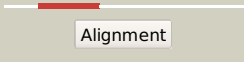

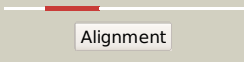
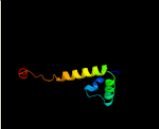
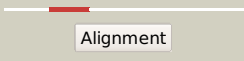

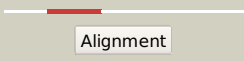
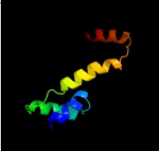
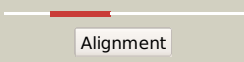
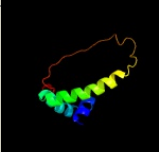
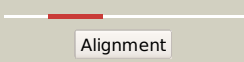

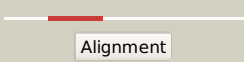

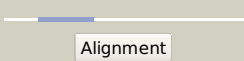

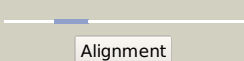
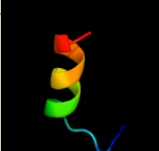
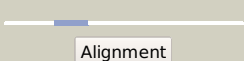

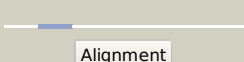
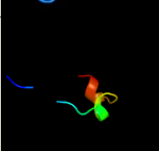


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0093c_(-)_102812_103660
Date	Tue Jul 23 14:50:13 BST 2019
Unique Job ID	c2a7bf8b391c1e7f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5frhA_</a>	 Alignment		99.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma factor rsra; <b>PDBTitle:</b> solution structure of oxidised rsra
2	<a href="#">c5wuqD_</a>	 Alignment		99.2	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> anti-sigma-w factor rsiw; <b>PDBTitle:</b> crystal structure of sigw in complex with its anti-sigma rsiw, a zinc2 binding form
3	<a href="#">c3hugJ_</a>	 Alignment		98.9	20	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> probable conserved membrane protein; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
4	<a href="#">c3vdoB_</a>	 Alignment		98.7	7	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anti-sigma-k factor rska; <b>PDBTitle:</b> structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
5	<a href="#">c2z2sD_</a>	 Alignment		98.5	22	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> anti-sigma factor chrr, transcriptional activator chrr; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
6	<a href="#">d1or7c_</a>	 Alignment		96.4	16	<b>Fold:</b> N-terminal, cytoplasmic domain of anti-sigmaE factor RseA <b>Superfamily:</b> N-terminal, cytoplasmic domain of anti-sigmaE factor RseA <b>Family:</b> N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
7	<a href="#">c1or7C_</a>	 Alignment		96.4	16	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> sigma-e factor negative regulatory protein; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
8	<a href="#">c6gh5M_</a>	 Alignment		24.3	18	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor,rna polymerase sigma-54 <b>PDBTitle:</b> cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
9	<a href="#">c2mugA_</a>	 Alignment		21.4	31	<b>PDB header:</b> ubiquitin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fanconi anemia-associated protein of 20 kda; <b>PDBTitle:</b> solution structure of the human faap20 ubz
10	<a href="#">c2murA_</a>	 Alignment		21.1	31	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fanconi anemia-associated protein of 20 kda; <b>PDBTitle:</b> solution structure of the human faap20 ubz-ubiquitin complex
11	<a href="#">c6fhsH_</a>	 Alignment		20.8	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> les2; <b>PDBTitle:</b> cryoem structure of ino80core

12	<a href="#">c2m0nA_</a>	Alignment		20.4	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
13	<a href="#">c3ol4B_</a>	Alignment		20.3	16	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
14	<a href="#">c4y2iA_</a>	Alignment		20.3	22	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-binding transport protein; <b>PDBTitle:</b> gold ion bound to golb
15	<a href="#">d2db7a1</a>	Alignment		19.9	24	<b>Fold:</b> Orange domain-like <b>Superfamily:</b> Orange domain-like <b>Family:</b> Hairy Orange domain
16	<a href="#">c2hh7A_</a>	Alignment		18.7	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein csor; <b>PDBTitle:</b> crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
17	<a href="#">c6cgaB_</a>	Alignment		18.4	50	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polycomb protein asx; <b>PDBTitle:</b> structure of the pr-dub complex
18	<a href="#">c2aj1A_</a>	Alignment		17.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cadmium-transporting atpase; <b>PDBTitle:</b> solution structure of apocada
19	<a href="#">c5camC_</a>	Alignment		17.7	10	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> pupr protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of the pseudomonas putida2 anti-sigma factor pupr (semet)
20	<a href="#">c6fmlH_</a>	Alignment		17.3	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> les2; <b>PDBTitle:</b> cryoem structure ino80core nucleosome complex
21	<a href="#">d1kvja_</a>	Alignment	not modelled	17.0	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
22	<a href="#">c1yg0A_</a>	Alignment	not modelled	17.0	5	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> cop associated protein; <b>PDBTitle:</b> solution structure of apo-copp from helicobacter pylori
23	<a href="#">c3fryB_</a>	Alignment	not modelled	16.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable copper-exporting p-type atpase a; <b>PDBTitle:</b> crystal structure of the copa c-terminal metal binding domain
24	<a href="#">c4m1pA_</a>	Alignment	not modelled	16.2	21	<b>PDB header:</b> transcription repressor <b>Chain:</b> A: <b>PDB Molecule:</b> copper-sensitive operon repressor (csor); <b>PDBTitle:</b> crystal structure of the copper-sensing repressor csor with cu(i) from2 geobacillus thermodenitrificans ng80-2
25	<a href="#">d2bcqa3</a>	Alignment	not modelled	15.3	22	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
26	<a href="#">c4adzA_</a>	Alignment	not modelled	15.2	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> csor; <b>PDBTitle:</b> crystal structure of the apo form of a copper-sensitive operon2 regulator (csor) protein from streptomyces lividans
27	<a href="#">d2e74f1</a>	Alignment	not modelled	14.8	11	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetM subunit of the cytochrome b6f complex <b>Family:</b> PetM subunit of the cytochrome b6f complex
28	<a href="#">c2ropA_</a>	Alignment	not modelled	14.8	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 2; <b>PDBTitle:</b> solution structure of domains 3 and 4 of human atp7b
29	<a href="#">c6e3vE_</a>	Alignment	not modelled	14.7	35	<b>PDB header:</b> signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> receptor activity-modifying protein 1;

29	<a href="#">c0e3yL_</a>	Alignment	not modelled	14.7	33	<b>PDBTitle:</b> cryo-em structure of the active, gs-protein complexed, human cgrp2 receptor
30	<a href="#">d1wjva1</a>	Alignment	not modelled	14.6	33	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> C2HC finger
31	<a href="#">c2wfbA_</a>	Alignment	not modelled	14.5	29	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein orp; <b>PDBTitle:</b> high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
32	<a href="#">c2l3mA_</a>	Alignment	not modelled	14.0	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> copper-ion-binding protein; <b>PDBTitle:</b> solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
33	<a href="#">c2re2A_</a>	Alignment	not modelled	13.8	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ta1041; <b>PDBTitle:</b> crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
34	<a href="#">c2mmuA_</a>	Alignment	not modelled	13.7	29	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein crga; <b>PDBTitle:</b> structure of crga, a cell division structural and regulatory protein2 from mycobacterium tuberculosis, in lipid bilayers
35	<a href="#">d2qifa1</a>	Alignment	not modelled	13.6	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
36	<a href="#">c2lqbA_</a>	Alignment	not modelled	13.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 2; <b>PDBTitle:</b> metal binding repeat 2 of the wilson disease protein (atp7b)
37	<a href="#">d2vana2</a>	Alignment	not modelled	13.0	19	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
38	<a href="#">c6ff2A_</a>	Alignment	not modelled	12.9	31	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> copper chaperone copz; <b>PDBTitle:</b> copz metallochaperone
39	<a href="#">c5fmnB_</a>	Alignment	not modelled	12.7	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> inrs; <b>PDBTitle:</b> the nickel-responsive transcriptional regulator inrs
40	<a href="#">c2ofhX_</a>	Alignment	not modelled	12.0	28	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
41	<a href="#">c4h44F_</a>	Alignment	not modelled	12.0	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> 2.70 a cytochrome b6f complex structure from nostoc pcc 7120
42	<a href="#">c4ogqF_</a>	Alignment	not modelled	12.0	18	<b>PDB header:</b> electron transport <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex
43	<a href="#">c2zt9F_</a>	Alignment	not modelled	12.0	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
44	<a href="#">d1s6ua_</a>	Alignment	not modelled	11.6	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
45	<a href="#">c5v2sA_</a>	Alignment	not modelled	11.5	17	<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
46	<a href="#">c2qdrA_</a>	Alignment	not modelled	11.5	38	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution
47	<a href="#">c2kyzA_</a>	Alignment	not modelled	11.4	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal binding protein; <b>PDBTitle:</b> nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
48	<a href="#">c2mrfA_</a>	Alignment	not modelled	11.4	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rad18; <b>PDBTitle:</b> nmr structure of the ubiquitin-binding zinc finger (ubz) domain from2 human rad18
49	<a href="#">c5tx8A_</a>	Alignment	not modelled	11.1	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> hh2; <b>PDBTitle:</b> solution structure of the de novo mini protein gh_h_44
50	<a href="#">d1p6ta2</a>	Alignment	not modelled	11.0	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
51	<a href="#">c3vthA_</a>	Alignment	not modelled	11.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
52	<a href="#">c5byhM_</a>	Alignment	not modelled	10.9	28	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor; <b>PDBTitle:</b> crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
53	<a href="#">c3dxxX_</a>	Alignment	not modelled	10.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> copper-transporting atpase ran1; <b>PDBTitle:</b> crystal structure of a copper binding domain from hma7, a p-2 type atpase
54	<a href="#">d2aw0a_</a>	Alignment	not modelled	10.3	36	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
55	<a href="#">d1cpza_</a>	Alignment	not modelled	10.1	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain

						<b>Family:</b> HMA, heavy metal-associated domain
56	<a href="#">c2ofgX_</a>	Alignment	not modelled	10.0	22	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
57	<a href="#">c5ze4A_</a>	Alignment	not modelled	9.8	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the structure of holo- structure of dhad complex with [2fe-2s] cluster
58	<a href="#">d2fmpa3</a>	Alignment	not modelled	9.7	22	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
59	<a href="#">c4g9iA_</a>	Alignment	not modelled	9.7	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation protein hypf; <b>PDBTitle:</b> crystal structure of t.kodakarensis hypf
60	<a href="#">c2l25A_</a>	Alignment	not modelled	9.5	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> np_888769.1
61	<a href="#">c3m92B_</a>	Alignment	not modelled	9.5	42	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein ycin; <b>PDBTitle:</b> the structure of ycin, an uncharacterized protein from shigella2 flexneri.
62	<a href="#">c2ldiA_</a>	Alignment	not modelled	9.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> nmr solution structure of ziaan sub mutant
63	<a href="#">c1nomA_</a>	Alignment	not modelled	9.2	20	<b>PDB header:</b> nucleotidyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase beta; <b>PDBTitle:</b> dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)
64	<a href="#">c2rmlA_</a>	Alignment	not modelled	9.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting p-type atpase copa; <b>PDBTitle:</b> solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
65	<a href="#">c3vhsB_</a>	Alignment	not modelled	8.7	42	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> atpase wrnip1; <b>PDBTitle:</b> crystal structure of ubz of human wrnip1
66	<a href="#">c2ga7A_</a>	Alignment	not modelled	8.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
67	<a href="#">c2k2pA_</a>	Alignment	not modelled	8.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1203; <b>PDBTitle:</b> solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
68	<a href="#">d1jroa1</a>	Alignment	not modelled	8.3	38	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
69	<a href="#">c3qd9D_</a>	Alignment	not modelled	8.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> qsox from trypanosoma brucei (tbqsox); <b>PDBTitle:</b> c72s/c353s mutant of trypanosoma brucei qsox containing an interdomain2 disulfide
70	<a href="#">c4nqa_</a>	Alignment	not modelled	8.1	21	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> I: <b>PDB Molecule:</b> liver x nuclear receptor beta; <b>PDBTitle:</b> crystal structure of liganded hrxr-alpha/hrxr-beta heterodimer on dna
71	<a href="#">c1y3kA_</a>	Alignment	not modelled	8.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the apo form of the fifth domain of2 menkes protein
72	<a href="#">d1p6ta1</a>	Alignment	not modelled	8.0	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
73	<a href="#">d2ggpb1</a>	Alignment	not modelled	7.9	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
74	<a href="#">d1v58a1</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
75	<a href="#">c5lcyD_</a>	Alignment	not modelled	7.8	24	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> frmr; <b>PDBTitle:</b> formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
76	<a href="#">d1v92a_</a>	Alignment	not modelled	7.7	11	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TAP-C domain-like
77	<a href="#">c4nsmA_</a>	Alignment	not modelled	7.7	46	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like protein sclb; <b>PDBTitle:</b> crystal structure of the streptococcal collagen-like protein 22 globular domain from invasive m3-type group a streptococcus
78	<a href="#">c5aj3k_</a>	Alignment	not modelled	7.6	56	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> mitoribosomal protein us11m, mrps11; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
79	<a href="#">c3aaib_</a>	Alignment	not modelled	7.4	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> copper homeostasis operon regulatory protein; <b>PDBTitle:</b> x-ray crystal structure of csor from thermus thermophilus hb8
80	<a href="#">c8icza_</a>	Alignment	not modelled	7.3	23	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase beta (e.c.2.7.7.7)); <b>PDBTitle:</b> dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)

81	<a href="#">c1yjrA</a>	Alignment	not modelled	7.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
82	<a href="#">c3dzuD</a>	Alignment	not modelled	7.2	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> peroxisome proliferator-activated receptor gamma; <b>PDBTitle:</b> intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with bvt.13, 9-cis retinoic acid and ncoa2 peptide
83	<a href="#">c2bcuA</a>	Alignment	not modelled	7.2	23	<b>PDB header:</b> transferase, lyase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase lambda; <b>PDBTitle:</b> dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
84	<a href="#">c2kxhA</a>	Alignment	not modelled	7.1	17	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative heavy metal transporter; <b>PDBTitle:</b> structure of the zinc binding domain of the atpase hma4
85	<a href="#">c5uanB</a>	Alignment	not modelled	7.1	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> retinoic acid receptor beta; <b>PDBTitle:</b> crystal structure of multi-domain rar-beta-rxr-alpha heterodimer on2 dna
86	<a href="#">c2kvcA</a>	Alignment	not modelled	7.1	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
87	<a href="#">c3dzyA</a>	Alignment	not modelled	7.0	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> retinoic acid receptor rxr-alpha; <b>PDBTitle:</b> intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with rosiglitazone, 9-cis retinoic acid and ncoa2 peptide
88	<a href="#">d1eysh2</a>	Alignment	not modelled	7.0	29	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
89	<a href="#">d1rzhh2</a>	Alignment	not modelled	7.0	33	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
90	<a href="#">c2epoB</a>	Alignment	not modelled	6.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetyl-beta-d-glucosaminidase; <b>PDBTitle:</b> n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
91	<a href="#">c5uanA</a>	Alignment	not modelled	6.9	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> retinoic acid receptor rxr-alpha; <b>PDBTitle:</b> crystal structure of multi-domain rar-beta-rxr-alpha heterodimer on2 dna
92	<a href="#">c5ac4A</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-beta-d-glucosaminidase; <b>PDBTitle:</b> gh20c, beta-hexosaminidase from streptococcus pneumoniae in complex2 with galnac
93	<a href="#">c2ihmA</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase mu; <b>PDBTitle:</b> polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
94	<a href="#">c3hd6A</a>	Alignment	not modelled	6.8	9	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter rh type c; <b>PDBTitle:</b> crystal structure of the human rhesus glycoprotein rhcg
95	<a href="#">d1osda</a>	Alignment	not modelled	6.7	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
96	<a href="#">d1lib8a2</a>	Alignment	not modelled	6.5	25	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> YhbC-like, N-terminal domain <b>Family:</b> YhbC-like, N-terminal domain
97	<a href="#">c3vhsA</a>	Alignment	not modelled	6.5	42	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase wrnip1; <b>PDBTitle:</b> crystal structure of ubz of human wrnip1
98	<a href="#">c6nmiC</a>	Alignment	not modelled	6.5	43	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general transcription factor iih subunit 1, p62; <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
99	<a href="#">c2lkyA</a>	Alignment	not modelled	6.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b