
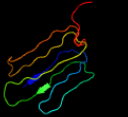


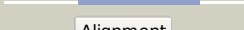


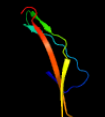

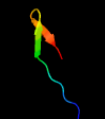

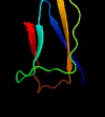
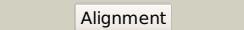

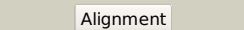

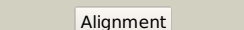

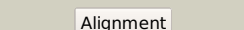

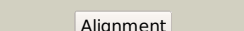



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0677c\_(mmpS5)\_778480\_778908  
 Date Fri Jul 26 01:50:24 BST 2019  
 Unique Job ID fdbdac23df1486c9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2lw3A_</a>	 Alignment		100.0	51	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein mmps4; <b>PDBTitle:</b> solution structure of the soluble domain of mmps4 from mycobacterium2 tuberculosis
2	<a href="#">d1qqda1</a>	 Alignment		27.0	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
3	<a href="#">d1fv1b1</a>	 Alignment		25.3	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
4	<a href="#">d3d85d2</a>	 Alignment		24.4	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
5	<a href="#">d1kona_</a>	 Alignment		23.4	25	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
6	<a href="#">d1muja1</a>	 Alignment		22.3	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
7	<a href="#">d1d5mb1</a>	 Alignment		21.4	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
8	<a href="#">d1ok0a_</a>	 Alignment		21.2	14	<b>Fold:</b> alpha-Amylase inhibitor tendamistat <b>Superfamily:</b> alpha-Amylase inhibitor tendamistat <b>Family:</b> alpha-Amylase inhibitor tendamistat
9	<a href="#">c3osvC_</a>	 Alignment		19.7	15	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> flagellar basal-body rod modification protein flgd; <b>PDBTitle:</b> the crytsal structure of flgd from p. aeruginosa
10	<a href="#">c4f3qA_</a>	 Alignment		17.9	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein cbu_1566; <b>PDBTitle:</b> structure of a yebc family protein (cbu_1566) from coxiella burnetii
11	<a href="#">d1c16a1</a>	 Alignment		17.6	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)

12	<a href="#">c5t9gD_</a>	Alignment		17.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glycoside hydrolase; <b>PDBTitle:</b> crystal structure of bugh2cwt in complex with galactoisofagomine
13	<a href="#">c2kerA_</a>	Alignment		17.3	20	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase inhibitor z-2685; <b>PDBTitle:</b> alpha-amylase inhibitor parvulstat (z-2685) from2 streptomyces parvulus
14	<a href="#">d1uvqb1</a>	Alignment		16.6	9	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
15	<a href="#">c3rolA_</a>	Alignment		16.4	18	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> h-2 class i histocompatibility antigen, k-b alpha chain; <b>PDBTitle:</b> murine class i major histocompatibility complex h-2kb in complex with2 post-translationally modified lcmv-derived gp34-41 peptide,3 comprising a nitrotyrosine at position 3
16	<a href="#">d1mw7a_</a>	Alignment		16.3	19	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
17	<a href="#">d1de4a1</a>	Alignment		16.1	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
18	<a href="#">d1neza1</a>	Alignment		15.8	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
19	<a href="#">d1k8da1</a>	Alignment		15.8	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
20	<a href="#">c5e09A_</a>	Alignment		15.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> structural insight of a trimodular halophilic cellulase with a family2 46 carbohydrate-binding module
21	<a href="#">c2amnA_</a>	Alignment	not modelled	15.2	57	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> cathelicidin; <b>PDBTitle:</b> solution structure of fowlicidin-1, a novel cathelicidin2 antimicrobial peptide from chicken
22	<a href="#">c2kvzA_</a>	Alignment	not modelled	14.9	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ispe; <b>PDBTitle:</b> structure of residues 161-235 of putative peptidoglycan binding2 protein lmo0835 from listeria monocytogenes: target lmr64b of the3 northeast structural genomics consortium
23	<a href="#">d1k5na1</a>	Alignment	not modelled	14.7	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
24	<a href="#">c5ee2A_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> hemoglobin-haptoglobin-utilization protein; <b>PDBTitle:</b> the crystal structure of the c-terminal beta-barrel of hpua from2 neisseria gonorrhoeae
25	<a href="#">d1vgka1</a>	Alignment	not modelled	14.1	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
26	<a href="#">d1kska3</a>	Alignment	not modelled	13.9	55	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Pseudouridine synthase RsuA N-terminal domain
27	<a href="#">c5aeoA_</a>	Alignment	not modelled	13.6	27	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> r. equi vapg protein; <b>PDBTitle:</b> virulence-associated protein vapg from the intracellular2 pathogen rhodococcus equi
28	<a href="#">c1sebB_</a>	Alignment	not modelled	12.4	11	<b>PDB header:</b> complex (mhc ii/peptide/toxin) <b>Chain:</b> B: <b>PDB Molecule:</b> hla class ii histocompatibility antigen; <b>PDBTitle:</b> complex of the human mhc class ii glycoprotein hla-dr1 and2 the bacterial superantigen seb

29	<a href="#">d2fa8a1</a>	Alignment	not modelled	12.4	42	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Selenoprotein W-related
30	<a href="#">d1lfpa_</a>	Alignment	not modelled	12.3	21	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
31	<a href="#">d1hx0a1</a>	Alignment	not modelled	12.0	17	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
32	<a href="#">c2zw3B_</a>	Alignment	not modelled	12.0	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> gap junction beta-2 protein; <b>PDBTitle:</b> structure of the connexin-26 gap junction channel at 3.52 angstrom resolution
33	<a href="#">c2obkE_</a>	Alignment	not modelled	12.0	47	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> selt/selw/selh selenoprotein domain; <b>PDBTitle:</b> x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
34	<a href="#">d3dhpa1</a>	Alignment	not modelled	11.3	20	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
35	<a href="#">c6b6B_</a>	Alignment	not modelled	11.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 2, sugar binding domain protein; <b>PDBTitle:</b> the crystal structure of glycosyl hydrolase family 2 (gh2) member from2 bacteroides cellulosilyticus dsm 14838
36	<a href="#">d1fnga1</a>	Alignment	not modelled	10.9	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
37	<a href="#">d1kjva1</a>	Alignment	not modelled	10.7	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
38	<a href="#">c6dxuA_</a>	Alignment	not modelled	10.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase family 2, tim barrel domain protein; <b>PDBTitle:</b> crystal structure of parabacteroides merdae beta-glucuronidase (gus)
39	<a href="#">d1uvqa1</a>	Alignment	not modelled	10.5	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
40	<a href="#">d1ywkA1</a>	Alignment	not modelled	10.4	38	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Kdul-like
41	<a href="#">c5lnkm_</a>	Alignment	not modelled	10.3	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> mitochondrial complex i, nd4 subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
42	<a href="#">c6d1pB_</a>	Alignment	not modelled	10.3	4	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolases family 2, sugar binding domain protein; <b>PDBTitle:</b> apo structure of bacteroides uniformis beta-glucuronidase 3
43	<a href="#">c3usaH_</a>	Alignment	not modelled	10.0	14	<b>PDB header:</b> immune system <b>Chain:</b> H: <b>PDB Molecule:</b> hla class ii histocompatibility antigen, do beta chain; <b>PDBTitle:</b> mhc class ii homolog structure
44	<a href="#">c6dxuB_</a>	Alignment	not modelled	9.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 2, tim barrel domain protein; <b>PDBTitle:</b> crystal structure of parabacteroides merdae beta-glucuronidase (gus)
45	<a href="#">d1zs8a1</a>	Alignment	not modelled	9.7	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
46	<a href="#">c3owrA_</a>	Alignment	not modelled	9.7	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative secreted protein (bf4250) from2 bacteroides fragilis nctc 9343 at 1.81 a resolution
47	<a href="#">c2kncA_</a>	Alignment	not modelled	9.7	29	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
48	<a href="#">c2kt7A_</a>	Alignment	not modelled	9.4	25	<b>PDB header:</b> cell adhesion, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidoglycan bound protein (lpxtg) <b>PDBTitle:</b> solution nmr structure of mucin-binding domain of protein2 lmo0835 from listeria monocytogenes, northeast structural3 genomics consortium target lmr64a
49	<a href="#">d1mhca1</a>	Alignment	not modelled	9.3	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
50	<a href="#">c2mgyA_</a>	Alignment	not modelled	9.1	28	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> translocator protein; <b>PDBTitle:</b> solution structure of the mitochondrial translocator protein (tspo) in2 complex with its high-affinity ligand pk11195
51	<a href="#">c1ywkE_</a>	Alignment	not modelled	9.0	38	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-deoxy-l-threo-5-hexosulose-uronate ketol- <b>PDBTitle:</b> crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
52	<a href="#">d1wbxa1</a>	Alignment	not modelled	8.9	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
53	<a href="#">c1q40C_</a>	Alignment	not modelled	8.8	33	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> mrna transport regulator mtr2; <b>PDBTitle:</b> crystal structure of the c. albicans mtr2-mex67 m domain

						complex
54	<a href="#">c4hhuA</a>	Alignment	not modelled	8.8	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> or280; <b>PDBTitle:</b> crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
55	<a href="#">d1s9va1</a>	Alignment	not modelled	8.8	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
56	<a href="#">c2p0gB</a>	Alignment	not modelled	8.8	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> selenoprotein w-related protein; <b>PDBTitle:</b> crystal structure of selenoprotein w-related protein from vibrio2 cholerae. northeast structural genomics target vcr75
57	<a href="#">d1klub1</a>	Alignment	not modelled	8.8	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
58	<a href="#">d1lk2a1</a>	Alignment	not modelled	8.7	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
59	<a href="#">d1es0b1</a>	Alignment	not modelled	8.7	7	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
60	<a href="#">c4kw3A</a>	Alignment	not modelled	8.5	29	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> ns1; <b>PDBTitle:</b> crystal structure of the non-structural protein 1 n-terminal origin-2 recognition/nickase domain from the emerging human bocavirus
61	<a href="#">d1u8ib2</a>	Alignment	not modelled	8.5	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
62	<a href="#">d1dr9a2</a>	Alignment	not modelled	8.3	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
63	<a href="#">d2cs4a1</a>	Alignment	not modelled	8.2	35	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
64	<a href="#">d1xrua1</a>	Alignment	not modelled	8.1	63	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Kdul-like
65	<a href="#">c3usaG</a>	Alignment	not modelled	8.1	10	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> hla class ii histocompatibility antigen, do alpha chain; <b>PDBTitle:</b> mhc class ii homolog structure
66	<a href="#">d2rb6a1</a>	Alignment	not modelled	7.8	22	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Ygd/YgdR-like
67	<a href="#">c3gebC</a>	Alignment	not modelled	7.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> eyes absent homolog 2; <b>PDBTitle:</b> crystal structure of edeya2
68	<a href="#">d1fngb1</a>	Alignment	not modelled	7.7	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
69	<a href="#">c2vdaB</a>	Alignment	not modelled	7.5	35	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> smaltoporin; <b>PDBTitle:</b> solution structure of the seca-signal peptide complex
70	<a href="#">d1jaea1</a>	Alignment	not modelled	7.4	21	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
71	<a href="#">d1jk8a1</a>	Alignment	not modelled	7.4	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
72	<a href="#">d1i4fa1</a>	Alignment	not modelled	7.3	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
73	<a href="#">d1dmla1</a>	Alignment	not modelled	7.3	20	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
74	<a href="#">c2nykA</a>	Alignment	not modelled	7.2	30	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> m157; <b>PDBTitle:</b> crystal structure of m157 from mouse cytomegalovirus
75	<a href="#">d1of5b</a>	Alignment	not modelled	6.9	27	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> NTF2-like
76	<a href="#">c4ypjB</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta galactosidase; <b>PDBTitle:</b> x-ray structure of the mutant of glycoside hydrolase
77	<a href="#">c2kppA</a>	Alignment	not modelled	6.7	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin0431 protein; <b>PDBTitle:</b> solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
78	<a href="#">d1k8ib1</a>	Alignment	not modelled	6.6	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
79	<a href="#">d1sawa</a>	Alignment	not modelled	6.6	22	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
80	<a href="#">c4ux5B</a>	Alignment	not modelled	6.5	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor mbp1; <b>PDBTitle:</b> structure of dna complex of pcg2

81	<a href="#">c6mhqE_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> gap junction alpha-3 protein, connexin-46; <b>PDBTitle:</b> structure of connexin-46 intercellular gap junction channel at 3.42 angstrom resolution by cryoem
82	<a href="#">d1dgja2</a>	Alignment	not modelled	6.3	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
83	<a href="#">c3a0hj_</a>	Alignment	not modelled	6.2	60	<b>PDB header:</b> electron transport <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
84	<a href="#">d2axtj1</a>	Alignment	not modelled	6.2	60	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, Psbj <b>Family:</b> Psbj-like
85	<a href="#">c1iebD_</a>	Alignment	not modelled	6.2	10	<b>PDB header:</b> histocompatibility antigen <b>Chain:</b> D; <b>PDB Molecule:</b> mhc class ii i-ek; <b>PDBTitle:</b> histocompatibility antigen
86	<a href="#">c2na6C_</a>	Alignment	not modelled	6.2	13	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
87	<a href="#">c2na6B_</a>	Alignment	not modelled	6.2	13	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
88	<a href="#">c2na6A_</a>	Alignment	not modelled	6.2	13	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
89	<a href="#">d1hyrc1</a>	Alignment	not modelled	6.2	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
90	<a href="#">d2oz4a2</a>	Alignment	not modelled	6.1	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
91	<a href="#">d1vlba2</a>	Alignment	not modelled	6.1	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
92	<a href="#">c2ojlB_</a>	Alignment	not modelled	6.0	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
93	<a href="#">d1iaka1</a>	Alignment	not modelled	6.0	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
94	<a href="#">c4gdzA_</a>	Alignment	not modelled	5.9	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4251 family protein (bacegg_02002) from2 bacteroides eggerthii dsm 20697 at 1.95 a resolution
95	<a href="#">c2npbA_</a>	Alignment	not modelled	5.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> selenoprotein w; <b>PDBTitle:</b> nmr solution structure of mouse selw
96	<a href="#">d1vcaa1</a>	Alignment	not modelled	5.9	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
97	<a href="#">c3s6pC_</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> virus <b>Chain:</b> C; <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> crystal structure of helicoverpa armigera stunt virus
98	<a href="#">d1r3ha1</a>	Alignment	not modelled	5.8	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
99	<a href="#">d1pkla1</a>	Alignment	not modelled	5.8	14	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain