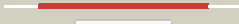



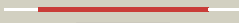






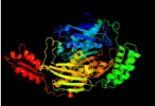


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2783c_(gpsl)_3090349_3092607
Date	Wed Aug 7 12:50:44 BST 2019
Unique Job ID	aaaa1942a2711c78

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4aimA_	 Alignment		100.0	46	PDB header: transferase/peptide Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rna e2 recognition peptide
2	c4nbqB_	 Alignment		100.0	45	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of the polynucleotide phosphorylase (cbu_0852) from coxiella2 burnetii
3	c1e3pA_	 Alignment		100.0	73	PDB header: polyribonucleotide transferase Chain: A: PDB Molecule: guanosine pentaphosphate synthetase; PDBTitle: tungstate derivative of streptomyces antibioticus pnpase/2 gpsi enzyme
4	c4am3A_	 Alignment		100.0	47	PDB header: transferase/rna Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rna
5	c1e3hA_	 Alignment		100.0	71	PDB header: polyribonucleotide transferase Chain: A: PDB Molecule: guanosine pentaphosphate synthetase; PDBTitle: semet derivative of streptomyces antibioticus pnpase/gpsi enzyme
6	c3u1kB_	 Alignment		100.0	36	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase 1, mitochondrial; PDBTitle: crystal structure of human pnpase
7	c6d6kB_	 Alignment		100.0	45	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of polyribonucleotide nucleotidyltransferase from2 acinetobacter baumannii
8	c4aidC_	 Alignment		100.0	47	PDB header: transferase/peptide Chain: C: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rna e2 recognition peptide
9	c3cdiA_	 Alignment		100.0	47	PDB header: transferase Chain: A: PDB Molecule: polynucleotide phosphorylase; PDBTitle: crystal structure of e. coli pnpase
10	c5xexC_	 Alignment		100.0	47	PDB header: transferase Chain: C: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of s.aureus pnpase catalytic domain
11	c5yjiE_	 Alignment		100.0	52	PDB header: cytosolic protein Chain: E: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of pnpase from staphylococcus epidermidis

12	c3cdjA	Alignment		100.0	47	PDB header: transferase Chain: A: PDB Molecule: polynucleotide phosphorylase; PDBTitle: crystal structure of the e. coli kh/s1 domain truncated2 pnpase
13	d1e3ha2	Alignment		100.0	80	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
14	c2po2A	Alignment		100.0	31	PDB header: hydrolase/hydrolase Chain: A: PDB Molecule: probable exosome complex exonuclease 1; PDBTitle: crystal structure of the p. abyssi exosome rnase ph ring2 complexed with cdp
15	c2wnrB	Alignment		100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: probable exosome complex exonuclease 1; PDBTitle: the structure of methanothermobacter thermautotrophicus2 exosome core assembly
16	c2ba1D	Alignment		100.0	30	PDB header: rna binding protein Chain: D: PDB Molecule: archaeal exosome complex exonuclease rrp41; PDBTitle: archaeal exosome core
17	c2nn6B	Alignment		100.0	24	PDB header: hydrolase/transferase Chain: B: PDB Molecule: exosome complex exonuclease rrp41; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
18	c2c37L	Alignment		100.0	32	PDB header: hydrolase Chain: L: PDB Molecule: probable exosome complex exonuclease 1; PDBTitle: rnase ph core of the archaeal exosome in complex with u82 rna
19	c6d6rF	Alignment		100.0	21	PDB header: hydrolase Chain: F: PDB Molecule: exosome complex component mtr3; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
20	c3dd6A	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of the rph, an exoribonuclease from bacillus anthracis2 at 1.7 a resolution
21	c6qh2A	Alignment	not modelled	100.0	45	PDB header: signaling protein Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: solution nmr ensemble for a chimeric kh-s1 domain construct of f2 exosomal polynucleotide phosphorylase at 298k compiled using the3 comand method
22	c1udsA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of the rna processing enzyme rnase ph r126a mutant2 from aquifex aeolicus
23	c2wp8B	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: exosome complex component ski6; PDBTitle: yeast rrp44 nuclease
24	c2pnzB	Alignment	not modelled	100.0	21	PDB header: hydrolase/hydrolase Chain: B: PDB Molecule: probable exosome complex exonuclease 2; PDBTitle: crystal structure of the p. abyssi exosome rnase ph ring2 complexed with udp and gmp
25	c4ifdF	Alignment	not modelled	100.0	16	PDB header: hydrolase/rna Chain: F: PDB Molecule: exosome complex component mtr3; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
26	c1r6mA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of the trna processing enzyme rnase ph from2 pseudomonas aeruginosa in complex with phosphate
27	c3b4tC	Alignment	not modelled	100.0	24	PDB header: transferase Chain: C: PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of mycobacterium tuberculosis rnase ph, the2 mycobacterium tuberculosis structural genomics consortium target3 rv1340
						PDB header: hydrolase/transferase

28	c2nn6C_	Alignment	not modelled	100.0	17	Chain: C: PDB Molecule: exosome complex exonuclease rrp43; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
29	d1e3ha6	Alignment	not modelled	100.0	75	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
30	c3hkmB_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: os03g0854200 protein; PDBTitle: crystal structure of rice(oryza sativa) rrp46
31	c2wnrC_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: probable exosome complex exonuclease 2; PDBTitle: the structure of methanothermobacter thermautotrophicus2 exosome core assembly
32	c2nn6E_	Alignment	not modelled	100.0	17	PDB header: hydrolase/transferase Chain: E: PDB Molecule: exosome complex exonuclease rrp42; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
33	c2ba0I_	Alignment	not modelled	100.0	22	PDB header: rna binding protein Chain: I: PDB Molecule: archaeal exosome rna binding protein rrp42; PDBTitle: archaeal exosome core
34	c2br2G_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: G: PDB Molecule: exosome complex exonuclease 2; PDBTitle: rnase ph core of the archaeal exosome
35	d1e3ha3	Alignment	not modelled	100.0	77	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
36	c2nn6D_	Alignment	not modelled	100.0	24	PDB header: hydrolase/transferase Chain: D: PDB Molecule: exosome complex exonuclease rrp46; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
37	c2nn6F_	Alignment	not modelled	100.0	22	PDB header: hydrolase/transferase Chain: F: PDB Molecule: exosome component 6; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
38	c1oysA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of the phosphorolytic exoribonuclease2 rnase ph from bacillus subtilis
39	c4ifdD_	Alignment	not modelled	100.0	21	PDB header: hydrolase/rna Chain: D: PDB Molecule: exosome complex component rrp46; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
40	d1e3ha5	Alignment	not modelled	100.0	64	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
41	c4ifdE_	Alignment	not modelled	100.0	12	PDB header: hydrolase/rna Chain: E: PDB Molecule: exosome complex component rrp42; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
42	d2je6b1	Alignment	not modelled	100.0	31	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
43	c2nn6A_	Alignment	not modelled	100.0	18	PDB header: hydrolase/transferase Chain: A: PDB Molecule: polymyositis/scleroderma autoantigen 1; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
44	d2ba0d1	Alignment	not modelled	100.0	27	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
45	c2wp8A_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: exosome complex component rrp45; PDBTitle: yeast rrp44 nuclease
46	d2nn6b1	Alignment	not modelled	99.9	27	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
47	d1r6la1	Alignment	not modelled	99.9	23	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
48	d1udsA1	Alignment	not modelled	99.9	19	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
49	d2ba0g1	Alignment	not modelled	99.9	24	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
50	d2je6a1	Alignment	not modelled	99.9	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
51	d2nn6e1	Alignment	not modelled	99.9	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
52	d2nn6a1	Alignment	not modelled	99.9	19	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
53	c3krnB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: protein c14a4.5, confirmed by transcript evidence; PDBTitle: crystal structure of c. elegans cell-death-related nuclease 5(crn-5)
54	d2nn6c1	Alignment	not modelled	99.9	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like

55	d1oysa1	Alignment	not modelled	99.9	23	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
56	d2nn6f1	Alignment	not modelled	99.9	27	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
57	d2nn6d1	Alignment	not modelled	99.9	25	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
58	d1udsa2	Alignment	not modelled	99.7	21	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
59	c4ifdC	Alignment	not modelled	99.7	19	PDB header: hydrolase/rna Chain: C: PDB Molecule: exosome complex component rrp43; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
60	d1r6la2	Alignment	not modelled	99.7	19	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
61	c2cqoA	Alignment	not modelled	99.6	32	PDB header: ribosome Chain: A: PDB Molecule: nucleolar protein of 40 kda; PDBTitle: solution structure of the s1 rna binding domain of human2 hypothetical protein flj11067
62	c1q46A	Alignment	not modelled	99.6	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
63	c4nnkA	Alignment	not modelled	99.6	36	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: structural basis for targeting the ribosomal protein s1 of2 mycobacterium tuberculosis by pyrazinamide
64	d1e3ha1	Alignment	not modelled	99.6	48	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 Family: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
65	c2eqsA	Alignment	not modelled	99.6	34	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8
66	c1q8kA	Alignment	not modelled	99.6	27	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 PDBTitle: solution structure of alpha subunit of human eif2
67	c1yz6A	Alignment	not modelled	99.5	28	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 alpha PDBTitle: crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
68	c5x8r8	Alignment	not modelled	99.5	30	PDB header: ribosome Chain: 8: PDB Molecule: 30s ribosomal protein s1, chloroplastic; PDBTitle: structure of the 30s small subunit of chloroplast ribosome from2 spinach
69	d1whua	Alignment	not modelled	99.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 Family: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
70	d1q46a2	Alignment	not modelled	99.5	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
71	c3j81j	Alignment	not modelled	99.5	24	PDB header: ribosome Chain: J: PDB Molecule: us4; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
72	d2ba0a1	Alignment	not modelled	99.5	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
73	d1kl9a2	Alignment	not modelled	99.5	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
74	d1oysa2	Alignment	not modelled	99.4	23	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
75	c2k4kA	Alignment	not modelled	99.4	31	PDB header: rna binding protein Chain: A: PDB Molecule: general stress protein 13; PDBTitle: solution structure of gsp13 from bacillus subtilis
76	c2khiA	Alignment	not modelled	99.4	36	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
77	d1go3e1	Alignment	not modelled	99.4	36	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
78	c2ahoB	Alignment	not modelled	99.4	27	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: structure of the archaeal initiation factor eif2 alpha-gamma2 heterodimer from sulfobolus solfataricus complexed with gdpnp
79	c5lm7A	Alignment	not modelled	99.4	13	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: crystal structure of the lambda n-nus factor complex
80	c2pcaA	Alignment	not modelled	99.4	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201;

80	c20c6A	Alignment	not modelled	99.4	33	PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa PDB header: ribosomal protein
81	c2khjA	Alignment	not modelled	99.4	28	Chain: A; PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
82	d2z0sa1	Alignment	not modelled	99.4	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
83	c1kl9A	Alignment	not modelled	99.4	27	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 2 subunit 1; PDBTitle: crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha
84	d2ba0d2	Alignment	not modelled	99.4	27	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
85	d1sroa	Alignment	not modelled	99.4	38	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
86	d2nn6h1	Alignment	not modelled	99.3	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
87	c2k52A	Alignment	not modelled	99.3	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein mj1198; PDBTitle: structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
88	c1hh2P	Alignment	not modelled	99.3	17	PDB header: transcription regulation Chain: P; PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima
89	d3bzka4	Alignment	not modelled	99.3	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
90	d2je6i1	Alignment	not modelled	99.3	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
91	d2je6b2	Alignment	not modelled	99.2	20	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
92	d2ahob2	Alignment	not modelled	99.2	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
93	c3psiA	Alignment	not modelled	99.2	9	PDB header: transcription Chain: A; PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
94	d2z0sa2	Alignment	not modelled	99.2	20	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
95	c2mf1A	Alignment	not modelled	99.2	21	PDB header: ribosomal protein Chain: A; PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 2 of e. coli ribosomal protein s1
96	c5xq5A	Alignment	not modelled	99.2	28	PDB header: ribosomal protein Chain: A; PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 5 of the e. coli ribosomal protein s1
97	d1wi5a	Alignment	not modelled	99.1	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
98	c2mf1A	Alignment	not modelled	99.1	18	PDB header: ribosomal protein Chain: A; PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 1 of e. coli ribosomal protein s1
99	d2br2b2	Alignment	not modelled	99.1	20	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
100	d1smxa	Alignment	not modelled	99.1	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
101	c6gmhM	Alignment	not modelled	99.1	21	PDB header: transcription Chain: M; PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
102	c2ba0A	Alignment	not modelled	99.1	21	PDB header: rna binding protein Chain: A; PDB Molecule: archaeal exosome rna binding protein rrp4; PDBTitle: archaeal exosome core
103	c2z0sA	Alignment	not modelled	99.0	15	PDB header: rna binding protein Chain: A; PDB Molecule: probable exosome complex rna-binding protein 1; PDBTitle: crystal structure of putative exosome complex rna-binding2 protein
104	d2nn6b2	Alignment	not modelled	99.0	16	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
105	d2ba0a3	Alignment	not modelled	99.0	24	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
106	d1y14b1	Alignment	not modelled	99.0	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins

						Family: Cold shock DNA-binding domain-like
107	c3go5A_	Alignment	not modelled	99.0	16	PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
108	c2bh8B_	Alignment	not modelled	99.0	41	PDB header: transcription Chain: B: PDB Molecule: 1b11; PDBTitle: combinatorial protein 1b11
109	d2nn6i1	Alignment	not modelled	98.9	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
110	c2je6l_	Alignment	not modelled	98.9	20	PDB header: hydrolase Chain: I: PDB Molecule: exosome complex rna-binding protein 1; PDBTitle: structure of a 9-subunit archaeal exosome
111	d2ctka1	Alignment	not modelled	98.8	18	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
112	d2je6a2	Alignment	not modelled	98.8	14	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
113	d1hh2p1	Alignment	not modelled	98.8	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
114	c5wwwA_	Alignment	not modelled	98.7	22	PDB header: rna binding protein/rna Chain: A: PDB Molecule: rna-binding e3 ubiquitin-protein ligase mex3c; PDBTitle: crystal structure of the kh1 domain of human rna-binding e3 ubiquitin-2 protein ligase mex-3c complex with rna
115	d1tuaa1	Alignment	not modelled	98.7	32	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
116	c2jzxA_	Alignment	not modelled	98.7	23	PDB header: rna binding protein Chain: A: PDB Molecule: poly(rc)-binding protein 2; PDBTitle: pcbp2 kh1-kh2 domains
117	c1go3E_	Alignment	not modelled	98.7	37	PDB header: transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: structure of an archeal homolog of the eukaryotic rna polymerase ii2 rpb4/rpb7 complex
118	c3n89B_	Alignment	not modelled	98.7	15	PDB header: cell cycle Chain: B: PDB Molecule: defective in germ line development protein 3, isoform a; PDBTitle: kh domains
119	d1we8a_	Alignment	not modelled	98.7	23	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
120	c2ba1B_	Alignment	not modelled	98.7	18	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core