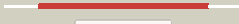



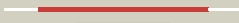


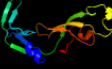

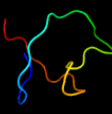



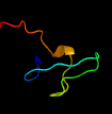

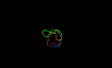






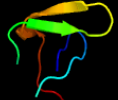
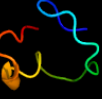

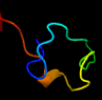







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1628c_(-)_1830077_1830568
Date	Fri Aug 2 13:30:22 BST 2019
Unique Job ID	be768d4c9e77010c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mg5W_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> W: <b>PDB Molecule:</b> 2,4-diacetylphloroglucinol biosynthesis protein; <b>PDBTitle:</b> a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (mapg)
2	<a href="#">c6et9H_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> pfam duf35; <b>PDBTitle:</b> structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
3	<a href="#">c6ok1B_</a>	 Alignment		100.0	28	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chsh2(duf35); <b>PDBTitle:</b> ltp2-chsh2(duf35) aldolase
4	<a href="#">d2gnra1</a>	 Alignment		100.0	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> SSO2064-like
5	<a href="#">c2kdxA_</a>	 Alignment		90.9	19	<b>PDB header:</b> metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein <b>PDBTitle:</b> solution structure of hypa protein
6	<a href="#">c3a44D_</a>	 Alignment		81.4	44	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> hydrogenase nickel incorporation protein hypa; <b>PDBTitle:</b> crystal structure of hypa in the dimeric form
7	<a href="#">c2kn9A_</a>	 Alignment		75.1	29	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
8	<a href="#">c4u3eA_</a>	 Alignment		74.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside triphosphate reductase; <b>PDBTitle:</b> anaerobic ribonucleotide reductase
9	<a href="#">c5ijlA_</a>	 Alignment		73.9	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase ii large subunit; <b>PDBTitle:</b> d-family dna polymerase - dp2 subunit (catalytic subunit)
10	<a href="#">d1lkoa2</a>	 Alignment		70.7	28	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
11	<a href="#">d2gmga1</a>	 Alignment		67.5	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF0610-like

12	<a href="#">c1dvbA</a>	Alignment		66.2	31	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
13	<a href="#">c2lcqA</a>	Alignment		66.0	45	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative toxin vapc6; <b>PDBTitle:</b> solution structure of the endonuclease nob1 from p.horikoshii
14	<a href="#">c6hmsB</a>	Alignment		63.9	41	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase ii large subunit,dna polymerase ii large <b>PDBTitle:</b> cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
15	<a href="#">d1s24a</a>	Alignment		62.9	28	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
16	<a href="#">c1s24A</a>	Alignment		62.9	28	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin 2; <b>PDBTitle:</b> rubredoxin domain ii from pseudomonas oleovorans
17	<a href="#">c6g5iy</a>	Alignment		62.6	22	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state r
18	<a href="#">c3j3v0</a>	Alignment		62.4	45	<b>PDB header:</b> ribosome <b>Chain:</b> 0: <b>PDB Molecule:</b> 50s ribosomal protein l32; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
19	<a href="#">d2zjr1</a>	Alignment		61.8	40	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
20	<a href="#">d6rxna</a>	Alignment		61.0	31	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
21	<a href="#">d2ayja1</a>	Alignment	not modelled	58.2	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L40e
22	<a href="#">c2ms3A</a>	Alignment	not modelled	57.5	25	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic nitric oxide reductase flavorubredoxin; <b>PDBTitle:</b> the nmr structure of the rubredoxin domain of the no reductase2 flavorubredoxin from escherichia coli
23	<a href="#">c4ce45</a>	Alignment	not modelled	57.1	29	<b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> mrpl32; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
24	<a href="#">d1iu5a</a>	Alignment	not modelled	57.0	38	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
25	<a href="#">d2fiya1</a>	Alignment	not modelled	56.9	19	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
26	<a href="#">d1brfa</a>	Alignment	not modelled	56.4	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
27	<a href="#">c2v3bB</a>	Alignment	not modelled	56.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rubredoxin 2; <b>PDBTitle:</b> crystal structure of the electron transfer complex rubredoxin -2 rubredoxin reductase from pseudomonas aeruginosa.
28	<a href="#">c2m4yA</a>	Alignment	not modelled	54.3	22	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> rubredoxin type protein from mycobacterium ulcerans
						<b>Fold:</b> Rubredoxin-like

29	<a href="#">d1dx8a_</a>	Alignment	not modelled	53.6	36	<b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
30	<a href="#">c2odxA</a>	Alignment	not modelled	53.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide iv; <b>PDBTitle:</b> solution structure of zn(ii)cox4
31	<a href="#">c3jc76_</a>	Alignment	not modelled	53.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> 6: <b>PDB Molecule:</b> dna replication licensing factor mcm6; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
32	<a href="#">c4v195_</a>	Alignment	not modelled	53.1	30	<b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> mitoribosomal protein bl32m, mrpl32; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
33	<a href="#">c6hu9p_</a>	Alignment	not modelled	52.7	22	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> P: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
34	<a href="#">d1h7va_</a>	Alignment	not modelled	52.5	40	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
35	<a href="#">c3wqyB_</a>	Alignment	not modelled	52.2	42	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> alanine--trna ligase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus alanyl-trna synthetase in2 complex with wild-type trna(ala) having g3.u70
36	<a href="#">d1qcva_</a>	Alignment	not modelled	51.0	26	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
37	<a href="#">d1iroa_</a>	Alignment	not modelled	50.8	37	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
38	<a href="#">d4rxna_</a>	Alignment	not modelled	49.0	39	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
39	<a href="#">d2j0151</a>	Alignment	not modelled	48.8	40	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
40	<a href="#">d2rdva_</a>	Alignment	not modelled	48.2	34	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
41	<a href="#">c1lttE_</a>	Alignment	not modelled	47.1	18	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> dna replication initiator (cdc21/cdc54); <b>PDBTitle:</b> the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
42	<a href="#">d1hk8a_</a>	Alignment	not modelled	47.0	27	<b>Fold:</b> PFL-like glycy radical enzymes <b>Superfamily:</b> PFL-like glycy radical enzymes <b>Family:</b> Class III anaerobic ribonucleotide reductase NRDD subunit
43	<a href="#">c1hk8A_</a>	Alignment	not modelled	47.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic ribonucleotide-triphosphate reductase; <b>PDBTitle:</b> structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dgtp
44	<a href="#">d1ltta_</a>	Alignment	not modelled	46.8	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA replication initiator (cdc21/cdc54) N-terminal domain
45	<a href="#">d1rb9a_</a>	Alignment	not modelled	46.7	34	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
46	<a href="#">d2ey4e1</a>	Alignment	not modelled	45.2	50	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
47	<a href="#">d2apob1</a>	Alignment	not modelled	44.7	52	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
48	<a href="#">c1vw4W_</a>	Alignment	not modelled	43.4	40	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 54s ribosomal protein l32, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
49	<a href="#">c2y69S_</a>	Alignment	not modelled	42.5	50	<b>PDB header:</b> electron transport <b>Chain:</b> S: <b>PDB Molecule:</b> cytochrome c oxidase subunit 5b; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
50	<a href="#">c2e9hA_</a>	Alignment	not modelled	42.0	24	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
51	<a href="#">d1k81a_</a>	Alignment	not modelled	41.5	24	<b>Fold:</b> Zinc-binding domain of translation initiation factor 2 beta <b>Superfamily:</b> Zinc-binding domain of translation initiation factor 2 beta <b>Family:</b> Zinc-binding domain of translation initiation factor 2 beta
52	<a href="#">d2cona1</a>	Alignment	not modelled	41.3	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> NOB1 zinc finger-like <b>Family:</b> NOB1 zinc finger-like
53	<a href="#">d1b8ta1</a>	Alignment	not modelled	40.7	30	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
54	<a href="#">c2gb5B_</a>	Alignment	not modelled	39.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh pyrophosphatase; <b>PDBTitle:</b> crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution <b>PDB header:</b> hydrolase

55	<a href="#">c3ja85_</a>	Alignment	not modelled	38.7	19	<b>Chain:</b> 5: <b>PDB Molecule:</b> minichromosome maintenance 5; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
56	<a href="#">d2dsxa1</a>	Alignment	not modelled	37.5	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
57	<a href="#">d2qam01</a>	Alignment	not modelled	37.4	16	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
58	<a href="#">c3ja86_</a>	Alignment	not modelled	37.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> 6: <b>PDB Molecule:</b> minichromosome maintenance 6; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
59	<a href="#">c1yuzB_</a>	Alignment	not modelled	34.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
60	<a href="#">c2ztgA_</a>	Alignment	not modelled	32.7	33	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa
61	<a href="#">c2zzfA_</a>	Alignment	not modelled	32.2	33	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of alanyl-trna synthetase without oligomerization2 domain
62	<a href="#">c2hr5B_</a>	Alignment	not modelled	31.7	28	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> pf1283- rubrerythrin from pyrococcus furiosus iron bound form
63	<a href="#">c2ysoA_</a>	Alignment	not modelled	31.0	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 95 homolog; <b>PDBTitle:</b> solution structure of the c2h2 type zinc finger (region 656-2 688) of human zinc finger protein 95 homolog
64	<a href="#">d1v54f_</a>	Alignment	not modelled	30.7	19	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Cytochrome c oxidase Subunit F
65	<a href="#">d1kn3a_</a>	Alignment	not modelled	30.4	15	<b>Fold:</b> PEBP-like <b>Superfamily:</b> PEBP-like <b>Family:</b> Phosphatidylethanolamine binding protein
66	<a href="#">d1hh2p1</a>	Alignment	not modelled	30.3	12	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
67	<a href="#">d2avue1</a>	Alignment	not modelled	29.7	16	<b>Fold:</b> FlhC-like <b>Superfamily:</b> FlhC-like <b>Family:</b> FlhC-like
68	<a href="#">c3lpeF_</a>	Alignment	not modelled	29.6	36	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> dna-directed rna polymerase subunit e"; <b>PDBTitle:</b> crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
69	<a href="#">d1vqo11</a>	Alignment	not modelled	28.5	26	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37e
70	<a href="#">c2lk1A_</a>	Alignment	not modelled	28.3	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein 5; <b>PDBTitle:</b> solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
71	<a href="#">c2lk0A_</a>	Alignment	not modelled	28.3	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein 5; <b>PDBTitle:</b> solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
72	<a href="#">d2qyqa1</a>	Alignment	not modelled	27.9	13	<b>Fold:</b> PEBP-like <b>Superfamily:</b> PEBP-like <b>Family:</b> Phosphatidylethanolamine binding protein
73	<a href="#">d1yuza2</a>	Alignment	not modelled	27.6	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
74	<a href="#">c6hv97_</a>	Alignment	not modelled	26.9	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
75	<a href="#">c3j21e_</a>	Alignment	not modelled	26.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 50s ribosomal protein l5p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
76	<a href="#">c2l55A_</a>	Alignment	not modelled	26.8	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> silb,silver efflux protein, mfp component of the three <b>PDBTitle:</b> solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
77	<a href="#">c4a1dK_</a>	Alignment	not modelled	26.5	38	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> ubiquitin-60s ribosomal protein l40; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rna and proteins of3 molecule 4.
78	<a href="#">c2avuF_</a>	Alignment	not modelled	25.9	16	<b>PDB header:</b> transcription activator <b>Chain:</b> F: <b>PDB Molecule:</b> flagellar transcriptional activator flhc; <b>PDBTitle:</b> structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription
79	<a href="#">d1nnqa2</a>	Alignment	not modelled	25.3	18	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
80	<a href="#">c2jufA_</a>	Alignment	not modelled	24.3	27	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> p53-associated parkin-like cytoplasmic protein; <b>PDBTitle:</b> nmr solution structure of parc cph domain. nesg target2

				hr3443b/sgc-toronto	
81	<a href="#">d1z8ga2</a>	Alignment	not modelled	24.0	25 <b>Fold:</b> SRCR-like <b>Superfamily:</b> SRCR-like <b>Family:</b> Hepsin, N-terminal domain
82	<a href="#">c2vl6C</a>	Alignment	not modelled	23.7	21 <b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> minichromosome maintenance protein mcm; <b>PDBTitle:</b> structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
83	<a href="#">d2jnga1</a>	Alignment	not modelled	23.3	27 <b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Tudor/PWWP/MBT <b>Family:</b> CPH domain
84	<a href="#">c3jc73</a>	Alignment	not modelled	23.2	15 <b>PDB header:</b> hydrolase <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
85	<a href="#">c5tvdA</a>	Alignment	not modelled	22.8	10 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tm16; <b>PDBTitle:</b> crystal structure of tm16
86	<a href="#">d1b8ta3</a>	Alignment	not modelled	22.4	42 <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
87	<a href="#">c5vbnB</a>	Alignment	not modelled	22.2	18 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase epsilon catalytic subunit a; <b>PDBTitle:</b> crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit
88	<a href="#">c2nchA</a>	Alignment	not modelled	22.0	13 <b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-1; <b>PDBTitle:</b> solution structure of translation initiation factor if1 from wolbachia2 endosymbiont strain trs of brugia malayi
89	<a href="#">c3j39m</a>	Alignment	not modelled	21.8	38 <b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
90	<a href="#">c3ndjA</a>	Alignment	not modelled	21.5	22 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
91	<a href="#">d1wjra</a>	Alignment	not modelled	21.5	29 <b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Tudor/PWWP/MBT <b>Family:</b> MBT repeat
92	<a href="#">d1p3ja2</a>	Alignment	not modelled	21.5	36 <b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain <b>Family:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain
93	<a href="#">d1s3ga2</a>	Alignment	not modelled	20.5	36 <b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain <b>Family:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain
94	<a href="#">d1zina2</a>	Alignment	not modelled	20.2	36 <b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain <b>Family:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain
95	<a href="#">c3vpbf</a>	Alignment	not modelled	19.7	38 <b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> alpha-aminoadipate carrier protein lysw; <b>PDBTitle:</b> argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
96	<a href="#">c5ij4A</a>	Alignment	not modelled	19.6	32 <b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cdc48-associated ubiquitin-like/zinc finger protein 1; <b>PDBTitle:</b> solution structure of an1-type zinc finger domain from cuz1 (cdc482 associated ubiquitin-like/zinc-finger protein-1)
97	<a href="#">c4tkoB</a>	Alignment	not modelled	18.9	18 <b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> emra; <b>PDBTitle:</b> structure of the periplasmic adaptor protein emra
98	<a href="#">c6hv96</a>	Alignment	not modelled	18.6	18 <b>PDB header:</b> dna binding protein <b>Chain:</b> 6: <b>PDB Molecule:</b> dna replication licensing factor mcm6; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
99	<a href="#">c2ytvA</a>	Alignment	not modelled	18.4	15 <b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold shock domain-containing protein e1; <b>PDBTitle:</b> solution structure of the fifth cold-shock domain of the human2 kiaa0885 protein (unr protein)