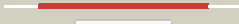
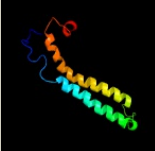

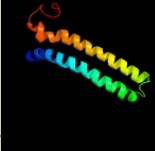
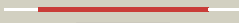
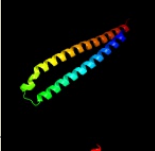





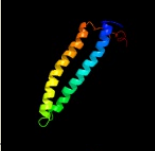



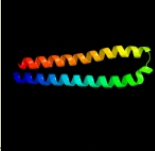



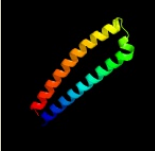



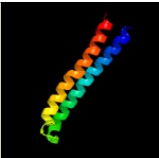
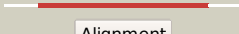

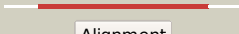
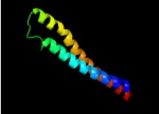







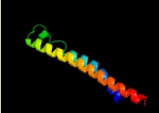

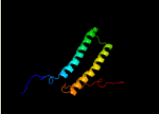
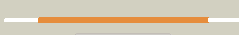
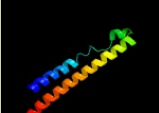

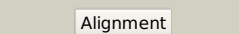
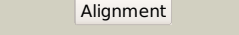

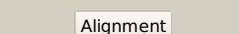


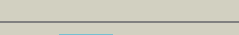


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0288\_(esxH)\_351848\_352138  
 Date Tue Jul 23 14:50:35 BST 2019  
 Unique Job ID 1249f39a097b9d28

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kg7B_</a>	 Alignment		99.9	100	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein esxh; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
2	<a href="#">d1wa8b1</a>	 Alignment		99.9	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
3	<a href="#">c4lwsA_</a>	 Alignment		99.8	18	<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
4	<a href="#">c3gvmA_</a>	 Alignment		99.8	15	<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
5	<a href="#">c3zbhC_</a>	 Alignment		99.8	13	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
6	<a href="#">d1wa8a1</a>	 Alignment		99.8	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
7	<a href="#">c4iogD_</a>	 Alignment		99.8	20	<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
8	<a href="#">c4lwsB_</a>	 Alignment		99.8	15	<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
9	<a href="#">c2vs0B_</a>	 Alignment		99.7	10	<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
10	<a href="#">c4i0xl_</a>	 Alignment		98.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J: <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
11	<a href="#">c4i0xA_</a>	 Alignment		98.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein mab_3112; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex

12	<a href="#">c3q4hB_</a>	 Alignment		98.5	66	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> low molecular weight protein antigen 7; <b>PDBTitle:</b> crystal structure of the mycobacterium smegmatis esxg complex2 (msmeg_0620-msmeg_0621)
13	<a href="#">d2g38b1</a>	 Alignment		97.5	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
14	<a href="#">c2g38B_</a>	 Alignment		97.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
15	<a href="#">d2gtsa1</a>	 Alignment		97.4	7	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> HP0062-like <b>Family:</b> HP0062-like
16	<a href="#">c3h6pD_</a>	 Alignment		97.0	83	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> esat-6-like protein esxr; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
17	<a href="#">c5xfsB_</a>	 Alignment		96.8	18	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp5 from m.2 tuberculosis
18	<a href="#">c4wj2A_</a>	 Alignment		93.5	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
19	<a href="#">c2kg7A_</a>	 Alignment		92.9	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein esxg (pe family protein); <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
20	<a href="#">c4xy3A_</a>	 Alignment		81.2	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
21	<a href="#">c5wlqA_</a>	 Alignment	not modelled	74.2	19	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid assembly scaffolding protein,myosin-7,microtubule- <b>PDBTitle:</b> crystal structure of amino acids 1677-1755 of human beta cardiac2 myosin fused to gp7 and eb1
22	<a href="#">c3h6pB_</a>	 Alignment	not modelled	69.1	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6 like protein esxs; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
23	<a href="#">d1aepa_</a>	 Alignment	not modelled	54.8	15	<b>Fold:</b> Apolipophorin-III <b>Superfamily:</b> Apolipophorin-III <b>Family:</b> Apolipophorin-III
24	<a href="#">c1ls4A_</a>	 Alignment	not modelled	54.5	15	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apolipophorin-iii; <b>PDBTitle:</b> nmr structure of apolipophorin-iii from locusta migratoria
25	<a href="#">c1wdfA_</a>	 Alignment	not modelled	46.2	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> crystal structure of mhv spike protein fusion core
26	<a href="#">c4nj1A_</a>	 Alignment	not modelled	44.5	8	<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
27	<a href="#">c6b3oB_</a>	 Alignment	not modelled	37.0	12	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
28	<a href="#">c1p68A_</a>	 Alignment	not modelled	30.5	26	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed protein s-824; <b>PDBTitle:</b> solution structure of s-824, a de novo designed four helix2 bundle

29	<a href="#">c3iv1F_</a>	Alignment	not modelled	29.1	12	<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
30	<a href="#">c4gzaA_</a>	Alignment	not modelled	27.1	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein 6; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxp2 (rv2346c-rv2347c) complex in space group c2221
31	<a href="#">d1st6a6</a>	Alignment	not modelled	26.3	8	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
32	<a href="#">c3ogiC_</a>	Alignment	not modelled	24.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative esat-6-like protein 6; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxp2 complex (rv2346c-rv2347c)
33	<a href="#">c5x5fC_</a>	Alignment	not modelled	24.8	8	<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
34	<a href="#">c6nb3B_</a>	Alignment	not modelled	23.6	8	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> mers-cov complex with human neutralizing Ica60 antibody fab fragment2 (state 1)
35	<a href="#">c6nzkB_</a>	Alignment	not modelled	23.6	10	<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
36	<a href="#">c1qu7A_</a>	Alignment	not modelled	22.8	15	<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
37	<a href="#">c4ug1A_</a>	Alignment	not modelled	22.7	11	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> gpsb n-terminal domain
38	<a href="#">c5i08A_</a>	Alignment	not modelled	21.3	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
39	<a href="#">c1nohB_</a>	Alignment	not modelled	20.5	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> head morphogenesis protein; <b>PDBTitle:</b> the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
40	<a href="#">c2bezC_</a>	Alignment	not modelled	19.6	10	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> structure of a proteolitically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein
41	<a href="#">d2j0na1</a>	Alignment	not modelled	19.2	12	<b>Fold:</b> IpaD-like <b>Superfamily:</b> IpaD-like <b>Family:</b> IpaD-like
42	<a href="#">c6gqaD_</a>	Alignment	not modelled	18.9	22	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> cell division regulator s. pneumoniae gpsb
43	<a href="#">c3jclC_</a>	Alignment	not modelled	18.6	12	<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
44	<a href="#">c2wukD_</a>	Alignment	not modelled	17.5	9	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> septum site-determining protein diviva; <b>PDBTitle:</b> diviva n-terminal domain, f17a mutant
45	<a href="#">c2pybC_</a>	Alignment	not modelled	17.4	13	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> neutrophil activating protein; <b>PDBTitle:</b> napa protein from borrelia burgdorferi
46	<a href="#">c5xlrC_</a>	Alignment	not modelled	16.6	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
47	<a href="#">c3vp8B_</a>	Alignment	not modelled	16.0	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general transcriptional corepressor tup1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the yeast general2 corepressor tup1p
48	<a href="#">c1zvaA_</a>	Alignment	not modelled	14.4	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> a structure-based mechanism of sars virus membrane fusion
49	<a href="#">c5wrgB_</a>	Alignment	not modelled	14.1	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
50	<a href="#">c5lkdB_</a>	Alignment	not modelled	14.1	6	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase omega-like 2; <b>PDBTitle:</b> crystal structure of the xi glutathione transferase ecm4 from2 saccharomyces cerevisiae in complex with glutathione
51	<a href="#">c5uxtA_</a>	Alignment	not modelled	13.6	16	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad; <b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad
52	<a href="#">c3ok8A_</a>	Alignment	not modelled	13.5	13	<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
53	<a href="#">c3g67A_</a>	Alignment	not modelled	13.0	8	<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
54	<a href="#">c6cs2A_</a>	Alignment	not modelled	12.9	10	<b>PDB header:</b> viral protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein,fibrin; <b>PDBTitle:</b> sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
55	<a href="#">d1icha_</a>	Alignment	not modelled	12.8	6	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain

						<b>Family:</b> DEATH domain, DD
56	<a href="#">c1ichA_</a>	Alignment	not modelled	12.8	6	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor-1; <b>PDBTitle:</b> solution structure of the tumor necrosis factor receptor-12 death domain
57	<a href="#">d1h6ga1</a>	Alignment	not modelled	12.8	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
58	<a href="#">c2of5K_</a>	Alignment	not modelled	12.3	11	<b>PDB header:</b> apoptosis <b>Chain:</b> K: <b>PDB Molecule:</b> leucine-rich repeat and death domain-containing protein; <b>PDBTitle:</b> oligomeric death domain complex
59	<a href="#">c2pnvA_</a>	Alignment	not modelled	12.2	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> small conductance calcium-activated potassium <b>PDBTitle:</b> crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
60	<a href="#">c3viqC_</a>	Alignment	not modelled	11.6	4	<b>PDB header:</b> recombination activator <b>Chain:</b> C: <b>PDB Molecule:</b> swi5-dependent recombination dna repair protein 1; <b>PDBTitle:</b> crystal structure of swi5-sfr1 complex from fission yeast
61	<a href="#">c2ym0B_</a>	Alignment	not modelled	10.9	12	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> cell invasion protein sipd; <b>PDBTitle:</b> truncated sipd from salmonella typhimurium
62	<a href="#">c1wyyB_</a>	Alignment	not modelled	10.7	10	<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
63	<a href="#">c1nfoA_</a>	Alignment	not modelled	10.3	6	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein e2; <b>PDBTitle:</b> apolipoprotein e2 (apoe2, d154a mutation)
64	<a href="#">c4y66D_</a>	Alignment	not modelled	10.2	7	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> putative tbp family protein; <b>PDBTitle:</b> crystal structure of giardia lamblia hop2-mnd1 complex
65	<a href="#">c3cazA_</a>	Alignment	not modelled	10.0	8	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bar protein; <b>PDBTitle:</b> crystal structure of a bar protein from galdieria sulphuraria
66	<a href="#">c3whlB_</a>	Alignment	not modelled	10.0	3	<b>PDB header:</b> hydrolase/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> probable 26s proteasome regulatory subunit p27; <b>PDBTitle:</b> crystal structure of nas2 n-terminal domain complexed with pan-rpt5c2 chimera
67	<a href="#">c5x5bB_</a>	Alignment	not modelled	9.9	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
68	<a href="#">c2yy0D_</a>	Alignment	not modelled	9.5	6	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> c-myc-binding protein; <b>PDBTitle:</b> crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
69	<a href="#">c2p90B_</a>	Alignment	not modelled	9.2	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein cgl1923; <b>PDBTitle:</b> the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
70	<a href="#">d1h6gb1</a>	Alignment	not modelled	9.0	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
71	<a href="#">c2ieqC_</a>	Alignment	not modelled	8.6	8	<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
72	<a href="#">c6h9mA_</a>	Alignment	not modelled	8.3	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil domain-containing protein 90b, mitochondrial, <b>PDBTitle:</b> coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor
73	<a href="#">c5ijnS_</a>	Alignment	not modelled	8.1	7	<b>PDB header:</b> transport protein <b>Chain:</b> S: <b>PDB Molecule:</b> nuclear pore complex protein nup58; <b>PDBTitle:</b> composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
74	<a href="#">c3tnuA_</a>	Alignment	not modelled	8.1	12	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> keratin, type i cytoskeletal 14; <b>PDBTitle:</b> heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
75	<a href="#">c1kmiZ_</a>	Alignment	not modelled	7.9	10	<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
76	<a href="#">d2p90a1</a>	Alignment	not modelled	7.8	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Cgl1923-like <b>Family:</b> Cgl1923-like
77	<a href="#">c6cv0C_</a>	Alignment	not modelled	7.7	4	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
78	<a href="#">c3swfA_</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-gated cation channel alpha-1; <b>PDBTitle:</b> cnga1 621-690 containing clz domain
79	<a href="#">c2j0oA_</a>	Alignment	not modelled	7.1	12	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> invasin ipad; <b>PDBTitle:</b> shigella flexneri ipad
80	<a href="#">d2j0oa1</a>	Alignment	not modelled	7.1	12	<b>Fold:</b> lpad-like <b>Superfamily:</b> lpad-like <b>Family:</b> lpad-like
						<b>PDB header:</b> structural protein

81	<a href="#">c2oszA_</a>	Alignment	not modelled	7.0	7	<b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin p58/p45; <b>PDBTitle:</b> structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
82	<a href="#">c3ci9B_</a>	Alignment	not modelled	6.8	3	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock factor-binding protein 1; <b>PDBTitle:</b> crystal structure of the human hsbp1
83	<a href="#">d1eq1a_</a>	Alignment	not modelled	6.7	6	<b>Fold:</b> Apolipoporphin-III <b>Superfamily:</b> Apolipoporphin-III <b>Family:</b> Apolipoporphin-III
84	<a href="#">d1gqaa_</a>	Alignment	not modelled	6.6	10	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Cytochromes <b>Family:</b> Cytochrome c'-like
85	<a href="#">c3n8uB_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> imelysin peptidase; <b>PDBTitle:</b> crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution
86	<a href="#">c2c6rA_</a>	Alignment	not modelled	6.3	15	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding stress response protein, dps family; <b>PDBTitle:</b> fe-soaked crystal structure of the dps92 from deinococcus2 radiodurans
87	<a href="#">c4modB_</a>	Alignment	not modelled	6.0	8	<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
88	<a href="#">c4iffC_</a>	Alignment	not modelled	5.8	19	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> fusion of phage phi29 gp7 protein and cell division protein <b>PDBTitle:</b> structural organization of ftsb, a transmembrane protein of the2 bacterial divisome
89	<a href="#">c1zv8l_</a>	Alignment	not modelled	5.6	11	<b>PDB header:</b> viral protein <b>Chain:</b> I: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> a structure-based mechanism of sars virus membrane fusion
90	<a href="#">c3kltB_</a>	Alignment	not modelled	5.5	9	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of a vimentin fragment
91	<a href="#">d2fjca1</a>	Alignment	not modelled	5.4	11	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
92	<a href="#">c3ogiD_</a>	Alignment	not modelled	5.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative esat-6-like protein 7; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esoxp2 complex (rv2346c-rv2347c)