

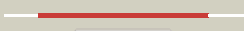






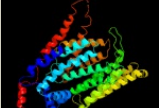












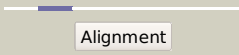

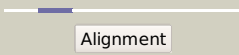

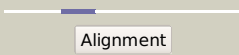
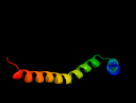
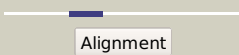
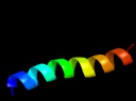
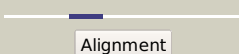
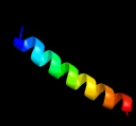
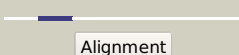
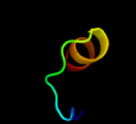


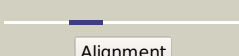
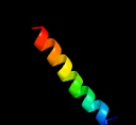
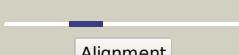


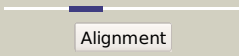

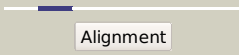

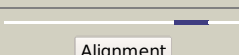
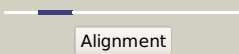


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1002c_(-)_1118432_1119943
Date	Wed Jul 31 22:05:07 BST 2019
Unique Job ID	bc23222bdb69e11b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6p25A_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dolichyl-phosphate-mannose--protein mannosyltransferase 1; <b>PDBTitle:</b> structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
2	<a href="#">c6p2rB_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dolichyl-phosphate-mannose--protein mannosyltransferase 2; <b>PDBTitle:</b> structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
3	<a href="#">c5f15A_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; <b>PDBTitle:</b> crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
4	<a href="#">c3rceA_</a>	 Alignment		99.8	10	<b>PDB header:</b> transferase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> oligosaccharide transferase to n-glycosylate proteins; <b>PDBTitle:</b> bacterial oligosaccharyltransferase pglb
5	<a href="#">c3wajA_</a>	 Alignment		99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane oligosaccharyl transferase; <b>PDBTitle:</b> crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
6	<a href="#">c6eznF_</a>	 Alignment		99.5	11	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
7	<a href="#">c5ir6B_</a>	 Alignment		19.5	8	<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
8	<a href="#">c5nf8A_</a>	 Alignment		16.2	6	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> respiratory supercomplex factor 1, mitochondrial; <b>PDBTitle:</b> solution structure of detergent-solubilized rcf1, a yeast2 mitochondrial inner membrane protein involved in respiratory complex3 iii/iv supercomplex formation
9	<a href="#">c5i6cB_</a>	 Alignment		13.4	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> uric acid-xanthine permease; <b>PDBTitle:</b> the structure of the eukaryotic purine/h+ symporter, uapa, in complex2 with xanthine
10	<a href="#">d1t33a2</a>	 Alignment		13.3	16	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
11	<a href="#">d1h5oa_</a>	 Alignment		10.9	44	<b>Fold:</b> Defensin-like <b>Superfamily:</b> Defensin-like <b>Family:</b> Myotoxin

12	<a href="#">c1z99A_</a>	 Alignment		10.9	44	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> crotamine; <b>PDBTitle:</b> solution structure of crotamine, a myotoxin from crotalus2 durissus terrificus
13	<a href="#">c3b6eA_</a>	 Alignment		10.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced helicase c domain-containing protein 1; <b>PDBTitle:</b> crystal structure of human dech-box rna helicase mda5 (melanoma2 differentiation-associated protein 5), dech-domain
14	<a href="#">c3hfxA_</a>	 Alignment		10.3	29	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
15	<a href="#">c2l34B_</a>	 Alignment		9.4	28	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12 transmembrane homodimer
16	<a href="#">c4wo1A_</a>	 Alignment		9.4	28	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
17	<a href="#">d1yksa1</a>	 Alignment		9.2	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
18	<a href="#">c4wo1B_</a>	 Alignment		9.2	28	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
19	<a href="#">c4wo1C_</a>	 Alignment		9.2	28	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
20	<a href="#">c4wo1B_</a>	 Alignment		9.2	28	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
21	<a href="#">c4wo1A_</a>	 Alignment	not modelled	9.2	28	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
22	<a href="#">c4wo1C_</a>	 Alignment	not modelled	9.2	28	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
23	<a href="#">c4wo1D_</a>	 Alignment	not modelled	9.2	28	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
24	<a href="#">c6ek1B_</a>	 Alignment	not modelled	9.1	70	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome alignment-maintaining phosphoprotein 1; <b>PDBTitle:</b> crystal structure of mammalian rev7 in complex with human chromosome2 alignment-maintaining phosphoprotein 1
25	<a href="#">c6ek1B_</a>	 Alignment	not modelled	9.1	70	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome alignment-maintaining phosphoprotein 1; <b>PDBTitle:</b> crystal structure of mammalian rev7 in complex with human chromosome2 alignment-maintaining phosphoprotein 1
26	<a href="#">c5gjqY_</a>	 Alignment	not modelled	8.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> Y: <b>PDB Molecule:</b> 26s proteasome complex subunit dss1; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
27	<a href="#">c6bvvB_</a>	 Alignment	not modelled	8.5	50	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein w; <b>PDBTitle:</b> nipah virus w protein c-terminus in complex with importin

						alpha 3
28	<a href="#">c5firH_</a>	Alignment	not modelled	7.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> paxt-1; <b>PDBTitle:</b> crystal structure of c. elegans xrn2 in complex with the2 xrn2-binding domain of paxt-1
29	<a href="#">c3c67B_</a>	Alignment	not modelled	7.7	6	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ygjk; <b>PDBTitle:</b> escherichia coli k12 ygjk in a complexed with glucose
30	<a href="#">c5xhbA_</a>	Alignment	not modelled	7.5	25	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> nisin immunity protein; <b>PDBTitle:</b> crystal structure of the full length of nisi in a lipid free form, the2 nisin immunity protein, from lactococcus lactis
31	<a href="#">c5d2mG_</a>	Alignment	not modelled	7.5	70	<b>PDB header:</b> ligase,protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> zinc finger protein 451; <b>PDBTitle:</b> complex between human sumo2-rangap1, ubc9 and znf451
32	<a href="#">c6hu9s_</a>	Alignment	not modelled	7.5	23	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> S: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 8; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
33	<a href="#">c6hu9g_</a>	Alignment	not modelled	7.5	23	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 7; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
34	<a href="#">d2e74a1</a>	Alignment	not modelled	7.3	16	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
35	<a href="#">d1pcfa_</a>	Alignment	not modelled	7.2	15	<b>Fold:</b> ssDNA-binding transcriptional regulator domain <b>Superfamily:</b> ssDNA-binding transcriptional regulator domain <b>Family:</b> Transcriptional coactivator PC4 C-terminal domain
36	<a href="#">d1e2wa1</a>	Alignment	not modelled	7.2	55	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Cytochrome f, large domain <b>Family:</b> Cytochrome f, large domain
37	<a href="#">c2l35B_</a>	Alignment	not modelled	7.1	30	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12- <i>nkq2c</i> transmembrane heterotrimer
38	<a href="#">d1hcza1</a>	Alignment	not modelled	7.1	27	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Cytochrome f, large domain <b>Family:</b> Cytochrome f, large domain
39	<a href="#">c2rbdB_</a>	Alignment	not modelled	7.0	16	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> bh2358 protein; <b>PDBTitle:</b> crystal structure of a putative spore coat protein (bh2358) from2 bacillus halodurans c-125 at 1.54 a resolution
40	<a href="#">c2l34A_</a>	Alignment	not modelled	7.0	30	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12 transmembrane homodimer
41	<a href="#">c5uxgB_</a>	Alignment	not modelled	6.9	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde deformylating oxygenase; <b>PDBTitle:</b> protein 84 with aldehyde deformylating oxygenase activity from2 sulfolobus tokodaii (monoclinic)
42	<a href="#">c6hwhb_</a>	Alignment	not modelled	6.7	7	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
43	<a href="#">d1tu2b1</a>	Alignment	not modelled	6.7	55	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Cytochrome f, large domain <b>Family:</b> Cytochrome f, large domain
44	<a href="#">c1q90A_</a>	Alignment	not modelled	6.7	55	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
45	<a href="#">c1e2vB_</a>	Alignment	not modelled	6.7	55	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> n153q mutant of cytochrome f from chlamydomonas reinhardtii
46	<a href="#">c3mhpC_</a>	Alignment	not modelled	6.6	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tic62_peptide; <b>PDBTitle:</b> fnr-recruitment to the thylakoid
47	<a href="#">d1ci3m1</a>	Alignment	not modelled	6.6	55	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Cytochrome f, large domain <b>Family:</b> Cytochrome f, large domain
48	<a href="#">c2momC_</a>	Alignment	not modelled	6.6	31	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
49	<a href="#">c2momB_</a>	Alignment	not modelled	6.6	31	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
50	<a href="#">c6iehB_</a>	Alignment	not modelled	6.5	75	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> exosome rna helicase mtr4; <b>PDBTitle:</b> crystal structures of the hmtr4-nrde2 complex
51	<a href="#">d2fwra2</a>	Alignment	not modelled	6.4	63	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
52	<a href="#">c5m0jH_</a>	Alignment	not modelled	6.4	50	<b>PDB header:</b> rna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> swi5-dependent ho expression protein 2,swi5-dependent ho

						<b>PDBTitle:</b> crystal structure of the cytoplasmic complex with she2p, she3p, and2 the ash1 mrna e3-localization element
53	<a href="#">d1vf5c1</a>	Alignment	not modelled	6.4	55	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Cytochrome f, large domain <b>Family:</b> Cytochrome f, large domain
54	<a href="#">c6iegA</a>	Alignment	not modelled	6.4	75	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exosome rna helicase mtr4; <b>PDBTitle:</b> crystal structure of human mtr4
55	<a href="#">c1zsgB</a>	Alignment	not modelled	6.3	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 1; <b>PDBTitle:</b> beta pix-sh3 complexed with an atypical peptide from alpha-2 pak
56	<a href="#">c2n1pA</a>	Alignment	not modelled	6.2	9	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 5b, ns5b; <b>PDBTitle:</b> structure of the c-terminal membrane domain of hcv ns5b protein
57	<a href="#">c6dhxC</a>	Alignment	not modelled	6.2	44	<b>PDB header:</b> antitoxin <b>Chain:</b> C: <b>PDB Molecule:</b> tipc2; <b>PDBTitle:</b> structure of tipc2 from streptococcus intermedius b196
58	<a href="#">c3t5jA</a>	Alignment	not modelled	6.1	21	<b>PDB header:</b> allergen, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pollen allergen phl p 4; <b>PDBTitle:</b> crystal structure of phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity
59	<a href="#">c2kwzA</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protease ns2-3; <b>PDBTitle:</b> solution structure of ns2 [60-99]
60	<a href="#">c4k05B</a>	Alignment	not modelled	6.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical exported protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0371) from2 bacteroides fragilis nctc 9343 at 1.65 a resolution
61	<a href="#">c4b19A</a>	Alignment	not modelled	6.0	17	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> pepa1; <b>PDBTitle:</b> s. aureus pepa1 nmr structure
62	<a href="#">c5l6nI</a>	Alignment	not modelled	6.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> thrombin inhibitor madanin 1; <b>PDBTitle:</b> disulfated madanin-thrombin complex
63	<a href="#">c2e75C</a>	Alignment	not modelled	5.9	55	<b>PDB header:</b> photosynthesis <b>Chain:</b> C: <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
64	<a href="#">c5fmfY</a>	Alignment	not modelled	5.8	42	<b>PDB header:</b> transcription <b>Chain:</b> Y: <b>PDB Molecule:</b> dna repair helicase rad3; <b>PDBTitle:</b> the p-lobe of rna polymerase ii pre-initiation complex
65	<a href="#">c2n73B</a>	Alignment	not modelled	5.7	50	<b>PDB header:</b> transferase/transferase regulator <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 4-kinase beta; <b>PDBTitle:</b> solution structure of the acbd3:pi4kb complex
66	<a href="#">c2mkvA</a>	Alignment	not modelled	5.7	23	<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
67	<a href="#">c1ctmA</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> electron transport(cytochrome) <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
68	<a href="#">c3iz3D</a>	Alignment	not modelled	5.7	14	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> viral structural protein 5; <b>PDBTitle:</b> cryoem structure of cytoplasmic polyhedrosis virus
69	<a href="#">c1tu2B</a>	Alignment	not modelled	5.6	55	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
70	<a href="#">c2n2eA</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> antibiotic-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nisin immunity protein; <b>PDBTitle:</b> nmr solution structure of the c-terminal domain of nisi, a lipoprotein2 from lactococcus lactis which confers immunity against nisin
71	<a href="#">d1dysa</a>	Alignment	not modelled	5.4	27	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycosyl hydrolases family 6, cellulases <b>Family:</b> Glycosyl hydrolases family 6, cellulases
72	<a href="#">c3l9oA</a>	Alignment	not modelled	5.4	75	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> crystal structure of mtr4, a co-factor of the nuclear exosome
73	<a href="#">c5fvjA</a>	Alignment	not modelled	5.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of tact (trna acetylating toxin) from salmonella
74	<a href="#">c2kluA</a>	Alignment	not modelled	5.3	14	<b>PDB header:</b> immune system, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
75	<a href="#">c2lomA</a>	Alignment	not modelled	5.3	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hig1 domain family member 1a; <b>PDBTitle:</b> backbone structure of human membrane protein hig1a
76	<a href="#">c4wvrE</a>	Alignment	not modelled	5.3	38	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> large proline-rich protein bag6; <b>PDBTitle:</b> crystal structure of bag6-ubl4a dimerization domain
77	<a href="#">c2jxmB</a>	Alignment	not modelled	5.3	36	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
						<b>PDB header:</b> oxidoreductase

78	<a href="#">c3chtA_</a>	Alignment	not modelled	5.3	21	<b>Chain:</b> A; <b>PDB Molecule:</b> p-aminobenzoate n-oxygenase; <b>PDBTitle:</b> crystal structure of di-iron aurf with partially bound ligand
79	<a href="#">d2eyqa3</a>	Alignment	not modelled	5.3	50	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
80	<a href="#">c1bzgA_</a>	Alignment	not modelled	5.3	23	<b>PDB header:</b> hormone <b>Chain:</b> A; <b>PDB Molecule:</b> parathyroid hormone-related protein; <b>PDBTitle:</b> the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
81	<a href="#">c4aghA_</a>	Alignment	not modelled	5.3	8	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> mosub1, transcription cofactor; <b>PDBTitle:</b> structural features of ssdna binding protein mosub1 from magnaporthe2 oryzae
82	<a href="#">c4xgtA_</a>	Alignment	not modelled	5.2	63	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> frq-interacting rna helicase; <b>PDBTitle:</b> structure of rna helicase frh a critical component of the neurospora2 crassa circadian clock
83	<a href="#">c4elnA_</a>	Alignment	not modelled	5.1	40	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> type iii effector xopai; <b>PDBTitle:</b> crystal structure of the type iii effector xopai from xanthomonas2 axonopodis pv. citri
84	<a href="#">c5cowA_</a>	Alignment	not modelled	5.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> c. remanei pgl-1 dimerization domain
85	<a href="#">c3bvdC_</a>	Alignment	not modelled	5.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 2a; <b>PDBTitle:</b> structure of surface-engineered cytochrome ba3 oxidase from thermus2 thermophilus under xenon pressure, 100psi 5min
86	<a href="#">d1xmec1</a>	Alignment	not modelled	5.1	24	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Bacterial ba3 type cytochrome c oxidase subunit IIa <b>Family:</b> Bacterial ba3 type cytochrome c oxidase subunit IIa