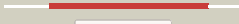























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3920c_(-)_4408511_4409074
Date	Sat Aug 10 22:05:11 BST 2019
Unique Job ID	cd13b61de8b04a2f

Detailed template information

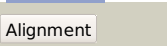
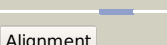
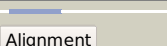
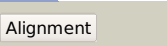
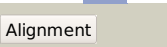
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gkuB_</a>	 Alignment		100.0	31	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> probable rna-binding protein; <b>PDBTitle:</b> crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
2	<a href="#">c2pt7G_</a>	 Alignment		100.0	18	<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)
3	<a href="#">c2cpmA_</a>	 Alignment		99.1	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> sperm-associated antigen 7; <b>PDBTitle:</b> solution structure of the r3h domain of human sperm-2 associated antigen 7
4	<a href="#">d1msza_</a>	 Alignment		98.9	21	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
5	<a href="#">c1mszA_</a>	 Alignment		98.9	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dna-binding protein smubp-2; <b>PDBTitle:</b> solution structure of the r3h domain from human smubp-2
6	<a href="#">d1whra_</a>	 Alignment		97.9	21	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
7	<a href="#">c3zeyX_</a>	 Alignment		96.8	18	<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
8	<a href="#">c5xyiD_</a>	 Alignment		96.1	13	<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
9	<a href="#">c2zkqc_</a>	 Alignment		96.1	12	<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="#">d1wh9a_</a>	 Alignment		95.7	14	<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)
11	<a href="#">d2qalc1</a>	 Alignment		95.5	16	<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)

12	<a href="#">c2xznC_</a>	Alignment		95.4	13	<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
13	<a href="#">c3j20C_</a>	Alignment		95.2	16	<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)
14	<a href="#">d2uubc1</a>	Alignment		95.1	20	<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)
15	<a href="#">c1s1hC_</a>	Alignment		94.7	16	<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.
16	<a href="#">d1egaa2</a>	Alignment		92.9	11	<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)
17	<a href="#">c3izbB_</a>	Alignment		92.8	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
18	<a href="#">c3j00C_</a>	Alignment		92.5	16	<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
19	<a href="#">c2fphX_</a>	Alignment		92.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> ylmh; <b>PDBTitle:</b> cell division protein ylmh from streptococcus pneumoniae
20	<a href="#">d1ug8a_</a>	Alignment		91.1	25	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
21	<a href="#">d1wf3a2</a>	Alignment	not modelled	89.5	19	<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)
22	<a href="#">c5o5jC_</a>	Alignment	not modelled	89.4	17	<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
23	<a href="#">d2asba3</a>	Alignment	not modelled	88.9	17	<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)
24	<a href="#">d1hh2p3</a>	Alignment	not modelled	87.6	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)
25	<a href="#">c3ievA_</a>	Alignment	not modelled	85.6	17	<b>PDB header:</b> nucleotide binding protein/rna <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
26	<a href="#">d2axya1</a>	Alignment	not modelled	84.6	14	<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)
27	<a href="#">c2qbfC_</a>	Alignment	not modelled	84.3	16	<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.
28	<a href="#">c1ztgD_</a>	Alignment	not modelled	84.0	12	<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

29	<a href="#">c1wf3A</a>	Alignment	not modelled	83.7	19	<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
30	<a href="#">c4b8tA</a>	Alignment	not modelled	81.8	17	<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.
31	<a href="#">c2cy1A</a>	Alignment	not modelled	81.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nusa protein homolog; <b>PDBTitle:</b> crystal structure of ape1850
32	<a href="#">c2asbA</a>	Alignment	not modelled	81.3	17	<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
33	<a href="#">d1tuaa2</a>	Alignment	not modelled	81.3	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)
34	<a href="#">d2z0sa2</a>	Alignment	not modelled	79.8	20	<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="#">c6emlp</a>	Alignment	not modelled	79.8	19	<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
36	<a href="#">c1k0rB</a>	Alignment	not modelled	78.9	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nusa; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis nusa
37	<a href="#">d1tuaa1</a>	Alignment	not modelled	78.8	25	<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="#">c1legaB</a>	Alignment	not modelled	78.5	14	<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
39	<a href="#">d1we8a</a>	Alignment	not modelled	78.5	12	<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="#">c1pnxC</a>	Alignment	not modelled	78.4	20	<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.
41	<a href="#">d1wvna1</a>	Alignment	not modelled	78.1	9	<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="#">c2gy9C</a>	Alignment	not modelled	77.1	16	<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
43	<a href="#">c1hh2P</a>	Alignment	not modelled	76.5	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
44	<a href="#">c2jzxA</a>	Alignment	not modelled	76.4	13	<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
45	<a href="#">c2hh3A</a>	Alignment	not modelled	75.9	16	<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
46	<a href="#">c5wwwA</a>	Alignment	not modelled	75.3	16	<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
47	<a href="#">c6qeyA</a>	Alignment	not modelled	74.4	5	<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
48	<a href="#">d1j4wa1</a>	Alignment	not modelled	74.2	16	<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)
49	<a href="#">c2hh2A</a>	Alignment	not modelled	73.8	30	<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
50	<a href="#">d1j4wa2</a>	Alignment	not modelled	72.7	9	<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="#">d1zzka1</a>	Alignment	not modelled	72.2	13	<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="#">d2ctea1</a>	Alignment	not modelled	71.0	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)
53	<a href="#">d1dt4a</a>	Alignment	not modelled	69.9	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)
54	<a href="#">c1j4wA</a>	Alignment	not modelled	69.6	18	<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
55	<a href="#">c4qmfB_</a>	Alignment	not modelled	68.7	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> krr1 small subunit processome component; <b>PDBTitle:</b> structure of the krr1 and faf1 complex from saccharomyces cerevisiae
56	<a href="#">d1x4na1</a>	Alignment	not modelled	68.6	13	<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="#">d1ec6a_</a>	Alignment	not modelled	66.8	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)
58	<a href="#">c3krmB_</a>	Alignment	not modelled	66.8	18	<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
59	<a href="#">c2dgrA_</a>	Alignment	not modelled	65.6	10	<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
60	<a href="#">c1hnwC_</a>	Alignment	not modelled	64.6	20	<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
61	<a href="#">d1dtja_</a>	Alignment	not modelled	64.4	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)
62	<a href="#">c2qndA_</a>	Alignment	not modelled	64.4	12	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fmr1 protein; <b>PDBTitle:</b> crystal structure of the kh1-kh2 domains from human fragile x mental2 retardation protein
63	<a href="#">c1l2fA_</a>	Alignment	not modelled	64.2	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
64	<a href="#">c6g18x_</a>	Alignment	not modelled	63.5	26	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 40s ribosomal protein s23; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state c
65	<a href="#">c5el3D_</a>	Alignment	not modelled	63.4	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> kh domain-containing, rna-binding, signal transduction- <b>PDBTitle:</b> structure of the kh domain of t-star
66	<a href="#">d2ctla1</a>	Alignment	not modelled	62.8	23	<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)
67	<a href="#">c2e3uA_</a>	Alignment	not modelled	62.0	15	<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
68	<a href="#">c2yqrA_</a>	Alignment	not modelled	61.7	16	<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
69	<a href="#">c2anrA_</a>	Alignment	not modelled	61.2	32	<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
70	<a href="#">c1tuaA_</a>	Alignment	not modelled	60.7	26	<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
71	<a href="#">c5udtD_</a>	Alignment	not modelled	59.9	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
72	<a href="#">d1x4ma1</a>	Alignment	not modelled	59.3	27	<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)
73	<a href="#">d2ba0a3</a>	Alignment	not modelled	59.1	7	<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)
74	<a href="#">d2ctka1</a>	Alignment	not modelled	58.8	13	<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="#">d1khma_</a>	Alignment	not modelled	57.9	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)
76	<a href="#">d1viga_</a>	Alignment	not modelled	57.2	13	<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="#">c2n8lA_</a>	Alignment	not modelled	55.8	18	<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
78	<a href="#">d2ctfa1</a>	Alignment	not modelled	53.5	11	<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)
79	<a href="#">c2jvzA_</a>	Alignment	not modelled	53.1	21	<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
80	<a href="#">c4mtaA_</a>	Alignment	not modelled	52.0	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination factor nusa;

80	<a href="#">c4mduA</a>	Alignment	not modelled	52.0	24	<b>PDBTitle:</b> crystal structure of transcription termination factor nusa from 2 planctomyces limnophilus dsm 3776
81	<a href="#">d2ctma1</a>	Alignment	not modelled	50.6	14	<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)
82	<a href="#">c2a1sC</a>	Alignment	not modelled	49.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> poly(a)-specific ribonuclease parn; <b>PDBTitle:</b> crystal structure of native parn nuclease domain
83	<a href="#">d2ctja1</a>	Alignment	not modelled	48.5	27	<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)
84	<a href="#">d1dk7a</a>	Alignment	not modelled	48.3	21	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
85	<a href="#">d1srva</a>	Alignment	not modelled	43.9	22	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
86	<a href="#">d1k1ga</a>	Alignment	not modelled	43.7	27	<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)
87	<a href="#">d1oela2</a>	Alignment	not modelled	43.5	19	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
88	<a href="#">d2bl5a1</a>	Alignment	not modelled	43.4	14	<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="#">c5lm7A</a>	Alignment	not modelled	43.0	13	<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
90	<a href="#">d1kida</a>	Alignment	not modelled	41.9	21	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
91	<a href="#">c4jvhA</a>	Alignment	not modelled	40.4	20	<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
92	<a href="#">c3m6cA</a>	Alignment	not modelled	40.1	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> 60 kda chaperonin 1; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis groel1 apical domain
93	<a href="#">c4jvyA</a>	Alignment	not modelled	39.3	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> female germline-specific tumor suppressor gld-1; <b>PDBTitle:</b> structure of the star (signal transduction and activation of rna)2 domain of gld-1 bound to rna
94	<a href="#">c4wala</a>	Alignment	not modelled	39.0	39	<b>PDB header:</b> protein binding/rna <b>Chain:</b> A: <b>PDB Molecule:</b> branchpoint-bridging protein; <b>PDBTitle:</b> crystal structure of selenomethionine msl5 protein in complex with rna2 at 2.2 a
95	<a href="#">c6qh2A</a>	Alignment	not modelled	38.8	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> solution nmr ensemble for a chimeric kh-s1 domain construct of 2 exosomal polynucleotide phosphrylase at 298k compiled using the3 comand method
96	<a href="#">c3af5A</a>	Alignment	not modelled	37.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph1404; <b>PDBTitle:</b> the crystal structure of an archaeal cpsf subunit, ph1404 from 2 pyrococcus horikoshii
97	<a href="#">d1sjpa2</a>	Alignment	not modelled	36.4	18	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
98	<a href="#">d1we3a2</a>	Alignment	not modelled	36.1	24	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
99	<a href="#">c5cdjA</a>	Alignment	not modelled	35.0	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco large subunit-binding protein subunit alpha, <b>PDBTitle:</b> apical domain of chloroplast chaperonin 60a
100	<a href="#">c5eltB</a>	Alignment	not modelled	34.6	47	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> kh domain-containing, rna-binding, signal transduction- <b>PDBTitle:</b> structure of the qua1-kh domain of t-star in complex with uaau rna
101	<a href="#">c5cffE</a>	Alignment	not modelled	34.3	19	<b>PDB header:</b> transcription/rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> staufen; <b>PDBTitle:</b> crystal structure of miranda/staufen dsrbd5 complex
102	<a href="#">d2je6i3</a>	Alignment	not modelled	29.7	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)
103	<a href="#">c2gtpD</a>	Alignment	not modelled	28.7	8	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> regulator of g-protein signaling 1; <b>PDBTitle:</b> crystal structure of the heterodimeric complex of human rgs1 and2 activated gi alpha 1
104	<a href="#">c4wyqB</a>	Alignment	not modelled	27.0	27	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> risc-loading complex subunit tarbp2; <b>PDBTitle:</b> crystal structure of the dicer-trbp interface
105	<a href="#">c2kkeA</a>	Alignment	not modelled	25.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5 <b>PDB header:</b> transcription

106	<a href="#">c6flqF_</a>	 Alignment	not modelled	25.2	15	<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
107	<a href="#">c2kkeB_</a>	 Alignment	not modelled	24.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
108	<a href="#">d2fug71</a>	 Alignment	not modelled	21.1	12	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Fratxin/Nqo15-like <b>Family:</b> Nqo15-like
109	<a href="#">c2dvkA_</a>	 Alignment	not modelled	21.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> upf0130 protein ape0816; <b>PDBTitle:</b> crystal structure of hypothetical protein from aeropyrum pernix
110	<a href="#">c2qw5B_</a>	 Alignment	not modelled	20.8	14	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> xylose isomerase-like tim barrel; <b>PDBTitle:</b> crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution