Phyre^2

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Description	P21499
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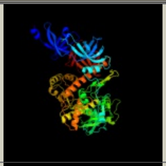
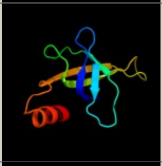
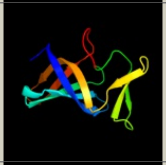
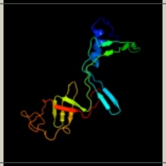
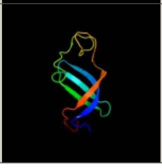
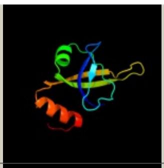
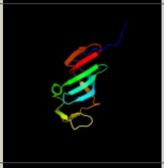
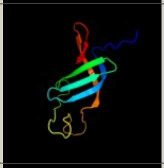
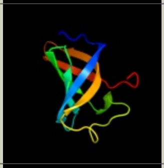
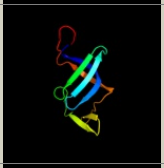
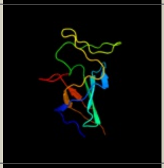
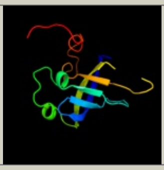
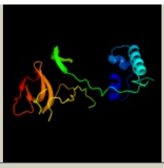
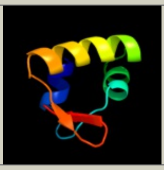
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ix1A_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant
2	c2wp8J_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
3	c2vnuD_	Alignment		100.0	25	**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 from2 deinococcus radiodurans, hexagonal crystal form. northeast3 structural genomics target drr63
5	d2r7da2	Alignment		100.0	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
6	d2ix0a4	Alignment		100.0	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
7	d2vnud4	Alignment		100.0	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
8	d2ix0a1	Alignment		99.7	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
9	d1go3e1	Alignment		99.6	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
10	c3h0gS_	Alignment		99.6	16	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
11	d2c35b1	Alignment		99.6	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

12	d2vnud1	Alignment		99.5	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
13	d2ix0a2	Alignment		99.4	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	c2b8kG_	Alignment		99.4	18	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
15	c2c35F_	Alignment		99.4	12	**PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii
16	c1go3E_	Alignment		99.3	29	**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
17	c2k52A_	Alignment		99.2	27	**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
18	d1y14b1	Alignment		99.2	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
19	c2pmzE_	Alignment		99.2	30	**PDB header:**translation, transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
20	d2vnud3	Alignment		99.2	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
21	c1nt9G_	Alignment	not modelled	99.2	20	**PDB header:**transcription, transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kd polypeptide; **PDBTitle:** complete 12-subunit rna polymerase ii
22	d1kl9a2	Alignment	not modelled	99.2	32	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	c2ckzB_	Alignment	not modelled	99.1	15	**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.
24	c2cqoA_	Alignment		99.1	20	**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
25	d1q46a2	Alignment	not modelled	99.1	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	c1yz6A_	Alignment	not modelled	99.1	22	**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
27	c1q46A_	Alignment	not modelled	99.1	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2

						saccharomyces cerevisia
28	c2khiA_	Alignment	not modelled	99.0	29	**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
29	c2khjA_	Alignment	not modelled	99.0	26	**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
30	c2k4kA_	Alignment	not modelled	98.9	35	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
31	c2eqsA_	Alignment	not modelled	98.9	27	**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
32	c1q8kA_	Alignment	not modelled	98.9	31	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 **PDBTitle:** solution structure of alpha subunit of human eif2
33	c2oceA_	Alignment	not modelled	98.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
34	d3bzka4	Alignment	not modelled	98.9	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	c3psiA_	Alignment	not modelled	98.8	12	**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	c2ahoB_	Alignment	not modelled	98.8	22	**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
37	c1kl9A_	Alignment	not modelled	98.8	30	**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
38	d1sroa_	Alignment	not modelled	98.7	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	d2z0sa1	Alignment	not modelled	98.7	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
40	d2ba0a1	Alignment	not modelled	98.7	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
41	d2je6i1	Alignment	not modelled	98.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	d2ahob2	Alignment	not modelled	98.6	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
43	d1wi5a_	Alignment	not modelled	98.6	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
44	c1l2fA_	Alignment	not modelled	98.6	14	**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	c3go5A_	Alignment	not modelled	98.6	25	**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
46	c1hh2P_	Alignment	not modelled	98.4	14	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
47	d1hh2p1	Alignment	not modelled	98.4	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
48	d2nn6h1	Alignment	not modelled	98.3	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
49	c3ayhB_	Alignment	not modelled	98.2	15	**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
50	c2z0sA_	Alignment	not modelled	98.2	19	**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

51	c3k2zA_	Alignment		98.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
52	c2bh8B_	Alignment	not modelled	97.8	51	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
53	d2ix0a3	Alignment	not modelled	97.7	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
54	d2vnud2	Alignment	not modelled	97.7	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
55	c2ba0A_	Alignment	not modelled	97.7	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
56	d1smxa_	Alignment	not modelled	97.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
57	d2nn6i1	Alignment	not modelled	97.6	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
58	c3aqqD_	Alignment	not modelled	97.4	18	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**calcium-regulated heat stable protein 1; **PDBTitle:** crystal structure of human crhsp-24
59	c2a8vA_	Alignment	not modelled	97.3	24	**PDB header:**protein/rna **Chain:** A: **PDB Molecule:**rna binding domain of rho transcription **PDBTitle:** rho transcription termination factor/rna complex
60	c2je6I_	Alignment	not modelled	97.2	17	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1; **PDBTitle:** structure of a 9-subunit archaeal exosome
61	c2nn6I_	Alignment	not modelled	97.0	19	**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
62	c2rf4A_	Alignment	not modelled	97.0	16	**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
63	c3a0jB_	Alignment	not modelled	96.9	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
64	d1a62a2	Alignment	not modelled	96.9	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
65	d1mjca_	Alignment	not modelled	96.9	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
66	c2ytxA_	Alignment	not modelled	96.8	24	**PDB header:**rna binding protein **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)
67	d1g6pa_	Alignment	not modelled	96.8	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
68	d1wfqa_	Alignment	not modelled	96.7	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
69	d1mkma1	Alignment		96.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
70	c2ytyA_	Alignment	not modelled	96.6	17	**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)
71	d1h95a_	Alignment	not modelled	96.6	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
72	c2ba1B_	Alignment	not modelled	96.6	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
73	c1mkmA_	Alignment		96.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
74	c3camB	Alignment	not modelled	96.5	23	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cold-shock domain family protein;

74	c3camB_	Alignment	not modelled	96.5	23	**PDBTitle:** crystal structure of the cold shock domain protein from neisseria2 meningitidis
75	c2k5nA_	Alignment	not modelled	96.3	22	**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
76	c2xroE_	Alignment	not modelled	95.9	15	**PDB header:**dna-binding protein/dna **Chain:** E: **PDB Molecule:**hth-type transcriptional regulator ttgv; **PDBTitle:** crystal structure of ttgv in complex with its dna operator
77	d1jhfa1	Alignment	not modelled	95.9	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
78	c1j5yA_	Alignment	not modelled	95.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, biotin repressor family; **PDBTitle:** crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
79	c3mq0A_	Alignment	not modelled	95.8	16	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**transcriptional repressor of the blcabc operon; **PDBTitle:** crystal structure of agobacterium tumefaciens repressor blcr
80	c3hruA_	Alignment	not modelled	95.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
81	d2es2a1	Alignment	not modelled	95.5	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
82	c2kcmA_	Alignment	not modelled	95.4	21	**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.
83	c1x65A_	Alignment	not modelled	95.2	18	**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)
84	d1c9oa_	Alignment	not modelled	95.2	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
85	d1biaa1	Alignment	not modelled	95.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
86	c2o0yB_	Alignment		95.0	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
87	d1j5ya1	Alignment	not modelled	95.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
88	c1uwvA_	Alignment	not modelled	94.9	16	**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
89	d1xmka1	Alignment	not modelled	94.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
90	c2g7uB_	Alignment	not modelled	94.8	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
91	d1uwva1	Alignment	not modelled	94.8	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
92	d1stza1	Alignment	not modelled	94.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
93	d2p4wa1	Alignment	not modelled	94.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like
94	d2nn6g1	Alignment	not modelled	94.4	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
95	c1z6rC_	Alignment	not modelled	94.3	10	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
96	d2d1ha1	Alignment	not modelled	94.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
97	c2it0A_	Alignment	not modelled	94.1	24	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
98	d2hr3a1	Alignment	not modelled	94.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators

99	c1f5tA_	Alignment	not modelled	94.0	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
100	c3trzE_	Alignment	not modelled	93.9	19	**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
101	c2ytvA_	Alignment	not modelled	93.9	23	**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)
102	d1z05a1	Alignment	not modelled	93.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
103	d1luza_	Alignment	not modelled	93.7	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
104	c2oqgA_	Alignment	not modelled	93.7	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
105	d1lvaa3	Alignment	not modelled	93.3	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
106	c3r4kD_	Alignment	not modelled	93.3	14	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcriptional regulator, iclr family; **PDBTitle:** crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
107	c1k0rB_	Alignment	not modelled	93.1	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa
108	c3pqkD_	Alignment	not modelled	93.0	26	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
109	c3f6vA_	Alignment	not modelled	92.9	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
110	d2htja1	Alignment	not modelled	92.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FaeA-like
111	c1wsuA_	Alignment	not modelled	92.8	21	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** c-terminal domain of elongation factor selb complexed with2 secis rna
112	c1fx7C_	Alignment	not modelled	92.7	25	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
113	c2h09A_	Alignment	not modelled	92.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
114	d1r1ua_	Alignment	not modelled	92.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
115	d1ku9a_	Alignment	not modelled	92.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
116	c2ewnA_	Alignment	not modelled	92.4	18	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
117	c1r22B_	Alignment	not modelled	92.2	17	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
118	c3cuoB_	Alignment	not modelled	92.0	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
119	c3b73A_	Alignment	not modelled	91.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phih1 repressor-like protein; **PDBTitle:** crystal structure of the phih1 repressor-like protein from2 haloarcula marismortui
120	c2fe3B_	Alignment	not modelled	91.9	20	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**peroxide operon regulator; **PDBTitle:** the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch