporidium hominis in complex with s-adenosyl-methionine
28	<a href="#">c6hwhX_</a>	Alignment	not modelled	14.9	23	<b>PDB header:</b> electron transport <b>Chain:</b> X; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory

						supercomplex from2 mycobacterium smegmatis
29	<a href="#">c3so4C_</a>	Alignment	not modelled	14.6	45	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> methionine-adenosyltransferase; <b>PDBTitle:</b> methionine-adenosyltransferase from entamoeba histolytica
30	<a href="#">c4le5A_</a>	Alignment	not modelled	14.5	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> structure of an unusual s-adenosylmethionine synthetase from2 campylobacter jejuni
31	<a href="#">c4k1cB_</a>	Alignment	not modelled	13.6	13	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger
32	<a href="#">d1k8ib2</a>	Alignment	not modelled	13.2	64	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
33	<a href="#">c4k1cA_</a>	Alignment	not modelled	13.1	13	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger
34	<a href="#">c3jlzP_</a>	Alignment	not modelled	12.7	13	<b>PDB header:</b> metal transport <b>Chain:</b> P: <b>PDB Molecule:</b> cation efflux family protein; <b>PDBTitle:</b> inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
35	<a href="#">d1u7ga_</a>	Alignment	not modelled	12.6	19	<b>Fold:</b> Ammonium transporter <b>Superfamily:</b> Ammonium transporter <b>Family:</b> Ammonium transporter
36	<a href="#">c2l9uB_</a>	Alignment	not modelled	11.7	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
37	<a href="#">c2l9uA_</a>	Alignment	not modelled	11.7	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
38	<a href="#">c2lx0A_</a>	Alignment	not modelled	11.1	29	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane fusion protein p14; <b>PDBTitle:</b> arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
39	<a href="#">c2zt9F_</a>	Alignment	not modelled	10.9	50	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
40	<a href="#">c4h44F_</a>	Alignment	not modelled	10.9	50	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> 2.70 a cytochrome b6f complex structure from nostoc pcc 7120
41	<a href="#">c4ogqF_</a>	Alignment	not modelled	10.9	50	<b>PDB header:</b> electron transport <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex
42	<a href="#">c4iu8A_</a>	Alignment	not modelled	10.8	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter (selenomethionine2 derivative)
43	<a href="#">c2ks1A_</a>	Alignment	not modelled	10.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
44	<a href="#">c2jwaA_</a>	Alignment	not modelled	10.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure
45	<a href="#">c5aj3m_</a>	Alignment	not modelled	9.9	50	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
46	<a href="#">d1yy9a4</a>	Alignment	not modelled	9.4	67	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Growth factor receptor domain <b>Family:</b> Growth factor receptor domain
47	<a href="#">c3uc8A_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - tetragonal crystal form
48	<a href="#">c3uc8B_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - tetragonal crystal form
49	<a href="#">c3uc7E_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
50	<a href="#">c2ll5A_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> cyclo-tc1 trp-cage
51	<a href="#">c3uc7A_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
52	<a href="#">c3uc7D_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
53	<a href="#">c3uc7C_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
54	<a href="#">c3uc7B_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form

55	<a href="#">c3uc7F_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
56	<a href="#">c3uc8C_</a>	Alignment	not modelled	9.3	86	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - tetragonal crystal form
57	<a href="#">c6nbxG_</a>	Alignment	not modelled	8.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
58	<a href="#">c3wi7A_</a>	Alignment	not modelled	8.4	70	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> oxidized polyvinyl alcohol hydrolase; <b>PDBTitle:</b> the complex structure of poph s172c with ligand, aca
59	<a href="#">d2de6a2</a>	Alignment	not modelled	8.1	40	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Ring hydroxylating alpha subunit catalytic domain
60	<a href="#">c4g5sZ_</a>	Alignment	not modelled	7.9	50	<b>PDB header:</b> cell cycle/signaling protein <b>Chain:</b> Z; <b>PDB Molecule:</b> g-protein-signaling modulator 2; <b>PDBTitle:</b> structure of lgn gl3/galphi3 complex
61	<a href="#">c5twaD_</a>	Alignment	not modelled	7.8	71	<b>PDB header:</b> apoptosis <b>Chain:</b> D; <b>PDB Molecule:</b> bak-2 protein; <b>PDBTitle:</b> crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
62	<a href="#">c5twaC_</a>	Alignment	not modelled	7.8	71	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> bak-2 protein; <b>PDBTitle:</b> crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
63	<a href="#">d1fft2</a>	Alignment	not modelled	7.8	14	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
64	<a href="#">c2qz5A_</a>	Alignment	not modelled	7.6	33	<b>PDB header:</b> signaling protein, lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> axin interactor, dorsalization associated <b>PDBTitle:</b> crystal structure of the c-terminal domain of aida
65	<a href="#">d1vpsa_</a>	Alignment	not modelled	7.3	21	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Group I dsDNA viruses <b>Family:</b> Papovaviridae-like VP
66	<a href="#">c4fmiN_</a>	Alignment	not modelled	7.1	18	<b>PDB header:</b> viral protein <b>Chain:</b> N; <b>PDB Molecule:</b> vp1; <b>PDBTitle:</b> merkel cell polyomavirus vp1 in complex with 3'-sialyllactosamine
67	<a href="#">c4g5sG_</a>	Alignment	not modelled	6.7	55	<b>PDB header:</b> cell cycle/signaling protein <b>Chain:</b> G; <b>PDB Molecule:</b> g-protein-signaling modulator 2; <b>PDBTitle:</b> structure of lgn gl3/galphi3 complex
68	<a href="#">c3a5pD_</a>	Alignment	not modelled	6.6	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> haemagglutinin i; <b>PDBTitle:</b> crystal structure of hemagglutinin
69	<a href="#">c2czsB_</a>	Alignment	not modelled	6.5	23	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> cytochrome c, putative; <b>PDBTitle:</b> crystal structure analysis of the diheme c-type cytochrome dhc2
70	<a href="#">c4s1kA_</a>	Alignment	not modelled	6.4	38	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> polyhedrin; <b>PDBTitle:</b> structure of uranotaenia sapphirina cypovirus (cpv17) polyhedrin at2 100 k
71	<a href="#">c3j39Q_</a>	Alignment	not modelled	6.3	31	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> 60s ribosomal protein l18; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
72	<a href="#">d1prtF_</a>	Alignment	not modelled	6.2	38	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
73	<a href="#">c2ka1B_</a>	Alignment	not modelled	6.2	42	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles
74	<a href="#">c2ka2A_</a>	Alignment	not modelled	6.2	42	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
75	<a href="#">d2bida_</a>	Alignment	not modelled	6.1	57	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
76	<a href="#">c5tcxA_</a>	Alignment	not modelled	6.1	20	<b>PDB header:</b> cell invasion <b>Chain:</b> A; <b>PDB Molecule:</b> cd81 antigen; <b>PDBTitle:</b> crystal structure of human tetraspanin cd81
77	<a href="#">c6g72A_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 3; <b>PDBTitle:</b> mouse mitochondrial complex i in the deactive state
78	<a href="#">c2n90A_</a>	Alignment	not modelled	5.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> high affinity nerve growth factor receptor; <b>PDBTitle:</b> trka transmembrane domain nmr structure in dpc micelles
79	<a href="#">c2n90B_</a>	Alignment	not modelled	5.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> high affinity nerve growth factor receptor; <b>PDBTitle:</b> trka transmembrane domain nmr structure in dpc micelles
80	<a href="#">c1bzka_</a>	Alignment	not modelled	5.7	25	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein (band 3 anion transport protein); <b>PDBTitle:</b> structural studies on the effects of the deletion in the2 red cell anion exchanger (band3, ae1) associated with3 south east asian ovalocytosis.

81	<a href="#">c2n4xA_</a>	Alignment	not modelled	5.7	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein (ccda); <b>PDBTitle:</b> structure of the transmembrane electron transporter ccda
82	<a href="#">c6qvcB_</a>	Alignment	not modelled	5.6	8	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride channel protein 1; <b>PDBTitle:</b> cryoem structure of the human clc-1 chloride channel, cbs state 1
83	<a href="#">d1ddba_</a>	Alignment	not modelled	5.3	57	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
84	<a href="#">c2lonA_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hig1 domain family member 1b; <b>PDBTitle:</b> backbone structure of human membrane protein higd1b
85	<a href="#">c5aexB_</a>	Alignment	not modelled	5.2	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> ammonium transporter mep2; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mep2
86	<a href="#">d1vd4a_</a>	Alignment	not modelled	5.2	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
87	<a href="#">c6iedA_</a>	Alignment	not modelled	5.2	6	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme a synthase; <b>PDBTitle:</b> crystal structure of heme a synthase from bacillus subtilis