

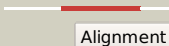

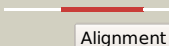







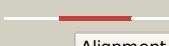












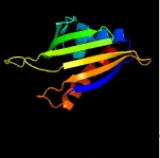
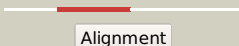


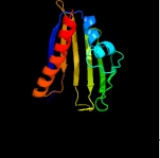

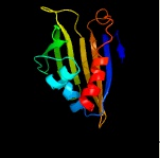


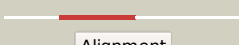




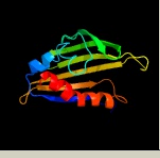

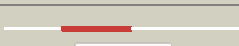
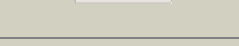






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0576 (-) _669851_671155
Date	Fri Jul 26 01:50:13 BST 2019
Unique Job ID	11f6118942e00dc2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lakA_	 Alignment		100.0	35	PDB header: structure genomics, unknown function Chain: A; PDB Molecule: ahsa1-like protein rhe_ch02687; PDBTitle: solution nmr structure of the ahsa1-like protein rhe_ch02687 (1-152)2 from rhizobium etli, northeast structural genomics consortium target3 rer242
2	c2nn5A_	 Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein ef_2215; PDBTitle: structure of conserved protein of unknown function ef2215 from2 enterococcus faecalis
3	c2luzA_	 Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: calu16; PDBTitle: solution nmr structure of calu16 from micromonospora echinospora,2 northeast structural genomics consortium (nesg) target mir12
4	d2nn5a1	 Alignment		100.0	19	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
5	d2k5ga1	 Alignment		100.0	20	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
6	d2il5a1	 Alignment		99.9	17	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
7	d1x53a1	 Alignment		99.9	20	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
8	c3q63F_	 Alignment		99.9	22	PDB header: structural genomics, unknown function Chain: F; PDB Molecule: mll2253 protein; PDBTitle: x-ray crystal structure of protein mll2253 from mesorhizobium loti,2 northeast structural genomics consortium target mlr404.
9	c2l8oA_	 Alignment		99.9	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of chr148 from cytophaga hutchinsonii, northeast2 structural genomics consortium target chr148
10	c2kewA_	 Alignment		99.9	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein yndb; PDBTitle: the solution structure of bacillus subtilis sr211 start domain by nmr2 spectroscopy
11	d3elia1	 Alignment		99.9	25	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain

12	c2m89A_	 Alignment		99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
13	c2lghA_	 Alignment		99.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein aha_2358 from aeromonas hydrophila refined with nh rdcs, northeast structural genomics consortium target ahr99.
14	c5z4eA_	 Alignment		99.9	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: txn09; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
15	c2leqA_	 Alignment		99.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: chemical shift assignment and solution structure of chr145 from cytophaga hutchinsonii, northeast structural genomics consortium3 target chr145
16	c2ldkA_	 Alignment		99.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein aaur_3427 from arthrobacter2 aureus, northeast structural genomics consortium target aar96
17	d1xfsa_	 Alignment		99.9	20	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
18	c2lcgA_	 Alignment		99.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115
19	c3otlA_	 Alignment		99.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: three-dimensional structure of the putative uncharacterized protein2 from rhizobium leguminosarum at the resolution 1.9a, northeast3 structural genomics consortium target rlr261
20	d1xn5a_	 Alignment		99.9	25	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
21	c3q6aH_	 Alignment	not modelled	99.9	17	PDB header: structure genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of the protein ssp2350 from staphylococcus2 saprophyticus, northeast structural genomics consortium target syr116
22	c3q64A_	 Alignment	not modelled	99.9	24	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: mll3774 protein; PDBTitle: x-ray crystal structure of protein mll3774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405.
23	c2lf2A_	 Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein chu_1110 from cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152
24	d1zxfa_1	 Alignment	not modelled	99.9	21	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
25	c3rd6A_	 Alignment	not modelled	99.9	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mll3558 protein; PDBTitle: crystal structure of mll3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403
26	c3ni8A_	 Alignment	not modelled	99.9	21	PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
27	c2l9pA_	 Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of q5hli9 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147

28	d1xn6a_	Alignment	not modelled	99.9	19	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
29	d1xuva_	Alignment	not modelled	99.9	16	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
30	d1z94a1	Alignment	not modelled	99.9	26	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
31	c3pu2G_	Alignment	not modelled	99.9	24	PDB header: structure genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics consortium target rhr263.
32	c3uidA_	Alignment	not modelled	99.9	19	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis
33	c3f6vA_	Alignment	not modelled	99.8	71	PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: crystal structure of possible transcriptional regulator for arsenical2 resistance
34	c2oqgA_	Alignment	not modelled	99.8	28	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
35	c2nsfA_	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein cgl3021; PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase
36	d2nsfa1	Alignment	not modelled	99.8	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: Maleylpyruvate isomerase-like
37	c3f6oB_	Alignment	not modelled	99.8	29	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
38	c3jthA_	Alignment	not modelled	99.7	34	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
39	c2kkoB_	Alignment	not modelled	99.7	35	PDB header: dna binding protein Chain: B: PDB Molecule: possible transcriptional regulatory protein PDBTitle: solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
40	c4omzG_	Alignment	not modelled	99.7	29	PDB header: transcription Chain: G: PDB Molecule: nlr; PDBTitle: crystal structure of nlr from sinorhizobium fredii
41	c1r22B_	Alignment	not modelled	99.7	38	PDB header: transcription repressor Chain: B: PDB Molecule: transcriptional repressor smtb; PDBTitle: crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
42	d1r1ta_	Alignment	not modelled	99.7	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
43	c3pqqD_	Alignment	not modelled	99.7	29	PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
44	c2lqpB_	Alignment	not modelled	99.7	33	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr
45	c6j0eB_	Alignment	not modelled	99.7	29	PDB header: transcription Chain: B: PDB Molecule: arsenic responsive repressor arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
46	c6j05B_	Alignment	not modelled	99.7	34	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
47	c2jscB_	Alignment	not modelled	99.7	36	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator rv1994c/mt2050; PDBTitle: nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
48	c2zkzC_	Alignment	not modelled	99.7	27	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
49	d1r1ua_	Alignment	not modelled	99.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
50	c3cuoB_	Alignment	not modelled	99.7	21	PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator ygav; PDBTitle: crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
51	c5xpgB_	Alignment	not modelled	99.7	33	PDB header: transcription Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator rv0081; PDBTitle: crystal structure of m.tuberculosis rv0081
						Fold: DNA/RNA-binding 3-helical bundle

52	d1u2wa1	Alignment	not modelled	99.5	25	Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
53	d2p4wa1	Alignment	not modelled	99.5	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like
54	d1ulya_	Alignment	not modelled	99.5	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932
55	d2b79a1	Alignment	not modelled	99.5	12	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like
56	c2m47A_	Alignment	not modelled	99.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein cgl2373; PDBTitle: solution nmr structure of the polyketide_cyc-like protein cgl2372 from2 corynebacterium glutamicum, northeast structural genomics consortium3 target cgr160
57	c4g6gA_	Alignment	not modelled	99.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein kfla_6221 from2 kribbella flavida dsm 17836
58	c5woxA_	Alignment	not modelled	99.3	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
59	c2qufB_	Alignment	not modelled	99.3	21	PDB header: transcription Chain: B: PDB Molecule: transcription factor pf0095; PDBTitle: crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
60	d2ns9a1	Alignment	not modelled	99.2	17	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
61	d2d1ha1	Alignment	not modelled	99.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
62	c5dukA_	Alignment	not modelled	99.1	25	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
63	c4xrwA_	Alignment	not modelled	99.1	17	PDB header: lyase Chain: A: PDB Molecule: bexl; PDBTitle: crystal structure of the di-domain aro/cyc bexl from the be-7585a2 biosynthetic pathway
64	d1ub9a_	Alignment	not modelled	99.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
65	d3cnwa1	Alignment	not modelled	99.0	16	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
66	d2rera1	Alignment	not modelled	99.0	16	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
67	d2pcsa1	Alignment	not modelled	99.0	19	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
68	c2kf2A_	Alignment	not modelled	98.9	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: solution nmr structure of of streptomyces coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365
69	d2d4ra1	Alignment	not modelled	98.9	18	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
70	c2kcZA_	Alignment	not modelled	98.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein dr_a0006; PDBTitle: solution nmr structure of the c-terminal domain of protein2 dr_a0006 from deinococcus radiodurans. northeast3 structural genomics consortium target drr147d
71	c4r7kA_	Alignment	not modelled	98.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein jhp0584; PDBTitle: 1.88 angstrom resolution crystal structure of hypothetical protein2 jhp0584 from helicobacter pylori.
72	c2le1A_	Alignment	not modelled	98.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of tfu_2981 from thermobifida fusca, northeast2 structural genomics consortium target tfr85a
73	c4xrtB_	Alignment	not modelled	98.7	16	PDB header: lyase Chain: B: PDB Molecule: stfq aromatase/cyclase; PDBTitle: crystal structure of the di-domain aro/cyc stfq from the steffimycin2 biosynthetic pathway
74	c3p9vA_	Alignment	not modelled	98.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: high resolution crystal structure of protein maqu_3174 from2 marinobacter aquaeolei, northeast structural genomics consortium3 target mqr197
75	c3tfzB_	Alignment	not modelled	98.6	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128
76	c3p51A_	Alignment	not modelled	98.6	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: three-dimensional structure of protein q2y8n9_nitmu from nitrosospira2 multiformis, northeast structural genomics consortium target nmr118
77	c2lioA_	Alignment	not modelled	98.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of bfr322 from bacteroides fragilis,

						northeast2 structural genomics consortium target bfr322
78	d1t17a	Alignment	not modelled	98.5	14	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
79	c4n0gC	Alignment	not modelled	98.4	11	PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex
80	c3ctaA	Alignment	not modelled	98.3	18	PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma acidophilum
81	c5z8oA	Alignment	not modelled	98.3	11	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis
82	c5vglA	Alignment	not modelled	98.3	10	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
83	c3r0aB	Alignment	not modelled	98.3	14	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazeri go1 (gi2 21227196)
84	d2qpva1	Alignment	not modelled	98.2	17	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
85	d3ctaa1	Alignment	not modelled	98.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
86	c6cmvA	Alignment	not modelled	98.1	25	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator Irs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from2 sulfolobus acidocaldarius
87	c4nb5D	Alignment	not modelled	98.1	18	PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator
88	d2etha1	Alignment	not modelled	97.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
89	c2nyxB	Alignment	not modelled	97.9	24	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
90	c2gxgA	Alignment	not modelled	97.8	26	PDB header: transcription Chain: A: PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
91	c2rdpA	Alignment	not modelled	97.8	23	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus
92	d2a61a1	Alignment	not modelled	97.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
93	d1lnwa	Alignment	not modelled	97.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
94	c3f3xA	Alignment	not modelled	97.8	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr from2 sulfolobus solfataricus
95	c5e4bB	Alignment	not modelled	97.8	14	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
96	c3zmdD	Alignment	not modelled	97.8	18	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor
97	d1y0ua	Alignment	not modelled	97.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
98	c5jlsA	Alignment	not modelled	97.7	19	PDB header: transcription Chain: A: PDB Molecule: adhesin competence repressor; PDBTitle: crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
99	c4fhtA	Alignment	not modelled	97.7	24	PDB header: transcription Chain: A: PDB Molecule: pcav transcriptional regulator; PDBTitle: crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand
100	c3oh8A	Alignment	not modelled	97.7	15	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
101	d2fbia1	Alignment	not modelled	97.7	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
102	c3cjinA	Alignment	not modelled	97.7	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi

103	c5jbrA_	Alignment	not modelled	97.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bcav_2135; PDBTitle: crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
104	c3k0IA_	Alignment	not modelled	97.7	15	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
105	c4xrfA_	Alignment	not modelled	97.7	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of mepr like protein complexed with pseudoligands
106	c3bpxB_	Alignment	not modelled	97.7	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr
107	c3qtjA_	Alignment	not modelled	97.7	14	PDB header: hormone receptor Chain: A: PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal strcuture of aba receptor pyl10 (apo)
108	d1lj9a_	Alignment	not modelled	97.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
109	c5yhxB_	Alignment	not modelled	97.6	22	PDB header: metal binding protein Chain: H: PDB Molecule: zinc transport transcriptional regulator; PDBTitle: structure of lactococcus lactis zitri, wild type
110	c3nrxC_	Alignment	not modelled	97.6	16	PDB header: transcription regulator Chain: C: PDB Molecule: putative transcriptional regulator (marr/emrr family); PDBTitle: crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
111	d1mkma1	Alignment	not modelled	97.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
112	c2nnnB_	Alignment	not modelled	97.6	24	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
113	c3e6mD_	Alignment	not modelled	97.6	30	PDB header: transcription regulator Chain: D: PDB Molecule: marr family transcriptional regulator; PDBTitle: the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
114	c3zplE_	Alignment	not modelled	97.6	26	PDB header: transcription/dna Chain: E: PDB Molecule: putative marr-family transcriptional repressor; PDBTitle: crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
115	d1sfxa_	Alignment	not modelled	97.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
116	c4esfA_	Alignment	not modelled	97.5	21	PDB header: transcription Chain: A: PDB Molecule: padr-like transcriptional regulator; PDBTitle: crystal structure of padr-like transcriptional regulator (bce3449)2 from bacillus cereus strain atcc 10987
117	c3k90C_	Alignment	not modelled	97.5	15	PDB header: hormone receptor, hydrolase regulator Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: the abscisic acid receptor pyr1 in complex with abscisic acid
118	d2bv6a1	Alignment	not modelled	97.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
119	c4mnuA_	Alignment	not modelled	97.5	13	PDB header: transcription regulator Chain: A: PDB Molecule: slya-like transcription regulator; PDBTitle: crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes
120	c3g3zA_	Alignment	not modelled	97.5	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis