
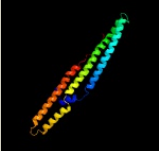
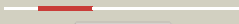
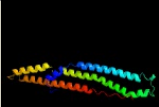

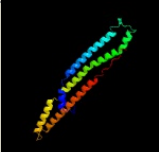



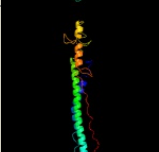



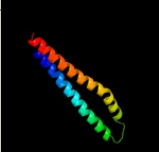



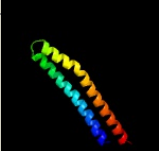

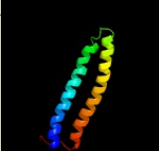




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1548c_(PPE21)_1751303_1753339
Date	Fri Aug 2 13:30:13 BST 2019
Unique Job ID	fda9f84e2d1c6314

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	54	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	<a href="#">d2g38b1</a>	 Alignment		100.0	33	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
3	<a href="#">c2g38B_</a>	 Alignment		100.0	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
5	<a href="#">c4wj2A_</a>	 Alignment		99.1	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
6	<a href="#">c2vs0B_</a>	 Alignment		98.2	13	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	<a href="#">c3gvmA_</a>	 Alignment		98.1	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	<a href="#">c4iogD_</a>	 Alignment		98.0	17	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
9	<a href="#">c3zbhC_</a>	 Alignment		98.0	15	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
10	<a href="#">d1wa8a1</a>	 Alignment		97.6	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsA_</a>	 Alignment		97.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	<a href="#">c4lwsB_</a>	Alignment		96.8	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	<a href="#">d1wa8b1</a>	Alignment		96.7	24	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		96.3	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein mab_3112; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	<a href="#">c2kg7B_</a>	Alignment		94.9	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein esxh; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	<a href="#">c3nb2B_</a>	Alignment		89.3	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> secreted effector protein; <b>PDBTitle:</b> crystal structure of e. coli o157:h7 effector protein nlel
17	<a href="#">c4i0xJ_</a>	Alignment		82.7	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J: <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
18	<a href="#">d1ui5a2</a>	Alignment		81.4	19	<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
19	<a href="#">c2ahmG_</a>	Alignment		33.9	18	<b>PDB header:</b> viral protein, replication <b>Chain:</b> G: <b>PDB Molecule:</b> replicase polyprotein 1ab, heavy chain; <b>PDBTitle:</b> crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
20	<a href="#">d1xkna_</a>	Alignment		32.3	13	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
21	<a href="#">c2lyyB_</a>	Alignment	not modelled	26.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein nb7890a from shewanella sp
22	<a href="#">c2kg7A_</a>	Alignment	not modelled	26.1	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein esxg (pe family protein); <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
23	<a href="#">c2iu1A_</a>	Alignment	not modelled	25.5	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of eif5 c-terminal domain
24	<a href="#">c3ub0D_</a>	Alignment	not modelled	23.6	14	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> non-structural protein 6, nsp6,; <b>PDBTitle:</b> crystal structure of the nonstructural protein 7 and 8 complex of f2 feline coronavirus
25	<a href="#">c3zfsA_</a>	Alignment	not modelled	22.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> f420-reducing hydrogenase, subunit alpha; <b>PDBTitle:</b> cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
26	<a href="#">c2qzaA_</a>	Alignment	not modelled	22.9	5	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted effector protein; <b>PDBTitle:</b> crystal structure of salmonella effector protein sopa
27	<a href="#">c5frgA_</a>	Alignment	not modelled	22.0	75	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
28	<a href="#">c3jywF_</a>	Alignment	not modelled	21.0	43	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 60s ribosomal protein l7(a); <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution

29	<a href="#">c2fulE_</a>	Alignment	not modelled	20.4	33	<b>PDB header:</b> translation <b>Chain:</b> E: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of the c-terminal domain of s. cerevisiae eif5
30	<a href="#">c3h6pB_</a>	Alignment	not modelled	20.0	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6 like protein exs5; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
31	<a href="#">c2l5bA_</a>	Alignment	not modelled	18.2	47	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> activator of apoptosis harakiri; <b>PDBTitle:</b> solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
32	<a href="#">c4n91A_</a>	Alignment	not modelled	18.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate
33	<a href="#">c1bkvA_</a>	Alignment	not modelled	17.4	56	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
34	<a href="#">c2hzkB_</a>	Alignment	not modelled	16.9	14	<b>PDB header:</b> ligand binding, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap-t family sorbitol/mannitol transporter, periplasmic <b>PDBTitle:</b> crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
35	<a href="#">c1bkvC_</a>	Alignment	not modelled	16.1	56	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
36	<a href="#">c1bkvB_</a>	Alignment	not modelled	16.1	56	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
37	<a href="#">d1paqa_</a>	Alignment	not modelled	15.2	20	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
38	<a href="#">c1paqA_</a>	Alignment	not modelled	15.2	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor eif-2b epsilon <b>PDBTitle:</b> crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
39	<a href="#">c2ke4A_</a>	Alignment	not modelled	14.6	75	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cdc42-interacting protein 4; <b>PDBTitle:</b> the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
40	<a href="#">c2kp7A_</a>	Alignment	not modelled	14.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crossover junction endonuclease mus81; <b>PDBTitle:</b> solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
41	<a href="#">c5lzkB_</a>	Alignment	not modelled	14.1	4	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> protein fam83b; <b>PDBTitle:</b> structure of the domain of unknown function duf1669 from human fam83b
42	<a href="#">c4mnpA_</a>	Alignment	not modelled	13.3	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminic acid-binding protein; <b>PDBTitle:</b> structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586
43	<a href="#">c5lc5a_</a>	Alignment	not modelled	12.5	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> snadh-ubiquinone oxidoreductase chain 3; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
44	<a href="#">c3gyyC_</a>	Alignment	not modelled	11.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
45	<a href="#">c3juia_</a>	Alignment	not modelled	11.5	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
46	<a href="#">c4p56C_</a>	Alignment	not modelled	11.1	16	<b>PDB header:</b> solute-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative extracellular solute-binding protein; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 bordetella bronchiseptica, target efi-510038 (bb2442), with bound3 (r)-mandelate and (s)-mandelate
47	<a href="#">c4tt1A_</a>	Alignment	not modelled	10.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deneddylase; <b>PDBTitle:</b> crystal structure of fragment 1600-1733 of hsv1 ul36, native
48	<a href="#">c2l5aA_</a>	Alignment	not modelled	10.4	16	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone h3-like centromeric protein cse4, protein scm3, <b>PDBTitle:</b> structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
49	<a href="#">c3a9rA_</a>	Alignment	not modelled	10.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-arabinose isomerase; <b>PDBTitle:</b> x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
50	<a href="#">c5i4rA_</a>	Alignment	not modelled	9.9	43	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> contact-dependent inhibitor a; <b>PDBTitle:</b> contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdi/ef-tu complex (trypsin-modified)
51	<a href="#">d1r76a_</a>	Alignment	not modelled	9.0	22	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Family 10 polysaccharide lyase <b>Family:</b> Family 10 polysaccharide lyase
52	<a href="#">c4y9ia_</a>	Alignment	not modelled	8.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis paralogous family 11; <b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
						<b>PDB header:</b> structural protein

53	<a href="#">c3du1X</a>	Alignment	not modelled	8.9	21	<b>Chain:</b> X: <b>PDB Molecule:</b> all3740 protein; <b>PDBTitle:</b> the 2.0 angstrom resolution crystal structure of het1, a pentapeptide2 repeat protein involved in heterocyst differentiation regulation from3 the cyanobacterium nostoc sp. strain pcc 7120
54	<a href="#">c6o9I6</a>	Alignment	not modelled	8.8	40	<b>PDB header:</b> transcription/dna <b>Chain:</b> 6: <b>PDB Molecule:</b> general transcription factor iih subunit 2; <b>PDBTitle:</b> human holo-pic in the closed state
55	<a href="#">c2kwuA</a>	Alignment	not modelled	7.9	46	<b>PDB header:</b> protein binding/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iota; <b>PDBTitle:</b> solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
56	<a href="#">c3qthA</a>	Alignment	not modelled	7.8	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a dinb-like protein (cps_3021) from colwellia2 psychrerythraea 34h at 2.20 a resolution
57	<a href="#">c5ec0A</a>	Alignment	not modelled	7.7	22	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> alp7a; <b>PDBTitle:</b> crystal structure of actin-like protein alp7a
58	<a href="#">c2yfwC</a>	Alignment	not modelled	7.7	15	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> histone h3-like centromeric protein cse4; <b>PDBTitle:</b> heterotetramer structure of kluyveromyces lactis cse4,h4
59	<a href="#">c3j21Y</a>	Alignment	not modelled	7.7	31	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 50s ribosomal protein l30p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
60	<a href="#">c3b50A</a>	Alignment	not modelled	7.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sialic acid-binding periplasmic protein siap; <b>PDBTitle:</b> structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
61	<a href="#">c3j3bF</a>	Alignment	not modelled	7.6	31	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 60s ribosomal protein l7; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
62	<a href="#">c6rdf7</a>	Alignment	not modelled	7.6	21	<b>PDB header:</b> proton transport <b>Chain:</b> 7: <b>PDB Molecule:</b> mitochondrial atp synthase associated protein asa7; <b>PDBTitle:</b> cryoem structure of polytomella f-atp synthase, primary rotary state2 3, monomer-masked refinement
63	<a href="#">d2fgga1</a>	Alignment	not modelled	7.4	40	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Rv2632c-like <b>Family:</b> Rv2632c-like
64	<a href="#">c4el8A</a>	Alignment	not modelled	7.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 48; <b>PDBTitle:</b> the unliganded structure of c.bescii cela gh48 module
65	<a href="#">c1e3aA</a>	Alignment	not modelled	7.3	23	<b>PDB header:</b> antibiotic resistance <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin amidase alpha subunit; <b>PDBTitle:</b> a slow processing precursor penicillin acylase from escherichia coli
66	<a href="#">c5hl8B</a>	Alignment	not modelled	7.2	12	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> type ii secretion system protein l; <b>PDBTitle:</b> 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
67	<a href="#">c4oanB</a>	Alignment	not modelled	7.0	17	<b>PDB header:</b> membrane protein/protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodospseudomonas palustris haa2 (rpb_2686), target efi-510221, with3 density modeled as (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-4 acetolactate)
68	<a href="#">c3j39F</a>	Alignment	not modelled	6.9	31	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 60s ribosomal protein l7; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
69	<a href="#">c2nviA</a>	Alignment	not modelled	6.9	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 25mer peptide from vacuolar atp synthase subunit <b>PDBTitle:</b> nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
70	<a href="#">c2dbfA</a>	Alignment	not modelled	6.8	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear factor nf-kappa-b p105 subunit; <b>PDBTitle:</b> solution structure of the death domain in human nuclear2 factor nf-kappa-b p105 subunit
71	<a href="#">c4yk2B</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bartonella effector protein (bep) substrate of virb t4ss; <b>PDBTitle:</b> crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
72	<a href="#">c1bzgA</a>	Alignment	not modelled	6.7	0	<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
73	<a href="#">c3bb9D</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative orphan protein; <b>PDBTitle:</b> crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
74	<a href="#">c2np3A</a>	Alignment	not modelled	6.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family regulator; <b>PDBTitle:</b> crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
75	<a href="#">c6hu9u</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> U: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 10; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
76	<a href="#">c2hu8B</a>	Alignment	not modelled	6.7	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> histone h3;

76	<a href="#">c210cB</a>	Alignment	not modelled	6.7	10	<b>PDBTitle:</b> structure of the h3-h4 chaperone asf1 bound to histones h3 and h4 <b>PDB header:</b> oxidoreductase
77	<a href="#">c4oo3A</a>	Alignment	not modelled	6.6	16	<b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (parmer_00841) from2 parabacteroides merdae atcc 43184 at 2.23 a resolution
78	<a href="#">c3r5zB</a>	Alignment	not modelled	6.6	16	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
79	<a href="#">c4wpyA</a>	Alignment	not modelled	6.6	20	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein dl-rv1738; <b>PDBTitle:</b> racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
80	<a href="#">c3h96B</a>	Alignment	not modelled	6.5	6	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeg_3358 f420 reductase
81	<a href="#">c3n6xA</a>	Alignment	not modelled	6.4	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glutathionylspermidine synthase; <b>PDBTitle:</b> crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methylobacillus flagellatus kt at 2.35 a resolution
82	<a href="#">c5kf6B</a>	Alignment	not modelled	6.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
83	<a href="#">d2apla1</a>	Alignment	not modelled	6.3	12	<b>Fold:</b> PG0816-like <b>Superfamily:</b> PG0816-like <b>Family:</b> PG0816-like
84	<a href="#">d1eqzg</a>	Alignment	not modelled	6.3	16	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
85	<a href="#">c4yk3B</a>	Alignment	not modelled	6.3	22	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bepe protein; <b>PDBTitle:</b> crystal structure of the bid domain of bepe from bartonella henselae
86	<a href="#">d1lua2</a>	Alignment	not modelled	6.2	29	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Methylene-tetrahydromethanopterin dehydrogenase
87	<a href="#">c4kkkA</a>	Alignment	not modelled	6.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exoglucanase s; <b>PDBTitle:</b> complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
88	<a href="#">c4i6jB</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> f-box/lrr-repeat protein 3; <b>PDBTitle:</b> a ubiquitin ligase-substrate complex
89	<a href="#">c2wybA</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-homoserine lactone acylase pvdq subunit <b>PDBTitle:</b> the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
90	<a href="#">c1l2aD</a>	Alignment	not modelled	6.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cellobiohydrolase; <b>PDBTitle:</b> the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
91	<a href="#">d1l1ya</a>	Alignment	not modelled	6.0	19	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
92	<a href="#">c4yicA</a>	Alignment	not modelled	5.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap transporter solute binding protein; <b>PDBTitle:</b> crystal structure of a trap transporter solute binding protein2 (ipr025997) from bordetella bronchiseptica rb50 (bb0280, target efi-3 500035) with bound picolinic acid
93	<a href="#">c4u0zH</a>	Alignment	not modelled	5.9	20	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> adenosine monophosphate-protein transferase ficd; <b>PDBTitle:</b> eukaryotic fic domain containing protein with bound apcpp
94	<a href="#">c3izce</a>	Alignment	not modelled	5.9	13	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 60s ribosomal protein rpl11 (l5p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
95	<a href="#">c2lkqA</a>	Alignment	not modelled	5.8	67	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin lambda-like polypeptide 1; <b>PDBTitle:</b> nmr structure of the lambda 5 22-45 peptide
96	<a href="#">c1d0rA</a>	Alignment	not modelled	5.8	30	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> glucagon-like peptide-1-(7-36)-amide; <b>PDBTitle:</b> solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water
97	<a href="#">d1vqow1</a>	Alignment	not modelled	5.8	13	<b>Fold:</b> Ribosomal protein L30p/L7e <b>Superfamily:</b> Ribosomal protein L30p/L7e <b>Family:</b> Ribosomal protein L30p/L7e
98	<a href="#">d1g9ga</a>	Alignment	not modelled	5.8	21	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
99	<a href="#">d2fug41</a>	Alignment	not modelled	5.7	18	<b>Fold:</b> HydB/Nqo4-like <b>Superfamily:</b> HydB/Nqo4-like <b>Family:</b> Nqo4-like