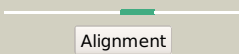

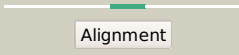
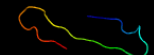
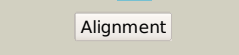
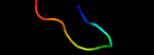
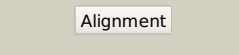
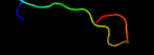
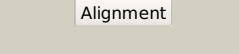
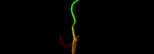
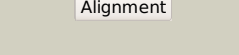
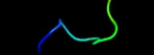
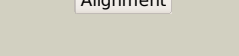

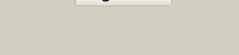





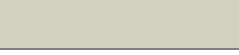

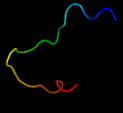







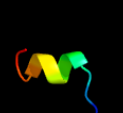


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1274\_(lprB)\_1424203\_1424760  
 Date Wed Jul 31 22:05:36 BST 2019  
 Unique Job ID 14ebf3300f73e5e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2re3A_</a>	 Alignment		47.6	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
2	<a href="#">d2b5ic2</a>	 Alignment		43.4	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
3	<a href="#">c2ra9A_</a>	 Alignment		34.6	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein duf1285; <b>PDBTitle:</b> crystal structure of a duf1285 family protein (sba1_2486) from2 shewanella baltica os155 at 1.40 a resolution
4	<a href="#">c2h0pA_</a>	 Alignment		34.4	37	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> nmr structure of the dengue-4 virus envelope protein domain2 iii
5	<a href="#">c2jqmA_</a>	 Alignment		31.1	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> envelope protein e; <b>PDBTitle:</b> yellow fever envelope protein domain iii nmr structure2 (s288-k398)
6	<a href="#">d1cc5a_</a>	 Alignment		21.8	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
7	<a href="#">d1e2rb1</a>	 Alignment		21.2	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
8	<a href="#">c2lqvA_</a>	 Alignment		20.0	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein yebf; <b>PDBTitle:</b> yebf
9	<a href="#">c3d8mA_</a>	 Alignment		18.6	18	<b>PDB header:</b> virus/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> baseplate protein, receptor binding protein; <b>PDBTitle:</b> crystal structure of a chimeric receptor binding protein from2 lactococcal phages subspecies tp901-1 and p2
10	<a href="#">d1lqsa1</a>	 Alignment		17.7	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
11	<a href="#">c4dixA_</a>	 Alignment		16.9	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> plectin-related protein; <b>PDBTitle:</b> crystal structure of the ig-ph domain of actin-binding protein scab1

12	<a href="#">c6iczX</a>	Alignment		16.2	4	<b>PDB header:</b> splicing <b>Chain:</b> X: <b>PDB Molecule:</b> prkr-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
13	<a href="#">c4j20B</a>	Alignment		16.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c-555; <b>PDBTitle:</b> x-ray structure of the cytochrome c-554 from chlorobaculum tepidum
14	<a href="#">d1kx7a</a>	Alignment		14.4	17	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
15	<a href="#">d1s6na</a>	Alignment		13.5	32	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Class II viral fusion proteins C-terminal domain
16	<a href="#">c4e6kG</a>	Alignment		11.2	24	<b>PDB header:</b> metal binding protein/electron transport <b>Chain:</b> G: <b>PDB Molecule:</b> bacterioferritin-associated ferredoxin; <b>PDBTitle:</b> 2.0 a resolution structure of pseudomonas aeruginosa bacterioferritin2 (bfrb) in complex with bacterioferritin associated ferredoxin (bfd)
17	<a href="#">c2ch8A</a>	Alignment		11.1	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> 33 kda early protein; <b>PDBTitle:</b> structure of the epstein-barr virus oncogene barf1
18	<a href="#">d2htja1</a>	Alignment		11.0	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FaeA-like
19	<a href="#">c1q1hA</a>	Alignment		10.8	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor e; <b>PDBTitle:</b> an extended winged helix domain in general transcription2 factor e/lie alpha
20	<a href="#">d1q1ha</a>	Alignment		10.8	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcription factor E/lie-alpha, N-terminal domain
21	<a href="#">c3l12A</a>	Alignment	not modelled	10.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution
22	<a href="#">d2jell2</a>	Alignment	not modelled	10.7	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
23	<a href="#">c3b5hB</a>	Alignment	not modelled	10.3	16	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> cervical emmprin; <b>PDBTitle:</b> crystal structure of the extracellular portion of hab18g/cd147
24	<a href="#">c4e6kI</a>	Alignment	not modelled	10.2	31	<b>PDB header:</b> metal binding protein/electron transport <b>Chain:</b> I: <b>PDB Molecule:</b> bacterioferritin-associated ferredoxin; <b>PDBTitle:</b> 2.0 a resolution structure of pseudomonas aeruginosa bacterioferritin2 (bfrb) in complex with bacterioferritin associated ferredoxin (bfd)
25	<a href="#">c2x3hA</a>	Alignment	not modelled	10.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> k5 lyase; <b>PDBTitle:</b> coliphage k5a lyase
26	<a href="#">d2i06a1</a>	Alignment	not modelled	10.0	21	<b>Fold:</b> Replication terminator protein (Tus) <b>Superfamily:</b> Replication terminator protein (Tus) <b>Family:</b> Replication terminator protein (Tus)
27	<a href="#">d1h9xa1</a>	Alignment	not modelled	9.9	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
28	<a href="#">d1eapb2</a>	Alignment	not modelled	9.6	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin

						<b>Family:</b> C1 set domains (antibody constant domain-like)
29	<a href="#">c1x9qA</a>	Alignment	not modelled	9.6	17	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> 4m5.3 anti-fluorescein single chain antibody fragment; <b>PDBTitle:</b> 4m5.3 anti-fluorescein single chain antibody fragment (scfv)
30	<a href="#">d1sm3h2</a>	Alignment	not modelled	9.5	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
31	<a href="#">d2ck0I2</a>	Alignment	not modelled	9.5	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
32	<a href="#">c4oi6A</a>	Alignment	not modelled	9.4	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nickel responsive protein; <b>PDBTitle:</b> crystal structure analysis of nickel-bound form sco4226 from2 streptomyces coelicolor a3(2)
33	<a href="#">d1igtb4</a>	Alignment	not modelled	9.3	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
34	<a href="#">c4jvwD</a>	Alignment	not modelled	9.2	17	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> sig mu chain c region secreted form; <b>PDBTitle:</b> igm c4-domain from mouse
35	<a href="#">c2xksA</a>	Alignment	not modelled	9.1	0	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> prion-like conversion during amyloid formation at atomic resolution
36	<a href="#">c5npiB</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> single chain variable fragment of the non-neutralizing <b>PDBTitle:</b> structure of the hepatitis c virus strain j4 glycoprotein e2 antigenic2 region 532-540 bound to the single chain variable fragment of the3 non-neutralizing antibody dao5
37	<a href="#">c2vifA</a>	Alignment	not modelled	9.1	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of cytokine signalling 6; <b>PDBTitle:</b> crystal structure of socs6 sh2 domain in complex with a c-kit2 phosphopeptide
38	<a href="#">c2druA</a>	Alignment	not modelled	9.0	23	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of cd48 antigen and t-cell surface antigen cd2; <b>PDBTitle:</b> crystal structure and binding properties of the cd2 and cd244 (2b4)2 binding protein, cd48
39	<a href="#">c1cczA</a>	Alignment	not modelled	9.0	23	<b>PDB header:</b> glycoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (cd58); <b>PDBTitle:</b> crystal structure of the cd2-binding domain of cd58 (lymphocyte2 function-associated antigen 3) at 1.8-a resolution
40	<a href="#">c2xglB</a>	Alignment	not modelled	8.8	25	<b>PDB header:</b> antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> colicin-m immunity protein; <b>PDBTitle:</b> the x-ray structure of the escherichia coli colicin m immunity protein2 demonstrates the presence of a disulphide bridge, which is3 functionally essential
41	<a href="#">d1deeb2</a>	Alignment	not modelled	8.6	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
42	<a href="#">c4o2hB</a>	Alignment	not modelled	8.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein bcam1869; <b>PDBTitle:</b> crystal structure of bcam1869 protein (rsam homolog) from burkholderia2 cenocepacia
43	<a href="#">d1uwel2</a>	Alignment	not modelled	8.5	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
44	<a href="#">c2jpwA</a>	Alignment	not modelled	8.3	32	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin i, cardiac muscle; <b>PDBTitle:</b> solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
45	<a href="#">c2x89F</a>	Alignment	not modelled	7.9	0	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> structure of the beta2_microglobulin involved in amyloidogenesis
46	<a href="#">d1bfoa2</a>	Alignment	not modelled	7.9	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
47	<a href="#">d1igyb4</a>	Alignment	not modelled	7.8	7	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
48	<a href="#">c5aonB</a>	Alignment	not modelled	7.6	27	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
49	<a href="#">d1mjul2</a>	Alignment	not modelled	7.5	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
50	<a href="#">d1bfob2</a>	Alignment	not modelled	7.4	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
51	<a href="#">c2pxgA</a>	Alignment	not modelled	7.4	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein; <b>PDBTitle:</b> nmr solution structure of omla
52	<a href="#">c4qycA</a>	Alignment	not modelled	7.4	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> carcinoembryonic antigen-related cell adhesion molecule 1, <b>PDBTitle:</b> crystal structure of the chimeric protein human ceacam1: human tim32 membrane distal amino terminal (n)-domain
53	<a href="#">d2ouwa1</a>	Alignment	not modelled	7.2	20	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> ITHA0727-like

54	<a href="#">c3alxB_</a>	Alignment	not modelled	7.2	22	<b>PDB header:</b> viral protein/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin,linker,cdw150; <b>PDBTitle:</b> crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (mv-h(1482r)-slam(n102h/r108y) fusion)
55	<a href="#">c2li5B_</a>	Alignment	not modelled	7.1	38	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme atg7; <b>PDBTitle:</b> nmr structure of atg8-atg7c30 complex
56	<a href="#">d1mhca1</a>	Alignment	not modelled	7.0	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
57	<a href="#">c3fomB_</a>	Alignment	not modelled	7.0	17	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of the class i mhc molecule h-2kwm7 with a single2 self peptide iqqsierl
58	<a href="#">c3fonD_</a>	Alignment	not modelled	7.0	17	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of the class i mhc molecule h-2kwm7 with a single2 self peptide vndifeai
59	<a href="#">d1c5cl2</a>	Alignment	not modelled	7.0	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
60	<a href="#">d2i8ga1</a>	Alignment	not modelled	6.9	19	<b>Fold:</b> Mog1p/PsbP-like <b>Superfamily:</b> Mog1p/PsbP-like <b>Family:</b> DIP2269-like
61	<a href="#">c3rwgB_</a>	Alignment	not modelled	6.9	0	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> rhesus macaque mhc class i molecule mamu-b*17-mw9
62	<a href="#">d1q72l2</a>	Alignment	not modelled	6.8	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
63	<a href="#">c2jtdA_</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> myomesin-1; <b>PDBTitle:</b> skelemin immunoglobulin c2 like domain 4
64	<a href="#">d1lk3l2</a>	Alignment	not modelled	6.7	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
65	<a href="#">d1s9va1</a>	Alignment	not modelled	6.7	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
66	<a href="#">d1pg7w2</a>	Alignment	not modelled	6.7	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
67	<a href="#">d1nira1</a>	Alignment	not modelled	6.6	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
68	<a href="#">d2fb4l2</a>	Alignment	not modelled	6.6	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
69	<a href="#">d1hdmb1</a>	Alignment	not modelled	6.5	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
70	<a href="#">d1mjuh2</a>	Alignment	not modelled	6.5	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
71	<a href="#">d1pskh2</a>	Alignment	not modelled	6.5	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
72	<a href="#">d1rzfl2</a>	Alignment	not modelled	6.4	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
73	<a href="#">c2mbhB_</a>	Alignment	not modelled	6.4	40	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> krueppel-like factor 1; <b>PDBTitle:</b> nmr structure of ekf(22-40)/ubiquitin complex
74	<a href="#">c3shsA_</a>	Alignment	not modelled	6.4	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hoc head outer capsid protein; <b>PDBTitle:</b> three n-terminal domains of the bacteriophage rb49 highly immunogenic2 outer capsid protein (hoc)
75	<a href="#">c4jgJB_</a>	Alignment	not modelled	6.3	43	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> carcinoembryonic antigen-related cell adhesion molecule 15; <b>PDBTitle:</b> crystal structure of the ig-like d1 domain from mouse2 carcinoembryogenic antigen-related cell adhesion molecule 153 (ceacam15) [psi-nysgrc-005691]
76	<a href="#">d1zs8a1</a>	Alignment	not modelled	6.3	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
77	<a href="#">d1l6xa2</a>	Alignment	not modelled	6.2	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
78	<a href="#">d1mo9a3</a>	Alignment	not modelled	6.2	15	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
79	<a href="#">d1osph2</a>	Alignment	not modelled	6.2	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)

80	<a href="#">d1lk2a1</a>	Alignment	not modelled	6.1	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
81	<a href="#">c5l87A_</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
82	<a href="#">c1cqkqB_</a>	Alignment	not modelled	6.1	8	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> ch3 domain of mak33 antibody; <b>PDBTitle:</b> crystal structure of the ch3 domain from the mak33 antibody
83	<a href="#">c1cqkqA_</a>	Alignment	not modelled	6.1	8	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> ch3 domain of mak33 antibody; <b>PDBTitle:</b> crystal structure of the ch3 domain from the mak33 antibody
84	<a href="#">d1cqka_</a>	Alignment	not modelled	6.1	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
85	<a href="#">c4liqC_</a>	Alignment	not modelled	6.1	25	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> beta-2-microglobulin, mhc class i-related protein; <b>PDBTitle:</b> crystal structure of a human mait tcr in complex with bovine mr1
86	<a href="#">c2mqsd_</a>	Alignment	not modelled	6.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> thp_t_chain; <b>PDBTitle:</b> transient collagen triple helix binding to a key metalloproteinase in2 invasion and development: spin labels to structure
87	<a href="#">d1zxqa1</a>	Alignment	not modelled	5.9	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
88	<a href="#">d1nfde2</a>	Alignment	not modelled	5.9	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
89	<a href="#">d2gysa1</a>	Alignment	not modelled	5.9	27	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
90	<a href="#">c2z0IA_</a>	Alignment	not modelled	5.9	15	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> early antigen protein d; <b>PDBTitle:</b> crystal structure of ebv-dna polymerase accessory protein2 bmrfl
91	<a href="#">c2zswD_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of h-2kb in complex with the q600y variant of jhmv2 epitope s598
92	<a href="#">c2zolB_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of h-2db in complex with the w513s variant of jhmv2 epitope s510
93	<a href="#">c2zswB_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of h-2kb in complex with the q600y variant of jhmv2 epitope s598
94	<a href="#">c1zt1B_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of class i mhc h-2kk in complex with an2 octapeptide
95	<a href="#">c3pqyQ_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> Q: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of 6218 tcr in complex with the h2db-pa224
96	<a href="#">c3pqyL_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> L: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of 6218 tcr in complex with the h2db-pa224
97	<a href="#">c2zswH_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> H: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of h-2kb in complex with the q600y variant of jhmv2 epitope s598
98	<a href="#">c1kpvB_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> high resolution crystal structure of the mhc class i complex h-2 2kb/sev9
99	<a href="#">c2zswF_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of h-2kb in complex with the q600y variant of jhmv2 epitope s598