












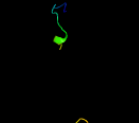

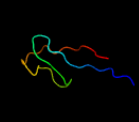








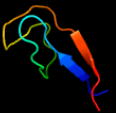
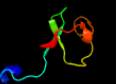
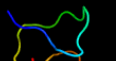






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3521 (-) _3957700_3958611
Date	Fri Aug 9 18:20:19 BST 2019
Unique Job ID	8e7e332a77f56635

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ok1B_</a>	 Alignment		100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chsh2(duf35); <b>PDBTitle:</b> ltp-2-chsh2(duf35) aldolase
2	<a href="#">c6et9H_</a>	 Alignment		100.0	28	<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
3	<a href="#">d2gnra1</a>	 Alignment		100.0	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> SSO2064-like
4	<a href="#">c5mg5W_</a>	 Alignment		100.0	17	<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 (magp)
5	<a href="#">c2lqqa_</a>	 Alignment		93.4	27	<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
6	<a href="#">c2kdxA_</a>	 Alignment		92.9	10	<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
7	<a href="#">c3a44D_</a>	 Alignment		92.8	20	<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
8	<a href="#">c6g5iy_</a>	 Alignment		91.8	13	<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
9	<a href="#">d2fiya1</a>	 Alignment		91.4	9	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
10	<a href="#">c1dvbA_</a>	 Alignment		91.3	27	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
11	<a href="#">c4u3eA_</a>	 Alignment		89.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside triphosphate reductase; <b>PDBTitle:</b> anaerobic ribonucleotide reductase

12	<a href="#">c5ijlA</a>	Alignment		89.1	32	<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)
13	<a href="#">d1lkoa2</a>	Alignment		87.7	31	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
14	<a href="#">d2cona1</a>	Alignment		87.3	14	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> NOB1 zinc finger-like <b>Family:</b> NOB1 zinc finger-like
15	<a href="#">c2hr5B</a>	Alignment		86.8	16	<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
16	<a href="#">d2ey4e1</a>	Alignment		86.7	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
17	<a href="#">d1hk8a</a>	Alignment		86.1	6	<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
18	<a href="#">c1hk8A</a>	Alignment		86.1	6	<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
19	<a href="#">d2apob1</a>	Alignment		85.8	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
20	<a href="#">d6rxna</a>	Alignment		85.5	21	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
21	<a href="#">c6hmsB</a>	Alignment	not modelled	85.0	32	<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
22	<a href="#">c2ms3A</a>	Alignment	not modelled	84.9	19	<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
23	<a href="#">c1s24A</a>	Alignment	not modelled	84.8	22	<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
24	<a href="#">d1s24a</a>	Alignment	not modelled	84.8	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
25	<a href="#">d1iu5a</a>	Alignment	not modelled	84.3	34	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
26	<a href="#">d1dx8a</a>	Alignment	not modelled	84.1	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
27	<a href="#">c2m4yA</a>	Alignment	not modelled	83.9	19	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> rubredoxin type protein from mycobacterium ulcerans
28	<a href="#">d2gmga1</a>	Alignment	not modelled	83.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF0610-like

29	<a href="#">d1brfa_</a>	Alignment	not modelled	83.0	35	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
30	<a href="#">c2v3bB_</a>	Alignment	not modelled	83.0	21	<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.
31	<a href="#">d1iroa_</a>	Alignment	not modelled	82.5	24	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
32	<a href="#">c2kn9A_</a>	Alignment	not modelled	81.9	28	<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
33	<a href="#">d1h7va_</a>	Alignment	not modelled	81.2	24	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
34	<a href="#">c4v195_</a>	Alignment	not modelled	81.2	9	<b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> mitoribosomal protein bl32m, mrpl32; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
35	<a href="#">d2rdva_</a>	Alignment	not modelled	81.1	31	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
36	<a href="#">c1yuzB_</a>	Alignment	not modelled	80.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
37	<a href="#">d4rxna_</a>	Alignment	not modelled	80.9	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
38	<a href="#">d1rb9a_</a>	Alignment	not modelled	80.6	31	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
39	<a href="#">d2zjrz1</a>	Alignment	not modelled	80.3	14	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
40	<a href="#">c3j3v0_</a>	Alignment	not modelled	80.2	19	<b>PDB header:</b> ribosome <b>Chain:</b> 0: <b>PDB Molecule:</b> 50s ribosomal protein l32; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
41	<a href="#">d1yuza2</a>	Alignment	not modelled	79.9	14	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
42	<a href="#">c3lpeF_</a>	Alignment	not modelled	79.6	8	<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
43	<a href="#">d1qcva_</a>	Alignment	not modelled	78.0	39	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
44	<a href="#">c1vw4W_</a>	Alignment	not modelled	77.2	5	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 54s ribosomal protein l32, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
45	<a href="#">c4ce45_</a>	Alignment	not modelled	77.0	10	<b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> mrpl32; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
46	<a href="#">d2dsxa1</a>	Alignment	not modelled	76.3	25	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
47	<a href="#">d2avue1</a>	Alignment	not modelled	74.2	20	<b>Fold:</b> FlhC-like <b>Superfamily:</b> FlhC-like <b>Family:</b> FlhC-like
48	<a href="#">c2avuF_</a>	Alignment	not modelled	72.2	20	<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
49	<a href="#">d2j0151</a>	Alignment	not modelled	71.9	24	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
50	<a href="#">c2f9iD_</a>	Alignment	not modelled	71.4	10	<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
51	<a href="#">c2k52A_</a>	Alignment	not modelled	70.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj1198; <b>PDBTitle:</b> structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
52	<a href="#">c2lk0A_</a>	Alignment	not modelled	65.6	13	<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
53	<a href="#">c5zb8B_</a>	Alignment	not modelled	65.5	17	<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
54	<a href="#">c2lk1A_</a>	Alignment	not modelled	65.3	13	<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

55	<a href="#">d1m2ka_</a>	Alignment	not modelled	64.9	18	<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
56	<a href="#">d1p3ja2</a>	Alignment	not modelled	63.4	33	<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="#">d1s3ga2</a>	Alignment	not modelled	63.2	33	<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
58	<a href="#">d1zina2</a>	Alignment	not modelled	62.6	33	<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
59	<a href="#">d2ak3a2</a>	Alignment	not modelled	61.4	52	<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
60	<a href="#">d1e4va2</a>	Alignment	not modelled	60.2	42	<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="#">d1nnaq2</a>	Alignment	not modelled	58.1	21	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
62	<a href="#">c3axtA_</a>	Alignment	not modelled	58.0	6	<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
63	<a href="#">d2qam01</a>	Alignment	not modelled	58.0	20	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
64	<a href="#">d1ryqa_</a>	Alignment	not modelled	57.9	9	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> RNA polymerase subunits <b>Family:</b> RpoE2-like
65	<a href="#">c6f42V_</a>	Alignment	not modelled	57.3	4	<b>PDB header:</b> transcription <b>Chain:</b> V: <b>PDB Molecule:</b> transcription factor iib 70 kda subunit; <b>PDBTitle:</b> rna polymerase iii closed complex cc1.
66	<a href="#">c2odxA_</a>	Alignment	not modelled	56.6	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide iv; <b>PDBTitle:</b> solution structure of zn(ii)cox4
67	<a href="#">d1k81a_</a>	Alignment	not modelled	56.3	12	<b>Fold:</b> Zinc-binding domain of translation initiation factor 2 beta <b>Superfamily:</b> Zinc-binding domain of translation initiation factor 2 beta <b>Family:</b> Zinc-binding domain of translation initiation factor 2 beta
68	<a href="#">c6hu9p_</a>	Alignment	not modelled	54.9	38	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> P: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
69	<a href="#">c3g9yA_</a>	Alignment	not modelled	54.3	9	<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
70	<a href="#">d2es2a1</a>	Alignment	not modelled	54.2	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
71	<a href="#">c4ldxB_</a>	Alignment	not modelled	53.4	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> auxin response factor 1; <b>PDBTitle:</b> crystal structure of the dna binding domain of arabidopsis thaliana2 auxin response factor 1 (arf1) in complex with protomor-like sequence3 er7
72	<a href="#">c1lttE_</a>	Alignment	not modelled	52.8	10	<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 archaean m.2 thermoautotrophicum
73	<a href="#">c2mqhA_</a>	Alignment	not modelled	52.5	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleic acid binding protein; <b>PDBTitle:</b> solution structure of the chlamydomonas reinhardtii nab1 cold shock2 domain, csd1
74	<a href="#">d2dkt1</a>	Alignment	not modelled	52.0	5	<b>Fold:</b> CHY zinc finger-like <b>Superfamily:</b> CHY zinc finger-like <b>Family:</b> CHY zinc finger
75	<a href="#">c3llkA_</a>	Alignment	not modelled	51.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfhydryl oxidase 1; <b>PDBTitle:</b> sulfhydryl oxidase fragment of human qsox1
76	<a href="#">c5ij4A_</a>	Alignment	not modelled	51.6	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cdc48-associated ubiquitin-like/zinc finger protein 1; <b>PDBTitle:</b> solution structure of an1-type zinc finger domain from cuz1 (cdc482 associated ubiquitin-like/zinc-finger protein-1)
77	<a href="#">d1c9oa_</a>	Alignment	not modelled	51.3	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
78	<a href="#">c3qd9D_</a>	Alignment	not modelled	50.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> qsox from trypanosoma brucei (tbqsox); <b>PDBTitle:</b> c72s/c353s mutant of trypanosoma brucei qsox containing an interdomain2 disulfide
79	<a href="#">d2f9yb1</a>	Alignment	not modelled	49.8	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
						<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl

80	<a href="#">c2f9yB_</a>	Alignment	not modelled	49.8	14	transferase subunit <b>PDBTitle:</b> the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli <b>PDB header:</b> transcription <b>Chain:</b> P: <b>PDB Molecule:</b> dna-directed rna polymerase subunit p; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
81	<a href="#">c4qiwp_</a>	Alignment	not modelled	49.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> sulfhydryl oxidase 1; <b>PDBTitle:</b> c76a/c455s mutant of mouse qsox1 containing an interdomain disulfide
82	<a href="#">c3t59D_</a>	Alignment	not modelled	48.8	23	<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
83	<a href="#">c2mxvA_</a>	Alignment	not modelled	48.3	25	<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
84	<a href="#">c4i5IA_</a>	Alignment	not modelled	47.9	14	<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
85	<a href="#">c6o3pA_</a>	Alignment	not modelled	47.6	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
86	<a href="#">d1q1aa_</a>	Alignment	not modelled	47.5	21	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L40e
87	<a href="#">d2ayja1</a>	Alignment	not modelled	47.2	9	<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
88	<a href="#">c4zlhB_</a>	Alignment	not modelled	46.1	17	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold shock domain family protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
89	<a href="#">c2kcmA_</a>	Alignment	not modelled	45.9	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA replication initiator (cdc21/cdc54) N-terminal domain
90	<a href="#">d1ltla_</a>	Alignment	not modelled	45.2	9	<b>PDB header:</b> translation <b>Chain:</b> P: <b>PDB Molecule:</b> eukaryotic translation initiation factor 2 subunit beta; <b>PDBTitle:</b> structure of eif2b-eif2 (phosphorylated at ser51) complex (model b)
91	<a href="#">c6qg3P_</a>	Alignment	not modelled	44.9	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> minichromosome maintenance protein mcm; <b>PDBTitle:</b> structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
92	<a href="#">c2vl6C_</a>	Alignment	not modelled	44.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c3 fumarate reductase; <b>PDBTitle:</b> the structure of the open conformation of a flavocytochrome c32 fumarate reductase
93	<a href="#">c1qo8A_</a>	Alignment	not modelled	44.4	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
94	<a href="#">d1akya2</a>	Alignment	not modelled	44.4	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c; <b>PDBTitle:</b> crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
95	<a href="#">c1jrxA_</a>	Alignment	not modelled	43.6	0	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 50s ribosomal protein l5p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
96	<a href="#">c3j2le_</a>	Alignment	not modelled	43.5	30	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
97	<a href="#">d1dl6a_</a>	Alignment	not modelled	43.2	10	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37e
98	<a href="#">d1vqo11</a>	Alignment	not modelled	42.9	15	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> solution structure of the eif-5 eif-2b domain from human2 eukaryotic translation initiation factor 5
99	<a href="#">c2e9hA_</a>	Alignment	not modelled	42.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic ribonucleotide-triphosphate reductase large <b>PDBTitle:</b> structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases, native nrdd
100	<a href="#">c1h7bA_</a>	Alignment	not modelled	42.3	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-protein ligase e3 mdm2; <b>PDBTitle:</b> solution structure of the c4 zinc-finger domain of hdm2
101	<a href="#">c2c6bA_</a>	Alignment	not modelled	40.6	4	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
102	<a href="#">d1mjca_</a>	Alignment	not modelled	39.9	16	<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
103	<a href="#">c3k35D_</a>	Alignment	not modelled	39.0	21	<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
104	<a href="#">c3cngC_</a>	Alignment	not modelled	37.3	20	

105	<a href="#">d1yc5a1</a>	Alignment	not modelled	37.2	8	<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
106	<a href="#">c5v8f3</a>	Alignment	not modelled	36.5	18	<b>PDB header:</b> replication <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
107	<a href="#">c3glsC</a>	Alignment	not modelled	36.4	8	<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
108	<a href="#">c5btrB</a>	Alignment	not modelled	36.3	10	<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
109	<a href="#">d1g6pa</a>	Alignment	not modelled	36.1	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
110	<a href="#">c2y69S</a>	Alignment	not modelled	35.1	30	<b>PDB header:</b> electron transport <b>Chain:</b> S: <b>PDB Molecule:</b> cytochrome c oxidase subunit 5b; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
111	<a href="#">d1b8ta1</a>	Alignment	not modelled	34.8	18	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
112	<a href="#">c5fmfR</a>	Alignment	not modelled	34.3	12	<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
113	<a href="#">c3pkiF</a>	Alignment	not modelled	34.3	21	<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
114	<a href="#">c2cr8A</a>	Alignment	not modelled	33.3	8	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> mdm4 protein; <b>PDBTitle:</b> solution structure of the zf-ranbp domain of p53-binding2 protein mdm4
115	<a href="#">c1q14A</a>	Alignment	not modelled	33.0	25	<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
116	<a href="#">c6cnbR</a>	Alignment	not modelled	33.0	4	<b>PDB header:</b> transcription/dna <b>Chain:</b> R: <b>PDB Molecule:</b> transcription factor iiib 70 kda subunit,tata-box-binding <b>PDBTitle:</b> yeast rna polymerase iii initial transcribing complex
117	<a href="#">c6nmiF</a>	Alignment	not modelled	32.9	0	<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
118	<a href="#">c2pziA</a>	Alignment	not modelled	32.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable serine/threonine-protein kinase pkng; <b>PDBTitle:</b> crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothioephene ax20017
119	<a href="#">c1s1iY</a>	Alignment	not modelled	32.3	14	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 60s ribosomal protein l37-a; <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.
120	<a href="#">c3ky9B</a>	Alignment	not modelled	32.2	23	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> autoinhibited vav1