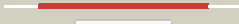



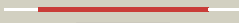




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0485 (-)_573987_575303
Date	Fri Jul 26 01:50:02 BST 2019
Unique Job ID	fc76f42c9fca8253

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z05A_	 Alignment		100.0	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
2	c1z6rC_	 Alignment		100.0	21	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
3	c4ijaA_	 Alignment		100.0	18	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecR2
4	c2hoeA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: n-acetylglucosamine kinase; PDBTitle: crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
5	c5f7pA_	 Alignment		100.0	20	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes
6	c3mcpA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
7	c5f7rA_	 Alignment		100.0	19	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
8	c2ap1A_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
9	c4htIA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
10	c3vgkB_	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
11	c3r8eA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: hypothetical sugar kinase; PDBTitle: crystal structure of a putative sugar kinase (chu_1875) from cytophaga2 hutchinsonii atcc 33406 at 1.65 a resolution

12	c2qm1D_	Alignment		100.0	22	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
13	c4db3A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-d-glucosamine kinase; PDBTitle: 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
14	c5nckA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
15	c1xc3A_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
16	c3vovC_	Alignment		100.0	25	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
17	c2aa4B_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: putative n-acetylmannosamine kinase; PDBTitle: crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
18	c3htvA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: d-allose kinase; PDBTitle: crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
19	c6ediA_	Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of leishmania braziliensis glucokinase
20	c2gupA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: rok family protein; PDBTitle: structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
21	c3eo3B_	Alignment	not modelled	100.0	20	PDB header: isomerase, transferase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
22	d1sz2a1	Alignment	not modelled	100.0	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
23	c3vpzA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
24	c1woqB_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B: PDB Molecule: inorganic polyphosphate/atp-glucomannokinase; PDBTitle: crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
25	c6da0A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from naegleria fowleri
26	c2ch5D_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
27	c2q2rA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
						PDB header: transferase

28	c3lm2B_	Alignment	not modelled	100.0	24	Chain: B: PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
29	c2e2pA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfobolus tokodaii hexokinase in2 complex with adp
30	d1z6ra3	Alignment	not modelled	100.0	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
31	d1z05a2	Alignment	not modelled	100.0	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
32	d2aa4a2	Alignment	not modelled	100.0	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
33	c1zc6A_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable n-acetylglucosamine kinase; PDBTitle: crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
34	d2ap1a1	Alignment	not modelled	100.0	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
35	d2h0ea2	Alignment	not modelled	100.0	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
36	d2gupa2	Alignment	not modelled	100.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
37	d1xc3a2	Alignment	not modelled	99.9	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
38	d1q18a2	Alignment	not modelled	99.9	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
39	d2h0ea3	Alignment	not modelled	99.9	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
40	d1z05a3	Alignment	not modelled	99.9	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
41	d1z6ra2	Alignment	not modelled	99.9	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
42	d2ap1a2	Alignment	not modelled	99.9	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
43	d1woqa2	Alignment	not modelled	99.9	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
44	d1woqa1	Alignment	not modelled	99.8	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
45	d2aa4a1	Alignment	not modelled	99.8	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
46	d1xc3a1	Alignment	not modelled	99.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
47	d2ews1	Alignment	not modelled	99.7	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
48	d2gupa1	Alignment	not modelled	99.7	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
49	d2ch5a1	Alignment	not modelled	99.7	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
50	d1huxa_	Alignment	not modelled	99.7	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
51	c3hm8D_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: D: PDB Molecule: hexokinase-3; PDBTitle: crystal structure of the c-terminal hexokinase domain of human hk3
52	c5zqtA_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A: PDB Molecule: hexokinase-6; PDBTitle: crystal structure of oryza sativa hexokinase 6
53	c1v4sA_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase isoform 2; PDBTitle: crystal structure of human glucokinase
54	d1z05a1	Alignment	not modelled	99.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
55	c1ig8A_	Alignment	not modelled	99.5	17	PDB header: transferase Chain: A: PDB Molecule: hexokinase pii;

55	c1qgA	Alignment	not modelled	99.5	17	PDBTitle: crystal structure of yeast hexokinase pii with the correct2 amino acid sequence PDB header: hexokinase
56	c1bdgA	Alignment	not modelled	99.5	15	Chain: A: PDB Molecule: hexokinase; PDBTitle: hexokinase from schistosoma mansoni complexed with glucose
57	c5hg1A	Alignment	not modelled	99.5	14	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hexokinase-2; PDBTitle: crystal structure of human hexokinase 2 with compd 1, a c-2-substituted2 glucosamine
58	c4ehtA	Alignment	not modelled	99.5	12	PDB header: electron transport Chain: A: PDB Molecule: activator of 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
59	d1q18a1	Alignment	not modelled	99.5	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
60	c1zbsA	Alignment	not modelled	99.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg1100; PDBTitle: crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
61	c1qhaA	Alignment	not modelled	99.5	13	PDB header: transferase Chain: A: PDB Molecule: protein (hexokinase); PDBTitle: human hexokinase type i complexed with atp analogue amp-pnp
62	c4qs9A	Alignment	not modelled	99.4	15	PDB header: transferase Chain: A: PDB Molecule: hexokinase-1; PDBTitle: arabidopsis hexokinase 1 (athxk1) mutant s177a structure in glucose-2 bound form
63	d1z6ra1	Alignment	not modelled	99.4	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
64	d1z6a1	Alignment	not modelled	99.3	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
65	c1zxoB	Alignment	not modelled	99.3	11	PDB header: unknown function Chain: B: PDB Molecule: conserved hypothetical protein q8a1p1; PDBTitle: x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
66	d2ch5a2	Alignment	not modelled	99.1	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
67	c3p4iA	Alignment	not modelled	99.0	14	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
68	c4ijnB	Alignment	not modelled	98.9	15	PDB header: transferase Chain: B: PDB Molecule: acetate kinase; PDBTitle: crystal structure of an acetate kinase from mycobacterium smegmatis2 bound to amp and sulfate
69	c6ioyD	Alignment	not modelled	98.8	12	PDB header: transferase Chain: D: PDB Molecule: acetate kinase; PDBTitle: crystal structure of porphyromonas gingivalis acetate kinase
70	c1sazA	Alignment	not modelled	98.7	15	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
71	d1saza2	Alignment	not modelled	98.6	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
72	c4e1jA	Alignment	not modelled	98.6	12	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
73	c1x3nA	Alignment	not modelled	98.6	11	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
74	c2iirJ	Alignment	not modelled	98.6	10	PDB header: transferase Chain: J: PDB Molecule: acetate kinase; PDBTitle: acetate kinase from a hypothermophile thermotoga maritima
75	c1tuuA	Alignment	not modelled	98.6	13	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: acetate kinase crystallized with atpgs
76	d2p3ra1	Alignment	not modelled	98.6	10	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
77	c3g25B	Alignment	not modelled	98.5	15	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
78	c1glbG	Alignment	not modelled	98.5	12	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase
79	c3khyA	Alignment	not modelled	98.5	10	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of a propionate kinase from francisella tularensis2 subsp. tularensis schu s4
80	c3ezwD	Alignment	not modelled	98.5	12	PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol

						kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
81	c2d4wA	Alignment	not modelled	98.5	16	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
82	c2dpnB	Alignment	not modelled	98.5	18	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
83	c3flcX	Alignment	not modelled	98.4	17	PDB header: transferase Chain: X: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
84	d2p4wa1	Alignment	not modelled	98.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like
85	c3h1qB	Alignment	not modelled	98.3	15	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrmus hydrogenoformans
86	d1zc6a2	Alignment	not modelled	98.3	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
87	c3hz6A	Alignment	not modelled	98.3	14	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
88	c2zf5O	Alignment	not modelled	98.3	14	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
89	c6cmvA	Alignment	not modelled	98.3	21	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator Irs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from2 sulfobolus acidocaldarius
90	c3gg4B	Alignment	not modelled	98.3	9	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
91	d1g99a2	Alignment	not modelled	98.3	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
92	c3wxiB	Alignment	not modelled	98.3	16	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
93	c5ya2A	Alignment	not modelled	98.3	10	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
94	c1hkgA	Alignment	not modelled	98.2	10	PDB header: transferase Chain: A: PDB Molecule: hexokinase a; PDBTitle: structural dynamics of yeast hexokinase during catalysis
95	c5htxA	Alignment	not modelled	98.2	16	PDB header: transferase Chain: A: PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp
96	c3ifrB	Alignment	not modelled	98.2	17	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
97	d1v4sa1	Alignment	not modelled	98.2	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
98	d2e1za2	Alignment	not modelled	98.2	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
99	c2nlxA	Alignment	not modelled	98.1	13	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
100	c5hv7A	Alignment	not modelled	98.1	23	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
101	c2w40C	Alignment	not modelled	98.1	13	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
102	c3gbtA	Alignment	not modelled	98.1	12	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
103	d1ub9a	Alignment	not modelled	98.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
104	c3slcA	Alignment	not modelled	98.1	11	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of apo form of acetate kinase (acka) from salmonella2 typhimurium
105	d1ulya	Alignment	not modelled	98.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932
106	d1bdga1	Alignment	not modelled	98.1	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase

107	c1xupO_	Alignment	not modelled	98.0	17	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
108	c5vm1A_	Alignment	not modelled	98.0	13	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylolyose kinase from brucella ovis
109	d1czan3	Alignment	not modelled	98.0	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
110	d1ig8a1	Alignment	not modelled	97.9	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
111	c4h0oB_	Alignment	not modelled	97.9	8	PDB header: transferase Chain: B: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from entamoeba histolytica
112	c3jvpA_	Alignment	not modelled	97.9	21	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
113	d2etha1	Alignment	not modelled	97.8	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
114	d1bg3a3	Alignment	not modelled	97.8	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
115	d2fbha1	Alignment	not modelled	97.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
116	d1lnwa_	Alignment	not modelled	97.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
117	c3bj6B_	Alignment	not modelled	97.8	10	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579
118	c3lmmB_	Alignment	not modelled	97.8	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the dip2311 protein from corynebacterium2 diphtheriae, northeast structural genomics consortium target cdr35
119	c2nyxB_	Alignment	not modelled	97.8	15	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
120	d1jgsa_	Alignment	not modelled	97.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators