Phyre2

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Description	P0A9J0
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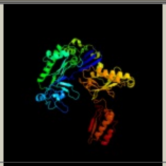
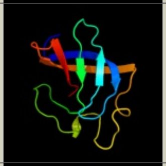
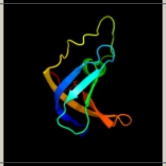
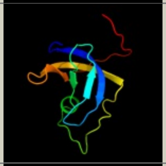
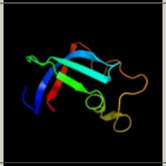
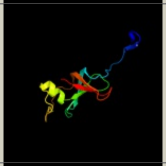
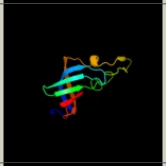
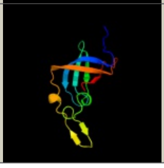
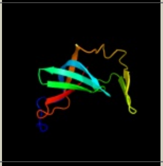
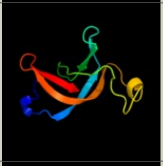
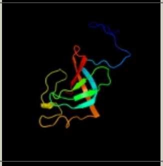
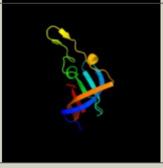
Unique Job ID	0ec622ab09a81cad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2c4rL_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
2	d1smxa_	Alignment		99.9	38	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
3	c1yz6A_	Alignment		98.3	20	**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
4	d2ba0a1	Alignment		98.1	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
5	d2z0sa1	Alignment		98.0	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
6	c2cqoA_	Alignment		98.0	23	**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
7	c2z0sA_	Alignment		97.9	23	**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
8	d2je6i1	Alignment		97.9	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
9	c2je6I_	Alignment		97.9	17	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1; **PDBTitle:** structure of a 9-subunit archaeal exosome
10	c2k4kA_	Alignment		97.9	27	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
11	d1q46a2	Alignment		97.9	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

12	c1q8kA_	Alignment		97.8	23	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 **PDBTitle:** solution structure of alpha subunit of human eif2
13	d1hh2p1	Alignment		97.8	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	c2khiA_	Alignment		97.8	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
15	c2khjA_	Alignment		97.8	19	**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
16	d2nn6h1	Alignment		97.8	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
17	c1q46A_	Alignment		97.7	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
18	c2ba0A_	Alignment		97.7	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
19	c1hh2P_	Alignment		97.7	25	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
20	d3bzka4	Alignment		97.7	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
21	d1wi5a_	Alignment	not modelled	97.7	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	c3go5A_	Alignment	not modelled	97.6	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
23	c2eqsA_	Alignment	not modelled	97.6	25	**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
24	c1l2fA_	Alignment	not modelled	97.6	25	**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
25	d1sroa_	Alignment	not modelled	97.5	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	d1go3e1	Alignment	not modelled	97.4	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
27	d1kl9a2	Alignment	not modelled	97.4	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
28	c2oceA_	Alignment	not modelled	97.3	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa

29	c2ahoB_	Alignment	not modelled	97.2	18	**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
30	c2k52A_	Alignment	not modelled	97.2	23	**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
31	c2ba1B_	Alignment	not modelled	97.1	23	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
32	d2nn6i1	Alignment	not modelled	97.1	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
33	c2c35F_	Alignment	not modelled	97.1	18	**PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii
34	d2ahob2	Alignment	not modelled	97.1	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	c1kl9A_	Alignment	not modelled	96.9	25	**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
36	d1y14b1	Alignment	not modelled	96.8	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
37	c3psiA_	Alignment	not modelled	96.8	14	**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)
38	c1go3E_	Alignment	not modelled	96.6	19	**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
39	c2nn6I_	Alignment	not modelled	96.5	21	**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
40	c2b8kG_	Alignment	not modelled	96.3	9	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
41	d2c35b1	Alignment	not modelled	96.3	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	c3h0gS_	Alignment	not modelled	96.3	17	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
43	d2nn6g1	Alignment	not modelled	96.0	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
44	c2pmzE_	Alignment	not modelled	95.6	18	**PDB header:**translation, transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
45	c1nt9G_	Alignment	not modelled	95.4	9	**PDB header:**transcription, transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kd polypeptide; **PDBTitle:** complete 12-subunit rna polymerase ii
46	d2asba1	Alignment	not modelled	95.0	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
47	c1k0rB_	Alignment	not modelled	94.9	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa
48	c2asbA_	Alignment	not modelled	94.5	24	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** structure of a mycobacterium tuberculosis nusa-rna complex
49	c2bh8B_	Alignment	not modelled	94.4	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
50	c2kcmA_	Alignment	not modelled	93.9	25	**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.
51	c2nn6G_	Alignment	not modelled	92.5	20	**PDB header:**hydrolase/transferase **Chain:** G: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
52	c3aqqD_	Alignment	not modelled	92.4	24	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**calcium-regulated heat stable protein 1; **PDBTitle:** crystal structure of human crhsp-24
53	d1c9oa_	Alignment	not modelled	92.2	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
54	c2lipA_	Alignment	not modelled	91.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease p protein component;

54	c2ljpA_	Alignment	not modelled	91.8	14	**PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for e.coli2 ribonuclease p protein
55	d2ja9a1	Alignment	not modelled	91.5	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
56	c2ckzB_	Alignment	not modelled	91.4	10	**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.
57	c2nn6H_	Alignment	not modelled	91.2	19	**PDB header:**hydrolase/transferase **Chain:** H: **PDB Molecule:**exosome complex exonuclease rrp4; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
58	d1a6fa_	Alignment	not modelled	89.9	22	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
59	d2es2a1	Alignment	not modelled	89.8	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
60	d1mjca_	Alignment	not modelled	89.3	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
61	d1h95a_	Alignment	not modelled	88.2	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
62	d1g6pa_	Alignment	not modelled	88.2	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	c2ja9A_	Alignment	not modelled	86.7	12	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40
64	d1nz0a_	Alignment	not modelled	85.8	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
65	d1d6ta_	Alignment	not modelled	84.8	15	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
66	d1k3ra1	Alignment	not modelled	83.6	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
67	c2ix1A_	Alignment	not modelled	83.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant
68	c3a0jB_	Alignment	not modelled	82.4	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
69	c2bx9J_	Alignment	not modelled	81.9	38	**PDB header:**transcription regulation **Chain:** J: **PDB Molecule:**tryptophan rna-binding attenuator protein-inhibitory **PDBTitle:** crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
70	c3ld0Q_	Alignment	not modelled	81.1	38	**PDB header:**gene regulation **Chain:** Q: **PDB Molecule:**inhibitor of trap, regulated by t-box (trp) sequence rtpa; **PDBTitle:** crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
71	c3ayhB_	Alignment	not modelled	80.2	10	**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
72	c2eqjA_	Alignment	not modelled	80.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
73	c2k5nA_	Alignment	not modelled	79.9	8	**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
74	c2hl7A_	Alignment	not modelled	78.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
75	c2wp8J_	Alignment	not modelled	74.4	23	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
76	d1nlta3	Alignment	not modelled	74.0	29	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
77	c3pihA_	Alignment	not modelled	72.1	21	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
78	c2hnkC_	Alignment	not modelled	68.4	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sam-dependent o-methyltransferase; **PDBTitle:** crystal structure of sam-dependent o-methyltransferase from2 pathogenic bacterium leptospira interrogans
79	c2kw0A_	Alignment	not modelled	67.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from

						escherichia.coli
80	c2e5pA_	Alignment	not modelled	65.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
81	c3camB_	Alignment	not modelled	64.9	23	**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
82	c3trzE_	Alignment	not modelled	62.4	21	**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
83	c3d0fA_	Alignment	not modelled	62.4	14	**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
84	c2ytvA_	Alignment	not modelled	59.6	27	**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)
85	c1nltA_	Alignment	not modelled	59.4	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** the crystal structure of hsp40 ydj1
86	d2ix0a2	Alignment	not modelled	58.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
87	c2pe4A_	Alignment	not modelled	57.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-1; **PDBTitle:** structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
88	c1x65A_	Alignment	not modelled	54.7	23	**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)
89	c2cttA_	Alignment	not modelled	54.6	36	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of zinc finger domain from human dnaj2 subfamily a member 3
90	c2d9tA_	Alignment	not modelled	52.0	18	**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
91	c3tr6A_	Alignment	not modelled	50.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-methyltransferase; **PDBTitle:** structure of a o-methyltransferase from coxiella burnetii
92	c2vy9A_	Alignment	not modelled	49.5	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**anti-sigma-factor antagonist; **PDBTitle:** molecular architecture of the stressosome, a signal2 integration and transduction hub
93	d2rdea2	Alignment	not modelled	48.8	23	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain-associated domain
94	c3d3rA_	Alignment	not modelled	44.6	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
95	c2e5qA_	Alignment	not modelled	44.5	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 19; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
96	d1we8a_	Alignment	not modelled	43.5	6	**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)
97	c2rf4A_	Alignment	not modelled	43.0	13	**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
98	d1exka_	Alignment	not modelled	42.4	46	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
99	c1tt9B_	Alignment	not modelled	42.2	24	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**formimidoyltransferase-cyclodeaminase **PDBTitle:** structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
100	d3d3ra1	Alignment	not modelled	41.8	19	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
101	c2hu9B_	Alignment	not modelled	35.0	30	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**mercuric transport protein periplasmic component; **PDBTitle:** x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
102	d1a62a2	Alignment	not modelled	34.8	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
103	c3nthA_	Alignment	not modelled	34.5	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**maternal protein tudor; **PDBTitle:** crystal structure of tudor and aubergine [r13(me2s)] complex
104	d1vc1a_	Alignment	not modelled	34.4	13	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa

105	d1x4ma1	Alignment	not modelled	34.3	8	**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	d1h9ma1	Alignment	not modelled	32.9	31	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
107	c3lz8A_	Alignment	not modelled	32.0	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.
108	d1p9ra_	Alignment	not modelled	31.9	40	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
109	c2vnuD_	Alignment	not modelled	31.6	19	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp44; **PDBTitle:** crystal structure of sc rrp44
110	c2ygrD_	Alignment	not modelled	30.9	50	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
111	c1h9sA_	Alignment	not modelled	29.9	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**molybdenum transport protein mode; **PDBTitle:** molybdate bound complex of dimop domain of mode from e.coli
112	d1h9ra1	Alignment	not modelled	29.6	15	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
113	d1xtda2	Alignment	not modelled	29.4	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
114	c2vkcA_	Alignment	not modelled	29.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nedd4-binding protein 2; **PDBTitle:** solution structure of the b3bp smr domain
115	c2dgyA_	Alignment	not modelled	28.5	32	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
116	d2ctma1	Alignment	not modelled	28.1	8	**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)
117	d2hqxa1	Alignment	not modelled	27.6	29	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
118	c2hqxB_	Alignment	not modelled	27.6	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**p100 co-activator tudor domain; **PDBTitle:** crystal structure of human p100 tudor domain conserved2 region
119	c2ytxA_	Alignment	not modelled	27.1	20	**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)
120	c2vf7B_	Alignment	not modelled	26.3	64	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans