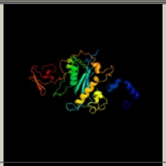
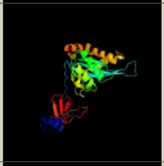
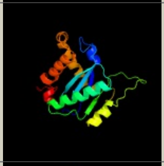
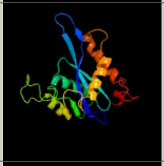
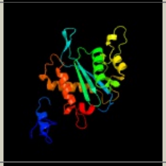
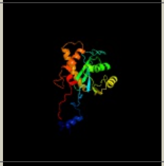
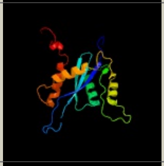
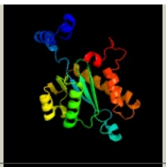
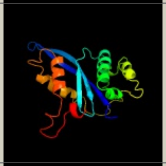
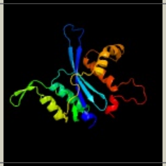
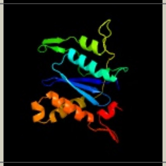
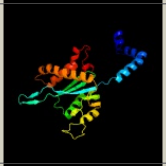
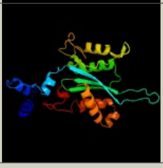
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3428c_(-)_3844918_3846150
Date	Fri Aug 9 18:20:10 BST 2019
Unique Job ID	a2c3ea645a62f1e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fcyA_	Alignment		100.0	15	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposase; **PDBTitle:** crystal structure of the bacteriophage mu transpososome
2	c1bcoA_	Alignment		99.9	9	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
3	d1bcoa2	Alignment		99.8	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**mu transposase, core domain
4	c5u1cA_	Alignment		99.8	8	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv-1 integrase, sso7d chimera; **PDBTitle:** structure of tetrameric hiv-1 strand transfer complex intasome
5	c5cz1B_	Alignment		99.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain of mmtv integrase
6	c1c0mA_	Alignment		99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
7	c3f9kV_	Alignment		99.8	12	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
8	c3nf9A_	Alignment		99.8	10	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
9	c3jcaE_	Alignment		99.8	15	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**integrase; **PDBTitle:** core model of the mouse mammary tumor virus intasome
10	d1asua_	Alignment		99.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
11	d1c0ma2	Alignment		99.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain

12	c5m0rF_	Alignment		99.7	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**integrase; **PDBTitle:** cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
13	c1ex4A_	Alignment		99.7	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
14	d1exqa_	Alignment		99.7	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
15	c3kksB_	Alignment		99.7	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii
16	c4mq3A_	Alignment		99.6	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** the 1.1 angstrom structure of catalytic core domain of fiv integrase
17	d1cxqa_	Alignment		99.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
18	d1hyva_	Alignment		99.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
19	c3hpgC_	Alignment		99.6	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**integrase; **PDBTitle:** visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
20	c1k6yB_	Alignment		99.6	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase
21	c5ejkG_	Alignment	not modelled	99.6	15	**PDB header:**transferase/dna **Chain:** G: **PDB Molecule:**gag-pro-pol polyprotein; **PDBTitle:** crystal structure of the rous sarcoma virus intasome
22	d1c6va_	Alignment	not modelled	99.5	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
23	c5u1cD_	Alignment	not modelled	99.3	9	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**hiv-1 integrase, sso7d chimera; **PDBTitle:** structure of tetrameric hiv-1 strand transfer complex intasome
24	c3l2tB_	Alignment	not modelled	99.3	14	**PDB header:**recombination/dna **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
25	c3dlrA_	Alignment	not modelled	99.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain from pfv integrase
26	c3l2uA_	Alignment	not modelled	98.1	14	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitegravir)
27	c3hosA_	Alignment	not modelled	97.6	12	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
28	d1bcoa1	Alignment	not modelled	97.0	20	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain

29	c5cr4B_	Alignment	not modelled	96.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sleeping beauty transposase, sb100x; **PDBTitle:** crystal structure of the sleeping beauty transposase catalytic domain
30	c3f2kB_	Alignment	not modelled	95.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone-lysine n-methyltransferase setmar; **PDBTitle:** structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
31	d2i5ua1	Alignment	not modelled	91.7	25	**Fold:**DnaD domain-like **Superfamily:**DnaD domain-like **Family:**DnaD domain
32	c2zc2A_	Alignment	not modelled	91.5	17	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnad-like replication protein; **PDBTitle:** crystal structure of dnad-like replication protein from streptococcus2 mutans ua159, gi 24377835, residues 127-199
33	c2f7tA_	Alignment	not modelled	82.0	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mos1 transposase; **PDBTitle:** crystal structure of the catalytic domain of mos1 mariner2 transposase
34	c5unkA_	Alignment	not modelled	63.7	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**sleeping beauty transposase; **PDBTitle:** nmr structure of the red subdomain of the sleeping beauty transposase
35	c6mzlM_	Alignment	not modelled	62.8	14	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor tfiid subunit 9, taf9; **PDBTitle:** human tfiid canonical state
36	d2ezia_	Alignment	not modelled	48.4	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
37	c2eqxA_	Alignment	not modelled	45.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kelch repeat and btb domain-containing protein 4; **PDBTitle:** solution structure of the back domain of kelch repeat and2 btb domain-containing protein 4
38	d2ezha_	Alignment	not modelled	45.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
39	d1mzba_	Alignment	not modelled	38.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
40	c2o03A_	Alignment	not modelled	36.1	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
41	c4i7hA_	Alignment	not modelled	34.6	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peroxide stress sensing regulator; **PDBTitle:** structural basis for peroxide sensing and gene regulation by perr from2 streptococcus pyogenes
42	c6dk4A_	Alignment	not modelled	34.3	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of campylobacter jejuni peroxide stress regulator
43	c2wbnA_	Alignment	not modelled	32.6	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**terminase large subunit; **PDBTitle:** crystal structure of the g2p (large terminase) nuclease2 domain from the bacteriophage spp1
44	c6hqaF_	Alignment	not modelled	32.2	14	**PDB header:**transcription **Chain:** F: **PDB Molecule:**subunit (17 kda) of tfiid and saga complexes, involved in **PDBTitle:** molecular structure of promoter-bound yeast tfiid
45	c2ahqA_	Alignment	not modelled	30.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
46	c3m5bA_	Alignment	not modelled	30.5	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** crystal structure of the btb domain from fazf/zbtb32
47	c2xigA_	Alignment	not modelled	29.7	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
48	c2yy9A_	Alignment	not modelled	29.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 48; **PDBTitle:** crystal structure of btb domain from mouse hkr3
49	c6gfcG_	Alignment	not modelled	26.9	19	**PDB header:**antiviral protein **Chain:** G: **PDB Molecule:**galectin-3-binding protein; **PDBTitle:** structure of the btb/poz domain of human 90k
50	c3mwmA_	Alignment	not modelled	26.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
51	c5nbcD_	Alignment	not modelled	26.6	17	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** structure of prokaryotic transcription factors
52	c4etsB_	Alignment	not modelled	25.4	8	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of campylobacter jejuni ferric uptake regulator
53	c3eyyA_	Alignment	not modelled	25.1	20	**PDB header:**transport **Chain:** A: **PDB Molecule:**putative iron uptake regulatory protein; **PDBTitle:** structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
54	d1stza1	Alignment	not modelled	24.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

54	d1stza1	Alignment	not modelled	24.6	15	**Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
55	c4eozC_	Alignment	not modelled	24.5	20	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**speckle-type poz protein; **PDBTitle:** crystal structure of the spop btb domain complexed with the cul3 n-2 terminal domain
56	c4uyiA_	Alignment	not modelled	24.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**structure-specific endonuclease subunit slx4; **PDBTitle:** crystal structure of the btb domain of human slx4 (btbd12)
57	c4dkwA_	Alignment	not modelled	23.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**large terminase protein; **PDBTitle:** structure of p22 large terminase nuclease domain
58	c5t9gD_	Alignment	not modelled	22.9	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycoside hydrolase; **PDBTitle:** crystal structure of bugh2cwt in complex with galactoisofagomine
59	c4ypjB_	Alignment	not modelled	22.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta galactosidase; **PDBTitle:** x-ray structure of the mutant of glycoside hydrolase
60	c6ed2A_	Alignment	not modelled	22.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase family 2, tim barrel domain protein; **PDBTitle:** faecalibacterium prausnitzii beta-glucuronidase
61	c2fu4B_	Alignment	not modelled	21.9	24	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
62	c5dmyA_	Alignment	not modelled	21.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** beta-galactosidase - construct 33-930
63	c2w57A_	Alignment	not modelled	21.9	20	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
64	c3hu6B_	Alignment	not modelled	20.6	20	**PDB header:**protein binding, ligase **Chain:** B: **PDB Molecule:**speckle-type poz protein; **PDBTitle:** structures of spop-substrate complexes: insights into2 molecular architectures of btb-cul3 ubiquitin ligases:3 spopmathx/btb/3-box-pucsbc1
65	c5l9wA_	Alignment	not modelled	20.1	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetophenone carboxylase delta subunit; **PDBTitle:** crystal structure of the apc core complex
66	c6dxuB_	Alignment	not modelled	20.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycosyl hydrolase family 2, tim barrel domain protein; **PDBTitle:** crystal structure of parabacteroides merdae beta-glucuronidase (gus)
67	d2p5ka1	Alignment	not modelled	19.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
68	c6d1pB_	Alignment	not modelled	19.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycosyl hydrolases family 2, sugar binding domain protein; **PDBTitle:** apo structure of bacteroides uniformis beta-glucuronidase 3
69	c5nl9B_	Alignment	not modelled	19.5	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**transcriptional regulator (fur family); **PDBTitle:** crystal structure of a peroxide stress regulator from leptospira2 interrogans
70	c6d0hB_	Alignment	not modelled	19.2	23	**PDB header:**toxin **Chain:** B: **PDB Molecule:**pars: cog5642 (duf2384) antitoxin; **PDBTitle:** part: prs adp-ribosylating toxin bound to cognate antitoxin pars
71	c4razB_	Alignment	not modelled	18.7	16	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**dna-binding transcriptional dual regulator of siderophore **PDBTitle:** crystal structure of magnetospirillum gryphiswaldense msr-1 holo-fur
72	c2mt3A_	Alignment	not modelled	18.7	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-54 factor; **PDBTitle:** structure of -24 dna binding domain of sigma 54 from e.coli
73	c1v85A_	Alignment	not modelled	18.3	15	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**similar to ring finger protein 36; **PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
74	c2fe3B_	Alignment	not modelled	17.7	16	**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
75	c2k4bA_	Alignment	not modelled	17.3	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** copr repressor structure
76	d1aoya_	Alignment	not modelled	17.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
77	c5fd6A_	Alignment	not modelled	16.9	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** zinc-bound manganese uptake regulator
78	c5xj2C_	Alignment	not modelled	16.3	11	**PDB header:**transferase/rna **Chain:** C: **PDB Molecule:**uncharacterized rna methyltransferase sp_1029; **PDBTitle:** structure of sprlmcd with u747 rna
						PDB header:immune system

79	c7ceiB_	Alignment	not modelled	16.1	15	**Chain:** B: **PDB Molecule:**protein (colicin e7 immunity protein); **PDBTitle:** the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
80	d1f9na1	Alignment	not modelled	15.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
81	d1b4aa1	Alignment	not modelled	15.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
82	c6bv7A_	Alignment	not modelled	15.5	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** nmr structure of sodium/calcium exchanger 1 (ncx1) two-helix bundle2 (thb) domain
83	c6ecaA_	Alignment	not modelled	15.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** lactobacillus rhamnosus beta-glucuronidase
84	d2jb0b1	Alignment	not modelled	15.3	14	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
85	c6hqaK_	Alignment	not modelled	15.2	24	**PDB header:**transcription **Chain:** K: **PDB Molecule:**subunit (61/68 kda) of tfiid and saga complexes; **PDBTitle:** molecular structure of promoter-bound yeast tfiid
86	c4qkoH_	Alignment	not modelled	15.2	9	**PDB header:**antimicrobial protein **Chain:** H: **PDB Molecule:**pyocin-s2; **PDBTitle:** the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
87	c4uhpA_	Alignment	not modelled	15.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**large component of pyocin ap41; **PDBTitle:** crystal structure of the pyocin ap41 dnase-immunity complex
88	c5ldrA_	Alignment	not modelled	15.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-d-galactosidase; **PDBTitle:** crystal structure of a cold-adapted dimeric beta-d-galactosidase from2 paracoccus sp. 32d strain in complex with galactose
89	c5nlbA_	Alignment	not modelled	15.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**kelch-like ech-associated protein 1; **PDBTitle:** crystal structure of human cul3 n-terminal domain bound to keap1 btb2 and 3-box
90	c4mtdA_	Alignment	not modelled	14.7	20	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**zinc uptake regulation protein; **PDBTitle:** zinc uptake regulator complexed with zinc and dna
91	c3htmB_	Alignment	not modelled	14.3	29	**PDB header:**protein binding, ligase **Chain:** A: **PDB Molecule:**speckle-type poz protein; **PDBTitle:** structures of spop-substrate complexes: insights into2 molecular architectures of btb-cul3 ubiquitin ligases:3 spopbtb/3-box
92	c6mvgB_	Alignment	not modelled	13.4	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** crystal structure of fmn-binding beta-glucuronidase from ruminococcus2 gnavus
93	d1buoa_	Alignment	not modelled	13.3	15	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
94	c5t98B_	Alignment	not modelled	13.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycoside hydrolase; **PDBTitle:** crystal structure of bugh2awt
95	c3djmA_	Alignment	not modelled	12.7	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf427; **PDBTitle:** crystal structure of a protein of unknown function from duf427 family2 (rsph17029_0682) from rhodobacter sphaeroides 2.4.1 at 2.51 a3 resolution
96	d2jn6a1	Alignment	not modelled	12.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
97	c2o8kA_	Alignment	not modelled	12.2	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
98	c5i4rA_	Alignment	not modelled	11.9	20	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**contact-dependent inhibitor a; **PDBTitle:** contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
99	c3cmgA_	Alignment	not modelled	11.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis