
























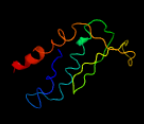




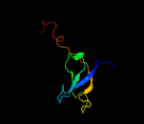


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2841c\_nusA\_3148395\_3149438  
 Date Wed Aug 7 12:50:50 BST 2019  
 Unique Job ID 2f137b905dab797a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6flqF_</a>	 Alignment		100.0	36	<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
2	<a href="#">c4mntA_</a>	 Alignment		100.0	36	<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
3	<a href="#">c1k0rB_</a>	 Alignment		100.0	100	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nusa; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis nusa
4	<a href="#">c5lm7A_</a>	 Alignment		100.0	36	<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
5	<a href="#">c1l2fA_</a>	 Alignment		100.0	42	<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
6	<a href="#">c1hh2P_</a>	 Alignment		100.0	42	<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
7	<a href="#">c2asbA_</a>	 Alignment		100.0	100	<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
8	<a href="#">c6j9eF_</a>	 Alignment		100.0	31	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> transcription termination/antitermination protein nusa; <b>PDBTitle:</b> cryo-em structure of xanthomonos oryzae transcription elongation2 complex with nusa and the bacteriophage protein p7
9	<a href="#">d2asba2</a>	 Alignment		100.0	100	<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)
10	<a href="#">d1hh2p2</a>	 Alignment		100.0	45	<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="#">c2kwpA_</a>	 Alignment		99.9	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation protein nusa; <b>PDBTitle:</b> solution structure of the aminoterminal domain of e. coli nusa

12	<a href="#">d1hh2p3</a>	Alignment		99.9	61	<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)
13	<a href="#">d2asba3</a>	Alignment		99.9	100	<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)
14	<a href="#">c2mt4A</a>	Alignment		99.9	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination/antitermination protein nusa; <b>PDBTitle:</b> solution structure of the n-terminal domain of nusa from b. subtilis
15	<a href="#">d1k0ra4</a>	Alignment		99.9	100	<b>Fold:</b> Transcription factor NusA, N-terminal domain <b>Superfamily:</b> Transcription factor NusA, N-terminal domain <b>Family:</b> Transcription factor NusA, N-terminal domain
16	<a href="#">d1hh2p4</a>	Alignment		99.9	43	<b>Fold:</b> Transcription factor NusA, N-terminal domain <b>Superfamily:</b> Transcription factor NusA, N-terminal domain <b>Family:</b> Transcription factor NusA, N-terminal domain
17	<a href="#">d2asba1</a>	Alignment		99.9	100	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
18	<a href="#">c2cy1A</a>	Alignment		99.8	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nusa protein homolog; <b>PDBTitle:</b> crystal structure of ape1850
19	<a href="#">d1hh2p1</a>	Alignment		99.7	28	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
20	<a href="#">c2mfiA</a>	Alignment		98.3	30	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> domain 1 of e. coli ribosomal protein s1
21	<a href="#">d1q46a2</a>	Alignment	not modelled	98.1	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
22	<a href="#">c1q46A</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 alpha subunit; <b>PDBTitle:</b> crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
23	<a href="#">d1go3e1</a>	Alignment	not modelled	98.1	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
24	<a href="#">c1yz6A</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> probable translation initiation factor 2 alpha <b>PDBTitle:</b> crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
25	<a href="#">d2ba0a1</a>	Alignment	not modelled	98.0	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
26	<a href="#">c2z0sA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable exosome complex rna-binding protein 1; <b>PDBTitle:</b> crystal structure of putative exosome complex rna-binding2 protein
27	<a href="#">c2khiA</a>	Alignment	not modelled	98.0	25	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
28	<a href="#">d1wi5a</a>	Alignment	not modelled	98.0	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like

29	<a href="#">c1q8kA</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 2 <b>PDBTitle:</b> solution structure of alpha subunit of human eif2
30	<a href="#">c6qh2A</a>	Alignment	not modelled	98.0	23	<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 of2 exosomal polynucleotide phosphrylase at 298k compiled using the3 comand method
31	<a href="#">c2k4kA</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> general stress protein 13; <b>PDBTitle:</b> solution structure of gsp13 from bacillus subtilis
32	<a href="#">c2khjA</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
33	<a href="#">c2k52A</a>	Alignment	not modelled	97.9	17	<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
34	<a href="#">c4nnkA</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> structural basis for targeting the ribosomal protein s1 of2 mycobacterium tuberculosis by pyrazinamide
35	<a href="#">d2z0sa1</a>	Alignment	not modelled	97.9	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
36	<a href="#">d2je6i1</a>	Alignment	not modelled	97.9	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
37	<a href="#">d1y14b1</a>	Alignment	not modelled	97.9	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
38	<a href="#">d1kl9a2</a>	Alignment	not modelled	97.8	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
39	<a href="#">c3j81j</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> us4; <b>PDBTitle:</b> cryoem structure of a partial yeast 48s preinitiation complex
40	<a href="#">c2eqsA</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase dhx8; <b>PDBTitle:</b> solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8
41	<a href="#">c2mflA</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> domain 2 of e. coli ribosomal protein s1
42	<a href="#">c2ahoB</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> translation initiation factor 2 alpha subunit; <b>PDBTitle:</b> structure of the archaeal initiation factor eif2 alpha-gamma2 heterodimer from sulfobolus solfataricus complexed with gdpnp
43	<a href="#">d1sroa</a>	Alignment	not modelled	97.7	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
44	<a href="#">d3bzka4</a>	Alignment	not modelled	97.7	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
45	<a href="#">d2ahob2</a>	Alignment	not modelled	97.7	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
46	<a href="#">c1go3E</a>	Alignment	not modelled	97.7	26	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> dna-directed rna polymerase subunit e; <b>PDBTitle:</b> structure of an archeal homolog of the eukaryotic rna polymerase ii2 rpb4/rpb7 complex
47	<a href="#">c2b8kG</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> transferase <b>Chain:</b> G; <b>PDB Molecule:</b> dna-directed rna polymerase ii 19 kda polypeptide; <b>PDBTitle:</b> 12-subunit rna polymerase ii
48	<a href="#">c2je6l</a>	Alignment	not modelled	97.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> I; <b>PDB Molecule:</b> exosome complex rna-binding protein 1; <b>PDBTitle:</b> structure of a 9-subunit archaeal exosome
49	<a href="#">d2nn6h1</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
50	<a href="#">c4q7jD</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> translation/transferase <b>Chain:</b> D; <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> complex structure of viral rna polymerase
51	<a href="#">c2cqoA</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> nucleolar protein of 40 kda; <b>PDBTitle:</b> solution structure of the s1 rna binding domain of human2 hypothetical protein flj11067
52	<a href="#">c4aimA</a>	Alignment	not modelled	97.5	23	<b>PDB header:</b> transferase/peptide <b>Chain:</b> A; <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of c. crescentus pnpase bound to rnase e2 recognition peptide
53	<a href="#">c5xq5A</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> nmr structure of the domain 5 of the e. coli ribosomal protein s1
54	<a href="#">c1kl9A</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 2 subunit 1; <b>PDBTitle:</b> crystal structure of the n-terminal segment of human

						eukaryotic2 initiation factor 2alpha <b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> dna-directed rna polymerase ii 19 kda polypeptide; <b>PDBTitle:</b> subunits rpb4 and rpb7 of human rna polymerase ii
55	<a href="#">c2c35F_</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> ribosome <b>Chain:</b> 8; <b>PDB Molecule:</b> 30s ribosomal protein s1, chloroplastic; <b>PDBTitle:</b> structure of the 30s small subunit of chloroplast ribosome from2 spinach
56	<a href="#">c5x8r8_</a>	Alignment	not modelled	97.3	22	<b>PDB header:</b> transferase <b>Chain:</b> G; <b>PDB Molecule:</b> rna polymerase ii subunit; <b>PDBTitle:</b> rna polymerase ii from komagataella pastoris (type-2 crystal)
57	<a href="#">c5x50G_</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> archaeal exosome rna binding protein rrp4; <b>PDBTitle:</b> archaeal exosome core
58	<a href="#">c2ba0A_</a>	Alignment	not modelled	97.3	21	<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
59	<a href="#">c2jzxA_</a>	Alignment	not modelled	97.2	26	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
60	<a href="#">d2c35b1</a>	Alignment	not modelled	97.1	19	<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
61	<a href="#">c2jvzA_</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> transcription, transferase <b>Chain:</b> G; <b>PDB Molecule:</b> dna-directed rna polymerase ii 19 kd polypeptide; <b>PDBTitle:</b> complete 12-subunit rna polymerase ii
62	<a href="#">c1nt9G_</a>	Alignment	not modelled	97.0	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> multidomain protein with s1 rna-binding domains; <b>PDBTitle:</b> crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
63	<a href="#">c3go5A_</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> transcription <b>Chain:</b> E; <b>PDB Molecule:</b> dna-directed rna polymerase, subunit e'; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
64	<a href="#">c4qiwE_</a>	Alignment	not modelled	96.9	24	<b>PDB header:</b> transcription <b>Chain:</b> S; <b>PDB Molecule:</b> dna-directed rna polymerase ii subunit rpb7; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
65	<a href="#">c3h0gS_</a>	Alignment	not modelled	96.9	22	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> I; <b>PDB Molecule:</b> 3'-5' exoribonuclease csl4 homolog; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
66	<a href="#">c2nn6I_</a>	Alignment	not modelled	96.8	17	<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
67	<a href="#">c3krmB_</a>	Alignment	not modelled	96.8	21	<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
68	<a href="#">c2n8lA_</a>	Alignment	not modelled	96.7	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
69	<a href="#">d2nn6i1</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcription elongation factor spt6; <b>PDBTitle:</b> crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
70	<a href="#">c3psiA_</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein pa5201; <b>PDBTitle:</b> crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
71	<a href="#">c2oceA_</a>	Alignment	not modelled	96.6	19	<b>PDB header:</b> transcription <b>Chain:</b> M; <b>PDB Molecule:</b> transcription elongation factor spt6,transcription <b>PDBTitle:</b> structure of activated transcription complex pol ii-dsif-paf-spt6
72	<a href="#">c6gmhM_</a>	Alignment	not modelled	96.6	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
73	<a href="#">c1j4wA_</a>	Alignment	not modelled	96.4	21	<b>PDB header:</b> translation, transferase <b>Chain:</b> E; <b>PDB Molecule:</b> dna-directed rna polymerase subunit e; <b>PDBTitle:</b> archaeal rna polymerase from sulfolobus solfataricus
74	<a href="#">c2pmzE_</a>	Alignment	not modelled	96.4	22	<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
75	<a href="#">c6qeyA_</a>	Alignment	not modelled	96.3	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
76	<a href="#">c2anrA_</a>	Alignment	not modelled	96.3	21	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc8; <b>PDBTitle:</b> crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
77	<a href="#">c3ayhB_</a>	Alignment	not modelled	96.0	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
78	<a href="#">d1smxa_</a>	Alignment	not modelled	96.0	26	

79	<a href="#">c2e3uA</a>	Alignment	not modelled	95.9	22	<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
80	<a href="#">c2qndA</a>	Alignment	not modelled	95.9	20	<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
81	<a href="#">c2ba1B</a>	Alignment	not modelled	95.5	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> archaeal exosome rna binding protein csl4; <b>PDBTitle:</b> archaeal exosome core
82	<a href="#">c2ja9A</a>	Alignment	not modelled	95.5	22	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exosome complex exonuclease rrp40; <b>PDBTitle:</b> structure of the n-terminal deletion of yeast exosome2 component rrp40
83	<a href="#">c2ckzB</a>	Alignment	not modelled	95.5	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna-directed rna polymerase iii 25 kd polypeptide; <b>PDBTitle:</b> x-ray structure of rna polymerase iii subcomplex c17-c25.
84	<a href="#">c4ifdI</a>	Alignment	not modelled	95.3	19	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> I: <b>PDB Molecule:</b> exosome complex component csl4; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
85	<a href="#">c4ifdG</a>	Alignment	not modelled	95.1	22	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> G: <b>PDB Molecule:</b> exosome complex component rrp40; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
86	<a href="#">c6emIp</a>	Alignment	not modelled	94.5	13	<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
87	<a href="#">d1x4ma1</a>	Alignment	not modelled	94.5	18	<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="#">c4oxpA</a>	Alignment	not modelled	94.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease e; <b>PDBTitle:</b> x-ray crystal structure of the s1 and 5'-sensor domains of rnaase e2 from caulobacter crescentus
89	<a href="#">d1j4wa1</a>	Alignment	not modelled	93.9	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)
90	<a href="#">c3af5A</a>	Alignment	not modelled	93.8	16	<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 from2 pyrococcus horikoshii
91	<a href="#">d1tuaa1</a>	Alignment	not modelled	93.8	24	<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)
92	<a href="#">c4ifdH</a>	Alignment	not modelled	93.8	24	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> exosome complex component rrp4; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
93	<a href="#">c6d6rH</a>	Alignment	not modelled	93.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> exosome complex component rrp4; <b>PDBTitle:</b> human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
94	<a href="#">c1ztgD</a>	Alignment	not modelled	93.5	26	<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
95	<a href="#">c2nn6G</a>	Alignment	not modelled	93.4	20	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> G: <b>PDB Molecule:</b> exosome complex exonuclease rrp40; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
96	<a href="#">d2nn6g1</a>	Alignment	not modelled	93.4	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
97	<a href="#">c4toiA</a>	Alignment	not modelled	93.4	25	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s2,ribosomal protein s1; <b>PDBTitle:</b> crystal structure of e.coli ribosomal protein s2 in complex with n-2 terminal domain of s1
98	<a href="#">d1dt4a</a>	Alignment	not modelled	93.3	24	<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)
99	<a href="#">d1j4wa2</a>	Alignment	not modelled	93.3	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)
100	<a href="#">c5xguB</a>	Alignment	not modelled	93.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease r; <b>PDBTitle:</b> escherichia coli. rnaase r
101	<a href="#">d2axyal</a>	Alignment	not modelled	93.0	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)
102	<a href="#">d2z0sa2</a>	Alignment	not modelled	93.0	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)
103	<a href="#">c5aj3f</a>	Alignment	not modelled	92.9	19	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> mitoribosomal protein bs6m, mrps6; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
104	<a href="#">d1dtja</a>	Alignment	not modelled	92.9	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)
						<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I)

105	<a href="#">d2ba0a3</a>	Alignment	not modelled	92.9	21	<b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
106	<a href="#">d1wvna1</a>	Alignment	not modelled	92.8	18	<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)
107	<a href="#">d1ec6a_</a>	Alignment	not modelled	92.6	24	<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)
108	<a href="#">c2hh2A_</a>	Alignment	not modelled	92.6	26	<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
109	<a href="#">c2dgrA_</a>	Alignment	not modelled	92.4	23	<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
110	<a href="#">c4b8tA_</a>	Alignment	not modelled	92.3	26	<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.
111	<a href="#">d2fmra_</a>	Alignment	not modelled	92.2	32	<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)
112	<a href="#">d1we8a_</a>	Alignment	not modelled	92.1	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)
113	<a href="#">c2hh3A_</a>	Alignment	not modelled	92.1	25	<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
114	<a href="#">d1x4na1</a>	Alignment	not modelled	92.1	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)
115	<a href="#">d1khma_</a>	Alignment	not modelled	91.9	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)
116	<a href="#">d2ja9a1</a>	Alignment	not modelled	91.6	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
117	<a href="#">d1viga_</a>	Alignment	not modelled	91.3	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)
118	<a href="#">d2ctla1</a>	Alignment	not modelled	91.3	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)
119	<a href="#">d2cpqa1</a>	Alignment	not modelled	91.2	32	<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)
120	<a href="#">c1tuaA_</a>	Alignment	not modelled	91.2	27	<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