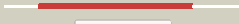


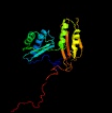
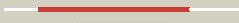










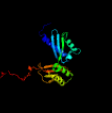








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0707_(rpsC)_804285_805109
Date	Fri Jul 26 01:50:28 BST 2019
Unique Job ID	b83cde38f49c8d10




















Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5o5jC_</a>	 Alignment		100.0	97	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 30s ribosomal protein s3; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	<a href="#">c3j00C_</a>	 Alignment		100.0	50	<b>PDB header:</b> ribosome/ribosomal protein <b>Chain:</b> C; <b>PDB Molecule:</b> 30s ribosomal protein s3; <b>PDBTitle:</b> structure of the ribosome-secye complex in the membrane environment
3	<a href="#">c2qbfC_</a>	 Alignment		100.0	54	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 30s ribosomal protein s3; <b>PDBTitle:</b> crystal structure of the bacterial ribosome from escherichia coli in2 complex with ribosome recycling factor (rrf). this file contains the3 30s subunit of the second 70s ribosome. the entire crystal structure4 contains two 70s ribosomes and is described in remark 400.
4	<a href="#">c1pnxC_</a>	 Alignment		100.0	56	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 30s ribosomal protein s3; <b>PDBTitle:</b> crystal structure of the wild type ribosome from e. coli, 30s subunit2 of 70s ribosome. this file, 1pnx, contains only molecules of the 30s3 ribosomal subunit. the 50s subunit is in the pdb file 1pny.
5	<a href="#">c1hnwC_</a>	 Alignment		100.0	56	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 30s ribosomal protein s3; <b>PDBTitle:</b> structure of the thermus thermophilus 30s ribosomal subunit2 in complex with tetracycline
6	<a href="#">c2gy9C_</a>	 Alignment		100.0	54	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 30s ribosomal subunit protein s3; <b>PDBTitle:</b> structure of the 30s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
7	<a href="#">c3bbnC_</a>	 Alignment		100.0	40	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> ribosomal protein s3; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
8	<a href="#">c2xznC_</a>	 Alignment		100.0	23	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> kh domain containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
9	<a href="#">c2zkaC_</a>	 Alignment		100.0	22	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> C; <b>PDB Molecule:</b> rna expansion segment es4; <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
10	<a href="#">c3j20C_</a>	 Alignment		100.0	31	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 30s ribosomal protein s3p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
11	<a href="#">c3zeyX_</a>	 Alignment		100.0	22	<b>PDB header:</b> ribosome <b>Chain:</b> X; <b>PDB Molecule:</b> 40s ribosomal protein s3, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

12	<a href="#">c5xyiD_</a>	Alignment		100.0	19	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s3, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
13	<a href="#">c1s1hC_</a>	Alignment		100.0	21	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> 40s ribosomal protein s3; <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, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
14	<a href="#">c3izbB_</a>	Alignment		100.0	21	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 40s ribosomal protein rps3 (s3p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
15	<a href="#">d2uubc2</a>	Alignment		100.0	53	<b>Fold:</b> Ribosomal protein S3 C-terminal domain <b>Superfamily:</b> Ribosomal protein S3 C-terminal domain <b>Family:</b> Ribosomal protein S3 C-terminal domain
16	<a href="#">d2qalc2</a>	Alignment		100.0	64	<b>Fold:</b> Ribosomal protein S3 C-terminal domain <b>Superfamily:</b> Ribosomal protein S3 C-terminal domain <b>Family:</b> Ribosomal protein S3 C-terminal domain
17	<a href="#">d2qalc1</a>	Alignment		100.0	42	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
18	<a href="#">d2uubc1</a>	Alignment		100.0	57	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
19	<a href="#">d1wh9a_</a>	Alignment		99.5	25	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
20	<a href="#">c3gkuB_</a>	Alignment		95.4	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable rna-binding protein; <b>PDBTitle:</b> crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
21	<a href="#">c2pt7G_</a>	Alignment	not modelled	93.9	15	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
22	<a href="#">c3j6vV_</a>	Alignment	not modelled	92.4	13	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 28s ribosomal protein s24, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
23	<a href="#">c2cy1A_</a>	Alignment	not modelled	79.6	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nusa protein homolog; <b>PDBTitle:</b> crystal structure of ape1850
24	<a href="#">d1egaa2</a>	Alignment	not modelled	77.5	21	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
25	<a href="#">c1egaB_</a>	Alignment	not modelled	75.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (gtp-binding protein era); <b>PDBTitle:</b> crystal structure of a widely conserved gtpase era
26	<a href="#">d1wf3a2</a>	Alignment	not modelled	72.2	21	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
27	<a href="#">d2asba3</a>	Alignment	not modelled	65.2	23	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
28	<a href="#">d1hh2p3</a>	Alignment	not modelled	64.7	23	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
29	<a href="#">c3af5A_</a>	Alignment	not modelled	63.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph1404;

29	<a href="#">c3d13A</a>	Alignment	not modelled	53.9	20	<b>PDBTitle:</b> the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii <b>PDB header:</b> nucleotide binding protein/rna
30	<a href="#">c3ievA</a>	Alignment	not modelled	57.7	25	<b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein era; <b>PDBTitle:</b> crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna
31	<a href="#">c1wf3A</a>	Alignment	not modelled	57.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
32	<a href="#">c2xr1A</a>	Alignment	not modelled	46.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor 100 kd <b>PDBTitle:</b> dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
33	<a href="#">c2hh2A</a>	Alignment	not modelled	45.7	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kh-type splicing regulatory protein; <b>PDBTitle:</b> solution structure of the fourth kh domain of ksrp
34	<a href="#">d2axya1</a>	Alignment	not modelled	41.4	26	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
35	<a href="#">c4b8tA</a>	Alignment	not modelled	41.0	33	<b>PDB header:</b> transcription/rna <b>Chain:</b> A: <b>PDB Molecule:</b> kh-type splicing regulatory protein; <b>PDBTitle:</b> rna binding protein solution structure of the third kh2 domain of ksrp in complex with the g-rich target sequence.
36	<a href="#">c2hh3A</a>	Alignment	not modelled	38.3	32	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kh-type splicing regulatory protein; <b>PDBTitle:</b> solution structure of the third kh domain of ksrp
37	<a href="#">d1we8a_</a>	Alignment	not modelled	37.8	22	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
38	<a href="#">c2asbA</a>	Alignment	not modelled	36.9	23	<b>PDB header:</b> transcription/rna <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation protein nusa; <b>PDBTitle:</b> structure of a mycobacterium tuberculosis nusa-rna complex
39	<a href="#">d1dt4a_</a>	Alignment	not modelled	36.9	15	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
40	<a href="#">d1tuaa1</a>	Alignment	not modelled	36.1	22	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
41	<a href="#">d1zzka1</a>	Alignment	not modelled	35.9	30	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
42	<a href="#">c1ztgD_</a>	Alignment	not modelled	33.9	18	<b>PDB header:</b> dna, rna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> poly(rc)-binding protein 1; <b>PDBTitle:</b> human alpha polyc binding protein kh1
43	<a href="#">d1j4wa1</a>	Alignment	not modelled	33.5	37	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
44	<a href="#">d1j4wa2</a>	Alignment	not modelled	33.0	22	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
45	<a href="#">d1dtja_</a>	Alignment	not modelled	31.6	15	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
46	<a href="#">c6qeyA</a>	Alignment	not modelled	30.4	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> insulin-like growth factor 2 mrna-binding protein 1; <b>PDBTitle:</b> imp1 kh1 and kh2 domains create a structural platform with unique rna2 recognition and re-modelling properties
47	<a href="#">c2anrA</a>	Alignment	not modelled	30.3	22	<b>PDB header:</b> rna-binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> neuro-oncological ventral antigen 1; <b>PDBTitle:</b> crystal structure (ii) of nova-1 kh1/kh2 domain tandem with 25nt rna2 hairpin
48	<a href="#">c3krmB_</a>	Alignment	not modelled	28.7	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> insulin-like growth factor 2 mrna-binding protein 1; <b>PDBTitle:</b> imp1 kh34
49	<a href="#">d1wvna1</a>	Alignment	not modelled	28.6	30	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
50	<a href="#">d1khma_</a>	Alignment	not modelled	28.0	26	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
51	<a href="#">d1ec6a_</a>	Alignment	not modelled	27.3	15	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
52	<a href="#">c1j4wA</a>	Alignment	not modelled	25.3	41	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> fuse binding protein; <b>PDBTitle:</b> complex of the kh3 and kh4 domains of fbp with a2 single_stranded 29mer dna oligonucleotide from the fuse3 element of the c-myc oncogene
53	<a href="#">c2n8IA</a>	Alignment	not modelled	23.4	26	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> insulin-like growth factor 2 mrna-binding protein 1; <b>PDBTitle:</b> zipcode-binding-protein-1 kh3kh4(dd) domains in complex with the kh32 rna target
54	<a href="#">d1x4na1</a>	Alignment	not modelled	23.1	26	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
						<b>PDB header:</b> unknown function

55	<a href="#">c4e0eB</a>	Alignment	not modelled	22.5	54	<b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4450 family protein (bt_4147) from2 bacteroides thetaiotaomicron vpi-5482 at 2.90 a resolution
56	<a href="#">d1x4ma1</a>	Alignment	not modelled	22.3	22	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
57	<a href="#">c2yqrA</a>	Alignment	not modelled	21.9	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa0907 protein; <b>PDBTitle:</b> solution structure of the kh domain in kiaa0907 protein
58	<a href="#">d2ba0a3</a>	Alignment	not modelled	21.7	28	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
59	<a href="#">c4mntnA</a>	Alignment	not modelled	21.7	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination factor nusa; <b>PDBTitle:</b> crystal structure of transcription termination factor nusa from2 planctomyces limnophilus dsm 3776
60	<a href="#">d1viga</a>	Alignment	not modelled	21.5	26	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
61	<a href="#">c1tuaA</a>	Alignment	not modelled	21.2	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ape0754; <b>PDBTitle:</b> 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix
62	<a href="#">c2jzxA</a>	Alignment	not modelled	21.1	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> poly(rc)-binding protein 2; <b>PDBTitle:</b> pcbp2 kh1-kh2 domains
63	<a href="#">c2ycbA</a>	Alignment	not modelled	20.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor; <b>PDBTitle:</b> structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
64	<a href="#">c5lm7A</a>	Alignment	not modelled	20.5	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination/antitermination protein nusa; <b>PDBTitle:</b> crystal structure of the lambda n-nus factor complex
65	<a href="#">d2ctja1</a>	Alignment	not modelled	20.3	26	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
66	<a href="#">d1myna</a>	Alignment	not modelled	20.0	42	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Insect defensins
67	<a href="#">c2dgrA</a>	Alignment	not modelled	19.5	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger and kh domain-containing protein 1; <b>PDBTitle:</b> solution structure of the second kh domain in ring finger2 and kh domain containing protein 1
68	<a href="#">d2ctla1</a>	Alignment	not modelled	19.3	26	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
69	<a href="#">c1k0rB</a>	Alignment	not modelled	19.0	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nusa; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis nusa
70	<a href="#">c1hh2P</a>	Alignment	not modelled	18.3	23	<b>PDB header:</b> transcription regulation <b>Chain:</b> P: <b>PDB Molecule:</b> n utilization substance protein a; <b>PDBTitle:</b> crystal structure of nusa from thermotoga maritima
71	<a href="#">c2jvzA</a>	Alignment	not modelled	18.2	24	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> far upstream element-binding protein 2; <b>PDBTitle:</b> solution nmr structure of the second and third kh domains2 of ksrp
72	<a href="#">c3e04A</a>	Alignment	not modelled	18.2	50	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate hydratase; <b>PDBTitle:</b> crystal structure of human fumarate hydratase
73	<a href="#">c5wwwA</a>	Alignment	not modelled	16.9	29	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding e3 ubiquitin-protein ligase mex3c; <b>PDBTitle:</b> crystal structure of the kh1 domain of human rna-binding e3 ubiquitin-2 protein ligase mex-3c complex with rna
74	<a href="#">d2fmra</a>	Alignment	not modelled	16.6	31	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
75	<a href="#">d1hsta</a>	Alignment	not modelled	16.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Linker histone H1/H5
76	<a href="#">d2ctea1</a>	Alignment	not modelled	15.9	22	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
77	<a href="#">c6flqF</a>	Alignment	not modelled	15.6	11	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> transcription termination/antitermination protein nusa; <b>PDBTitle:</b> cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
78	<a href="#">c1l2fA</a>	Alignment	not modelled	14.1	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> n utilization substance protein a; <b>PDBTitle:</b> crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
79	<a href="#">d2ctka1</a>	Alignment	not modelled	13.4	17	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
80	<a href="#">d2ctma1</a>	Alignment	not modelled	13.3	22	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)

81	<a href="#">c2fenA_</a>	 Alignment	not modelled	11.5	50	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-carboxy-cis,cis-muconate lactonizing enzyme; <b>PDBTitle:</b> 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2
82	<a href="#">d1b33n_</a>	 Alignment	not modelled	11.5	14	<b>Fold:</b> Allophycocyanin linker chain (domain) <b>Superfamily:</b> Allophycocyanin linker chain (domain) <b>Family:</b> Allophycocyanin linker chain (domain)
83	<a href="#">d2cmea1</a>	 Alignment	not modelled	11.3	42	<b>Fold:</b> SARS ORF9b-like <b>Superfamily:</b> SARS ORF9b-like <b>Family:</b> SARS ORF9b-like
84	<a href="#">d2ctfa1</a>	 Alignment	not modelled	11.3	19	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
85	<a href="#">d1tuaa2</a>	 Alignment	not modelled	10.9	29	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
86	<a href="#">d2gysa1</a>	 Alignment	not modelled	10.4	40	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
87	<a href="#">d2cpqa1</a>	 Alignment	not modelled	10.2	31	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
88	<a href="#">d2z0sa2</a>	 Alignment	not modelled	9.7	21	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
89	<a href="#">c4hgvC_</a>	 Alignment	not modelled	9.1	38	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> crystal structure of a fumarate hydratase
90	<a href="#">c2e3uA_</a>	 Alignment	not modelled	9.0	35	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1566; <b>PDBTitle:</b> crystal structure analysis of dim2p from pyrococcus horikoshii ot3
91	<a href="#">c6emlp_</a>	 Alignment	not modelled	9.0	8	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein s0-a; <b>PDBTitle:</b> cryo-em structure of a late pre-40s ribosomal subunit from2 saccharomyces cerevisiae
92	<a href="#">c4jvhA_</a>	 Alignment	not modelled	8.9	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein quaking; <b>PDBTitle:</b> structure of the star domain of quaking protein in complex with rna
93	<a href="#">c3n89B_</a>	 Alignment	not modelled	8.6	20	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> defective in germ line development protein 3, isoform a; <b>PDBTitle:</b> kh domains
94	<a href="#">c2pfmA_</a>	 Alignment	not modelled	8.1	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
95	<a href="#">c5vkwB_</a>	 Alignment	not modelled	8.1	38	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase ade13 from candida2 albicans
96	<a href="#">c3gtdB_</a>	 Alignment	not modelled	8.1	38	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
97	<a href="#">c5xnzA_</a>	 Alignment	not modelled	7.8	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cred; <b>PDBTitle:</b> crystal structure of cred complex with fumarate
98	<a href="#">d1c3ca_</a>	 Alignment	not modelled	7.7	43	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
99	<a href="#">c2w2rA_</a>	 Alignment	not modelled	7.7	5	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein; <b>PDBTitle:</b> structure of the vesicular stomatitis virus matrix protein