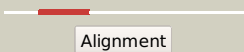
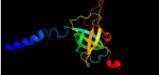
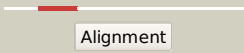

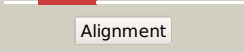

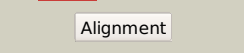



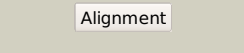

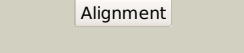



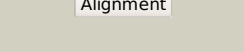
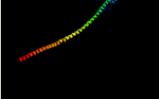
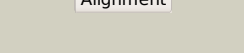
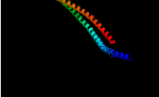
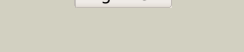
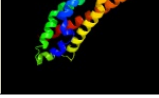
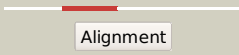
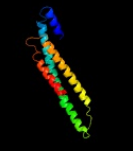
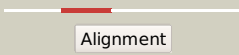

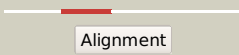
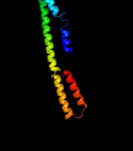
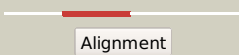
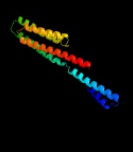
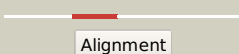
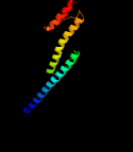

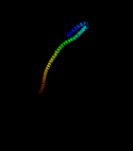
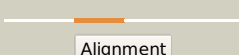


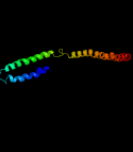


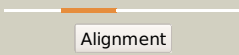
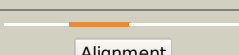

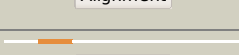
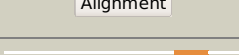
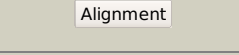
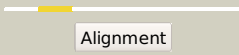



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3494c_(mce4F)_3911854_3913548
Date	Fri Aug 9 18:20:17 BST 2019
Unique Job ID	02ddfd512aaa258d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4C_</a>	 Alignment		99.9	35	<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		99.8	26	<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="#">c5uvnA_</a>	 Alignment		99.3	13	<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
4	<a href="#">c5uvnE_</a>	 Alignment		99.3	13	<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
5	<a href="#">c5uvnC_</a>	 Alignment		99.3	13	<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
6	<a href="#">c5uvnB_</a>	 Alignment		99.3	13	<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
7	<a href="#">c5uvnD_</a>	 Alignment		99.3	13	<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
8	<a href="#">c5uvnF_</a>	 Alignment		99.3	13	<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
9	<a href="#">c1qu7A_</a>	 Alignment		96.4	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
10	<a href="#">c3g67A_</a>	 Alignment		95.7	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
11	<a href="#">c6e6aB_</a>	 Alignment		95.3	13	<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

12	<a href="#">c3cwgA</a>	 Alignment		92.9	13	<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
13	<a href="#">c5xbjA</a>	 Alignment		92.7	11	<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
14	<a href="#">c4ut1A</a>	 Alignment		91.9	17	<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
15	<a href="#">c2yfaA</a>	 Alignment		91.2	13	<b>PDB header:</b> receptor <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis transducer; <b>PDBTitle:</b> x-ray structure of mcps ligand binding domain in complex with malate
16	<a href="#">c3lnrA</a>	 Alignment		90.1	9	<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
17	<a href="#">c2ch7A</a>	 Alignment		90.0	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
18	<a href="#">c3zx6A</a>	 Alignment		87.8	11	<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
19	<a href="#">c5u0pU</a>	 Alignment		83.3	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
20	<a href="#">d1quua1</a>	 Alignment		82.4	13	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
21	<a href="#">c4abxB</a>	 Alignment	not modelled	82.1	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
22	<a href="#">c3ojaB</a>	 Alignment	not modelled	82.1	13	<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
23	<a href="#">d1st6a4</a>	 Alignment	not modelled	81.1	12	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
24	<a href="#">c2j5uB</a>	 Alignment	not modelled	80.6	23	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
25	<a href="#">c4n16C</a>	 Alignment	not modelled	80.0	19	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> survival motor neuron protein; <b>PDBTitle:</b> structure of the full-length form of the protein smn found in healthy2 patients
26	<a href="#">c2qf4A</a>	 Alignment	not modelled	79.9	20	<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)
27	<a href="#">c4rh7A</a>	 Alignment	not modelled	79.3	7	<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
28	<a href="#">d1ykhb1</a>	 Alignment	not modelled	79.2	5	<b>Fold:</b> Mediator hinge subcomplex-like <b>Superfamily:</b> Mediator hinge subcomplex-like <b>Family:</b> CSE2-like

29	<a href="#">d1eq1a_</a>	Alignment	not modelled	77.5	11	<b>Fold:</b> Apolipophorin-III <b>Superfamily:</b> Apolipophorin-III <b>Family:</b> Apolipophorin-III
30	<a href="#">c1wyyB_</a>	Alignment	not modelled	76.4	14	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
31	<a href="#">c4e40A_</a>	Alignment	not modelled	75.2	5	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the haptoglobin-hemoglobin receptor of trypanosoma congolense
32	<a href="#">c2p22A_</a>	Alignment	not modelled	74.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor protein stp22 of temperature-sensitive alpha- <b>PDBTitle:</b> structure of the yeast escrt-i heterotetramer core
33	<a href="#">c1deqF_</a>	Alignment	not modelled	72.4	10	<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)
34	<a href="#">c3euhB_</a>	Alignment	not modelled	72.3	16	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome partition protein mukf; <b>PDBTitle:</b> crystal structure of the muke-mukf complex
35	<a href="#">c6b7nC_</a>	Alignment	not modelled	72.0	13	<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
36	<a href="#">c1kmiZ_</a>	Alignment	not modelled	69.8	12	<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
37	<a href="#">c2d4yA_</a>	Alignment	not modelled	69.8	11	<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)
38	<a href="#">c5j65A_</a>	Alignment	not modelled	67.4	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
39	<a href="#">c3gvmA_</a>	Alignment	not modelled	66.9	7	<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
40	<a href="#">c2dnxA_</a>	Alignment	not modelled	66.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> syntaxin-12; <b>PDBTitle:</b> solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
41	<a href="#">c6nzkB_</a>	Alignment	not modelled	66.7	11	<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
42	<a href="#">c6grjG_</a>	Alignment	not modelled	65.9	8	<b>PDB header:</b> toxin <b>Chain:</b> G: <b>PDB Molecule:</b> ahlb; <b>PDBTitle:</b> structure of the ahlb pore of the tripartite alpha-pore forming toxin,2 ahl, from aeromonas hydrophila.
43	<a href="#">c5yixA_</a>	Alignment	not modelled	65.0	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> caulobacter crescentus gcrs sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
44	<a href="#">c2wpgA_</a>	Alignment	not modelled	64.6	9	<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 (sada3, in-2 register fusion)
45	<a href="#">c3ur1C_</a>	Alignment	not modelled	64.2	11	<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.
46	<a href="#">c5wwlN_</a>	Alignment	not modelled	64.0	12	<b>PDB header:</b> cell cycle <b>Chain:</b> N: <b>PDB Molecule:</b> kinetochore protein nnf1; <b>PDBTitle:</b> crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
47	<a href="#">c3zbhC_</a>	Alignment	not modelled	63.8	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
48	<a href="#">c6gaoC_</a>	Alignment	not modelled	63.4	9	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t11 reovirus sigma1 coiled coil tail and body
49	<a href="#">c6gajA_</a>	Alignment	not modelled	61.5	7	<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 t11 reovirus sigma1 coiled coil tail (iodide)
50	<a href="#">c6g7oA_</a>	Alignment	not modelled	61.2	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline ceramidase 3,soluble cytochrome b562; <b>PDBTitle:</b> crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
51	<a href="#">c1bf5A_</a>	Alignment	not modelled	60.2	10	<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
52	<a href="#">c5i08A_</a>	Alignment	not modelled	60.0	11	<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
53	<a href="#">c2qihA_</a>	Alignment	not modelled	59.8	10	<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
						<b>Fold:</b> OB-fold

54	<a href="#">d1h9ra2</a>	Alignment	not modelled	58.6	16	<b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
55	<a href="#">c4iogD</a>	Alignment	not modelled	57.3	8	<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
56	<a href="#">c5x5bB</a>	Alignment	not modelled	57.2	13	<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
57	<a href="#">c2vs0B</a>	Alignment	not modelled	57.2	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
58	<a href="#">c6iiuA</a>	Alignment	not modelled	56.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, <b>PDBTitle:</b> crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
59	<a href="#">c4f7gB</a>	Alignment	not modelled	56.5	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> tal1n-1; <b>PDBTitle:</b> crystal structure of talin autoinhibition complex
60	<a href="#">c2ieqC</a>	Alignment	not modelled	56.5	11	<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
61	<a href="#">c1bg1A</a>	Alignment	not modelled	55.8	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (transcription factor stat3b); <b>PDBTitle:</b> transcription factor stat3b/dna complex
62	<a href="#">c5xlrC</a>	Alignment	not modelled	55.6	13	<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
63	<a href="#">c3jclC</a>	Alignment	not modelled	55.4	11	<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
64	<a href="#">d1guta</a>	Alignment	not modelled	55.0	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> Molybdate/tungstate binding protein MOP
65	<a href="#">c6cs2A</a>	Alignment	not modelled	54.5	13	<b>PDB header:</b> viral protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein,fibrinin; <b>PDBTitle:</b> sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
66	<a href="#">c4l6rA</a>	Alignment	not modelled	54.4	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562 and glucagon receptor chimera; <b>PDBTitle:</b> structure of the class b human glucagon g protein coupled receptor
67	<a href="#">c6gy8B</a>	Alignment	not modelled	54.2	10	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> xaxa; <b>PDBTitle:</b> crystal structure of xaxa from xenorhabdus nematophila
68	<a href="#">d1u5pa1</a>	Alignment	not modelled	53.7	9	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
69	<a href="#">c4lwsA</a>	Alignment	not modelled	53.5	12	<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
70	<a href="#">c1ei3C</a>	Alignment	not modelled	53.4	8	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
71	<a href="#">c5zhyA</a>	Alignment	not modelled	52.8	7	<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
72	<a href="#">c6nb3B</a>	Alignment	not modelled	52.2	13	<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)
73	<a href="#">c3s90B</a>	Alignment	not modelled	51.6	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> vinculin; <b>PDBTitle:</b> human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
74	<a href="#">c5n76C</a>	Alignment	not modelled	51.2	23	<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
75	<a href="#">d1hcia4</a>	Alignment	not modelled	50.8	8	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
76	<a href="#">c3vkhA</a>	Alignment	not modelled	50.2	13	<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
77	<a href="#">c5cwsC</a>	Alignment	not modelled	49.9	8	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> nucleoporin nsp1; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
78	<a href="#">c1zvzA</a>	Alignment	not modelled	49.7	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> vinculin; <b>PDBTitle:</b> vinculin head (0-258) in complex with the talin rod residue2 820-844
79	<a href="#">d1h9ma1</a>	Alignment	not modelled	49.0	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain

80	<a href="#">d1h9ma2</a>	Alignment	not modelled	48.1	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
81	<a href="#">d1wa8a1</a>	Alignment	not modelled	48.1	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
82	<a href="#">c1deqO</a>	Alignment	not modelled	47.3	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)
83	<a href="#">c1yv1B</a>	Alignment	not modelled	47.2	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
84	<a href="#">c5jxpA</a>	Alignment	not modelled	47.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
85	<a href="#">c3s90A</a>	Alignment	not modelled	47.0	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> vinculin; <b>PDBTitle:</b> human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
86	<a href="#">c1ei3E</a>	Alignment	not modelled	46.8	6	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
87	<a href="#">c4qkvB</a>	Alignment	not modelled	46.0	20	<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
88	<a href="#">c3fyqA</a>	Alignment	not modelled	45.8	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cg6831-pa (talin); <b>PDBTitle:</b> structure of drosophila melanogaster talin ibs2 domain (residues 1981-2 2168)
89	<a href="#">c3rfr1</a>	Alignment	not modelled	44.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> pmob; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
90	<a href="#">c5tgyA</a>	Alignment	not modelled	43.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ps1; <b>PDBTitle:</b> nmr structure of holo-ps1
91	<a href="#">c5eh4D</a>	Alignment	not modelled	43.0	36	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
92	<a href="#">c5eh4A</a>	Alignment	not modelled	43.0	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
93	<a href="#">c5eh4C</a>	Alignment	not modelled	43.0	36	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
94	<a href="#">c5eh4B</a>	Alignment	not modelled	43.0	36	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
95	<a href="#">c3dyjA</a>	Alignment	not modelled	42.9	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> taln-1; <b>PDBTitle:</b> crystal structure a talin rod fragment
96	<a href="#">c5eh6A</a>	Alignment	not modelled	42.8	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane monomer in2 lipidic cubic phase
97	<a href="#">c2mgxA</a>	Alignment	not modelled	42.4	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> steroid receptor rna activator 1; <b>PDBTitle:</b> nmr structure of sra1p c-terminal domain
98	<a href="#">c217nA</a>	Alignment	not modelled	41.8	9	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> taln-1; <b>PDBTitle:</b> nmr structure of the b domain of talin
99	<a href="#">c5t58B</a>	Alignment	not modelled	41.7	13	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> klla0e05809p; <b>PDBTitle:</b> structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
100	<a href="#">d1s35a1</a>	Alignment	not modelled	41.6	10	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
101	<a href="#">c6gy6Q</a>	Alignment	not modelled	41.2	10	<b>PDB header:</b> toxin <b>Chain:</b> Q: <b>PDB Molecule:</b> xaxa; <b>PDBTitle:</b> xaxab pore complex from xenorhabdus nematophila
102	<a href="#">c6ezvX</a>	Alignment	not modelled	41.2	13	<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
103	<a href="#">c4lwsB</a>	Alignment	not modelled	41.1	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
104	<a href="#">c5y2gA</a>	Alignment	not modelled	40.9	12	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,protein b; <b>PDBTitle:</b> structure of mbp tagged gbs camp
105	<a href="#">c6el1F</a>	Alignment	not modelled	40.8	8	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> yaxa; <b>PDBTitle:</b> yaxab pore complex
106	<a href="#">c5tvbB</a>	Alianment	not modelled	40.2	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein tpr;

						<b>PDBTitle:</b> structure of the tpr oligomerization domain
107	<a href="#">c5dfzA_</a>	Alignment	not modelled	40.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 38; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
108	<a href="#">c5wrgB_</a>	Alignment	not modelled	39.7	11	<b>PDB header:</b> virus like particle <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> sars-cov spike glycoprotein
109	<a href="#">c4qkwB_</a>	Alignment	not modelled	39.7	10	<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
110	<a href="#">c2nrjA_</a>	Alignment	not modelled	39.3	10	<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
111	<a href="#">c2iakA_</a>	Alignment	not modelled	38.8	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> bullous pemphigoid antigen 1, isoform 5; <b>PDBTitle:</b> crystal structure of a protease resistant fragment of the plakin2 domain of bullous pemphigoid antigen1 (bpag1)
112	<a href="#">c3ok8A_</a>	Alignment	not modelled	38.1	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> brain-specific angiogenesis inhibitor 1-associated protein <b>PDBTitle:</b> i-bar of pinkbar
113	<a href="#">c5x5fC_</a>	Alignment	not modelled	37.7	13	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> s protein; <b>PDBTitle:</b> prefusion structure of mers-cov spike glycoprotein, conformation 2
114	<a href="#">c5szsC_</a>	Alignment	not modelled	37.6	14	<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
115	<a href="#">c3tj5A_</a>	Alignment	not modelled	37.6	14	<b>PDB header:</b> protein binding/toxin <b>Chain:</b> A: <b>PDB Molecule:</b> vinculin; <b>PDBTitle:</b> human vinculin head domain (vh1, residues 1-258) in complex with the2 vinculin binding site of the surface cell antigen 4 (sca4-vbs-n;3 residues 412-434) from rickettsia rickettsii
116	<a href="#">c1rkeA_</a>	Alignment	not modelled	36.8	14	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> vinculin; <b>PDBTitle:</b> human vinculin head (1-258) in complex with human vinculin2 tail (879-1066)
117	<a href="#">d1wa8b1</a>	Alignment	not modelled	36.2	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
118	<a href="#">d1cuna2</a>	Alignment	not modelled	34.9	10	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
119	<a href="#">d1fr3a_</a>	Alignment	not modelled	34.9	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> Molybdate/tungstate binding protein MOP
120	<a href="#">d1t98a2</a>	Alignment	not modelled	34.3	18	<b>Fold:</b> STAT-like <b>Superfamily:</b> MukF C-terminal domain-like <b>Family:</b> MukF C-terminal domain-like