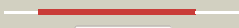


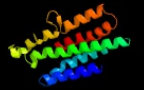





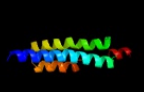



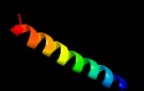

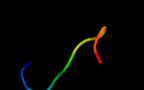



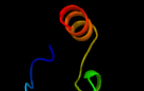


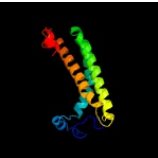

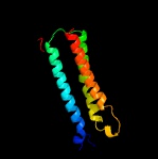

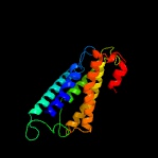



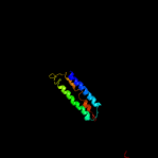


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2154c\_(ftsW)\_2413356\_2414930  
 Date Mon Aug 5 13:25:27 BST 2019  
 Unique Job ID 1af6d1312dd15a2d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6basA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> peptidoglycan glycosyltransferase roda; <b>PDBTitle:</b> crystal structure of thermus thermophilus rod shape determining2 protein roda d255a mutant (q5six3_thet8)
2	<a href="#">c5mg3D_</a>	 Alignment		76.3	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
3	<a href="#">c2kncB_</a>	 Alignment		65.3	30	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
4	<a href="#">c4dveA_</a>	 Alignment		43.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> biotin transporter bioy; <b>PDBTitle:</b> crystal structure at 2.1 a of the s-component for biotin from an ecf-2 type abc transporter
5	<a href="#">c2v50A_</a>	 Alignment		42.3	25	<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
6	<a href="#">c2mr7A_</a>	 Alignment		42.1	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> apo structure of the peptidyl carrier protein domain 7 of the2 teicoplanin producing non-ribosomal peptide synthetase
7	<a href="#">c5zazA_</a>	 Alignment		36.5	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin beta-2; <b>PDBTitle:</b> solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
8	<a href="#">d2azea1</a>	 Alignment		33.3	40	<b>Fold:</b> E2F-DP heterodimerization region <b>Superfamily:</b> E2F-DP heterodimerization region <b>Family:</b> DP dimerization segment
9	<a href="#">c2rmzA_</a>	 Alignment		29.5	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> bicelle-embedded integrin beta3 transmembrane segment
10	<a href="#">c4pxhF_</a>	 Alignment		29.2	23	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> F; <b>PDB Molecule:</b> peptide synthetase; <b>PDBTitle:</b> structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis in complex with a peptidyl carrier protein domain
11	<a href="#">c5lq3F_</a>	 Alignment		28.9	11	<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

12	<a href="#">c6iedA_</a>	Alignment		27.2	17	<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
13	<a href="#">c4quvB_</a>	Alignment		27.1	10	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> delta(14)-sterol reductase; <b>PDBTitle:</b> structure of an integral membrane delta(14)-sterol reductase
14	<a href="#">c5vreB_</a>	Alignment		26.7	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative integral membrane protein; <b>PDBTitle:</b> crystal structure of a lysosomal potassium-selective channel tmem1752 homolog from chamaesiphon minutus
15	<a href="#">c5u3hA_</a>	Alignment		26.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> hmwp2 nonribosomal peptide synthetase; <b>PDBTitle:</b> solution structure of apo pcp1 from yersiniabactin synthetase
16	<a href="#">d3dtua1</a>	Alignment		25.1	21	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
17	<a href="#">d2pnga1</a>	Alignment		24.7	21	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
18	<a href="#">c5zk4D_</a>	Alignment		22.7	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> disa protein; <b>PDBTitle:</b> the structure of dszs acyltransferase with carrier protein
19	<a href="#">c4il3B_</a>	Alignment		21.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ste24p; <b>PDBTitle:</b> crystal structure of s. mikatae ste24p
20	<a href="#">c4aq5A_</a>	Alignment		20.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholine receptor subunit alpha; <b>PDBTitle:</b> gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
21	<a href="#">c2bg9A_</a>	Alignment	not modelled	20.3	18	<b>PDB header:</b> ion channel/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholine receptor protein, alpha chain; <b>PDBTitle:</b> refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
22	<a href="#">d2gdwa1</a>	Alignment	not modelled	19.5	26	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Peptidyl carrier domain
23	<a href="#">c2mawA_</a>	Alignment	not modelled	19.2	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> neuronal acetylcholine receptor subunit alpha-7; <b>PDBTitle:</b> nmr structures of the alpha7 nachr transmembrane domain.
24	<a href="#">c1m56G_</a>	Alignment	not modelled	17.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)
25	<a href="#">c5ejdK_</a>	Alignment	not modelled	16.8	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> K: <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of holo t3ct
26	<a href="#">c5mtiA_</a>	Alignment	not modelled	16.8	27	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine-binding protein; <b>PDBTitle:</b> bamb_5917 acyl-carrier protein
27	<a href="#">c4aq9E_</a>	Alignment	not modelled	15.3	15	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> acetylcholine receptor gamma subunit; <b>PDBTitle:</b> gating movement in acetylcholine receptor analysed by time- resolved2 electron cryo-microscopy (open class)
28	<a href="#">c2bg9E_</a>	Alignment	not modelled	15.3	15	<b>PDB header:</b> ion channel/receptor <b>Chain:</b> E: <b>PDB Molecule:</b> acetylcholine receptor protein, gamma chain;

						<b>PDBTitle:</b> refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
29	<a href="#">c5msvB_</a>	Alignment	not modelled	13.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioester reductase domain-containing protein; <b>PDBTitle:</b> structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp
30	<a href="#">c6iu3A_</a>	Alignment	not modelled	13.7	15	<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
31	<a href="#">c4rfsT_</a>	Alignment	not modelled	13.5	8	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> T: <b>PDB Molecule:</b> energy-coupling factor transporter transmembrane protein <b>PDBTitle:</b> structure of a pantothenate energy coupling factor transporter
32	<a href="#">c4i4dA_</a>	Alignment	not modelled	13.5	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide synthetase nrps type ii-pcp; <b>PDBTitle:</b> structure of blmi, a type-ii acyl-carrier-protein from streptomyces2 verticillus involved in bleomycin biosynthesis
33	<a href="#">c2m59A_</a>	Alignment	not modelled	13.1	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
34	<a href="#">c2m59B_</a>	Alignment	not modelled	13.1	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
35	<a href="#">c4ev6E_</a>	Alignment	not modelled	12.9	24	<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
36	<a href="#">c6ithA_</a>	Alignment	not modelled	12.9	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> syndecan-2; <b>PDBTitle:</b> structure of the transmembrane domain of syndecan 2 in micelles
37	<a href="#">c6o7xa_</a>	Alignment	not modelled	12.8	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a; <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3
38	<a href="#">c5gasN_</a>	Alignment	not modelled	12.6	14	<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
39	<a href="#">c3rkoL_</a>	Alignment	not modelled	12.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit l; <b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
40	<a href="#">c2zzeG_</a>	Alignment	not modelled	12.0	41	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
41	<a href="#">c1oy8A_</a>	Alignment	not modelled	12.0	15	<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
42	<a href="#">c4qndA_</a>	Alignment	not modelled	11.7	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemical transport protein; <b>PDBTitle:</b> crystal structure of a semisweet
43	<a href="#">c5kxiC_</a>	Alignment	not modelled	11.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> neuronal acetylcholine receptor subunit beta-2; <b>PDBTitle:</b> x-ray structure of the human alpha4beta2 nicotinic receptor
44	<a href="#">c2jo1A_</a>	Alignment	not modelled	11.3	41	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
45	<a href="#">c4knbE_</a>	Alignment	not modelled	11.2	36	<b>PDB header:</b> transcription/replication <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein spt16d; <b>PDBTitle:</b> structure of the spt16d pob3n heterodimer
46	<a href="#">c2ywxA_</a>	Alignment	not modelled	11.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
47	<a href="#">c3n23E_</a>	Alignment	not modelled	10.6	47	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
48	<a href="#">c2cq8A_</a>	Alignment	not modelled	10.5	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> solution structure of rsgi ruh-033, a pp-binding domain of2 10-ftfhdh from human cdna
49	<a href="#">c2mkvA_</a>	Alignment	not modelled	10.5	35	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles
50	<a href="#">c2jp3A_</a>	Alignment	not modelled	10.1	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
51	<a href="#">c4heaT_</a>	Alignment	not modelled	9.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> T: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 12; <b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus
						<b>PDB header:</b> signaling protein

52	<a href="#">c2e8mA</a>	Alignment	not modelled	9.6	15	<b>Chain:</b> A; <b>PDB Molecule:</b> epidermal growth factor receptor kinase <b>PDBTitle:</b> solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
53	<a href="#">d1qlec</a>	Alignment	not modelled	9.4	16	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like
54	<a href="#">c6b2zA</a>	Alignment	not modelled	9.3	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> atp synthase protein 8; <b>PDBTitle:</b> cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
55	<a href="#">c6b2zL</a>	Alignment	not modelled	9.3	14	<b>PDB header:</b> membrane protein <b>Chain:</b> L; <b>PDB Molecule:</b> atp synthase protein 8; <b>PDBTitle:</b> cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
56	<a href="#">d1q90b</a>	Alignment	not modelled	9.3	8	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
57	<a href="#">c6hcyA</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> metalloreductase steap4; <b>PDBTitle:</b> human steap4 bound to nadp, fad, heme and fe(iii)-nta.
58	<a href="#">c5zgbL</a>	Alignment	not modelled	9.2	54	<b>PDB header:</b> photosynthesis <b>Chain:</b> I; <b>PDB Molecule:</b> psai; <b>PDBTitle:</b> cryo-em structure of the red algal psi-lhcr
59	<a href="#">c5zghL</a>	Alignment	not modelled	9.2	54	<b>PDB header:</b> photosynthesis <b>Chain:</b> I; <b>PDB Molecule:</b> psai; <b>PDBTitle:</b> cryo-em structure of the red algal psi-lhcr
60	<a href="#">c1v55B</a>	Alignment	not modelled	9.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> bovine heart cytochrome c oxidase at the fully reduced state
61	<a href="#">c2kogA</a>	Alignment	not modelled	8.7	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure
62	<a href="#">c5d7tH</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> H; <b>PDB Molecule:</b> energy-coupling factor transporter transmembrane protein <b>PDBTitle:</b> folate ecf transporter: apo state
63	<a href="#">c1q90G</a>	Alignment	not modelled	8.5	70	<b>PDB header:</b> photosynthesis <b>Chain:</b> G; <b>PDB Molecule:</b> cytochrome b6f complex subunit petg; <b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
64	<a href="#">d1q90g</a>	Alignment	not modelled	8.5	70	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
65	<a href="#">c2y69Q</a>	Alignment	not modelled	8.4	7	<b>PDB header:</b> electron transport <b>Chain:</b> Q; <b>PDB Molecule:</b> cytochrome c oxidase subunit 4 isoform 1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
66	<a href="#">c6btmC</a>	Alignment	not modelled	8.2	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> alternative complex iii subunit c; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
67	<a href="#">c4wd7A</a>	Alignment	not modelled	8.2	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> bestrophin domain protein; <b>PDBTitle:</b> crystal structure of a bacterial bestrophin homolog from klebsiella2 pneumoniae by zn-sad phasing
68	<a href="#">c6owsB</a>	Alignment	not modelled	8.0	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
69	<a href="#">c6fosl</a>	Alignment	not modelled	7.9	54	<b>PDB header:</b> photosynthesis <b>Chain:</b> I; <b>PDB Molecule:</b> photosystem i reaction center subunit viii; <b>PDBTitle:</b> cyanidioschyzon merolae photosystem i
70	<a href="#">d1v54d</a>	Alignment	not modelled	7.8	7	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV <b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV
71	<a href="#">c4kppA</a>	Alignment	not modelled	7.6	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax
72	<a href="#">c6d0hB</a>	Alignment	not modelled	7.6	21	<b>PDB header:</b> toxin <b>Chain:</b> B; <b>PDB Molecule:</b> pars: cog5642 (duf2384) antitoxin; <b>PDBTitle:</b> part: prs adp-ribosylating toxin bound to cognate antitoxin pars
73	<a href="#">c2micA</a>	Alignment	not modelled	7.6	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
74	<a href="#">c2micB</a>	Alignment	not modelled	7.6	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
75	<a href="#">c2fq1A</a>	Alignment	not modelled	7.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> isochorismatase; <b>PDBTitle:</b> crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
76	<a href="#">c6hwhX</a>	Alignment	not modelled	7.4	16	<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
77	<a href="#">c4byt7</a>	Alignment	not modelled	7.3	12	<b>PDB header:</b> ribosome <b>Chain:</b> 7; <b>PDB Molecule:</b> suppressor protein stm1; <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnmet2 eukaryotic translation initiation complex

78	<a href="#">c3u5ch_</a>	Alignment	not modelled	7.3	12	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 40s ribosomal protein s7-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
79	<a href="#">c4byl7_</a>	Alignment	not modelled	7.3	12	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> suppressor protein stm1; <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnramet2 eukaryotic translation initiation complex
80	<a href="#">c2zqpY_</a>	Alignment	not modelled	7.3	15	<b>PDB header:</b> protein transport <b>Chain:</b> Y: <b>PDB Molecule:</b> preprotein translocase secy subunit; <b>PDBTitle:</b> crystal structure of secye translocon from thermus2 thermophilus
81	<a href="#">c5wb5A_</a>	Alignment	not modelled	7.3	25	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> putative eukaryotic translation initiation factor eif-4e; <b>PDBTitle:</b> leishmania if4e-1 bound to leishmania 4e-ip1
82	<a href="#">c5mjrA_</a>	Alignment	not modelled	7.0	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> protein thf1; <b>PDBTitle:</b> structure of psb29 at 1.55a
83	<a href="#">c1m57H_</a>	Alignment	not modelled	7.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
84	<a href="#">c4mt1A_</a>	Alignment	not modelled	6.8	13	<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
85	<a href="#">c5ujqA_</a>	Alignment	not modelled	6.6	62	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin; <b>PDBTitle:</b> nmr solution structure of the two-component bacteriocin cbnxy
86	<a href="#">d2e74a1</a>	Alignment	not modelled	6.6	8	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
87	<a href="#">c2ifmA_</a>	Alignment	not modelled	6.6	17	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> pf1 filamentous bacteriophage; <b>PDBTitle:</b> pf1 filamentous bacteriophage: refinement of a molecular2 model by simulated annealing using 3.3 angstroms3 resolution x-ray fibre diffraction data
88	<a href="#">c1q11A_</a>	Alignment	not modelled	6.6	17	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> pf1 bacteriophage coat protein b; <b>PDBTitle:</b> inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
89	<a href="#">c5sxpG_</a>	Alignment	not modelled	6.6	30	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> G: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> structural basis for the interaction between itch prr and beta-pix
90	<a href="#">c6j5bC_</a>	Alignment	not modelled	6.5	35	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> protein phosphate starvation response 1; <b>PDBTitle:</b> structural basis for the target dna recognition and binding by the myb2 domain of phosphate starvation response regulator 1
91	<a href="#">c5x3xq_</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> transport protein <b>Chain:</b> Q: <b>PDB Molecule:</b> uncharacterized protein cbiq; <b>PDBTitle:</b> 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo
92	<a href="#">d1xmeb2</a>	Alignment	not modelled	6.5	35	<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
93	<a href="#">c5kxiA_</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> neuronal acetylcholine receptor subunit alpha-4; <b>PDBTitle:</b> x-ray structure of the human alpha4beta2 nicotinic receptor
94	<a href="#">c1ar1B_</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> complex (oxidoreductase/antibody) <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
95	<a href="#">c1qleB_</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> oxidoreductase/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> cryo-structure of the paracoccus denitrificans four-subunit cytochrome2 c oxidase in the completely oxidized state complexed with an antibody3 fv fragment
96	<a href="#">d2h8pc1</a>	Alignment	not modelled	6.4	22	<b>Fold:</b> Voltage-gated potassium channels <b>Superfamily:</b> Voltage-gated potassium channels <b>Family:</b> Voltage-gated potassium channels
97	<a href="#">c5sxpF_</a>	Alignment	not modelled	6.4	37	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> F: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> structural basis for the interaction between itch prr and beta-pix
98	<a href="#">c5n6mA_</a>	Alignment	not modelled	6.3	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein n-acyltransferase; <b>PDBTitle:</b> structure of the membrane integral lipoprotein n-acyltransferase lnt2 from p. aeruginosa
99	<a href="#">c6dmoA_</a>	Alignment	not modelled	6.3	12	<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