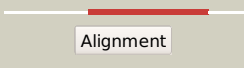

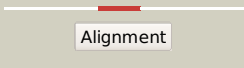

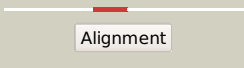
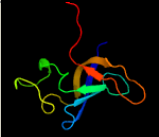
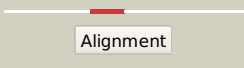
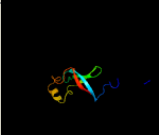
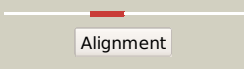
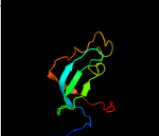
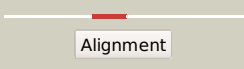
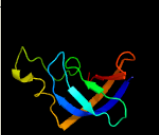
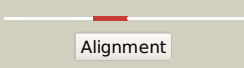
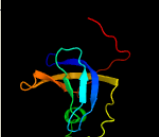
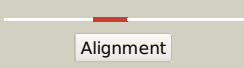

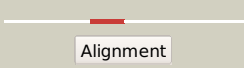
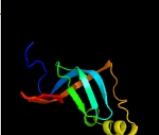
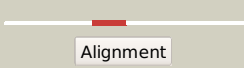
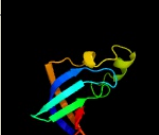
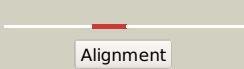
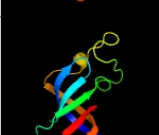






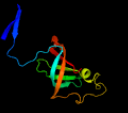




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2444c_(rne)_2742133_2744994
Date	Wed Aug 7 12:50:07 BST 2019
Unique Job ID	fa0bd31411b4d20f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2c4rL_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> ribonuclease e; <b>PDBTitle:</b> catalytic domain of e. coli rna se
2	<a href="#">c4oxpA_</a>	 Alignment		100.0	39	<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 rna se2 from caulobacter crescentus
3	<a href="#">d1smxa_</a>	 Alignment		99.9	44	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
4	<a href="#">c6qh2A_</a>	 Alignment		98.4	26	<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 phosphorylase at 298k compiled using the3 comand method
5	<a href="#">c4aimA_</a>	 Alignment		98.3	26	<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 rna se2 recognition peptide
6	<a href="#">d2ba0a1</a>	 Alignment		98.2	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
7	<a href="#">c2z0sA_</a>	 Alignment		98.2	25	<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
8	<a href="#">d2z0sa1</a>	 Alignment		98.2	28	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
9	<a href="#">c2cqoA_</a>	 Alignment		98.2	18	<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
10	<a href="#">c4nnkA_</a>	 Alignment		98.2	25	<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
11	<a href="#">c1yz6A_</a>	 Alignment		98.1	23	<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

12	<a href="#">d1q46a2</a>	Alignment		98.1	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
13	<a href="#">d2je6i1</a>	Alignment		98.0	26	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
14	<a href="#">c2ba0A_</a>	Alignment		98.0	19	<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
15	<a href="#">c3j81j_</a>	Alignment		98.0	19	<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
16	<a href="#">c2k4kA_</a>	Alignment		98.0	27	<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
17	<a href="#">c2khjA_</a>	Alignment		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 6 of the e. coli ribosomal2 protein s1
18	<a href="#">c2je6l_</a>	Alignment		98.0	17	<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
19	<a href="#">c1q8kA_</a>	Alignment		97.9	21	<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
20	<a href="#">d2nn6h1</a>	Alignment		97.9	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
21	<a href="#">c2eqsA_</a>	Alignment	not modelled	97.9	23	<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
22	<a href="#">c2khiA_</a>	Alignment	not modelled	97.9	22	<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
23	<a href="#">c5x8r8_</a>	Alignment	not modelled	97.9	31	<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
24	<a href="#">d3bzka4</a>	Alignment	not modelled	97.9	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
25	<a href="#">c1q46A_</a>	Alignment	not modelled	97.9	22	<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
26	<a href="#">d1sroa_</a>	Alignment	not modelled	97.8	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
27	<a href="#">d1wi5a_</a>	Alignment	not modelled	97.8	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
28	<a href="#">d1go3e1</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
						<b>PDB header:</b> transcription

29	<a href="#">c5lm7A</a>	Alignment	not modelled	97.7	24	<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
30	<a href="#">c3go5A</a>	Alignment	not modelled	97.7	19	<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
31	<a href="#">c2mfIA</a>	Alignment	not modelled	97.7	23	<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
32	<a href="#">c2oceA</a>	Alignment	not modelled	97.6	27	<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
33	<a href="#">d1hh2p1</a>	Alignment	not modelled	97.6	26	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
34	<a href="#">c2ba1B</a>	Alignment	not modelled	97.6	21	<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
35	<a href="#">c1hh2P</a>	Alignment	not modelled	97.5	26	<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
36	<a href="#">d2nn6i1</a>	Alignment	not modelled	97.5	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
37	<a href="#">c2k52A</a>	Alignment	not modelled	97.4	24	<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
38	<a href="#">c2ahoB</a>	Alignment	not modelled	97.4	28	<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 sulfolobus solfataricus complexed with gdnpp
39	<a href="#">d1y14b1</a>	Alignment	not modelled	97.3	12	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
40	<a href="#">d1kl9a2</a>	Alignment	not modelled	97.3	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
41	<a href="#">c1l2fA</a>	Alignment	not modelled	97.3	27	<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
42	<a href="#">d2ahob2</a>	Alignment	not modelled	97.1	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
43	<a href="#">c3psiA</a>	Alignment	not modelled	97.1	13	<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)
44	<a href="#">c2nn6I</a>	Alignment	not modelled	97.1	25	<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
45	<a href="#">c5xq5A</a>	Alignment	not modelled	97.0	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
46	<a href="#">c5x50G</a>	Alignment	not modelled	96.9	15	<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)
47	<a href="#">c6gmhM</a>	Alignment	not modelled	96.9	17	<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
48	<a href="#">c6flqF</a>	Alignment	not modelled	96.8	23	<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
49	<a href="#">c2mfIA</a>	Alignment	not modelled	96.8	16	<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
50	<a href="#">c6d6rH</a>	Alignment	not modelled	96.8	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
51	<a href="#">c2c35F</a>	Alignment	not modelled	96.8	13	<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
52	<a href="#">c4ifdH</a>	Alignment	not modelled	96.7	23	<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
53	<a href="#">c2b8kG</a>	Alignment	not modelled	96.7	11	<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

54	<a href="#">d2nn6g1</a>	Alignment	not modelled	96.6	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
55	<a href="#">c3h0gS_</a>	Alignment	not modelled	96.6	19	<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
56	<a href="#">c1kl9A_</a>	Alignment	not modelled	96.6	24	<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
57	<a href="#">c4q7jD_</a>	Alignment	not modelled	96.6	24	<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
58	<a href="#">c4ifdl_</a>	Alignment	not modelled	96.5	32	<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
59	<a href="#">c1go3E_</a>	Alignment	not modelled	96.2	18	<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
60	<a href="#">d2c35b1</a>	Alignment	not modelled	96.2	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
61	<a href="#">c4qiwe_</a>	Alignment	not modelled	96.2	23	<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
62	<a href="#">c2bh8B_</a>	Alignment	not modelled	96.0	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> 1b11; <b>PDBTitle:</b> combinatorial protein 1b11
63	<a href="#">c1nt9G_</a>	Alignment	not modelled	96.0	11	<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
64	<a href="#">c4mntA_</a>	Alignment	not modelled	96.0	23	<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
65	<a href="#">c4nbqB_</a>	Alignment	not modelled	95.7	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> structure of the polynucleotide phosphorylase (cbu_0852) from coxiella2 burnetii
66	<a href="#">c2pmzE_</a>	Alignment	not modelled	95.7	19	<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
67	<a href="#">c3d0fA_</a>	Alignment	not modelled	94.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding 1 transmembrane protein mrca; <b>PDBTitle:</b> structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
68	<a href="#">d2ja9a1</a>	Alignment	not modelled	94.8	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="#">c2nn6H_</a>	Alignment	not modelled	94.8	19	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> H: <b>PDB Molecule:</b> exosome complex exonuclease rrp4; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
70	<a href="#">c2nn6G_</a>	Alignment	not modelled	94.8	18	<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
71	<a href="#">c3aqqD_</a>	Alignment	not modelled	94.4	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> calcium-regulated heat stable protein 1; <b>PDBTitle:</b> crystal structure of human crhsp-24
72	<a href="#">c5xguB_</a>	Alignment	not modelled	94.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease r; <b>PDBTitle:</b> escherichia coli. rnase r
73	<a href="#">d2asba1</a>	Alignment	not modelled	94.2	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
74	<a href="#">c2ja9A_</a>	Alignment	not modelled	93.7	20	<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
75	<a href="#">c1k0rB_</a>	Alignment	not modelled	93.7	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nusa; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis nusa
76	<a href="#">c2asbA_</a>	Alignment	not modelled	93.7	22	<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
77	<a href="#">c2kcmA_</a>	Alignment	not modelled	91.4	27	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold shock domain family protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
78	<a href="#">c4pmwB_</a>	Alignment	not modelled	91.0	16	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> dis3-like exonuclease 2; <b>PDBTitle:</b> structure of mouse dis3l2 in complex with oligou rna substrate
79	<a href="#">c5c0wj_</a>	Alignment	not modelled	90.9	23	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> J: <b>PDB Molecule:</b> exosome complex exonuclease dis3; <b>PDBTitle:</b> structure of a 12-subunit nuclear exosome complex

						bound to single-2 stranded rna substrates
80	<a href="#">c4a4iA_</a>	Alignment	not modelled	90.6	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lin-28 homolog b; <b>PDBTitle:</b> crystal structure of the human lin28b cold shock domain
81	<a href="#">d1c9oa_</a>	Alignment	not modelled	90.2	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
82	<a href="#">c2wp8J_</a>	Alignment	not modelled	90.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> exosome complex exonuclease dis3; <b>PDBTitle:</b> yeast rrp44 nuclease
83	<a href="#">d1h95a_</a>	Alignment	not modelled	89.2	14	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
84	<a href="#">c2ljpA_</a>	Alignment	not modelled	88.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease p protein component; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for e.coli2 ribonuclease p protein
85	<a href="#">c2hnkC_</a>	Alignment	not modelled	87.9	24	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent o-methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent o-methyltransferase from pathogenic2 bacterium leptospira interrogans
86	<a href="#">d1mjca_</a>	Alignment	not modelled	87.7	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
87	<a href="#">c2ckzB_</a>	Alignment	not modelled	87.5	9	<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.
88	<a href="#">d2es2a1</a>	Alignment	not modelled	87.3	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
89	<a href="#">d1g6pa_</a>	Alignment	not modelled	86.8	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
90	<a href="#">c4ifdG_</a>	Alignment	not modelled	86.7	18	<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
91	<a href="#">c3ayhB_</a>	Alignment	not modelled	86.5	12	<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
92	<a href="#">c2lssA_</a>	Alignment	not modelled	85.4	16	<b>PDB header:</b> rna binding protein, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold shock-like protein; <b>PDBTitle:</b> solution structure of the r. rickettsii cold shock-like protein
93	<a href="#">c4zu9A_</a>	Alignment	not modelled	83.7	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor selb; <b>PDBTitle:</b> crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
94	<a href="#">c2eqjA_</a>	Alignment	not modelled	82.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metal-response element-binding transcription <b>PDBTitle:</b> solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
95	<a href="#">c3pihA_</a>	Alignment	not modelled	80.8	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> t. maritima uvra in complex with fluorescein-modified dna
96	<a href="#">c2bx9J_</a>	Alignment	not modelled	79.6	53	<b>PDB header:</b> transcription regulation <b>Chain:</b> J: <b>PDB Molecule:</b> tryptophan rna-binding attenuator protein-inhibitory <b>PDBTitle:</b> crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
97	<a href="#">c3ld0Q_</a>	Alignment	not modelled	79.5	46	<b>PDB header:</b> gene regulation <b>Chain:</b> Q: <b>PDB Molecule:</b> inhibitor of trap, regulated by t-box (trp) sequence rtpa; <b>PDBTitle:</b> crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
98	<a href="#">c6j9eF_</a>	Alignment	not modelled	79.3	30	<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
99	<a href="#">d1k3ra1</a>	Alignment	not modelled	79.1	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Hypothetical protein MTH1 (MT0001), insert domain
100	<a href="#">c2mqhA_</a>	Alignment	not modelled	78.9	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleic acid binding protein; <b>PDBTitle:</b> solution structure of the chlamydomonas reinhardtii nab1 cold shock2 domain, csd1
101	<a href="#">c2e5pA_</a>	Alignment	not modelled	78.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 1; <b>PDBTitle:</b> solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
102	<a href="#">d1nlta3</a>	Alignment	not modelled	77.3	30	<b>Fold:</b> Dnaj/Hsp40 cysteine-rich domain <b>Superfamily:</b> Dnaj/Hsp40 cysteine-rich domain <b>Family:</b> Dnaj/Hsp40 cysteine-rich domain
103	<a href="#">d1nz0a_</a>	Alignment	not modelled	76.8	28	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> RNase P protein
104	<a href="#">c4toiA_</a>	Alignment	not modelled	76.8	24	<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

105	<a href="#">c5o6fA_</a>	Alignment	not modelled	76.7	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold-shock protein; <b>PDBTitle:</b> nmr structure of cold shock protein a from corynebacterium2 pseudotuberculosis
106	<a href="#">c3izq1_</a>	Alignment	not modelled	75.8	17	<b>PDB header:</b> ribosomal protein,hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> structure of the dom34-hbs1-gdnpn complex bound to a translating2 ribosome
107	<a href="#">d1d6ta_</a>	Alignment	not modelled	75.4	22	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> RNase P protein
108	<a href="#">c2k5nA_</a>	Alignment	not modelled	75.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative cold-shock protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal domain of protein eca15802 from erwinia carotovora, northeast structural genomics consortium3 target ewr156a
109	<a href="#">d1a6fa_</a>	Alignment	not modelled	75.1	24	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> RNase P protein
110	<a href="#">c4mo1B_</a>	Alignment	not modelled	74.8	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> antitermination protein q; <b>PDBTitle:</b> crystal structure of antitermination protein q from bacteriophage2 lambda. northeast structural genomics consortium target or18a.
111	<a href="#">c3pnwX_</a>	Alignment	not modelled	72.8	17	<b>PDB header:</b> protein binding/immune system <b>Chain:</b> X: <b>PDB Molecule:</b> tudor domain-containing protein 3; <b>PDBTitle:</b> crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
112	<a href="#">c2pe4A_</a>	Alignment	not modelled	72.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronidase-1; <b>PDBTitle:</b> structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
113	<a href="#">c3zqiC_</a>	Alignment	not modelled	72.0	60	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
114	<a href="#">c2ytvA_</a>	Alignment	not modelled	71.9	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold shock domain-containing protein e1; <b>PDBTitle:</b> solution structure of the fifth cold-shock domain of the human2 kiaa0885 protein (unr protein)
115	<a href="#">c5udbD_</a>	Alignment	not modelled	71.8	16	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
116	<a href="#">c2m0oA_</a>	Alignment	not modelled	70.8	19	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 1; <b>PDBTitle:</b> the solution structure of human phf1 in complex with h3k36me3
117	<a href="#">c1nltA_</a>	Alignment	not modelled	68.5	28	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial protein import protein mas5; <b>PDBTitle:</b> the crystal structure of hsp40 ydj1
118	<a href="#">c3tr6A_</a>	Alignment	not modelled	67.8	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> structure of a o-methyltransferase from coxiella burnetii
119	<a href="#">d2ix0a2</a>	Alignment	not modelled	67.0	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
120	<a href="#">d1fcqa_</a>	Alignment	not modelled	66.5	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Bee venom hyaluronidase