

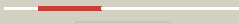




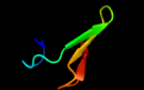



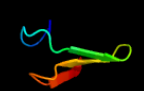










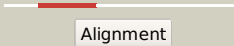



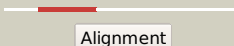


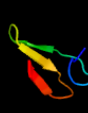
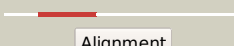
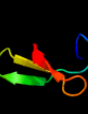
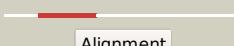







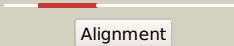


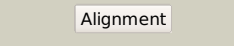
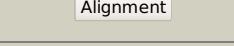
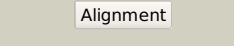




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0829 (-) _921578_921868
Date	Fri Jul 26 01:50:41 BST 2019
Unique Job ID	9ea61741b4c6252d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2akla2</a>	 Alignment		94.5	16	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> PhnA zinc-binding domain
2	<a href="#">c2gb5B_</a>	 Alignment		94.2	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
3	<a href="#">c6e7aY_</a>	 Alignment		94.0	29	<b>PDB header:</b> dna binding protein/dna/rna <b>Chain:</b> Y; <b>PDB Molecule:</b> casx; <b>PDBTitle:</b> casx-grna-dna(30bp) state ii
4	<a href="#">c2qa4Z_</a>	 Alignment		93.5	27	<b>PDB header:</b> ribosome <b>Chain:</b> Z; <b>PDB Molecule:</b> 50s ribosomal protein l37ae; <b>PDBTitle:</b> a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
5	<a href="#">c2aklA_</a>	 Alignment		93.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> phna-like protein pa0128; <b>PDBTitle:</b> solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
6	<a href="#">d1vqoz1</a>	 Alignment		93.0	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
7	<a href="#">d1ffkw_</a>	 Alignment		92.7	19	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
8	<a href="#">c1hk8A_</a>	 Alignment		92.6	17	<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
9	<a href="#">d1hk8a_</a>	 Alignment		92.6	17	<b>Fold:</b> PFL-like glycyl radical enzymes <b>Superfamily:</b> PFL-like glycyl radical enzymes <b>Family:</b> Class III anaerobic ribonucleotide reductase NRDD subunit
10	<a href="#">c4b6ap_</a>	 Alignment		92.6	27	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> 60s ribosomal protein l17-a; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
11	<a href="#">c4a17Y_</a>	 Alignment		92.5	23	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> rpl37a; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.

12	<a href="#">c3cc4Z_</a>	 Alignment		92.4	27	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae; <b>PDBTitle:</b> co-crystal structure of anisomycin bound to the 50s ribosomal subunit
13	<a href="#">c2zkrz_</a>	 Alignment		92.3	27	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> Z: <b>PDB Molecule:</b> e site t-rna; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an 3.7 a cryo-em map
14	<a href="#">d1jj2y_</a>	 Alignment		92.3	19	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
15	<a href="#">c3j21i_</a>	 Alignment		92.2	31	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l13p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
16	<a href="#">c3izrm_</a>	 Alignment		92.2	19	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l23 (l14p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
17	<a href="#">c1yshD_</a>	 Alignment		92.2	19	<b>PDB header:</b> structural protein/rna <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein l37a; <b>PDBTitle:</b> localization and dynamic behavior of ribosomal protein l30e
18	<a href="#">c3j39p_</a>	 Alignment		92.1	27	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
19	<a href="#">d1pfta_</a>	 Alignment		91.9	19	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
20	<a href="#">c3zf7o_</a>	 Alignment		91.8	35	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l13a, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
21	<a href="#">c1s1i9_</a>	 Alignment	not modelled	91.1	27	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l43; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
22	<a href="#">c3jyw9_</a>	 Alignment	not modelled	90.4	27	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l43; <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
23	<a href="#">c3k7aM_</a>	 Alignment	not modelled	89.1	16	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> crystal structure of an rna polymerase ii-tfiib complex
24	<a href="#">c5fz5M_</a>	 Alignment	not modelled	88.8	16	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> transcription initiation complex structures elucidate dna opening (cc)
25	<a href="#">d1dl6a_</a>	 Alignment	not modelled	88.3	13	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
26	<a href="#">c3k1fM_</a>	 Alignment	not modelled	88.1	17	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> crystal structure of rna polymerase ii in complex with tfiib
27	<a href="#">d1twfi2</a>	 Alignment	not modelled	87.7	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
28	<a href="#">c3ky9B_</a>	 Alignment	not modelled	87.3	16	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> proto-oncogene vav;

						<b>PDBTitle:</b> autoinhibited vav1
29	<a href="#">c5iy9Q_</a>	Alignment	not modelled	87.3	22	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> Q; <b>PDB Molecule:</b> general transcription factor iie subunit 1; <b>PDBTitle:</b> human holo-pic in the initial transcribing state (no iis)
30	<a href="#">c5iy9M_</a>	Alignment	not modelled	87.3	14	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> M; <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> human holo-pic in the initial transcribing state (no iis)
31	<a href="#">c2lcqA_</a>	Alignment	not modelled	86.8	15	<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
32	<a href="#">c5x51X_</a>	Alignment	not modelled	86.6	27	<b>PDB header:</b> transferase <b>Chain:</b> X; <b>PDB Molecule:</b> rna polymerase subunit, found in rna polymerase complexes <b>PDBTitle:</b> rna polymerase ii from komagataella pastoris (type-3 crystal)
33	<a href="#">c5flmI_</a>	Alignment	not modelled	86.1	25	<b>PDB header:</b> transcription <b>Chain:</b> I; <b>PDB Molecule:</b> dna-directed rna polymerase ii subunit rpb9; <b>PDBTitle:</b> structure of transcribing mammalian rna polymerase ii
34	<a href="#">c1yuzB_</a>	Alignment	not modelled	85.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
35	<a href="#">c4v1oM_</a>	Alignment	not modelled	85.6	22	<b>PDB header:</b> transcription <b>Chain:</b> M; <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> architecture of the rna polymerase ii-mediator core transcription2 initiation complex
36	<a href="#">c2vrwB_</a>	Alignment	not modelled	85.6	15	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> critical structural role for the ph and c1 domains of the2 vav1 exchange factor
37	<a href="#">c1i3qI_</a>	Alignment	not modelled	85.2	20	<b>PDB header:</b> transcription <b>Chain:</b> I; <b>PDB Molecule:</b> dna-directed rna polymerase ii 14.2kd <b>PDBTitle:</b> rna polymerase ii crystal form i at 3.1 a resolution
38	<a href="#">c6f42V_</a>	Alignment	not modelled	85.0	15	<b>PDB header:</b> transcription <b>Chain:</b> V; <b>PDB Molecule:</b> transcription factor iiib 70 kda subunit; <b>PDBTitle:</b> rna polymerase iii closed complex cc1.
39	<a href="#">c4u3eA_</a>	Alignment	not modelled	84.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonucleoside triphosphate reductase; <b>PDBTitle:</b> anaerobic ribonucleotide reductase
40	<a href="#">c2kdxA_</a>	Alignment	not modelled	84.8	22	<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
41	<a href="#">c3cngC_</a>	Alignment	not modelled	84.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from nitrosomonas europaea
42	<a href="#">c2ja6L_</a>	Alignment	not modelled	84.7	16	<b>PDB header:</b> transferase <b>Chain:</b> L; <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii 7.7 kda <b>PDBTitle:</b> cpd lesion containing rna polymerase ii elongation complex b
43	<a href="#">c3h0gI_</a>	Alignment	not modelled	84.6	24	<b>PDB header:</b> transcription <b>Chain:</b> L; <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc4; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
44	<a href="#">c5flmL_</a>	Alignment	not modelled	83.8	20	<b>PDB header:</b> transcription <b>Chain:</b> L; <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc4; <b>PDBTitle:</b> structure of transcribing mammalian rna polymerase ii
45	<a href="#">c6hv8A_</a>	Alignment	not modelled	83.4	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dna polymerase epsilon catalytic subunit a; <b>PDBTitle:</b> cryo-em structure of s. cerevisiae polymerase epsilon deltatcat mutant
46	<a href="#">c6cnbR_</a>	Alignment	not modelled	83.1	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> R; <b>PDB Molecule:</b> transcription factor iiib 70 kda subunit,tata-box-binding <b>PDBTitle:</b> yeast rna polymerase iii initial transcribing complex
47	<a href="#">d2ct7a1</a>	Alignment	not modelled	83.1	20	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> !BR domain
48	<a href="#">c4c2mX_</a>	Alignment	not modelled	82.3	14	<b>PDB header:</b> transcription <b>Chain:</b> X; <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa12; <b>PDBTitle:</b> structure of rna polymerase i at 2.8 a resolution
49	<a href="#">c6g5iy_</a>	Alignment	not modelled	81.8	24	<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
50	<a href="#">c3h0gI_</a>	Alignment	not modelled	80.9	18	<b>PDB header:</b> transcription <b>Chain:</b> I; <b>PDB Molecule:</b> dna-directed rna polymerase ii subunit rpb9; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
51	<a href="#">c3bjjA_</a>	Alignment	not modelled	80.1	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
52	<a href="#">c5iycU_</a>	Alignment	not modelled	79.2	17	<b>PDB header:</b> transcription, transferase/dna <b>Chain:</b> U; <b>PDB Molecule:</b> transcription elongation factor a protein 1; <b>PDBTitle:</b> human core-pic in the initial transcribing state
53	<a href="#">c2f9yB_</a>	Alignment	not modelled	78.2	21	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli

54	<a href="#">d2f9yb1</a>	Alignment	not modelled	78.2	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
55	<a href="#">c4qiwp_</a>	Alignment	not modelled	78.0	16	<b>PDB header:</b> transcription <b>Chain:</b> P: <b>PDB Molecule:</b> dna-directed rna polymerase subunit p; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
56	<a href="#">c2f9iD_</a>	Alignment	not modelled	77.7	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
57	<a href="#">c5vbnB_</a>	Alignment	not modelled	77.2	19	<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
58	<a href="#">c1y1yS_</a>	Alignment	not modelled	76.8	16	<b>PDB header:</b> transferase/transcription/dna-rna hybrid <b>Chain:</b> S: <b>PDB Molecule:</b> transcription elongation factor s-ii; <b>PDBTitle:</b> rna polymerase ii-tfiis-dna/rna complex
59	<a href="#">c5ijlA_</a>	Alignment	not modelled	76.6	20	<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)
60	<a href="#">c5wtiZ_</a>	Alignment	not modelled	76.2	31	<b>PDB header:</b> hydrolase/dna/rna <b>Chain:</b> Z: <b>PDB Molecule:</b> crispr-associated protein; <b>PDBTitle:</b> crystal structure of the crispr-associated protein in complex with2 crrna and dna
61	<a href="#">c3wwnB_</a>	Alignment	not modelled	76.0	23	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orff; <b>PDBTitle:</b> crystal structure of lysz from thermus thermophilus complex with lysw
62	<a href="#">c2hr5B_</a>	Alignment	not modelled	75.3	19	<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="#">c1pqvS_</a>	Alignment	not modelled	75.0	23	<b>PDB header:</b> transferase/transcription <b>Chain:</b> S: <b>PDB Molecule:</b> transcription elongation factor s-ii; <b>PDBTitle:</b> rna polymerase ii-tfiis complex
64	<a href="#">c5xonU_</a>	Alignment	not modelled	73.4	13	<b>PDB header:</b> transcription/rna <b>Chain:</b> U: <b>PDB Molecule:</b> general transcription elongation factor tfiis; <b>PDBTitle:</b> rna polymerase ii elongation complex bound with spt4/5 and tfiis
65	<a href="#">c2nb9A_</a>	Alignment	not modelled	73.4	26	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of zitp zinc finger
66	<a href="#">d2fiya1</a>	Alignment	not modelled	72.8	19	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
67	<a href="#">c5fjal_</a>	Alignment	not modelled	72.4	14	<b>PDB header:</b> transcription <b>Chain:</b> I: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc10; <b>PDBTitle:</b> cryo-em structure of yeast rna polymerase iii at 4.7 a
68	<a href="#">c2m4yA_</a>	Alignment	not modelled	72.3	35	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> rubredoxin type protein from mycobacterium ulcerans
69	<a href="#">d1qypa_</a>	Alignment	not modelled	72.2	30	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
70	<a href="#">d1pfva3</a>	Alignment	not modelled	72.2	30	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Methionyl-tRNA synthetase (MetRS), Zn-domain <b>Family:</b> Methionyl-tRNA synthetase (MetRS), Zn-domain
71	<a href="#">c6hmsB_</a>	Alignment	not modelled	72.1	20	<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
72	<a href="#">d1k81a_</a>	Alignment	not modelled	72.0	16	<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
73	<a href="#">d2zjrz1</a>	Alignment	not modelled	71.9	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
74	<a href="#">d1tfia_</a>	Alignment	not modelled	71.5	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
75	<a href="#">c5fywW_</a>	Alignment	not modelled	71.4	14	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha; <b>PDBTitle:</b> transcription initiation complex structures elucidate dna opening (oc)
76	<a href="#">c2enzA_</a>	Alignment	not modelled	70.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c theta type; <b>PDBTitle:</b> solution structure of the second c1 domain from human2 protein kinase c theta
77	<a href="#">c3j3v0_</a>	Alignment	not modelled	69.9	20	<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)
78	<a href="#">d1yuza2</a>	Alignment	not modelled	69.1	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
79	<a href="#">d2j0151</a>	Alianment	not modelled	69.0	20	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins

						Family:Ribosomal protein L32p
80	<a href="#">c2qkdA_</a>	Alignment	not modelled	68.2	22	<b>PDB header:</b> signaling protein, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein zpr1; <b>PDBTitle:</b> crystal structure of tandem zpr1 domains
81	<a href="#">d1nnga2</a>	Alignment	not modelled	68.0	19	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
82	<a href="#">c2eliA_</a>	Alignment	not modelled	67.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c alpha type; <b>PDBTitle:</b> solution structure of the second phorbol2 esters/diacylglycerol binding domain of human protein3 kinase c alpha type
83	<a href="#">c4rvga_</a>	Alignment	not modelled	67.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-mycarose 3-c-methyltransferase; <b>PDBTitle:</b> crystal structure of mtmc in complex with sam and tdp
84	<a href="#">d1lkoa2</a>	Alignment	not modelled	66.9	36	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
85	<a href="#">c3zyga_</a>	Alignment	not modelled	66.8	25	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine kinase <b>PDBTitle:</b> crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
86	<a href="#">d1tbna_</a>	Alignment	not modelled	66.8	18	<b>Fold:</b> Cysteine-rich domain <b>Superfamily:</b> Cysteine-rich domain <b>Family:</b> Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
87	<a href="#">c3ndjA_</a>	Alignment	not modelled	65.6	34	<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
88	<a href="#">c2ba1B_</a>	Alignment	not modelled	65.4	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> archaeal exosome rna binding protein csl4; <b>PDBTitle:</b> archaeal exosome core
89	<a href="#">c1nuiA_</a>	Alignment	not modelled	65.0	21	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna primase/helicase; <b>PDBTitle:</b> crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
90	<a href="#">d2g45a1</a>	Alignment	not modelled	64.9	15	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> Zf-UBP
91	<a href="#">d1ptqa_</a>	Alignment	not modelled	64.4	15	<b>Fold:</b> Cysteine-rich domain <b>Superfamily:</b> Cysteine-rich domain <b>Family:</b> Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
92	<a href="#">c3a44D_</a>	Alignment	not modelled	64.3	22	<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
93	<a href="#">c5xogM_</a>	Alignment	not modelled	64.1	23	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription elongation factor 1 homolog; <b>PDBTitle:</b> rna polymerase ii elongation complex bound with spt5 kow5 and elf1
94	<a href="#">c1dvaA_</a>	Alignment	not modelled	63.7	45	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
95	<a href="#">c1z2qa_</a>	Alignment	not modelled	63.1	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lm5-1; <b>PDBTitle:</b> high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major
96	<a href="#">d1xa6a3</a>	Alignment	not modelled	63.1	13	<b>Fold:</b> Cysteine-rich domain <b>Superfamily:</b> Cysteine-rich domain <b>Family:</b> Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
97	<a href="#">d1wjva1</a>	Alignment	not modelled	62.9	27	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> C2HC finger
98	<a href="#">c1y8fA_</a>	Alignment	not modelled	62.9	13	<b>PDB header:</b> endocytosis/exocytosis,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> unc-13 homolog a; <b>PDBTitle:</b> solution structure of the munc13-1 c1-domain
99	<a href="#">c2ennA_</a>	Alignment	not modelled	62.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c theta type; <b>PDBTitle:</b> solution structure of the first c1 domain from human2 protein kinase c theta
100	<a href="#">c5y06A_</a>	Alignment	not modelled	61.9	34	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> msmeg_4306; <b>PDBTitle:</b> structural characterization of msmeg_4306 from mycobacterium smegmatis
101	<a href="#">c2kn9A_</a>	Alignment	not modelled	61.8	11	<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
102	<a href="#">c6gymW_</a>	Alignment	not modelled	61.1	20	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha, <b>PDBTitle:</b> structure of a yeast closed complex with distorted dna (ccd1st)
103	<a href="#">c2yqqa_</a>	Alignment	not modelled	60.2	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger hit domain-containing protein 3; <b>PDBTitle:</b> solution structure of the zf-hit domain in zinc finger hit2 domain-containing protein 3 (trip-3)
104	<a href="#">d1rb9a_</a>	Alignment	not modelled	60.0	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like

						<b>Family:</b> Rubredoxin
105	<a href="#">c2db6A</a>	Alignment	not modelled	59.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 and cysteine rich domain 3; <b>PDBTitle:</b> solution structure of rsgi ruh-051, a c1 domain of stac32 from human cdna
106	<a href="#">c1ee8A</a>	Alignment	not modelled	57.9	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mutm (fpg) protein; <b>PDBTitle:</b> crystal structure of mutm (fpg) protein from thermus thermophilus hb8
107	<a href="#">c2cszA</a>	Alignment	not modelled	57.9	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> synaptotagmin-like protein 4; <b>PDBTitle:</b> solution structure of the ring domain of the synaptotagmin-2 like protein 4
108	<a href="#">c3bvoA</a>	Alignment	not modelled	57.4	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> co-chaperone protein hscb, mitochondrial precursor; <b>PDBTitle:</b> crystal structure of human co-chaperone protein hscb
109	<a href="#">c6o9lQ</a>	Alignment	not modelled	56.7	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> Q: <b>PDB Molecule:</b> general transcription factor iie subunit 1; <b>PDBTitle:</b> human holo-pic in the closed state
110	<a href="#">d1k3xa3</a>	Alignment	not modelled	55.8	22	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
111	<a href="#">c2ctuA</a>	Alignment	not modelled	55.7	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 483; <b>PDBTitle:</b> solution structure of zinc finger domain from human zn2 finger protein 483
112	<a href="#">d1x3za1</a>	Alignment	not modelled	55.7	28	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
113	<a href="#">d1wiia</a>	Alignment	not modelled	55.2	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Putative zinc binding domain
114	<a href="#">c5u31A</a>	Alignment	not modelled	54.9	29	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease c2c1; <b>PDBTitle:</b> crystal structure of aacc2c1-sgrna-8mer substrate dna ternary complex
115	<a href="#">c5fmfR</a>	Alignment	not modelled	54.7	18	<b>PDB header:</b> transcription <b>Chain:</b> R: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha, tfa1; <b>PDBTitle:</b> the p-lobe of rna polymerase ii pre-initiation complex
116	<a href="#">d1s24a</a>	Alignment	not modelled	54.5	31	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
117	<a href="#">c1s24A</a>	Alignment	not modelled	54.5	31	<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
118	<a href="#">c3nw0A</a>	Alignment	not modelled	54.3	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural maintenance of chromosomes element 1 <b>PDBTitle:</b> crystal structure of mageg1 and nse1 complex
119	<a href="#">c5wqeA</a>	Alignment	not modelled	53.9	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease c2c1; <b>PDBTitle:</b> crystal structure of alicyclobacillus acidoterrestris c2c1 in complex2 with single-guide rna at 3.1 angstrom resolution
120	<a href="#">c3c5kA</a>	Alignment	not modelled	53.5	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histone deacetylase 6; <b>PDBTitle:</b> crystal structure of human hdac6 zinc finger domain