
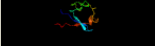
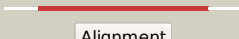

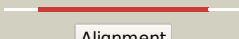


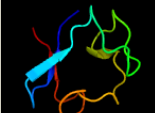

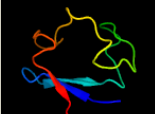

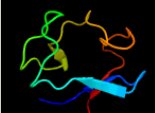










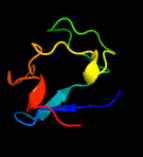
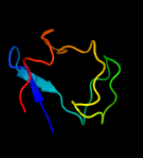
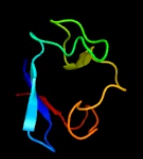
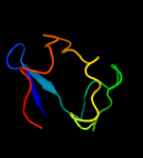
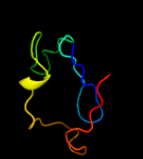
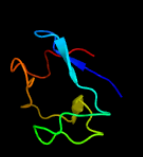





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3250c_(rubB)_3630381_3630563
Date	Thu Aug 8 16:20:45 BST 2019
Unique Job ID	3a34d736ebac323b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kn9A_</a>	 Alignment		100.0	98	<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
2	<a href="#">c1s24A_</a>	 Alignment		99.9	57	<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
3	<a href="#">d1s24a_</a>	 Alignment		99.9	57	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
4	<a href="#">d1iroa_</a>	 Alignment		99.9	47	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
5	<a href="#">c2v3bB_</a>	 Alignment		99.9	66	<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.
6	<a href="#">d4rxna_</a>	 Alignment		99.9	51	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
7	<a href="#">d1h7va_</a>	 Alignment		99.9	31	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
8	<a href="#">d2rdva_</a>	 Alignment		99.9	51	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
9	<a href="#">d1dx8a_</a>	 Alignment		99.9	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
10	<a href="#">d1qcva_</a>	 Alignment		99.9	42	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
11	<a href="#">d1brfa_</a>	 Alignment		99.9	51	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin

12	<a href="#">d2dsxa1</a>	Alignment		99.9	51	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
13	<a href="#">d1rb9a_</a>	Alignment		99.9	54	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
14	<a href="#">d1iu5a_</a>	Alignment		99.9	49	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
15	<a href="#">c2ms3A_</a>	Alignment		99.9	38	<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
16	<a href="#">c2m4yA_</a>	Alignment		99.9	54	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> rubredoxin type protein from mycobacterium ulcerans
17	<a href="#">d6rxna_</a>	Alignment		99.8	43	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
18	<a href="#">c5xpdA_</a>	Alignment		99.7	45	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transporter; <b>PDBTitle:</b> sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
19	<a href="#">c2hr5B_</a>	Alignment		98.6	34	<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
20	<a href="#">d1lkoa2</a>	Alignment		98.6	34	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
21	<a href="#">d1yuza2</a>	Alignment	not modelled	98.4	31	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
22	<a href="#">c1dvaA_</a>	Alignment	not modelled	98.4	35	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
23	<a href="#">c1yuzB_</a>	Alignment	not modelled	98.4	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
24	<a href="#">d1nnaq2</a>	Alignment	not modelled	98.3	38	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
25	<a href="#">c4tpuA_</a>	Alignment	not modelled	98.0	37	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> crystal structure of ferredoxin-dependent disulfide reductase from2 methanosarcina acetivorans
26	<a href="#">d2gmga1</a>	Alignment	not modelled	92.9	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF0610-like
27	<a href="#">c5fywW_</a>	Alignment	not modelled	91.8	19	<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)
28	<a href="#">c5zb8B_</a>	Alignment	not modelled	91.5	38	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pfuendoq; <b>PDBTitle:</b> crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus <b>PDB header:</b> transcription

29	<a href="#">c6gymW_</a>	Alignment	not modelled	91.0	18	<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 (ccdist)
30	<a href="#">c5iy9O_</a>	Alignment	not modelled	90.2	21	<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)
31	<a href="#">c5oqmW_</a>	Alignment	not modelled	88.6	18	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription factor tfiie subunit; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
32	<a href="#">c5oqjW_</a>	Alignment	not modelled	88.4	18	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih
33	<a href="#">c3h0gl_</a>	Alignment	not modelled	88.0	19	<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
34	<a href="#">c2kdxA_</a>	Alignment	not modelled	87.5	30	<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
35	<a href="#">c5fmfR_</a>	Alignment	not modelled	87.5	20	<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
36	<a href="#">c3a44D_</a>	Alignment	not modelled	87.5	21	<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
37	<a href="#">c2lqgA_</a>	Alignment	not modelled	86.6	48	<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
38	<a href="#">c6o9lQ_</a>	Alignment	not modelled	86.6	23	<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
39	<a href="#">c1i3gl_</a>	Alignment	not modelled	83.2	27	<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
40	<a href="#">d1m2ka_</a>	Alignment	not modelled	81.9	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
41	<a href="#">c4c2mX_</a>	Alignment	not modelled	80.3	19	<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
42	<a href="#">c5flml_</a>	Alignment	not modelled	79.9	21	<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
43	<a href="#">c5j9wC_</a>	Alignment	not modelled	79.8	20	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> acetophenone carboxylase beta subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
44	<a href="#">c2m6oA_</a>	Alignment	not modelled	79.0	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
45	<a href="#">c4u3eA_</a>	Alignment	not modelled	77.9	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside triphosphate reductase; <b>PDBTitle:</b> anaerobic ribonucleotide reductase
46	<a href="#">c3glsC_</a>	Alignment	not modelled	73.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-3, <b>PDBTitle:</b> crystal structure of human sirt3
47	<a href="#">c5fjal_</a>	Alignment	not modelled	73.7	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
48	<a href="#">d1vd4a_</a>	Alignment	not modelled	71.5	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
49	<a href="#">c4zlhB_</a>	Alignment	not modelled	70.8	45	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide assembly protein b; <b>PDBTitle:</b> structure of the lapb cytoplasmic domain at 2 angstroms
50	<a href="#">c5m45l_</a>	Alignment	not modelled	70.4	22	<b>PDB header:</b> ligase <b>Chain:</b> I: <b>PDB Molecule:</b> acetone carboxylase gamma subunit; <b>PDBTitle:</b> structure of acetone carboxylase purified from xanthobacter2 autotrophicus
51	<a href="#">d1q1aa_</a>	Alignment	not modelled	69.4	26	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
52	<a href="#">d1hk8a_</a>	Alignment	not modelled	69.2	24	<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
53	<a href="#">c1hk8A_</a>	Alignment	not modelled	69.2	24	<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
54	<a href="#">c4o64C_</a>	Alignment	not modelled	67.9	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> lysine-specific demethylase 2b; <b>PDBTitle:</b> zinc fingers of kdm2b

55	<a href="#">c5iy9M_</a>	Alignment	not modelled	67.8	23	<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)
56	<a href="#">d2ak3a2</a>	Alignment	not modelled	66.5	10	<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
57	<a href="#">c6et9H_</a>	Alignment	not modelled	65.9	34	<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
58	<a href="#">d1yc5a1</a>	Alignment	not modelled	65.5	23	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
59	<a href="#">c5vbnB_</a>	Alignment	not modelled	64.0	33	<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
60	<a href="#">d1e4va2</a>	Alignment	not modelled	63.3	10	<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
61	<a href="#">c6g5iy_</a>	Alignment	not modelled	62.5	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
62	<a href="#">c5mg5W_</a>	Alignment	not modelled	62.4	13	<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 (magg)
63	<a href="#">c4i5iA_</a>	Alignment	not modelled	62.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-1; <b>PDBTitle:</b> crystal structure of the sirt1 catalytic domain bound to nad and an2 ex527 analog
64	<a href="#">d1akya2</a>	Alignment	not modelled	61.1	16	<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
65	<a href="#">c1q14A_</a>	Alignment	not modelled	61.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hst2 protein; <b>PDBTitle:</b> structure and autoregulation of the yeast hst2 homolog of sir2
66	<a href="#">c3g9yA_</a>	Alignment	not modelled	59.7	40	<b>PDB header:</b> transcription/rna <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger ran-binding domain-containing protein 2; <b>PDBTitle:</b> crystal structure of the second zinc finger from zranb2/znf265 bound2 to 6 nt srna sequence agguaa
67	<a href="#">d1zina2</a>	Alignment	not modelled	59.0	23	<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
68	<a href="#">d1p3ja2</a>	Alignment	not modelled	58.0	19	<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
69	<a href="#">c5o10B_</a>	Alignment	not modelled	57.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative silent information regulator 2,putative silent <b>PDBTitle:</b> structure of leishmania infantum silent information regulator 22 related protein 1 (lisir2rp1) in complex with acetylated p53 peptide
70	<a href="#">d1s3ga2</a>	Alignment	not modelled	56.3	19	<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
71	<a href="#">c2d9gA_</a>	Alignment	not modelled	55.5	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yy1-associated factor 2; <b>PDBTitle:</b> solution structure of the zf-ranbp domain of yy1-associated2 factor 2
72	<a href="#">c5a1vK_</a>	Alignment	not modelled	55.3	16	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> the structure of the cop1 coat linkage i
73	<a href="#">c6ok1B_</a>	Alignment	not modelled	55.1	33	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chsh2(duf35); <b>PDBTitle:</b> itp2-chsh2(duf35) aldolase
74	<a href="#">d1fp0a1</a>	Alignment	not modelled	54.3	30	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> PHD domain
75	<a href="#">d1dl6a_</a>	Alignment	not modelled	54.1	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
76	<a href="#">c2k5cA_</a>	Alignment	not modelled	53.9	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf0385; <b>PDBTitle:</b> nmr structure for pf0385
77	<a href="#">c3lpeF_</a>	Alignment	not modelled	53.8	37	<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
78	<a href="#">d2akla2</a>	Alignment	not modelled	53.6	25	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> PhnA zinc-binding domain
						<b>PDB header:</b> transcription

79	<a href="#">c1fp0A_</a>	Alignment	not modelled	52.8	31	<b>Chain:</b> A; <b>PDB Molecule:</b> kap-1 corepressor; <b>PDBTitle:</b> solution structure of the phd domain from the kap-12 corepressor
80	<a href="#">c6nmiF_</a>	Alignment	not modelled	52.8	27	<b>PDB header:</b> transcription <b>Chain:</b> F; <b>PDB Molecule:</b> general transcription factor iih subunit 3, p34; <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
81	<a href="#">c2lk1A_</a>	Alignment	not modelled	51.8	40	<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
82	<a href="#">c2lk0A_</a>	Alignment	not modelled	50.1	40	<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
83	<a href="#">c5btrB_</a>	Alignment	not modelled	49.7	22	<b>PDB header:</b> hydrolase/substrate <b>Chain:</b> B; <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-1; <b>PDBTitle:</b> crystal structure of sirt1 in complex with resveratrol and an amc-2 containing peptide
84	<a href="#">c4bbqA_</a>	Alignment	not modelled	48.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> lysine-specific demethylase 2a; <b>PDBTitle:</b> crystal structure of the cxxc and phd domain of human lysine-specific2 demethylase 2a (kdm2a)(fbx111)
85	<a href="#">c3k1fM_</a>	Alignment	not modelled	48.4	27	<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
86	<a href="#">c3mv2A_</a>	Alignment	not modelled	48.1	16	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> crystal structure of a-cop in complex with e-cop
87	<a href="#">c2mxvA_</a>	Alignment	not modelled	47.9	50	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> rna-binding protein 10; <b>PDBTitle:</b> nmr structure of the first zinc finger domain of rbm10
88	<a href="#">c5oqdB_</a>	Alignment	not modelled	47.4	13	<b>PDB header:</b> gene regulation <b>Chain:</b> B; <b>PDB Molecule:</b> polycomb protein pcl; <b>PDBTitle:</b> phd2 and winged-helix domain of polycomblike
89	<a href="#">d1wila_</a>	Alignment	not modelled	47.3	22	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> variant PHD-like domain
90	<a href="#">d1wgma_</a>	Alignment	not modelled	47.2	15	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> U-box
91	<a href="#">c3k7aM_</a>	Alignment	not modelled	47.1	24	<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
92	<a href="#">c5ijlA_</a>	Alignment	not modelled	46.2	24	<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)
93	<a href="#">c1n0zA_</a>	Alignment	not modelled	45.5	64	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> zfn265; <b>PDBTitle:</b> solution structure of the first zinc-finger domain from2 znf265
94	<a href="#">c3mkrB_</a>	Alignment	not modelled	45.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
95	<a href="#">d2gnra1</a>	Alignment	not modelled	44.7	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> SSO2064-like
96	<a href="#">d1t1ha_</a>	Alignment	not modelled	44.7	27	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> U-box
97	<a href="#">c3zg6A_</a>	Alignment	not modelled	44.5	16	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-6; <b>PDBTitle:</b> the novel de-long chain fatty acid function of human sirt6
98	<a href="#">c3jb9T_</a>	Alignment	not modelled	44.2	19	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> T; <b>PDB Molecule:</b> pre-mrna-processing factor 19; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
99	<a href="#">c2f9iD_</a>	Alignment	not modelled	43.8	24	<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
100	<a href="#">c4me3A_</a>	Alignment	not modelled	43.4	20	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> dna replication licensing factor mcm related protein; <b>PDBTitle:</b> 1.8 angstrom crystal structure of the n-terminal domain of an archaeal2 mcm
101	<a href="#">c4pogC_</a>	Alignment	not modelled	43.4	24	<b>PDB header:</b> replication, dna binding protein/dna <b>Chain:</b> C; <b>PDB Molecule:</b> cell division control protein 21; <b>PDBTitle:</b> mcm-ssdna co-crystal structure
102	<a href="#">c3o70A_</a>	Alignment	not modelled	42.7	20	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> phd finger protein 13; <b>PDBTitle:</b> phd-type zinc finger of human phd finger protein 13
103	<a href="#">c3u5pF_</a>	Alignment	not modelled	42.6	27	<b>PDB header:</b> transcription <b>Chain:</b> F; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase trim33; <b>PDBTitle:</b> crystal structure of the complex of trim33 phd-bromo and h3(1-28)2 k9me3k14ack18ack23ac histone peptide
104	<a href="#">c4a17Y_</a>	Alignment	not modelled	42.6	15	<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.

105	<a href="#">c5hh7A_</a>	Alignment	not modelled	42.4	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> origin of replication complex subunit 1b; <b>PDBTitle:</b> crystal structure of arabidopsis orc1b bah-phd cassette in complex2 with unmodified h3 peptide
106	<a href="#">c5fz5M_</a>	Alignment	not modelled	42.2	24	<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)
107	<a href="#">c2e61A_</a>	Alignment	not modelled	42.1	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger cw-type pwwp domain protein 1; <b>PDBTitle:</b> solution structure of the zf-cw domain in zinc finger cw-type pwwp2 domain protein 1
108	<a href="#">c2epsA_</a>	Alignment	not modelled	42.0	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> poz-, at hook-, and zinc finger-containing <b>PDBTitle:</b> solution structure of the 4th zinc finger domain of zinc2 finger protein 278
109	<a href="#">d1mm3a_</a>	Alignment	not modelled	41.6	26	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> PHD domain
110	<a href="#">c2avuF_</a>	Alignment	not modelled	41.5	30	<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
111	<a href="#">c5jneA_</a>	Alignment	not modelled	40.3	40	<b>PDB header:</b> ligase/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> e3 sumo-protein ligase siz1,ubiquitin-like protein smt3; <b>PDBTitle:</b> e2-sumo-siz1 e3-sumo-pcna complex
112	<a href="#">d2avue1</a>	Alignment	not modelled	40.2	30	<b>Fold:</b> FlhC-like <b>Superfamily:</b> FlhC-like <b>Family:</b> FlhC-like
113	<a href="#">c6hmsB_</a>	Alignment	not modelled	40.1	24	<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
114	<a href="#">c4mvtC_</a>	Alignment	not modelled	39.8	40	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> e3 sumo-protein ligase pias3; <b>PDBTitle:</b> crystal structure of sumo e3 ligase pias3
115	<a href="#">d1ffkw_</a>	Alignment	not modelled	39.7	25	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
116	<a href="#">d1mm2a_</a>	Alignment	not modelled	39.6	33	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> PHD domain
117	<a href="#">c3izrM_</a>	Alignment	not modelled	39.4	25	<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
118	<a href="#">c3a1bA_</a>	Alignment	not modelled	39.1	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 3a, histone h3.1; <b>PDBTitle:</b> crystal structure of the dnmt3a add domain in complex with histone h3
119	<a href="#">c3cc4Z_</a>	Alignment	not modelled	38.9	17	<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
120	<a href="#">c3wvnB_</a>	Alignment	not modelled	38.7	31	<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