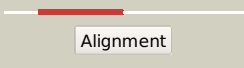
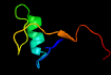
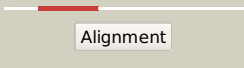

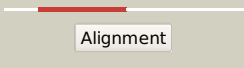

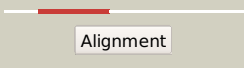

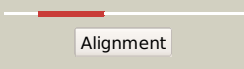

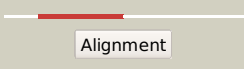

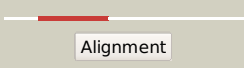
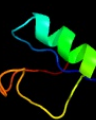
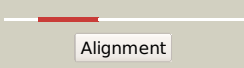

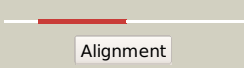

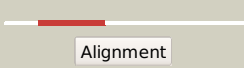

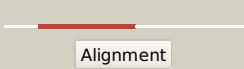
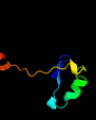



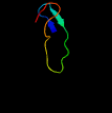


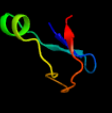
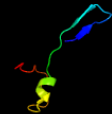
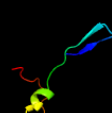


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0991c_(-)_1108176_1108508
Date	Wed Jul 31 22:05:06 BST 2019
Unique Job ID	f26fcc7049265ec1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kdxA_</a>	 Alignment		96.4	18	<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
2	<a href="#">c2hr5B_</a>	 Alignment		96.0	36	<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
3	<a href="#">d1m2ka_</a>	 Alignment		96.0	38	<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
4	<a href="#">c2lqA_</a>	 Alignment		96.0	18	<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
5	<a href="#">c2m6oA_</a>	 Alignment		95.5	18	<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
6	<a href="#">c3a44D_</a>	 Alignment		95.3	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> hydrogenase nickel incorporation protein hypa; <b>PDBTitle:</b> crystal structure of hypa in the dimeric form
7	<a href="#">c6g5iy_</a>	 Alignment		94.4	26	<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
8	<a href="#">c1dvbA_</a>	 Alignment		94.2	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
9	<a href="#">c3glsC_</a>	 Alignment		93.9	33	<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
10	<a href="#">d1yuza2</a>	 Alignment		93.3	14	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
11	<a href="#">d1dx8a_</a>	 Alignment		93.0	21	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin

12	<a href="#">d1lkoa2</a>	Alignment		92.9	19	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
13	<a href="#">c5ol0B_</a>	Alignment		92.7	26	<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
14	<a href="#">d1yc5a1</a>	Alignment		92.6	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
15	<a href="#">d1ltla_</a>	Alignment		92.2	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA replication initiator (cdc21/cdc54) N-terminal domain
16	<a href="#">c4i5iA_</a>	Alignment		92.0	21	<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
17	<a href="#">d1nnqa2</a>	Alignment		92.0	34	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
18	<a href="#">c4pogC_</a>	Alignment		92.0	22	<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
19	<a href="#">d2jneal</a>	Alignment		91.9	26	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Yfgj-like <b>Family:</b> Yfgj-like
20	<a href="#">c2jneA_</a>	Alignment		91.9	26	<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.
21	<a href="#">c3axtA_</a>	Alignment	not modelled	91.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable n(2),n(2)-dimethylguanosine trna methyltransferase <b>PDBTitle:</b> complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
22	<a href="#">c2kn9A_</a>	Alignment	not modelled	91.6	23	<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
23	<a href="#">d1iu5a_</a>	Alignment	not modelled	91.5	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
24	<a href="#">d2dsxa1</a>	Alignment	not modelled	91.3	30	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
25	<a href="#">c5fywW_</a>	Alignment	not modelled	91.3	24	<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)
26	<a href="#">d1brfa_</a>	Alignment	not modelled	91.3	20	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
27	<a href="#">d1h7va_</a>	Alignment	not modelled	91.1	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
28	<a href="#">d4rxna_</a>	Alignment	not modelled	91.1	30	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like

						<b>Family:</b> Rubredoxin
29	<a href="#">c6hmsB_</a>	Alignment	not modelled	90.9	27	<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
30	<a href="#">d1qcva_</a>	Alignment	not modelled	90.9	7	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
31	<a href="#">d1lroa_</a>	Alignment	not modelled	90.6	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
32	<a href="#">c1ltiE_</a>	Alignment	not modelled	90.6	29	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> dna replication initiator (cdc21/cdc54); <b>PDBTitle:</b> the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
33	<a href="#">d6rxna_</a>	Alignment	not modelled	90.6	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
34	<a href="#">d1rb9a_</a>	Alignment	not modelled	90.5	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
35	<a href="#">d1s24a_</a>	Alignment	not modelled	90.5	20	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
36	<a href="#">c1s24A_</a>	Alignment	not modelled	90.5	20	<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
37	<a href="#">c2ms3A_</a>	Alignment	not modelled	90.3	23	<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
38	<a href="#">d2rdva_</a>	Alignment	not modelled	90.1	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
39	<a href="#">c2v3bB_</a>	Alignment	not modelled	89.8	20	<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.
40	<a href="#">c3wwnB_</a>	Alignment	not modelled	89.7	22	<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
41	<a href="#">c3pkIF_</a>	Alignment	not modelled	89.7	31	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> human sirt6 crystal structure in complex with adp ribose
42	<a href="#">c5btrB_</a>	Alignment	not modelled	89.6	21	<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
43	<a href="#">c3vpbF_</a>	Alignment	not modelled	89.4	11	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> alpha-aminoadipate carrier protein lysw; <b>PDBTitle:</b> argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
44	<a href="#">c4me3A_</a>	Alignment	not modelled	88.8	24	<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
45	<a href="#">c2jrpA_</a>	Alignment	not modelled	88.7	33	<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
46	<a href="#">c1q14A_</a>	Alignment	not modelled	88.1	21	<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
47	<a href="#">c5oj7A_</a>	Alignment	not modelled	88.1	26	<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
48	<a href="#">c2m4yA_</a>	Alignment	not modelled	87.6	26	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> rubredoxin type protein from mycobacterium ulcerans
49	<a href="#">c5iy9Q_</a>	Alignment	not modelled	87.5	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)
50	<a href="#">d1q1aa_</a>	Alignment	not modelled	87.4	13	<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
51	<a href="#">d1ma3a_</a>	Alignment	not modelled	87.2	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
52	<a href="#">c6gymW_</a>	Alignment	not modelled	86.6	24	<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 (cddist)
53	<a href="#">d2gmga1</a>	Alignment	not modelled	86.4	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF0610-like

54	<a href="#">c3zg6A</a>	Alignment	not modelled	85.9	23	<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
55	<a href="#">c5fmfR</a>	Alignment	not modelled	85.7	24	<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
56	<a href="#">c5oqiW</a>	Alignment	not modelled	85.5	24	<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
57	<a href="#">c2m4vA</a>	Alignment	not modelled	85.3	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> mycobacterium tuberculosis rna polymerase binding protein a (rbpa) and2 its interactions with sigma factors
58	<a href="#">d1ywsa1</a>	Alignment	not modelled	85.2	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> CSL zinc finger <b>Family:</b> CSL zinc finger
59	<a href="#">c5oqmW</a>	Alignment	not modelled	85.1	24	<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
60	<a href="#">c3ja82</a>	Alignment	not modelled	84.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> 2: <b>PDB Molecule:</b> minichromosome maintenance 2; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
61	<a href="#">c5tw1J</a>	Alignment	not modelled	84.2	24	<b>PDB header:</b> transcription activator/transferase/dna <b>Chain:</b> J: <b>PDB Molecule:</b> rna polymerase-binding protein rbpa; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
62	<a href="#">c6c04J</a>	Alignment	not modelled	83.9	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> J: <b>PDB Molecule:</b> rna polymerase-binding protein rbpa; <b>PDBTitle:</b> mtb rnap holo/rbpa/double fork dna -closed clamp
63	<a href="#">c3jwpA</a>	Alignment	not modelled	83.8	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein sir2 homologue; <b>PDBTitle:</b> crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
64	<a href="#">d1wgea1</a>	Alignment	not modelled	82.7	26	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> CSL zinc finger <b>Family:</b> CSL zinc finger
65	<a href="#">c3k35D</a>	Alignment	not modelled	81.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> crystal structure of human sirt6
66	<a href="#">d2cona1</a>	Alignment	not modelled	81.6	26	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> NOB1 zinc finger-like <b>Family:</b> NOB1 zinc finger-like
67	<a href="#">c4tpuA</a>	Alignment	not modelled	81.4	27	<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
68	<a href="#">c6o9IQ</a>	Alignment	not modelled	80.5	21	<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
69	<a href="#">c4c2mX</a>	Alignment	not modelled	78.4	31	<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
70	<a href="#">c5fyqB</a>	Alignment	not modelled	78.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-2; <b>PDBTitle:</b> sirt2 in complex with a 13-mer trifluoroacetylated ran peptide
71	<a href="#">c3cngC</a>	Alignment	not modelled	78.3	14	<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
72	<a href="#">d1qypa</a>	Alignment	not modelled	76.0	30	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
73	<a href="#">c5x51X</a>	Alignment	not modelled	75.8	30	<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)
74	<a href="#">c3hkpP</a>	Alignment	not modelled	75.7	15	<b>PDB header:</b> transferase <b>Chain:</b> P: <b>PDB Molecule:</b> dna-directed rna polymerase subunit p; <b>PDBTitle:</b> the x-ray crystal structure of rna polymerase from archaea
75	<a href="#">c3f2cA</a>	Alignment	not modelled	75.3	25	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> geobacillus kaustophilus dna polc; <b>PDBTitle:</b> dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
76	<a href="#">c2jr7A</a>	Alignment	not modelled	75.1	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dph3 homolog; <b>PDBTitle:</b> solution structure of human desr1
77	<a href="#">c2ktvA</a>	Alignment	not modelled	75.1	8	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic peptide chain release factor subunit 1; <b>PDBTitle:</b> human erf1 c-domain, "open" conformer
78	<a href="#">c3jc55</a>	Alignment	not modelled	74.2	10	<b>PDB header:</b> hydrolase <b>Chain:</b> 5: <b>PDB Molecule:</b> minichromosome maintenance protein 5; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
						<b>Fold:</b> DHS-like NAD/FAD-binding domain

79	<a href="#">d1s5pa_</a>	Alignment	not modelled	73.9	23	<b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
80	<a href="#">c4u3eA_</a>	Alignment	not modelled	73.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside triphosphate reductase; <b>PDBTitle:</b> anaerobic ribonucleotide reductase
81	<a href="#">d2b4ya1</a>	Alignment	not modelled	73.6	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
82	<a href="#">c5m45l_</a>	Alignment	not modelled	72.6	29	<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
83	<a href="#">c3h0gL_</a>	Alignment	not modelled	72.5	26	<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
84	<a href="#">c2gb5B_</a>	Alignment	not modelled	72.3	16	<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
85	<a href="#">c3ja86_</a>	Alignment	not modelled	71.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> 6: <b>PDB Molecule:</b> minichromosome maintenance 6; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
86	<a href="#">c5flmL_</a>	Alignment	not modelled	70.7	21	<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
87	<a href="#">c1hk8A_</a>	Alignment	not modelled	70.5	16	<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
88	<a href="#">d1hk8a_</a>	Alignment	not modelled	70.5	16	<b>Fold:</b> PFL-like glycol radical enzymes <b>Superfamily:</b> PFL-like glycol radical enzymes <b>Family:</b> Class III anaerobic ribonucleotide reductase NRDD subunit
89	<a href="#">c5j9wC_</a>	Alignment	not modelled	70.3	18	<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
90	<a href="#">d1vd4a_</a>	Alignment	not modelled	70.2	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
91	<a href="#">c3jc54_</a>	Alignment	not modelled	69.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> dna replication licensing factor mcm4; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
92	<a href="#">c5h7i7_</a>	Alignment	not modelled	68.1	30	<b>PDB header:</b> hydrolase <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> cryo-em structure of the cdt1-mcm2-7 complex in amppnp state
93	<a href="#">c2ja6L_</a>	Alignment	not modelled	68.0	22	<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
94	<a href="#">c2hjhB_</a>	Alignment	not modelled	67.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent histone deacetylase sir2; <b>PDBTitle:</b> crystal structure of the sir2 deacetylase
95	<a href="#">d1dfxa2</a>	Alignment	not modelled	67.1	35	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Desulforedoxin
96	<a href="#">c6hv97_</a>	Alignment	not modelled	66.2	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
97	<a href="#">c1x68A_</a>	Alignment	not modelled	66.1	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fhf5 protein; <b>PDBTitle:</b> solution structures of the c-terminal lim domain of human2 fhf5 protein
98	<a href="#">c4zlhB_</a>	Alignment	not modelled	66.0	23	<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
99	<a href="#">c4iaoB_</a>	Alignment	not modelled	65.8	16	<b>PDB header:</b> hydrolase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent histone deacetylase sir2; <b>PDBTitle:</b> crystal structure of sir2 c543s mutant in complex with sid domain of2 sir4
100	<a href="#">c1vzhB_</a>	Alignment	not modelled	65.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> desulfoferrodoxin; <b>PDBTitle:</b> structure of superoxide reductase bound to ferrocyanide and active2 site expansion upon x-ray induced photoreduction
101	<a href="#">c5u8s4_</a>	Alignment	not modelled	64.9	23	<b>PDB header:</b> replication <b>Chain:</b> 4: <b>PDB Molecule:</b> dna replication licensing factor mcm4; <b>PDBTitle:</b> structure of eukaryotic cmg helicase at a replication fork
102	<a href="#">d1tfia_</a>	Alignment	not modelled	64.8	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
103	<a href="#">c5a3aA_</a>	Alignment	not modelled	64.7	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)
104	<a href="#">c5mg5W_</a>	Alignment	not modelled	64.3	18	<b>PDB header:</b> transferase <b>Chain:</b> W: <b>PDB Molecule:</b> 2,4-diacetylphloroglucinol biosynthesis protein; <b>PDBTitle:</b> a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol

						(mapg)
105	<a href="#">c5xonU_</a>	Alignment	not modelled	64.3	34	<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
106	<a href="#">c1y1yS_</a>	Alignment	not modelled	64.3	31	<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
107	<a href="#">c3pihA_</a>	Alignment	not modelled	64.2	24	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> svrabc system protein a; <b>PDBTitle:</b> t. maritima uvra in complex with fluorescein-modified dna
108	<a href="#">c1rikA_</a>	Alignment	not modelled	64.1	42	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> e6apc1 peptide; <b>PDBTitle:</b> e6-binding zinc finger (e6apc1)
109	<a href="#">c5ijjA_</a>	Alignment	not modelled	64.0	22	<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)
110	<a href="#">c4af1A_</a>	Alignment	not modelled	63.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide chain release factor subunit 1; <b>PDBTitle:</b> archeal release factor arf1
111	<a href="#">c6hv96_</a>	Alignment	not modelled	62.2	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> 6: <b>PDB Molecule:</b> dna replication licensing factor mcm6; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
112	<a href="#">d1j8fa_</a>	Alignment	not modelled	61.8	16	<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
113	<a href="#">d1x6ea2</a>	Alignment	not modelled	60.9	40	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
114	<a href="#">c3ja84_</a>	Alignment	not modelled	60.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> minichromosome maintenance 4; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
115	<a href="#">d2cota1</a>	Alignment	not modelled	59.4	40	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
116	<a href="#">c1pqvS_</a>	Alignment	not modelled	58.4	31	<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
117	<a href="#">d1twfi2</a>	Alignment	not modelled	58.3	31	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
118	<a href="#">c5fjaI_</a>	Alignment	not modelled	58.1	21	<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
119	<a href="#">d2akla2</a>	Alignment	not modelled	57.8	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> PhnA zinc-binding domain
120	<a href="#">c5udb7_</a>	Alignment	not modelled	57.6	21	<b>PDB header:</b> replication <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1