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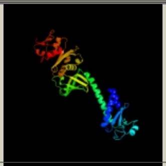
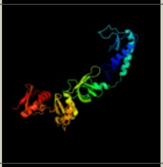
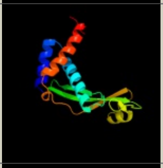
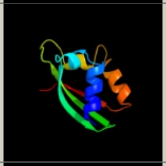
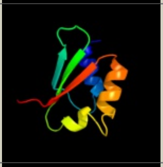
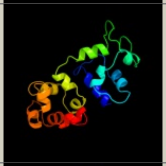
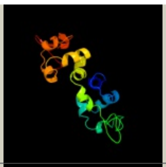
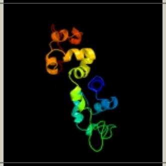
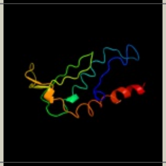
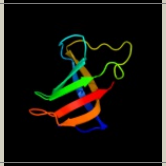
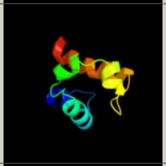
Description	P0AFF6
Date	Thu Jan 5 11:26:07 GMT 2012
Unique Job ID	f8574ffcb15887fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1l2fA_	Alignment		100.0	35	**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
2	c1hh2P_	Alignment		100.0	35	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
3	c1k0rB_	Alignment		100.0	38	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa
4	c2asbA_	Alignment		100.0	39	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** structure of a mycobacterium tuberculosis nusa-rna complex
5	d2asba2	Alignment		100.0	47	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
6	c2kwpA_	Alignment		100.0	98	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** solution structure of the aminoterminal domain of e. coli nusa
7	d1hh2p2	Alignment		100.0	47	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
8	d1hh2p4	Alignment		100.0	34	**Fold:**Transcription factor NusA, N-terminal domain **Superfamily:**Transcription factor NusA, N-terminal domain **Family:**Transcription factor NusA, N-terminal domain
9	d1hh2p3	Alignment		99.9	36	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
10	c2owoA_	Alignment		99.9	20	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
11	d2asba3	Alignment		99.9	41	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)

12	c1dgsB_	Alignment		99.9	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
13	c1v9pB_	Alignment		99.9	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
14	d1dgsa1	Alignment		99.9	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
15	d1k0ra4	Alignment		99.8	35	**Fold:**Transcription factor NusA, N-terminal domain **Superfamily:**Transcription factor NusA, N-terminal domain **Family:**Transcription factor NusA, N-terminal domain
16	d2asba1	Alignment		99.8	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
17	d1hh2p1	Alignment		99.8	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
18	c2cy1A_	Alignment		99.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nusa protein homolog; **PDBTitle:** crystal structure of ape1850
19	c1wcnA_	Alignment		99.5	100	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** nmr structure of the carboxyterminal domains of escherichia2 coli nusa
20	d1u9la_	Alignment		99.1	100	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**NusA extra C-terminal domains
21	c3go5A_	Alignment	not modelled	98.9	19	**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
22	d1q46a2	Alignment	not modelled	98.8	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	c1q46A_	Alignment	not modelled	98.8	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
24	c2khjA_	Alignment	not modelled	98.8	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
25	c1yz6A_	Alignment	not modelled	98.8	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
26	c2k4kA_	Alignment	not modelled	98.8	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
27	c2khiA_	Alignment	not modelled	98.8	18	**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
						Fold:OB-fold

28	d2ba0a1	Alignment	not modelled	98.8	16	**Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
29	d1go3e1	Alignment	not modelled	98.8	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
30	c2z0sA_	Alignment	not modelled	98.8	17	**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
31	c1q8kA_	Alignment	not modelled	98.8	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 **PDBTitle:** solution structure of alpha subunit of human eif2
32	d2z0sa1	Alignment	not modelled	98.7	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
33	c2k52A_	Alignment	not modelled	98.7	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
34	d1wi5a_	Alignment	not modelled	98.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	d2je6i1	Alignment	not modelled	98.7	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
36	d1kl9a2	Alignment	not modelled	98.7	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
37	d2i1qa1	Alignment	not modelled	98.7	35	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
38	d1y14b1	Alignment	not modelled	98.7	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	d1pzna1	Alignment	not modelled	98.7	32	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
40	d2a1jb1	Alignment	not modelled	98.7	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
41	c2cqoA_	Alignment	not modelled	98.6	18	**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
42	d2nn6h1	Alignment	not modelled	98.6	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
43	d1szpa1	Alignment	not modelled	98.6	29	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
44	c2ahoB_	Alignment	not modelled	98.6	15	**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
45	d3bzka4	Alignment	not modelled	98.5	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	d1sroa_	Alignment	not modelled	98.5	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
47	d1x2ia1	Alignment	not modelled	98.5	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
48	c2je6I_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1; **PDBTitle:** structure of a 9-subunit archaeal exosome
49	c1go3E_	Alignment	not modelled	98.4	22	**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
50	d2ahob2	Alignment	not modelled	98.4	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	c1kl9A_	Alignment	not modelled	98.4	24	**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
52	c2ba0A_	Alignment	not modelled	98.4	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
53	d2bgwa1	Alignment	not modelled	98.4	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
						PDB header:transferase

54	c2b8kG_	Alignment	not modelled	98.4	12	**Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
55	d1kfta_	Alignment	not modelled	98.4	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
56	c1kftA_	Alignment	not modelled	98.4	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
57	c2eqsA_	Alignment	not modelled	98.3	17	**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
58	c2oceA_	Alignment	not modelled	98.3	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
59	c1b22A_	Alignment	not modelled	98.3	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
60	d1b22a_	Alignment	not modelled	98.3	25	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
61	c3psiA_	Alignment	not modelled	98.3	16	**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)
62	c2c35F_	Alignment	not modelled	98.3	22	**PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii
63	d2c35b1	Alignment	not modelled	98.2	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
64	d2nn6i1	Alignment	not modelled	98.1	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
65	d1szpb1	Alignment	not modelled	98.1	30	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
66	c1nt9G_	Alignment	not modelled	98.0	12	**PDB header:**transcription, transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kd polypeptide; **PDBTitle:** complete 12-subunit rna polymerase ii
67	d1smxa_	Alignment	not modelled	98.0	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
68	c2w9mB_	Alignment	not modelled	98.0	21	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
69	c3h0gS_	Alignment	not modelled	97.9	22	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
70	c2nn6I_	Alignment	not modelled	97.9	27	**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
71	c2nrzB_	Alignment	not modelled	97.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
72	c2pmzE_	Alignment	not modelled	97.9	21	**PDB header:**translation, transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
73	c2ba1B_	Alignment	not modelled	97.7	15	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
74	c2bhnD_	Alignment	not modelled	97.7	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xpf endonuclease; **PDBTitle:** xpf from aeropyrum pernix
75	c2ckzB_	Alignment	not modelled	97.5	23	**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.
76	c2ihmA_	Alignment	not modelled	97.4	18	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
77	d2aq0a1	Alignment	not modelled	97.4	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
78	c3ayhB_	Alignment	not modelled	97.4	17	**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
79	c2ja9A_	Alignment	not modelled	97.4	20	**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
80	c1kdhA_	Alignment	not modelled	97.4	13	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short

							PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
81	c2bcuA_		Alignment	not modelled	97.2	16	**PDB header:**transferase, lyase/dna **Chain:** A: **PDB Molecule:**dna polymerase lambda; **PDBTitle:** dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
82	c3c1zA_		Alignment	not modelled	97.2	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna integrity scanning protein disa; **PDBTitle:** structure of the ligand-free form of a bacterial dna damage2 sensor protein
83	d2p6ra2		Alignment	not modelled	97.1	16	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
84	c1ixrA_		Alignment	not modelled	97.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
85	d2nn6g1		Alignment	not modelled	97.0	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
86	d1doqa_		Alignment	not modelled	97.0	25	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
87	d1lb2b_		Alignment	not modelled	97.0	17	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
88	d1cuka2		Alignment	not modelled	96.9	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
89	c8iczA_		Alignment	not modelled	96.9	21	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase beta (e.c.2.7.7.7)); **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
90	c2nn6G_		Alignment	not modelled	96.9	18	**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
91	c2jvzA_		Alignment	not modelled	96.9	16	**PDB header:**splicing **Chain:** A: **PDB Molecule:**far upstream element-binding protein 2; **PDBTitle:** solution nmr structure of the second and third kh domains2 of ksrp
92	d1z3eb1		Alignment	not modelled	96.9	19	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
93	c2jzxA_		Alignment	not modelled	96.8	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2; **PDBTitle:** pcbp2 kh1-kh2 domains
94	d1cooa_		Alignment	not modelled	96.8	17	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
95	d1ixra1		Alignment	not modelled	96.8	21	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
96	d2ja9a1		Alignment	not modelled	96.7	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
97	c2bh8B_		Alignment	not modelled	96.7	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
98	c2va8A_		Alignment	not modelled	96.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
99	c2wp8J_		Alignment	not modelled	96.5	22	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
100	c2csdB_		Alignment	not modelled	96.5	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
101	c2nn6H_		Alignment	not modelled	96.4	18	**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
102	c2ix1A_		Alignment	not modelled	96.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant
103	d1pu6a_		Alignment	not modelled	96.4	22	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
104	c1hjpA_		Alignment	not modelled	96.3	21	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
105	c1d8lA_		Alignment	not modelled	96.3	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva); **PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
106	d1bvsa2		Alignment	not modelled	96.2	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like

						Family:DNA helicase RuvA subunit, middle domain
107	c2h5xA_	Alignment	not modelled	96.1	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
108	c2rf4A_	Alignment	not modelled	96.0	14	**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
109	c2p6uA_	Alignment	not modelled	95.8	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
110	c1j4wA_	Alignment	not modelled	95.8	26	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**fuse binding protein; **PDBTitle:** complex of the kh3 and kh4 domains of fbp with a2 single_stranded 29mer dna oligonucleotide from the fuse3 element of the c-myc oncogene
111	c3krmB_	Alignment	not modelled	95.7	22	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**insulin-like growth factor 2 mrna-binding protein **PDBTitle:** imp1 kh34
112	c2anrA_	Alignment	not modelled	95.4	20	**PDB header:**rna-binding protein/rna **Chain:** A: **PDB Molecule:**neuro-oncological ventral antigen 1; **PDBTitle:** crystal structure (ii) of nova-1 kh1/kh2 domain tandem with 25nt rna2 hairpin
113	c2c4rL_	Alignment	not modelled	95.3	16	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
114	c1t4gA_	Alignment	not modelled	95.1	25	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** atpase in complex with amp-pnp
115	d1keaa_	Alignment	not modelled	95.0	17	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
116	c1s5lu_	Alignment	not modelled	95.0	30	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
117	c2qndA_	Alignment	not modelled	94.8	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**fmr1 protein; **PDBTitle:** crystal structure of the kh1-kh2 domains from human fragile x mental2 retardation protein
118	d2ba0a3	Alignment	not modelled	94.6	15	**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)
119	d1x4ma1	Alignment	not modelled	94.5	15	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
120	d2axtu1	Alignment	not modelled	94.5	26	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like