Phyre^2

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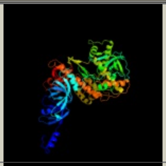
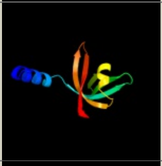
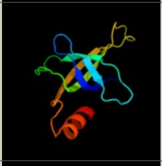
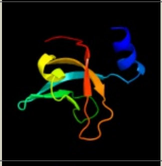
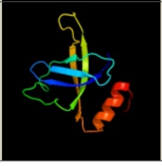
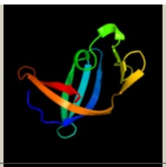
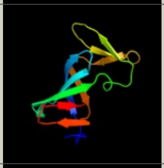
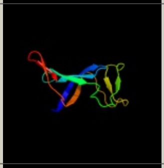
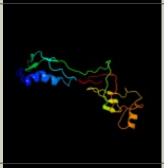
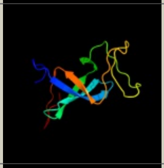
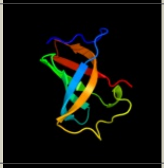
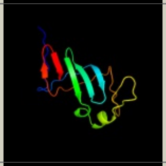
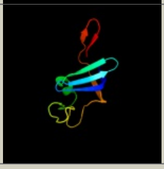
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ix1A_	Alignment		100.0	99	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant
2	c2wp8J_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
3	c2vnuD_	Alignment		100.0	20	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp44; **PDBTitle:** crystal structure of sc rrp44
4	c2r7fA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease ii family protein; **PDBTitle:** crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63
5	d2ix0a4	Alignment		100.0	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
6	d2vnud4	Alignment		100.0	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
7	d2r7da2	Alignment		100.0	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
8	d2ix0a2	Alignment		99.6	96	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
9	d2ix0a1	Alignment		99.5	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
10	d2vnud3	Alignment		99.3	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
11	d2vnud1	Alignment		99.1	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

12	d2ix0a3	Alignment		98.9	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
13	d1go3e1	Alignment		98.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	d2c35b1	Alignment		98.8	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
15	c3h0gS_	Alignment		98.8	13	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
16	d1kl9a2	Alignment		98.5	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
17	c2c35F_	Alignment		98.5	16	**PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii
18	c2k52A_	Alignment		98.5	22	**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
19	c2b8kG_	Alignment		98.5	20	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
20	d1y14b1	Alignment		98.5	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
21	c1q46A_	Alignment	not modelled	98.4	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
22	c1yz6A_	Alignment	not modelled	98.4	19	**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
23	d1q46a2	Alignment	not modelled	98.3	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
24	c1go3E_	Alignment	not modelled	98.3	16	**PDB header:**transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** structure of an archeal homolog of the eukaryotic rna2 polymerase ii rpb4/rpb7 complex
25	c2khiA_	Alignment	not modelled	98.3	21	**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
26	c2cqoA_	Alignment	not modelled	98.2	13	**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
27	c1q8kA_	Alignment	not modelled	98.2	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 **PDBTitle:** solution structure of alpha subunit of human eif2
28	c1nt9G_	Alignment	not modelled	98.1	21	**PDB header:**transcription, transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kd polypeptide;

						PDBTitle: complete 12-subunit rna polymerase ii
29	c2k4kA_	Alignment	not modelled	98.0	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
30	c2ahoB_	Alignment	not modelled	98.0	26	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** structure of the archaeal initiation factor eif2 alpha-2 gamma heterodimer from sulfolobus solfataricus complexed3 with gdpnp
31	c2khjA_	Alignment	not modelled	98.0	23	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
32	d3bzka4	Alignment	not modelled	98.0	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
33	c1kl9A_	Alignment	not modelled	98.0	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
34	c2pmzE_	Alignment	not modelled	98.0	12	**PDB header:**translation, transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
35	c3psiA_	Alignment	not modelled	97.9	4	**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)
36	c2eqsA_	Alignment	not modelled	97.9	14	**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
37	c2oceA_	Alignment	not modelled	97.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
38	d2ahob2	Alignment	not modelled	97.9	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	c2ckzB_	Alignment	not modelled	97.8	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii 25 kd **PDBTitle:** x-ray structure of rna polymerase iii subcomplex c17-c25.
40	d2vnud2	Alignment	not modelled	97.8	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
41	d2ba0a1	Alignment	not modelled	97.8	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	c3go5A_	Alignment	not modelled	97.7	18	**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
43	d1sroa_	Alignment	not modelled	97.7	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
44	c1l2fA_	Alignment	not modelled	97.6	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
45	d2je6i1	Alignment	not modelled	97.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	d1wi5a_	Alignment	not modelled	97.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
47	d2z0sa1	Alignment	not modelled	97.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
48	d1hh2p1	Alignment	not modelled	97.4	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
49	c1hh2P_	Alignment	not modelled	97.2	23	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
50	d2nn6h1	Alignment	not modelled	97.1	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	d1g6pa_	Alignment	not modelled	97.0	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
52	d1a62a2	Alignment	not modelled	96.9	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
53	c2z0sA_	Alignment	not modelled	96.8	18	**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
						PDB header:rna binding protein

54	c2ytxA_	Alignment	not modelled	96.6	28	**Chain:** A: **PDB Molecule:**cold shock domain-containing protein e1; **PDBTitle:** solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein)
55	c2k5nA_	Alignment	not modelled	96.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cold-shock protein; **PDBTitle:** solution nmr structure of the n-terminal domain of protein2 eca1580 from erwinia carotovora, northeast structural3 genomics consortium target ewr156a
56	c2a8vA_	Alignment	not modelled	96.5	23	**PDB header:**protein/rna **Chain:** A: **PDB Molecule:**rna binding domain of rho transcription **PDBTitle:** rho transcription termination factor/rna complex
57	d1smxa_	Alignment	not modelled	96.5	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
58	c3a0jB_	Alignment	not modelled	96.4	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
59	d1mjca_	Alignment	not modelled	96.4	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
60	c3aqqD_	Alignment	not modelled	96.3	23	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**calcium-regulated heat stable protein 1; **PDBTitle:** crystal structure of human crhsp-24
61	c2kcmA_	Alignment	not modelled	96.2	23	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**cold shock domain family protein; **PDBTitle:** solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
62	d2nn6i1	Alignment	not modelled	96.1	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	c2ba0A_	Alignment	not modelled	96.1	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
64	d2es2a1	Alignment	not modelled	96.1	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
65	d1h95a_	Alignment	not modelled	96.1	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
66	c3ayhB_	Alignment	not modelled	96.0	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc8; **PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
67	d1wfqa_	Alignment	not modelled	95.9	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
68	c3camB_	Alignment	not modelled	95.7	25	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cold-shock domain family protein; **PDBTitle:** crystal structure of the cold shock domain protein from neisseria2 meningitidis
69	d1c9oa_	Alignment	not modelled	95.6	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
70	c1uwvA_	Alignment	not modelled	95.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**23s rrna (uracil-5-)-methyltransferase ruma; **PDBTitle:** crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
71	c2rf4A_	Alignment	not modelled	95.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
72	c2bh8B_	Alignment	not modelled	95.3	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
73	c2nn6I_	Alignment	not modelled	95.2	13	**PDB header:**hydrolase/transferase **Chain:** I: **PDB Molecule:**3'-5' exoribonuclease csl4 homolog; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
74	d1uwva1	Alignment	not modelled	95.1	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
75	c2ytyA_	Alignment	not modelled	94.9	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**cold shock domain-containing protein e1; **PDBTitle:** solution structure of the fourth cold-shock domain of the human2 kiaa0885 protein (unr protein)
76	c2je6I_	Alignment	not modelled	94.8	18	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1; **PDBTitle:** structure of a 9-subunit archaeal exosome
77	d1luza_	Alignment	not modelled	94.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
78	c3trzE_	Alignment	not modelled	94.1	23	**PDB header:**rna binding protein/rna **Chain:** E: **PDB Molecule:**protein lin-28 homolog a; **PDBTitle:** mouse lin28a in complex with let-7d microrna pre-element
						PDB header:transcription/rna **Chain:** B: **PDB Molecule:**rho transcription termination factor;

79	c1xpuB_	Alignment	not modelled	92.9	31	**PDBTitle:** structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
80	c2ba1B_	Alignment	not modelled	92.3	16	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
81	c1x65A_	Alignment	not modelled	91.6	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**unr protein; **PDBTitle:** solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)
82	c2vs1A_	Alignment	not modelled	89.7	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized rna methyltransferase pyrab10780; **PDBTitle:** the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine
83	d1yvca1	Alignment	not modelled	89.4	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
84	d1jjga_	Alignment	not modelled	89.1	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
85	d1jt8a_	Alignment	not modelled	87.4	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
86	d1yeza1	Alignment	not modelled	84.4	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
87	c2ytvA_	Alignment	not modelled	84.0	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**cold shock domain-containing protein e1; **PDBTitle:** solution structure of the fifth cold-shock domain of the human2 kiaa0885 protein (unr protein)
88	c3i4oA_	Alignment	not modelled	83.2	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
89	c2oqkA_	Alignment	not modelled	82.4	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
90	d1u0la1	Alignment	not modelled	81.9	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
91	c2yv5A_	Alignment	not modelled	81.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
92	d1ah9a_	Alignment	not modelled	81.3	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
93	c3l0oB_	Alignment	not modelled	80.1	41	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
94	c2dgyA_	Alignment	not modelled	69.6	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
95	d2nn6g1	Alignment	not modelled	68.1	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
96	c2i38A_	Alignment	not modelled	67.1	16	**PDB header:**rna binding protein/chimera **Chain:** A: **PDB Molecule:**fusion protein consists of immunoglobin g- **PDBTitle:** solution structure of the rrm of srp20
97	c2eqkA_	Alignment	not modelled	65.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tudor domain-containing protein 4; **PDBTitle:** solution structure of the tudor domain of tudor domain-2 containing protein 4
98	d1hr0w_	Alignment	not modelled	64.9	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
99	c2rcnA_	Alignment	not modelled	62.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
100	c2hqxB_	Alignment	not modelled	61.9	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**p100 co-activator tudor domain; **PDBTitle:** crystal structure of human p100 tudor domain conserved2 region
101	d2hqxa1	Alignment	not modelled	61.9	14	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
102	c3d0fA_	Alignment	not modelled	60.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
103	c1k0rB_	Alignment	not modelled	59.3	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa
104	d1t9ha1	Alignment	not modelled	59.3	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

105	d1f39a_	Alignment	not modelled	56.6	12	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
106	c2wacA_	Alignment	not modelled	52.7	17	**PDB header:**splicing **Chain:** A: **PDB Molecule:**cg7008-pa; **PDBTitle:** extended tudor domain of drosophila melanogaster tudor-sn (2 p100)
107	c4a4fA_	Alignment	not modelled	51.0	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**survival of motor neuron-related-splicing factor 30; **PDBTitle:** solution structure of spf30 tudor domain in complex with2 symmetrically dimethylated arginine
108	d1e3pa2	Alignment	not modelled	50.4	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
109	d1mhna_	Alignment	not modelled	49.0	17	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
110	c2xnqA_	Alignment	not modelled	49.0	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nuclear polyadenylated rna-binding protein 3; **PDBTitle:** structural insights into cis element recognition of non-2 polyadenylated rnas by the nab3-rrm
111	d2diqa1	Alignment	not modelled	48.9	20	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
112	c3metB_	Alignment	not modelled	48.5	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**saga-associated factor 29 homolog; **PDBTitle:** crystal structure of sgf29 in complex with h3k4me2
113	d1d7qa_	Alignment	not modelled	48.0	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
114	c2d9tA_	Alignment	not modelled	43.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tudor domain-containing protein 3; **PDBTitle:** solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse
115	c2c4rL_	Alignment	not modelled	43.0	18	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
116	c3pnwX_	Alignment	not modelled	42.8	17	**PDB header:**protein binding/immune system **Chain:** X: **PDB Molecule:**tudor domain-containing protein 3; **PDBTitle:** crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
117	c1g5vA_	Alignment	not modelled	38.4	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**survival motor neuron protein 1; **PDBTitle:** solution structure of the tudor domain of the human smn2 protein
118	d2ja9a1	Alignment	not modelled	37.3	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
119	d2cqda1	Alignment	not modelled	36.9	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
120	d2asba1	Alignment	not modelled	35.8	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like