






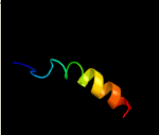






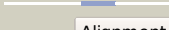

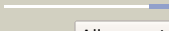







# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3288c\_(usfY)\_3669583\_3669996  
 Date Thu Aug 8 16:20:49 BST 2019  
 Unique Job ID 7fa89d68d32dec0d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4wgiA_</a>	 Alignment		46.4	19	<b>PDB header:</b> apoptosis/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,induced myeloid <b>PDBTitle:</b> a single diastereomer of a macrolactam core binds specifically to2 myeloid cell leukemia 1 (mcl1)
2	<a href="#">c5ua4A_</a>	 Alignment		36.7	19	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> 5-hl; <b>PDBTitle:</b> crystal structure of a179l:bid bh3 complex
3	<a href="#">c5v2sA_</a>	 Alignment		35.1	27	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type i
4	<a href="#">c2lx0A_</a>	 Alignment		30.7	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane fusion protein p14; <b>PDBTitle:</b> arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
5	<a href="#">c5ohdB_</a>	 Alignment		30.1	30	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> growth hormone receptor; <b>PDBTitle:</b> putative inactive (dormant) dimeric state of ghr transmembrane domain
6	<a href="#">d1q59a_</a>	 Alignment		27.2	18	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
7	<a href="#">c2a3lA_</a>	 Alignment		22.2	56	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amp deaminase; <b>PDBTitle:</b> x-ray structure of adenosine 5'-monophosphate deaminase from2 arabidopsis thaliana in complex with coformycin 5'-phosphate
8	<a href="#">d2a3la1</a>	 Alignment		22.2	56	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenosine/AMP deaminase
9	<a href="#">c2mkvA_</a>	 Alignment		21.2	27	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles
10	<a href="#">c5wddA_</a>	 Alignment		21.0	18	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-2-related ovarian killer protein; <b>PDBTitle:</b> crystal structure of chicken bok
11	<a href="#">c5f5uE_</a>	 Alignment		20.2	33	<b>PDB header:</b> splicing <b>Chain:</b> E: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum

12	<a href="#">c2jp3A_</a>	Alignment		16.9	11	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
13	<a href="#">c2jo1A_</a>	Alignment		15.8	14	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A; <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
14	<a href="#">c2a5yA_</a>	Alignment		15.6	21	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> apoptosis regulator ced-9; <b>PDBTitle:</b> structure of a ced-4/ced-9 complex
15	<a href="#">c4xz6A_</a>	Alignment		15.5	19	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> glycine betaine/proline abc transporter, periplasmic <b>PDBTitle:</b> tmox in complex with tmao
16	<a href="#">c6hwhX_</a>	Alignment		14.3	23	<b>PDB header:</b> electron transport <b>Chain:</b> X; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
17	<a href="#">c6ijjF_</a>	Alignment		13.6	27	<b>PDB header:</b> membrane protein <b>Chain:</b> F; <b>PDB Molecule:</b> psaf; <b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii
18	<a href="#">c1ciiA_</a>	Alignment		13.2	13	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
19	<a href="#">c3kj2B_</a>	Alignment		13.0	41	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> mcl-1 in complex with bim bh3 mutant f4ae
20	<a href="#">c2yv6A_</a>	Alignment		12.1	22	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> bcl-2 homologous antagonist/killer; <b>PDBTitle:</b> crystal structure of human bcl-2 family protein bak
21	<a href="#">d1gzga_</a>	Alignment	not modelled	12.0	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
22	<a href="#">c3l6gA_</a>	Alignment	not modelled	11.8	11	<b>PDB header:</b> glycine betaine-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> betaine abc transporter permease and substrate binding <b>PDBTitle:</b> crystal structure of lactococcal opuac in its open conformation
23	<a href="#">c5f5uB_</a>	Alignment	not modelled	11.6	41	<b>PDB header:</b> splicing <b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
24	<a href="#">c2xa0A_</a>	Alignment	not modelled	11.6	24	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> apoptosis regulator bcl-2; <b>PDBTitle:</b> crystal structure of bcl-2 in complex with a bax bh32 peptide
25	<a href="#">c2ks1B_</a>	Alignment	not modelled	11.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
26	<a href="#">c3kdpG_</a>	Alignment	not modelled	11.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
27	<a href="#">c3kdpH_</a>	Alignment	not modelled	11.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
28	<a href="#">c2rgwD_</a>	Alignment	not modelled	11.0	32	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
						<b>PDB header:</b> hydrolase/transport protein

29	<a href="#">c2zxeG</a>	Alignment	not modelled	10.9	26	<b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
30	<a href="#">c2o2fA</a>	Alignment	not modelled	10.6	26	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis regulator bcl-2; <b>PDBTitle:</b> solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
31	<a href="#">d5easa1</a>	Alignment	not modelled	10.5	13	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases <b>Family:</b> Terpenoid cyclase N-terminal domain
32	<a href="#">c5ujqA</a>	Alignment	not modelled	10.3	20	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin; <b>PDBTitle:</b> nmr solution structure of the two-component bacteriocin cbnxy
33	<a href="#">d2c1ha1</a>	Alignment	not modelled	10.2	37	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
34	<a href="#">d1pq1a</a>	Alignment	not modelled	10.2	20	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
35	<a href="#">d1h7na</a>	Alignment	not modelled	10.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
36	<a href="#">d1l6sa</a>	Alignment	not modelled	10.0	37	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
37	<a href="#">c4hqjE</a>	Alignment	not modelled	9.7	21	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of na+,k+-atpase in the na+-bound state
38	<a href="#">c5f5uH</a>	Alignment	not modelled	9.7	41	<b>PDB header:</b> splicing <b>Chain:</b> H: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
39	<a href="#">c4deyB</a>	Alignment	not modelled	9.5	33	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker.
40	<a href="#">c2ip6A</a>	Alignment	not modelled	8.8	23	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> papb; <b>PDBTitle:</b> crystal structure of pedb
41	<a href="#">d1ysga1</a>	Alignment	not modelled	8.8	24	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
42	<a href="#">d2v0ea1</a>	Alignment	not modelled	8.8	30	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
43	<a href="#">c4hqjG</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of na+,k+-atpase in the na+-bound state
44	<a href="#">c2ckaA</a>	Alignment	not modelled	8.3	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding protein 8; <b>PDBTitle:</b> solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
45	<a href="#">d2ckaa1</a>	Alignment	not modelled	8.3	40	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
46	<a href="#">c6igzF</a>	Alignment	not modelled	8.1	22	<b>PDB header:</b> plant protein <b>Chain:</b> F: <b>PDB Molecule:</b> psaf; <b>PDBTitle:</b> structure of psi-lhci
47	<a href="#">c3d7vB</a>	Alignment	not modelled	8.1	44	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of mcl-1 in complex with an mcl-1 selective bh32 ligand
48	<a href="#">c2jpkA</a>	Alignment	not modelled	8.1	63	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit beta; <b>PDBTitle:</b> lactococcin g-b in dpc
49	<a href="#">c6f2dI</a>	Alignment	not modelled	8.1	19	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> flagellar biosynthetic protein flq; <b>PDBTitle:</b> a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
50	<a href="#">c6f2dJ</a>	Alignment	not modelled	8.1	19	<b>PDB header:</b> protein transport <b>Chain:</b> J: <b>PDB Molecule:</b> flagellar biosynthetic protein flq; <b>PDBTitle:</b> a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
51	<a href="#">c5tn2B</a>	Alignment	not modelled	8.1	50	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator sinr; <b>PDBTitle:</b> solution structure of the c-terminal multimerization domain of the2 master biofilm-regulator sinr from bacillus subtilis
52	<a href="#">c2ckcA</a>	Alignment	not modelled	8.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding protein 7; <b>PDBTitle:</b> solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
53	<a href="#">d2ckca1</a>	Alignment	not modelled	8.0	30	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
54	<a href="#">c4p5aB</a>	Alignment	not modelled	8.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidylate synthase thyx;

54	<a href="#">c9p3aB</a>	Alignment	not modelled	8.0	29	<b>PDBTitle:</b> crystal structure of a ump/dump methylase polb from streptomyces2 cacaoi bound with 5-br ump
55	<a href="#">d1kfia4</a>	Alignment	not modelled	8.0	83	<b>Fold:</b> TBP-like <b>Superfamily:</b> Phosphoglucomutase, C-terminal domain <b>Family:</b> Phosphoglucomutase, C-terminal domain
56	<a href="#">d1m4a1</a>	Alignment	not modelled	7.9	30	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
57	<a href="#">d3pmga4</a>	Alignment	not modelled	7.9	83	<b>Fold:</b> TBP-like <b>Superfamily:</b> Phosphoglucomutase, C-terminal domain <b>Family:</b> Phosphoglucomutase, C-terminal domain
58	<a href="#">c4ymkA</a>	Alignment	not modelled	7.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase 1; <b>PDBTitle:</b> crystal structure of stearyl-coenzyme a desaturase 1
59	<a href="#">d2dl6a1</a>	Alignment	not modelled	7.7	40	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
60	<a href="#">c4zyoA</a>	Alignment	not modelled	7.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase; <b>PDBTitle:</b> crystal structure of human integral membrane stearyl-coa desaturase2 with substrate
61	<a href="#">d1pv8a</a>	Alignment	not modelled	7.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
62	<a href="#">c3io8D</a>	Alignment	not modelled	7.5	67	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> biml12f in complex with bcl-xl
63	<a href="#">c4atyA</a>	Alignment	not modelled	7.4	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> terephthalate 1,2-cis-dihydrodiol dehydrogenase; <b>PDBTitle:</b> crystal structure of a terephthalate 1,2-cis-2 dihydrodioldehydrogenase from burkholderia xenovorans3 lb400
64	<a href="#">c6r6bl</a>	Alignment	not modelled	7.3	16	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> surface presentation of antigens protein spaq; <b>PDBTitle:</b> structure of the core shigella flexneri type iii secretion system2 export gate complex sctrst (spa24/spa9/spa29).
65	<a href="#">c5t3pB</a>	Alignment	not modelled	7.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal coenzyme a diphosphatase nudt7; <b>PDBTitle:</b> crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
66	<a href="#">c3n23E</a>	Alignment	not modelled	7.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
67	<a href="#">c1ml4A</a>	Alignment	not modelled	7.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate transcarbamoylase; <b>PDBTitle:</b> the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
68	<a href="#">c2voyB</a>	Alignment	not modelled	6.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
69	<a href="#">c4jo8B</a>	Alignment	not modelled	6.9	36	<b>PDB header:</b> immune system/viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> killer cell lectin-like receptor 8; <b>PDBTitle:</b> crystal structure of the activating ly49h receptor in complex with2 m157 (g1f strain)
70	<a href="#">c6akfC</a>	Alignment	not modelled	6.9	27	<b>PDB header:</b> membrane protein/toxin <b>Chain:</b> C: <b>PDB Molecule:</b> claudin-3; <b>PDBTitle:</b> crystal structure of mouse claudin-3 p134a mutant in complex with c-2 terminal fragment of clostridium perfringens enterotoxin
71	<a href="#">c5ir6B</a>	Alignment	not modelled	6.8	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bd-type quinol oxidase subunit ii; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans
72	<a href="#">c3io8B</a>	Alignment	not modelled	6.7	35	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> biml12f in complex with bcl-xl
73	<a href="#">c4zr0A</a>	Alignment	not modelled	6.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ceramide very long chain fatty acid hydroxylase scs7; <b>PDBTitle:</b> full length scs7p (only hydroxylase domain visible)
74	<a href="#">c5f5tD</a>	Alignment	not modelled	6.5	33	<b>PDB header:</b> splicing <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the prp38-mfap1 complex of chaetomium2 thermophilum
75	<a href="#">c1p58E</a>	Alignment	not modelled	6.4	25	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
76	<a href="#">c4k7eA</a>	Alignment	not modelled	6.3	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> crystal structure of junin virus nucleoprotein
77	<a href="#">c3ah5E</a>	Alignment	not modelled	6.2	17	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> thymidylate synthase thyx; <b>PDBTitle:</b> crystal structure of flavin dependent thymidylate synthase thyx from2 helicobacter pylori complexed with fad and dump
78	<a href="#">c5zzjC</a>	Alignment	not modelled	6.1	43	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> santalene synthase; <b>PDBTitle:</b> crystal structure of a enzyme from santalum album
79	<a href="#">c5wpcB</a>	Alignment	not modelled	6.1	67	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11;

79	<a href="#">cJw05B_</a>	Alignment	not modelled	6.1	67	<b>PDBTitle:</b> structural and functional insights into canarypox virus cnp0582 regulation of apoptosis
80	<a href="#">c2v6qB_</a>	Alignment	not modelled	6.0	67	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of a bhrf-1 : bim bh3 complex
81	<a href="#">c1vytE_</a>	Alignment	not modelled	5.9	33	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
82	<a href="#">c2wh6B_</a>	Alignment	not modelled	5.9	67	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> crystal structure of anti-apoptotic bhrf1 in complex with the bim bh32 domain
83	<a href="#">c4d2mD_</a>	Alignment	not modelled	5.9	67	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> vaccinia virus f1l bound to bim bh3
84	<a href="#">d1h21a_</a>	Alignment	not modelled	5.8	18	<b>Fold:</b> Multiheme cytochromes <b>Superfamily:</b> Multiheme cytochromes <b>Family:</b> Di-heme elbow motif
85	<a href="#">d1vlva1</a>	Alignment	not modelled	5.7	27	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
86	<a href="#">c5ilqA_</a>	Alignment	not modelled	5.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> crystal structure of truncated unliganded aspartate transcarbamoylase2 from plasmodium falciparum
87	<a href="#">c3b9bA_</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium <b>PDBTitle:</b> structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
88	<a href="#">d1y5ic1</a>	Alignment	not modelled	5.4	23	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Respiratory nitrate reductase 1 gamma chain <b>Family:</b> Respiratory nitrate reductase 1 gamma chain
89	<a href="#">c6nhwB_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
90	<a href="#">c6nhwF_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
91	<a href="#">c6nhwC_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
92	<a href="#">c6nhwE_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
93	<a href="#">c6nhwA_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
94	<a href="#">c6nhwD_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
95	<a href="#">c2hi1A_</a>	Alignment	not modelled	5.3	80	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxythreonine-4-phosphate dehydrogenase 2; <b>PDBTitle:</b> the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
96	<a href="#">d2v0fa1</a>	Alignment	not modelled	5.3	50	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
97	<a href="#">d1e43a1</a>	Alignment	not modelled	5.3	36	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
98	<a href="#">c2d35A_</a>	Alignment	not modelled	5.2	37	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division activator ceda; <b>PDBTitle:</b> solution structure of cell division reactivation factor,2 ceda
99	<a href="#">d1jb0f_</a>	Alignment	not modelled	5.1	31	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit III of photosystem I reaction centre, PsaF <b>Family:</b> Subunit III of photosystem I reaction centre, PsaF