





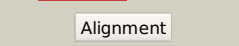



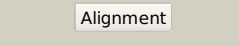

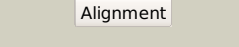

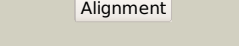

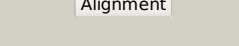
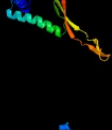
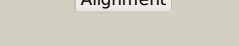
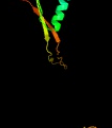
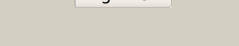




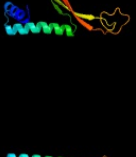

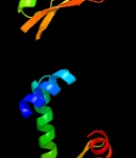

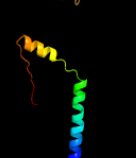
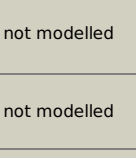


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2986c_(hupB)_3343186_3343830
Date	Thu Aug 8 16:20:15 BST 2019
Unique Job ID	21714b3fb40bd708

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lifA_	 Alignment		99.9	39	PDB header: recombination/dna Chain: A: PDB Molecule: integration host factor; PDBTitle: single chain integration host factor mutant protein (scihf2-k45ae) in2 complex with dna
2	c3c4iA_	 Alignment		99.9	100	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein hu homolog; PDBTitle: crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
3	d1p71a_	 Alignment		99.9	43	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
4	c2np2B_	 Alignment		99.9	31	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hbb; PDBTitle: hbb-dna complex
5	d1owfb_	 Alignment		99.9	31	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
6	d1owfa_	 Alignment		99.9	38	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
7	c5lvtC_	 Alignment		99.9	40	PDB header: dna binding protein Chain: C: PDB Molecule: dna-binding protein hu; PDBTitle: structure of hu protein from lactococcus lactis
8	c4qujB_	 Alignment		99.9	39	PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna-binding protein hu; PDBTitle: crystal structure of dna-bound nucleoid associated protein, sav1473
9	c4n1vA_	 Alignment		99.9	36	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein hu-beta; PDBTitle: structure of dna-binding protein hu from micoplasma spiroplasma2 melliferum
10	c2ndpA_	 Alignment		99.9	12	PDB header: dna binding protein Chain: A: PDB Molecule: histone-like dna-binding superfamily protein; PDBTitle: structure of dna-binding hu protein from micoplasma mycoplasma2 gallisepticum
11	d1exea_	 Alignment		99.9	32	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein

12	c3rhiB	Alignment		99.9	42	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein hu; PDBTitle: dna-binding protein hu from bacillus anthracis
13	c6n2IA	Alignment		99.8	38	PDB header: dna binding protein Chain: A: PDB Molecule: histone family protein dna-binding protein; PDBTitle: crystal structure of a histone family protein dna-binding protein from2 burkholderia ambifaria
14	d1mula	Alignment		99.8	43	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
15	d1huua	Alignment		99.8	49	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
16	c5ekaA	Alignment		99.8	39	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein hu; PDBTitle: hu dna-binding protein from thermus thermophilus
17	d2o97b1	Alignment		99.7	37	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
18	d1b8za	Alignment		99.6	47	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
19	c4fmrB	Alignment		98.2	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized hypothetical protein; PDBTitle: crystal structure of a putative bacterial dna binding protein2 (bvq_2165) from bacteroides vulgatus atcc 8482 at 2.25 a resolution
20	c4s12C	Alignment		79.2	14	PDB header: lyase Chain: C: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: 1.55 angstrom crystal structure of n-acetylmuramic acid 6-phosphate2 etherase from yersinia enterocolitica.
21	c3cvjB	Alignment	not modelled	77.2	15	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
22	d1nria	Alignment	not modelled	75.7	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
23	c1nriA	Alignment	not modelled	75.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
24	c6jx3B	Alignment	not modelled	67.4	18	PDB header: peptide binding protein Chain: B: PDB Molecule: tfub1; PDBTitle: lasso peptide synthetase b1 complexed with the leader peptide
25	c4lzdD	Alignment	not modelled	67.0	16	PDB header: lyase/lyase inhibitor Chain: D: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: crystal structure of murq from h.influenzae with bound inhibitor
26	d1z67a1	Alignment	not modelled	65.2	26	Fold: YidB-like Superfamily: YidB-like Family: YidB-like
27	c5uqiA	Alignment	not modelled	61.5	16	PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
28	d1ussa	Alignment	not modelled	61.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5

29	d1o17a1	Alignment	not modelled	58.0	20	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
30	c5v1uB	Alignment	not modelled	56.8	12	PDB header: protein binding Chain: B: PDB Molecule: tbib1; PDBTitle: tbib1 in complex with the tbia(beta) leader peptide
31	c5by2A	Alignment	not modelled	56.5	19	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
32	c2lsoA	Alignment	not modelled	56.4	13	PDB header: nuclear protein Chain: A: PDB Molecule: histone h1x; PDBTitle: solution nmr structure of the globular domain of human histone h1x,2 northeast structural genomics consortium (nesg) target hr7057a
33	c2mxfA	Alignment	not modelled	55.3	33	PDB header: transcription regulator/dna Chain: A: PDB Molecule: mvat; PDBTitle: structure of the dna complex of the c-terminal domain of mvat
34	d1brwa1	Alignment	not modelled	54.8	13	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
35	c1o17A	Alignment	not modelled	53.7	20	PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyl-transferase (trpd)
36	c4hkmA	Alignment	not modelled	51.1	0	PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure of an anthranilate phosphoribosyltransferase (target2 id nysgrc-016600) from xanthomonas campestris
37	d1tk9a	Alignment	not modelled	50.4	20	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
38	d1x92a	Alignment	not modelled	50.3	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
39	c5sxyA	Alignment	not modelled	50.1	12	PDB header: chaperone Chain: A: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
40	c3twkB	Alignment	not modelled	48.8	15	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
41	c2yskA	Alignment	not modelled	48.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ttha1432; PDBTitle: crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
42	c2ma3A	Alignment	not modelled	48.2	9	PDB header: replication Chain: A: PDB Molecule: dna replication initiator (cdc21/cdc54); PDBTitle: nmr solution structure of the c-terminus of the minichromosome2 maintenance protein mcm from methanothermobacter thermautotrophicus
43	c3g2bA	Alignment	not modelled	46.6	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: coenzyme pqq synthesis protein d; PDBTitle: crystal structure of pqqd from xanthomonas campestris
44	d1khdA1	Alignment	not modelled	46.6	7	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
45	d2tptA1	Alignment	not modelled	43.2	10	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
46	c2yvaB	Alignment	not modelled	42.1	16	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
47	d1v74a	Alignment	not modelled	42.1	22	Fold: Colicin D/E5 nuclease domain Superfamily: Colicin D/E5 nuclease domain Family: Colicin D nuclease domain
48	d1yqaa1	Alignment	not modelled	41.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
49	c1tk0A	Alignment	not modelled	40.9	16	PDB header: transferase/electron transport/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: t7 dna polymerase ternary complex with 8 oxo guanosine and ddctp at2 the insertion site
50	d1aipc1	Alignment	not modelled	40.5	25	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
51	c1otpA	Alignment	not modelled	39.4	10	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
52	c1hkgA	Alignment	not modelled	39.3	13	PDB header: transferase Chain: A: PDB Molecule: hexokinase a; PDBTitle: structural dynamics of yeast hexokinase during catalysis

53	d1nh2d1	Alignment	not modelled	38.6	11	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
54	d1uoua1	Alignment	not modelled	38.5	22	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
55	d1i27a_	Alignment	not modelled	38.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of the rap74 subunit of TFIIF
56	d1vola2	Alignment	not modelled	37.4	12	Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain
57	c5tdyD_	Alignment	not modelled	36.6	6	PDB header: motor protein Chain: D: PDB Molecule: flagellar motor switch protein flig; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
58	c6deeA_	Alignment	not modelled	36.4	24	PDB header: endocytosis Chain: A: PDB Molecule: nck-interacting protein with sh3 domain; PDBTitle: crystal structure of the c-terminus of homo sapiens spin90 (sh3-2 protein interacting with nck), residues 306-722
59	c2krcA_	Alignment	not modelled	36.4	10	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit delta; PDBTitle: solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
60	c4eqqA_	Alignment	not modelled	35.8	32	PDB header: protein binding Chain: A: PDB Molecule: putative host cell surface-exposed lipoprotein; PDBTitle: structure of ltp, a superinfection exclusion protein from the2 streptococcus thermophilus temperate phage tp-j34
61	c1tr8A_	Alignment	not modelled	35.6	21	PDB header: chaperone Chain: A: PDB Molecule: conserved protein (mth177); PDBTitle: crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
62	c1brwB_	Alignment	not modelled	34.3	13	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
63	d1xb2b1	Alignment	not modelled	34.2	24	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
64	d1aisb2	Alignment	not modelled	33.2	18	Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain
65	c5i01B_	Alignment	not modelled	33.1	7	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
66	d2o4ta1	Alignment	not modelled	32.6	10	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
67	d2cp9a1	Alignment	not modelled	32.5	24	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
68	c2dsjA_	Alignment	not modelled	32.1	17	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
69	d1r2za1	Alignment	not modelled	30.9	28	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
70	c1vquB_	Alignment	not modelled	30.1	17	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase 2; PDBTitle: crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
71	d1v8ga1	Alignment	not modelled	29.8	4	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
72	c3mzyA_	Alignment	not modelled	29.8	3	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
73	d1g8ia_	Alignment	not modelled	29.3	17	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
74	d2elca1	Alignment	not modelled	29.1	4	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
75	c2v79B_	Alignment	not modelled	29.0	8	PDB header: dna binding protein Chain: B: PDB Molecule: dna replication protein dnad; PDBTitle: crystal structure of the n-terminal domain of dnad from bacillus2 subtilis
76	c4kt3B_	Alignment	not modelled	29.0	14	PDB header: hydrolase Chain: B: PDB Molecule: putative lipoprotein; PDBTitle: structure of a type vi secretion system effector-immunity complex from2 pseudomonas protegens
						Fold: SIS domain

77	d1m3sa_	Alignment	not modelled	28.7	16	Superfamily: SIS domain Family: mono-SIS domain
78	d1hh2p4	Alignment	not modelled	28.7	22	Fold: Transcription factor NusA, N-terminal domain Superfamily: Transcription factor NusA, N-terminal domain Family: Transcription factor NusA, N-terminal domain
79	c2mt4A_	Alignment	not modelled	28.6	16	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: solution structure of the n-terminal domain of nusa from b. subtilis
80	c1ywwA_	Alignment	not modelled	28.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa4738; PDBTitle: nmr structure of p. aeruginosa protein pa4738: northeast2 structural genomics consortium target pap2
81	c2rv8A_	Alignment	not modelled	28.0	22	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: solution structure of the phop dna-binding domain from mycobacterium2 tuberculosis
82	d1vr3a1	Alignment	not modelled	27.8	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Acireductone dioxygenase
83	c5zqtA_	Alignment	not modelled	27.8	14	PDB header: transferase Chain: A: PDB Molecule: hexokinase-6; PDBTitle: crystal structure of oryza sativa hexokinase 6
84	c5iw7D_	Alignment	not modelled	27.7	26	PDB header: translation Chain: D: PDB Molecule: ribosome biogenesis protein tsr1,ribosome biogenesis PDBTitle: crystal structure of yeast tsr1, a pre-40s ribosome synthesis factor
85	c5iw7A_	Alignment	not modelled	27.5	26	PDB header: translation Chain: A: PDB Molecule: ribosome biogenesis protein tsr1,ribosome biogenesis PDBTitle: crystal structure of yeast tsr1, a pre-40s ribosome synthesis factor
86	c5nofB_	Alignment	not modelled	27.1	8	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyltransferase from thermococcus kodakaraensis
87	c1khdD_	Alignment	not modelled	26.8	7	PDB header: transferase Chain: D: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.9 resolution3 (current name, pectobacterium carotovorum)
88	c5wwnA_	Alignment	not modelled	26.7	26	PDB header: rna binding protein Chain: A: PDB Molecule: ribosome biogenesis protein tsr1; PDBTitle: crystal structure of tsr1
89	c2w7nA_	Alignment	not modelled	26.6	18	PDB header: transcription/dna Chain: A: PDB Molecule: trfb transcriptional repressor protein; PDBTitle: crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
90	c5nclA_	Alignment	not modelled	26.4	13	PDB header: signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase cbk1; PDBTitle: crystal structure of the cbk1-mob2 kinase-coactivator complex with an2 ssd1 peptide
91	c4qg5D_	Alignment	not modelled	26.4	16	PDB header: isomerase Chain: D: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
92	d1bjfa_	Alignment	not modelled	26.0	8	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
93	c6g51u_	Alignment	not modelled	25.7	21	PDB header: ribosome Chain: U: PDB Molecule: 40s ribosomal protein s20; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state d
94	c3wy0A_	Alignment	not modelled	25.7	11	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein csyb; PDBTitle: the i375w mutant of csyb complexed with coa-sh
95	d1dula_	Alignment	not modelled	25.3	10	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
96	c1v8gB_	Alignment	not modelled	25.2	4	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
97	c2vn2B_	Alignment	not modelled	24.9	8	PDB header: replication Chain: B: PDB Molecule: chromosome replication initiation protein; PDBTitle: crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
98	d1nvpd1	Alignment	not modelled	24.7	17	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
99	c2bpgB_	Alignment	not modelled	24.7	22	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
100	d1z6ra1	Alignment	not modelled	24.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
101	c6h9mA_	Alignment	not modelled	24.4	22	PDB header: membrane protein Chain: A: PDB Molecule: coiled-coil domain-containing protein 90b, mitochondrial, PDBTitle: coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor
102	c3w6kC_	Alignment	not modelled	24.2	10	PDB header: cell cycle Chain: C: PDB Molecule: scpb;

102	c3w6kC_	Alignment	not modelled	24.2	19	PDBTitle: crystal structure of dimer of scpb n-terminal domain complexed with2 scpa peptide
103	d1efub3	Alignment	not modelled	23.8	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
104	c3thgA_	Alignment	not modelled	21.3	11	PDB header: protein binding Chain: A: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: crystal structure of the creosote rubisco activase c-domain
105	c5dukA_	Alignment	not modelled	21.1	12	PDB header: transcription Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
106	d1ctfa_	Alignment	not modelled	20.8	28	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
107	d1smf2	Alignment	not modelled	20.3	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
108	c2zjq5_	Alignment	not modelled	20.3	19	PDB header: ribosome Chain: 5: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: interaction of l7 with l11 induced by micrococin binding to the2 deinococcus radiodurans 50s subunit
109	d2zjq51	Alignment	not modelled	20.3	19	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
110	c2e5nA_	Alignment	not modelled	20.1	18	PDB header: transcription Chain: A: PDB Molecule: rna polymerase ii elongation factor ell2; PDBTitle: solution structure of the ell_n2 domain of target of rna2 polymerase ii elongation factor ell2
111	c6iu8C_	Alignment	not modelled	20.1	19	PDB header: metal transport Chain: C: PDB Molecule: vit1; PDBTitle: crystal structure of cytoplasmic metal binding domain with cobalt ions