
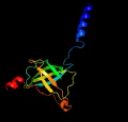





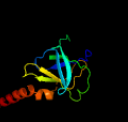









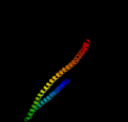

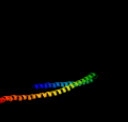

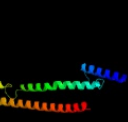
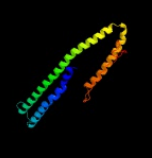

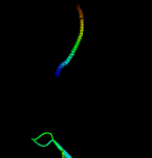
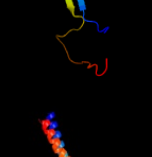
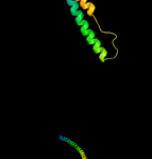
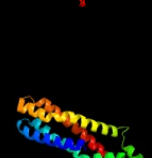


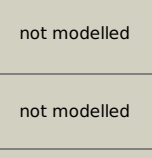


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3497c_(mce4C)_3916062_3917135
Date	Fri Aug 9 18:20:17 BST 2019
Unique Job ID	081a595261895b89

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4C_</a>	 Alignment		99.9	30	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> toluene tolerance efflux transporter (abc superfamily, <b>PDBTitle:</b> cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
2	<a href="#">c5uw8C_</a>	 Alignment		99.6	21	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> probable phospholipid abc transporter-binding protein mlad; <b>PDBTitle:</b> structure of e. coli mce protein mlad, core mce domain
3	<a href="#">c5uvc_</a>	 Alignment		99.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
4	<a href="#">c5uvcF_</a>	 Alignment		99.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
5	<a href="#">c5uvcB_</a>	 Alignment		99.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
6	<a href="#">c5uvcD_</a>	 Alignment		99.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
7	<a href="#">c5uvcA_</a>	 Alignment		99.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
8	<a href="#">c5uvcE_</a>	 Alignment		99.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
9	<a href="#">c3g67A_</a>	 Alignment		92.9	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of a soluble chemoreceptor from thermotoga2 maritima
10	<a href="#">c1qu7A_</a>	 Alignment		89.5	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
11	<a href="#">c6b7nC_</a>	 Alignment		85.9	15	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike protein; <b>PDBTitle:</b> cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state

12	<a href="#">c6evzX_</a>	Alignment		84.5	11	<b>PDB header:</b> toxin <b>Chain:</b> X: <b>PDB Molecule:</b> non-hemolytic enterotoxin lytic component I1; <b>PDBTitle:</b> the cytotoxin maka from vibrio cholerae
13	<a href="#">c3lnrA_</a>	Alignment		83.6	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> aerotaxis transducer aer2; <b>PDBTitle:</b> crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
14	<a href="#">c2ch7A_</a>	Alignment		83.4	13	<b>PDB header:</b> chemotaxis <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
15	<a href="#">c2j5uB_</a>	Alignment		80.6	12	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
16	<a href="#">c2ieqC_</a>	Alignment		80.0	14	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
17	<a href="#">c3zx6A_</a>	Alignment		77.7	13	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hamp, methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
18	<a href="#">c6e6aB_</a>	Alignment		76.9	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> inclusion membrane protein a; <b>PDBTitle:</b> triclinic crystal form of inca g144a point mutant
19	<a href="#">c2d4yA_</a>	Alignment		75.9	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook-associated protein 1; <b>PDBTitle:</b> crystal structure of a 49k fragment of hap1 (flgk)
20	<a href="#">c6gajA_</a>	Alignment		75.5	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
21	<a href="#">c3ojaB_</a>	Alignment	not modelled	72.9	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
22	<a href="#">c1kmiZ_</a>	Alignment	not modelled	71.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> Z: <b>PDB Molecule:</b> chemotaxis protein chez; <b>PDBTitle:</b> crystal structure of an e.coli chemotaxis protein, chez
23	<a href="#">c4tkoB_</a>	Alignment	not modelled	71.5	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> emra; <b>PDBTitle:</b> structure of the periplasmic adaptor protein emra
24	<a href="#">c5xbjA_</a>	Alignment	not modelled	69.4	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook-associated protein flgk; <b>PDBTitle:</b> the structure of the flagellar hook junction protein hap1 (flgk) from2 campylobacter jejuni
25	<a href="#">c1deqO_</a>	Alignment	not modelled	68.6	8	<b>PDB header:</b> blood clotting <b>Chain:</b> O: <b>PDB Molecule:</b> fibrinogen (beta chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
26	<a href="#">c1deqF_</a>	Alignment	not modelled	68.1	12	<b>PDB header:</b> blood clotting <b>Chain:</b> F: <b>PDB Molecule:</b> fibrinogen (gamma chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
27	<a href="#">c1ei3C_</a>	Alignment	not modelled	67.9	7	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
28	<a href="#">d1st6a4</a>	Alignment	not modelled	66.8	13	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin <b>PDB header:</b> viral protein, inhibitor

29	<a href="#">c5zuvB_</a>	Alignment	not modelled	65.7	16	<b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein,spike glycoprotein,inhibitor ek1; <b>PDBTitle:</b> crystal structure of the human coronavirus 229e hr1 motif in complex2 with pan-covs inhibitor ek1
30	<a href="#">c4ut1A_</a>	Alignment	not modelled	65.2	14	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook-associated protein; <b>PDBTitle:</b> the structure of the flagellar hook junction protein flgk2 from burkholderia pseudomallei
31	<a href="#">c5lp5F_</a>	Alignment	not modelled	62.0	13	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> F: <b>PDB Molecule:</b> rod shape-determining protein (mrec); <b>PDBTitle:</b> complex between penicillin-binding protein (pbp2) and mrec from2 helicobacter pylori
32	<a href="#">c1ei3E_</a>	Alignment	not modelled	59.9	12	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
33	<a href="#">c2wpgA_</a>	Alignment	not modelled	59.2	5	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> trimeric autotransporter adhesin fragment; <b>PDBTitle:</b> salmonella enterica sada 479-519 fused to gcn4 adaptors (sadak3, in-2 register fusion)
34	<a href="#">c6gapB_</a>	Alignment	not modelled	58.3	12	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t3d reovirus sigma1 coiled coil tail and body
35	<a href="#">c5n76C_</a>	Alignment	not modelled	56.0	18	<b>PDB header:</b> nickel-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> coot; <b>PDBTitle:</b> crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
36	<a href="#">c5szsC_</a>	Alignment	not modelled	55.7	13	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
37	<a href="#">c2gl2B_</a>	Alignment	not modelled	54.9	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> adhesion a; <b>PDBTitle:</b> crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
38	<a href="#">c2qihA_</a>	Alignment	not modelled	53.1	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> protein uspa1; <b>PDBTitle:</b> crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
39	<a href="#">d1eq1a_</a>	Alignment	not modelled	52.5	17	<b>Fold:</b> Apolipophorin-III <b>Superfamily:</b> Apolipophorin-III <b>Family:</b> Apolipophorin-III
40	<a href="#">d1rh5b_</a>	Alignment	not modelled	51.1	17	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Preprotein translocase SecE subunit <b>Family:</b> Preprotein translocase SecE subunit
41	<a href="#">c3cwgA_</a>	Alignment	not modelled	50.9	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment
42	<a href="#">c5x5bB_</a>	Alignment	not modelled	48.0	10	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> prefusion structure of sars-cov spike glycoprotein, conformation 2
43	<a href="#">c2vs0B_</a>	Alignment	not modelled	46.6	13	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
44	<a href="#">c4iogD_</a>	Alignment	not modelled	46.5	11	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
45	<a href="#">c3j99M_</a>	Alignment	not modelled	46.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> synaptosomal-associated protein 25; <b>PDBTitle:</b> structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iiib)
46	<a href="#">c4abxB_</a>	Alignment	not modelled	45.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein recn; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans recn coiled-2 coil domain
47	<a href="#">d2cp6a1</a>	Alignment	not modelled	44.8	20	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
48	<a href="#">c4qkvB_</a>	Alignment	not modelled	43.1	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase i and transcript release factor; <b>PDBTitle:</b> crystal structure of the mouse cavin1 hr1 domain
49	<a href="#">c5xlrC_</a>	Alignment	not modelled	42.8	10	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> structure of sars-cov spike glycoprotein
50	<a href="#">d1szia_</a>	Alignment	not modelled	42.4	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain <b>Family:</b> Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
51	<a href="#">c5zhyA_</a>	Alignment	not modelled	41.5	8	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein, spike glycoprotein; <b>PDBTitle:</b> structural characterization of the hcov-229e fusion core
52	<a href="#">c6nzkB_</a>	Alignment	not modelled	41.2	15	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> spike surface glycoprotein; <b>PDBTitle:</b> structural basis for human coronavirus attachment to sialic acid2 receptors
53	<a href="#">c1cz5A_</a>	Alignment	not modelled	39.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
54	<a href="#">c5u0pU_</a>	Alignment	not modelled	38.2	9	<b>PDB header:</b> transcription <b>Chain:</b> U: <b>PDB Molecule:</b> mediator complex subunit 21; <b>PDBTitle:</b> cryo-em structure of the transcriptional mediator

55	<a href="#">c6cs2A_</a>	Alignment	not modelled	37.0	10	<b>PDB header:</b> viral protein/hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> spike glycoprotein,fibritin; <b>PDBTitle:</b> sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
56	<a href="#">c3vkhA_</a>	Alignment	not modelled	36.4	12	<b>PDB header:</b> motor protein <b>Chain:</b> A; <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of a functional full-length dynein motor domain
57	<a href="#">c1bf5A_</a>	Alignment	not modelled	34.4	6	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A; <b>PDB Molecule:</b> signal transducer and activator of transcription 1- <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
58	<a href="#">c3qr8A_</a>	Alignment	not modelled	33.1	15	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> baseplate assembly protein v; <b>PDBTitle:</b> crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
59	<a href="#">c5i08A_</a>	Alignment	not modelled	33.0	14	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> spike glycoprotein, envelope glycoprotein chimera; <b>PDBTitle:</b> prefusion structure of a human coronavirus spike protein
60	<a href="#">d1st6a3</a>	Alignment	not modelled	32.2	10	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
61	<a href="#">c3jclC_</a>	Alignment	not modelled	32.0	13	<b>PDB header:</b> viral protein <b>Chain:</b> C; <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
62	<a href="#">c6nb3B_</a>	Alignment	not modelled	31.7	14	<b>PDB header:</b> virus <b>Chain:</b> B; <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
63	<a href="#">d1h9ra2</a>	Alignment	not modelled	30.5	12	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
64	<a href="#">c6ewyA_</a>	Alignment	not modelled	30.2	10	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> peptidoglycan endopeptidase ripa; <b>PDBTitle:</b> ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
65	<a href="#">c5wrgB_</a>	Alignment	not modelled	28.5	10	<b>PDB header:</b> virus like particle <b>Chain:</b> B; <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> sars-cov spike glycoprotein
66	<a href="#">d1wa8a1</a>	Alignment	not modelled	28.1	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
67	<a href="#">c1yvlB_</a>	Alignment	not modelled	27.9	9	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> structure of unphosphorylated stat1
68	<a href="#">d1h9ma2</a>	Alignment	not modelled	27.4	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
69	<a href="#">c4xa3A_</a>	Alignment	not modelled	26.6	11	<b>PDB header:</b> motor protein <b>Chain:</b> A; <b>PDB Molecule:</b> gp7-myh7(1361-1425)-eb1 chimera protein; <b>PDBTitle:</b> crystal structure of the coiled-coil surrounding skip 2 of myh7
70	<a href="#">c2qf4A_</a>	Alignment	not modelled	26.3	17	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> cell shape determining protein mrec; <b>PDBTitle:</b> high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
71	<a href="#">d1guta_</a>	Alignment	not modelled	25.8	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> Molybdate/tungstate binding protein MOP
72	<a href="#">c3gvmA_</a>	Alignment	not modelled	25.4	13	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
73	<a href="#">c5yfpG_</a>	Alignment	not modelled	25.3	9	<b>PDB header:</b> exocytosis <b>Chain:</b> G; <b>PDB Molecule:</b> exocyst complex component exo70; <b>PDBTitle:</b> cryo-em structure of the exocyst complex
74	<a href="#">c5j9qH_</a>	Alignment	not modelled	24.2	10	<b>PDB header:</b> transferase <b>Chain:</b> H; <b>PDB Molecule:</b> chromatin modification-related protein yng2; <b>PDBTitle:</b> crystal structure of the nua4 core complex
75	<a href="#">c4lwsA_</a>	Alignment	not modelled	24.0	6	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
76	<a href="#">c3zrwB_</a>	Alignment	not modelled	23.8	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> af1503 protein, osmolarity sensor protein envz; <b>PDBTitle:</b> the structure of the dimeric hamp-dhp fusion a291v mutant
77	<a href="#">c3pe0B_</a>	Alignment	not modelled	23.7	10	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> structure of the central region of the plakin domain of plectin
78	<a href="#">d1h9ma1</a>	Alignment	not modelled	23.6	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
79	<a href="#">c3iv1F_</a>	Alignment	not modelled	23.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> tumor susceptibility gene 101 protein; <b>PDBTitle:</b> coiled-coil domain of tumor susceptibility gene 101
80	<a href="#">c5ew5C_</a>	Alignment	not modelled	22.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> colicin-e9;

80	<a href="#">cJewJC_</a>	Alignment	not modelled	22.8	11	<b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9 <b>PDB header:</b> viral protein
81	<a href="#">c1wywB_</a>	Alignment	not modelled	22.5	16	<b>Chain:</b> B: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
82	<a href="#">c4rh7A_</a>	Alignment	not modelled	22.1	13	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein/cytoplasmic dynein 2 heavy chain <b>PDBTitle:</b> crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
83	<a href="#">c4s37F_</a>	Alignment	not modelled	21.9	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> phage baseplate protein; <b>PDBTitle:</b> crystal structure of r2 pyocin membrane-piercing spike
84	<a href="#">c2dq3A_</a>	Alignment	not modelled	21.8	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of aq_298
85	<a href="#">c4qkwB_</a>	Alignment	not modelled	21.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> muscle-related coiled-coil protein; <b>PDBTitle:</b> crystal structure of the zebrafish cavin4a hr1 domain
86	<a href="#">c5j65A_</a>	Alignment	not modelled	20.4	11	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> pesticidal crystal protein cry6aa; <b>PDBTitle:</b> crystal structure of trypsin activated cry6aa
87	<a href="#">d1hcia4</a>	Alignment	not modelled	20.2	9	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
88	<a href="#">c4modB_</a>	Alignment	not modelled	20.1	13	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hr1 of s protein, linker, hr2 of s protein; <b>PDBTitle:</b> structure of the mers-cov fusion core
89	<a href="#">c3ghgK_</a>	Alignment	not modelled	20.0	9	<b>PDB header:</b> blood clotting <b>Chain:</b> K: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
90	<a href="#">c2l8sA_</a>	Alignment	not modelled	19.6	8	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
91	<a href="#">c4lwsB_</a>	Alignment	not modelled	19.5	11	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
92	<a href="#">c3pltB_</a>	Alignment	not modelled	19.2	11	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> sphingolipid long chain base-responsive protein lsp1; <b>PDBTitle:</b> crystal structure of lsp1 from saccharomyces cerevisiae
93	<a href="#">d2cu6a1</a>	Alignment	not modelled	18.6	13	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
94	<a href="#">c3ur1C_</a>	Alignment	not modelled	17.8	9	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> the structure of a ternary complex between chea domains p4 and p5 with2 chew and with a truncated fragment of tm14, a chemoreceptor analog3 from thermotoga maritima.
95	<a href="#">c5dmaA_</a>	Alignment	not modelled	17.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase pcra; <b>PDBTitle:</b> crystal structure of c-terminal tudor domain in pcra/uvrd helicase
96	<a href="#">c4njlA_</a>	Alignment	not modelled	17.6	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> s protein; <b>PDBTitle:</b> crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
97	<a href="#">c5b0oB_</a>	Alignment	not modelled	17.3	39	<b>PDB header:</b> hydrolase/motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellum-specific atp synthase; <b>PDBTitle:</b> structure of the flih-flii complex
98	<a href="#">c3zbhC_</a>	Alignment	not modelled	16.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
99	<a href="#">c2nrjA_</a>	Alignment	not modelled	16.5	14	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> hbl b protein; <b>PDBTitle:</b> crystal structure of hemolysin binding component from2 bacillus cereus