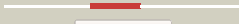



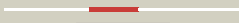




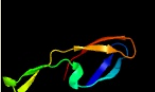









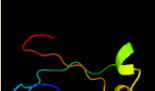

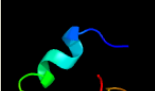





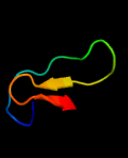





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2811 (- )_3116149_3116757
Date	Wed Aug 7 12:50:47 BST 2019
Unique Job ID	0b22dfc69f58dbe1

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2jn6a1</a>	 Alignment		93.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
2	<a href="#">c3gn5B</a>	 Alignment		92.9	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygit/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygit/b3021)
3	<a href="#">d2coba1</a>	 Alignment		90.6	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
4	<a href="#">d1pdnc</a>	 Alignment		86.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
5	<a href="#">c2nb9A</a>	 Alignment		83.5	25	<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
6	<a href="#">c6paxA</a>	 Alignment		83.5	11	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
7	<a href="#">d2fiya1</a>	 Alignment		82.5	26	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
8	<a href="#">c2rn7A</a>	 Alignment		81.9	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
9	<a href="#">c1u78A</a>	 Alignment		81.5	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
10	<a href="#">c3eswA</a>	 Alignment		80.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine <b>PDBTitle:</b> complex of yeast pngase with glcnac2-iac.
11	<a href="#">c3glsC</a>	 Alignment		79.4	23	<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

12	<a href="#">d1x3za1</a>	Alignment		78.6	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
13	<a href="#">d1j8fa_</a>	Alignment		77.7	12	<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
14	<a href="#">c1hlvA_</a>	Alignment		77.5	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
15	<a href="#">c3hefB_</a>	Alignment		77.2	10	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small subunit
16	<a href="#">d1k78a1</a>	Alignment		76.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
17	<a href="#">c2gb5B_</a>	Alignment		75.9	23	<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
18	<a href="#">c5o10B_</a>	Alignment		75.5	27	<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
19	<a href="#">c5xonU_</a>	Alignment		75.3	16	<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
20	<a href="#">d1yc5a1</a>	Alignment		74.8	19	<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
21	<a href="#">d1bw6a_</a>	Alignment	not modelled	73.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
22	<a href="#">c3ndjA_</a>	Alignment	not modelled	71.7	23	<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
23	<a href="#">c3cngC_</a>	Alignment	not modelled	70.1	32	<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
24	<a href="#">d6paxa1</a>	Alignment	not modelled	69.0	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
25	<a href="#">c2cg4B_</a>	Alignment	not modelled	68.9	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
26	<a href="#">c2p6tH_</a>	Alignment	not modelled	68.7	14	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
27	<a href="#">c2jvnA_</a>	Alignment	not modelled	67.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly [adp-ribose] polymerase 1; <b>PDBTitle:</b> domain c of human parp-1
28	<a href="#">c2cfxD_</a>	Alignment	not modelled	67.0	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
29	<a href="#">c2albA_</a>	Alignment	not modelled	66.8	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa;

29	<a href="#">c2cnaA</a>	Alignment	not modelled	66.8	22	<b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
30	<a href="#">d1hlva1</a>	Alignment	not modelled	65.5	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
31	<a href="#">c2e1cA</a>	Alignment	not modelled	65.0	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
32	<a href="#">d1p91a</a>	Alignment	not modelled	64.7	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA methyltransferase RlmA
33	<a href="#">d1twf2</a>	Alignment	not modelled	64.4	18	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
34	<a href="#">c4pccC</a>	Alignment	not modelled	64.2	27	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> possible transcriptional regulatory protein (probably <b>PDBTitle:</b> crystal structure of mtbaldr (rv2779c)
35	<a href="#">c2riqA</a>	Alignment	not modelled	64.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly [adp-ribose] polymerase 1; <b>PDBTitle:</b> crystal structure of the third zinc-binding domain of human parp-1
36	<a href="#">c6o3pA</a>	Alignment	not modelled	63.8	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal nadh pyrophosphatase nudt12; <b>PDBTitle:</b> crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
37	<a href="#">c1i1gA</a>	Alignment	not modelled	62.8	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpa; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
38	<a href="#">c2ia0A</a>	Alignment	not modelled	62.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
39	<a href="#">c2ak1A</a>	Alignment	not modelled	59.9	24	<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
40	<a href="#">d2jneA1</a>	Alignment	not modelled	59.6	25	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Yfgj-like <b>Family:</b> Yfgj-like
41	<a href="#">c2jneA</a>	Alignment	not modelled	59.6	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yfgj; <b>PDBTitle:</b> nmr structure of e.coli yfgj modelled with two zn+2 bound. northeast2 structural genomics consortium target er317.
42	<a href="#">c2dbbA</a>	Alignment	not modelled	59.2	11	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
43	<a href="#">c4opxD</a>	Alignment	not modelled	58.5	32	<b>PDB header:</b> transferase/dna/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> poly [adp-ribose] polymerase 1; <b>PDBTitle:</b> structure of human parp-1 bound to a dna double strand break in2 complex with (2r)-5-fluoro-2-methyl-2,3-dihydro-1-benzofuran-7-3 carboxamide
44	<a href="#">c5btrB</a>	Alignment	not modelled	57.0	19	<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
45	<a href="#">c4kisA</a>	Alignment	not modelled	56.8	13	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative integrase [bacteriophage a118]; <b>PDBTitle:</b> crystal structure of a lsr-dna complex
46	<a href="#">c2qkdA</a>	Alignment	not modelled	56.0	24	<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
47	<a href="#">d1q1aa</a>	Alignment	not modelled	55.1	19	<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
48	<a href="#">c2gqqB</a>	Alignment	not modelled	54.9	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
49	<a href="#">d1zs4a1</a>	Alignment	not modelled	54.3	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Bacteriophage CII protein
50	<a href="#">c4rulA</a>	Alignment	not modelled	54.3	18	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 1; <b>PDBTitle:</b> crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
51	<a href="#">d2f4ma1</a>	Alignment	not modelled	53.7	20	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
52	<a href="#">d1qypa</a>	Alignment	not modelled	52.4	32	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
53	<a href="#">c4czdA</a>	Alignment	not modelled	52.0	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway. <b>PDB header:</b> transcription regulator

54	<a href="#">c2e7xA</a>	Alignment	not modelled	51.4	19	<b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
55	<a href="#">d1dgsa1</a>	Alignment	not modelled	51.4	45	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> NAD+-dependent DNA ligase, domain 3
56	<a href="#">c1pqvS</a>	Alignment	not modelled	51.3	18	<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
57	<a href="#">c3i4pA</a>	Alignment	not modelled	50.8	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
58	<a href="#">d1ma3a</a>	Alignment	not modelled	50.3	15	<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="#">c1q14A</a>	Alignment	not modelled	49.5	19	<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
60	<a href="#">d1i27a</a>	Alignment	not modelled	49.4	35	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of the rap74 subunit of TFIIF
61	<a href="#">c5a3aA</a>	Alignment	not modelled	49.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sir2 family protein; <b>PDBTitle:</b> crystal structure of the adp-ribosylating sirtuin (sirtm)2 from streptococcus pyogenes (apo form)
62	<a href="#">c5fjaL</a>	Alignment	not modelled	49.2	29	<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
63	<a href="#">c2xroE</a>	Alignment	not modelled	48.8	26	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgv; <b>PDBTitle:</b> crystal structure of ttgv in complex with its dna operator
64	<a href="#">c1y1yS</a>	Alignment	not modelled	48.2	18	<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
65	<a href="#">c3a44D</a>	Alignment	not modelled	48.1	15	<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
66	<a href="#">c2vbzA</a>	Alignment	not modelled	47.2	25	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
67	<a href="#">c5iycU</a>	Alignment	not modelled	47.0	19	<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
68	<a href="#">c3h0gl</a>	Alignment	not modelled	45.9	25	<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
69	<a href="#">c2jrpA</a>	Alignment	not modelled	44.3	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
70	<a href="#">c3e7ID</a>	Alignment	not modelled	44.1	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
71	<a href="#">c6k0bH</a>	Alignment	not modelled	43.3	30	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> H: <b>PDB Molecule:</b> ribonuclease p protein component 4; <b>PDBTitle:</b> cryo-em structure of archaeal ribonuclease p with mature trna
72	<a href="#">c4czdD</a>	Alignment	not modelled	43.0	15	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
73	<a href="#">d2akla2</a>	Alignment	not modelled	42.6	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> PhnA zinc-binding domain
74	<a href="#">c5iy9M</a>	Alignment	not modelled	42.3	30	<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)
75	<a href="#">d1tfia</a>	Alignment	not modelled	41.5	18	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
76	<a href="#">c4i5iA</a>	Alignment	not modelled	41.2	19	<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
77	<a href="#">c3cc4Z</a>	Alignment	not modelled	41.1	36	<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
78	<a href="#">c2zaeB</a>	Alignment	not modelled	40.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease p protein component 4; <b>PDBTitle:</b> crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
						<b>PDB header:</b> transferase

79	<a href="#">c3floD_</a>	Alignment	not modelled	39.8	28	<b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase alpha catalytic subunit a; <b>PDBTitle:</b> crystal structure of the carboxyl-terminal domain of yeast dna2 polymerase alpha in complex with its b subunit
80	<a href="#">d1pzra_</a>	Alignment	not modelled	39.6	19	<b>Fold:</b> HLH-like <b>Superfamily:</b> Docking domain B of the erythromycin polyketide synthase (DEBS) <b>Family:</b> Docking domain B of the erythromycin polyketide synthase (DEBS)
81	<a href="#">c2kdxA_</a>	Alignment	not modelled	39.4	21	<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
82	<a href="#">c3zf7o_</a>	Alignment	not modelled	39.3	52	<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
83	<a href="#">c4rvqA_</a>	Alignment	not modelled	39.3	13	<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="#">c3alrA_</a>	Alignment	not modelled	39.3	31	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nanos protein; <b>PDBTitle:</b> crystal structure of nanos
85	<a href="#">d1dl6a_</a>	Alignment	not modelled	39.1	30	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
86	<a href="#">c2qa4Z_</a>	Alignment	not modelled	38.4	36	<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
87	<a href="#">c4c2mX_</a>	Alignment	not modelled	38.2	28	<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
88	<a href="#">c5zwnY_</a>	Alignment	not modelled	38.0	32	<b>PDB header:</b> splicing <b>Chain:</b> Y: <b>PDB Molecule:</b> protein luc7; <b>PDBTitle:</b> cryo-em structure of the yeast pre-b complex at an average resolution2 of 3.3 angstrom (part ii: u1 snrp region)
89	<a href="#">c1i3ql_</a>	Alignment	not modelled	37.9	17	<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
90	<a href="#">c2epqA_</a>	Alignment	not modelled	37.7	46	<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 third zinc finger domain of zinc2 finger protein 278
91	<a href="#">c4b6ap_</a>	Alignment	not modelled	37.5	40	<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
92	<a href="#">c5oj7A_</a>	Alignment	not modelled	37.3	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacylase; <b>PDBTitle:</b> sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
93	<a href="#">d2cg4a1</a>	Alignment	not modelled	37.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
94	<a href="#">c3wwnB_</a>	Alignment	not modelled	37.1	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
95	<a href="#">c4a17Y_</a>	Alignment	not modelled	36.5	40	<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.
96	<a href="#">c3vdoA_</a>	Alignment	not modelled	35.7	8	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor sigk; <b>PDBTitle:</b> structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
97	<a href="#">c2o8xA_</a>	Alignment	not modelled	35.3	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
98	<a href="#">d1ffkw_</a>	Alignment	not modelled	35.2	44	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
99	<a href="#">c5kl1B_</a>	Alignment	not modelled	34.9	23	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> protein nanos; <b>PDBTitle:</b> crystal structure of the pumilio-nos-hunchback rna complex
100	<a href="#">c2ctdA_</a>	Alignment	not modelled	33.9	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 512; <b>PDBTitle:</b> solution structure of two zf-c2h2 domains from human zinc2 finger protein 512
101	<a href="#">d1pvma3</a>	Alignment	not modelled	33.9	88	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Hypothetical protein Ta0289 C-terminal domain <b>Family:</b> Hypothetical protein Ta0289 C-terminal domain
102	<a href="#">c4v1oM_</a>	Alignment	not modelled	33.8	31	<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
103	<a href="#">c6g90H_</a>	Alignment	not modelled	33.5	19	<b>PDB header:</b> splicing <b>Chain:</b> H: <b>PDB Molecule:</b> protein luc7,protein luc7,protein luc7; <b>PDBTitle:</b> prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)
104	<a href="#">c2l4aA_</a>	Alignment	not modelled	33.5	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp

105	<a href="#">c1s1i9_</a>	Alignment	not modelled	33.2	40	<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.
106	<a href="#">c3jyw9_</a>	Alignment	not modelled	33.0	40	<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
107	<a href="#">c3izrm_</a>	Alignment	not modelled	32.9	40	<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
108	<a href="#">d2gnra1</a>	Alignment	not modelled	32.4	58	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> SSO2064-like
109	<a href="#">c3j21i_</a>	Alignment	not modelled	31.4	44	<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)
110	<a href="#">d1qxfa_</a>	Alignment	not modelled	31.3	35	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein S27e
111	<a href="#">c3j39p_</a>	Alignment	not modelled	31.3	36	<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
112	<a href="#">c1umqA_</a>	Alignment	not modelled	31.2	13	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
113	<a href="#">d1umqa_</a>	Alignment	not modelled	31.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
114	<a href="#">d1vqoz1</a>	Alignment	not modelled	31.0	36	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
115	<a href="#">c1yshD_</a>	Alignment	not modelled	30.6	40	<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
116	<a href="#">c2zkrz_</a>	Alignment	not modelled	30.5	40	<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 an3 8.7 a cryo-em map
117	<a href="#">d1m2ka_</a>	Alignment	not modelled	30.4	42	<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
118	<a href="#">c4glxA_</a>	Alignment	not modelled	30.3	36	<b>PDB header:</b> ligase/ligase inhibitor/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> dna ligase a in complex with inhibitor
119	<a href="#">c3iz6X_</a>	Alignment	not modelled	30.3	20	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 40s ribosomal protein s27 (s27e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
120	<a href="#">c3zf7t_</a>	Alignment	not modelled	30.1	15	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein l19, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome