

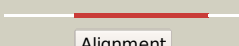



















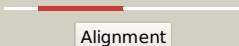







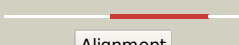




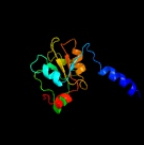




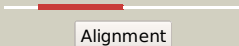

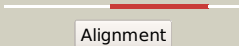



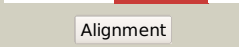



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0324 (-) _391352_392032
Date	Tue Jul 23 14:50:39 BST 2019
Unique Job ID	92fc887c59554a24

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kkoB_	 Alignment		99.9	100	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.
2	c3tp9B_	 Alignment		99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase and rhodanese domain protein; PDBTitle: crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
3	d1yt8a1	 Alignment		99.9	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
4	c1yt8A_	 Alignment		99.9	26	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
5	d1yt8a3	 Alignment		99.9	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
6	c3nhvE_	 Alignment		99.9	29	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: bh2092 protein; PDBTitle: crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
7	c5ve5C_	 Alignment		99.9	41	PDB header: oxidoreductase, transferase Chain: C: PDB Molecule: bpprf; PDBTitle: crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytofirmans in complex with glutathione
8	c2hhgA_	 Alignment		99.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa3614; PDBTitle: structure of protein of unknown function rpa3614, possible tyrosine2 phosphatase, from rhodopseudomonas palustris cga009
9	c3ilmD_	 Alignment		99.9	32	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr3790 protein; PDBTitle: crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
10	c3emeA_	 Alignment		99.9	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rhodanese-like domain protein; PDBTitle: crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
11	c3gk5A_	 Alignment		99.9	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized rhodanese-related protein tvg0868615; PDBTitle: crystal structure of rhodanese-related protein (tvg0868615) from2 thermoplasma volcanium, northeast structural genomics consortium3 target tvr109a

12	dlr1ua_	 Alignment		99.9	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
13	dle0ca1	 Alignment		99.9	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
14	c1r22B_	 Alignment		99.8	27	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
15	c2lkpB_	 Alignment		99.8	28	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr
16	dlyt8a4	 Alignment		99.8	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
17	c4omzG_	 Alignment		99.8	30	PDB header: transcription Chain: G: PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii
18	dlqxna_	 Alignment		99.8	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
19	c1e0cA_	 Alignment		99.8	26	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
20	dlgmxa_	 Alignment		99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
21	dlr1ta_	 Alignment	not modelled	99.8	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
22	c2oqgA_	 Alignment	not modelled	99.8	26	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
23	c2moiA_	 Alignment	not modelled	99.8	25	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the cytoplasmic rhodanese domain of the inner2 membrane protein ygap from escherichia coli
24	c3aaxB_	 Alignment	not modelled	99.8	24	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
25	c6mxvA_	 Alignment	not modelled	99.8	18	PDB header: unknown function Chain: A: PDB Molecule: rhodanese-like family protein; PDBTitle: the crystal structure of a rhodanese-like family protein from2 francisella tularensis subsp. tularensis schu s4
26	c3hzuA_	 Alignment	not modelled	99.8	24	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
27	c3fojA_	 Alignment	not modelled	99.8	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
		 Alignment				PDB header: transferase

28	c1uarA_	Alignment	not modelled	99.8	26	Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermophilus hb8
29	c3k9rA_	Alignment	not modelled	99.8	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: alr3790 protein; PDBTitle: x-ray structure of the rhodanese-like domain of the alr3790 protein2 from anaebaena sp. northeast structural genomics consortium target3 nsr437c.
30	c3pqkD_	Alignment	not modelled	99.8	26	PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
31	c1urhA_	Alignment	not modelled	99.8	32	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: the "rhodanese" fold and catalytic mechanism of 2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli
32	d1t3ka_	Alignment	not modelled	99.8	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
33	d1tq1a_	Alignment	not modelled	99.8	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
34	d1yt8a2_	Alignment	not modelled	99.8	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
35	c3jthA_	Alignment	not modelled	99.8	30	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
36	c6bevB_	Alignment	not modelled	99.8	31	PDB header: transferase Chain: B: PDB Molecule: thiosulfate sulfurtransferase/rhodanese-like domain- PDBTitle: human single domain sulfurtransferase tstd1
37	c2fsxA_	Alignment	not modelled	99.8	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
38	c2k0zA_	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein hp1203; PDBTitle: solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
39	c1boiA_	Alignment	not modelled	99.8	27	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
40	c2zkzC_	Alignment	not modelled	99.8	25	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
41	d1rha1_	Alignment	not modelled	99.8	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
42	c3d1pA_	Alignment	not modelled	99.8	24	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
43	c5xpqB_	Alignment	not modelled	99.8	35	PDB header: transcription Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator rv0081; PDBTitle: crystal structure of m.tuberculosis rv0081
44	d1okga1_	Alignment	not modelled	99.8	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
45	c3f6vA_	Alignment	not modelled	99.8	27	PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: crystal structure of possible transcriptional regulator for arsenical2 resistance
46	d1urha1_	Alignment	not modelled	99.8	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
47	c3i2vA_	Alignment	not modelled	99.8	26	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
48	c3olhA_	Alignment	not modelled	99.8	24	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
49	d1uara1_	Alignment	not modelled	99.8	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
50	c6h98A_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.
51	c3cuoB_	Alignment	not modelled	99.8	26	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
52	d1uara2_	Alignment	not modelled	99.8	33	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)

53	c6j05B_	Alignment	not modelled	99.8	35	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
54	c3icrA_	Alignment	not modelled	99.8	35	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
55	c3ippA_	Alignment	not modelled	99.8	28	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynjc; PDBTitle: crystal structure of sulfur-free ynjc
56	c6j0eB_	Alignment	not modelled	99.8	27	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
57	c2jscB_	Alignment	not modelled	99.8	30	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator rv1994c/mt2050; PDBTitle: nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
58	c3f6oB_	Alignment	not modelled	99.8	20	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
59	d1u2wa1	Alignment	not modelled	99.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
60	c3utnX_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: X: PDB Molecule: thiosulfate sulfurtransferase tum1; PDBTitle: crystal structure of tum1 protein from saccharomyces cerevisiae
61	c4f67A_	Alignment	not modelled	99.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0176 protein lpg2838; PDBTitle: three dimensional structure of the double mutant of upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nsg) target lgr82
62	d1e0ca2	Alignment	not modelled	99.7	31	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
63	c1okgA_	Alignment	not modelled	99.7	19	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
64	c3g5jA_	Alignment	not modelled	99.7	26	PDB header: nucleotide binding protein Chain: A: PDB Molecule: putative atp/gtp binding protein; PDBTitle: crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
65	c2dcqA_	Alignment	not modelled	99.7	14	PDB header: unknown function Chain: A: PDB Molecule: putative protein at4g01050; PDBTitle: fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
66	c3ntaA_	Alignment	not modelled	99.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
67	c2jtqA_	Alignment	not modelled	99.7	29	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
68	c3f4aA_	Alignment	not modelled	99.7	25	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
69	d1rha2	Alignment	not modelled	99.7	26	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
70	d1c25a_	Alignment	not modelled	99.7	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
71	d1ymka1	Alignment	not modelled	99.6	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
72	d2p4wa1	Alignment	not modelled	99.6	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like
73	c2eg4B_	Alignment	not modelled	99.6	29	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
74	d1okga2	Alignment	not modelled	99.6	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
75	c2j6pF_	Alignment	not modelled	99.6	23	PDB header: oxidoreductase Chain: F: PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major
76	c2uzqE_	Alignment	not modelled	99.6	25	PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
77	c3op3A_	Alignment	not modelled	99.6	24	PDB header: hydrolase Chain: A: PDB Molecule: m-phase inducer phosphatase 3; PDBTitle: crystal structure of cell division cycle 25c protein isoform a from2 homo sapiens Fold: Rhodanese/Cell cycle control phosphatase

78	d1whba_	Alignment	not modelled	99.5	20	Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
79	d1ulya_	Alignment	not modelled	99.5	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932
80	c2vswB_	Alignment	not modelled	99.5	29	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 16; PDBTitle: the structure of the rhodanese domain of the human dual specificity2 phosphatase 16
81	c1wv9B_	Alignment	not modelled	99.5	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
82	c2oucB_	Alignment	not modelled	99.4	23	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the map kinase binding domain of mkp5
83	d1urha2	Alignment	not modelled	99.4	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
84	d1hzma_	Alignment	not modelled	99.4	29	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
85	c4g6gA_	Alignment	not modelled	99.4	20	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
86	d2gwfa1	Alignment	not modelled	99.4	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
87	c3r2uC_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
88	d2d1ha1	Alignment	not modelled	99.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
89	c2qufB_	Alignment	not modelled	99.3	15	PDB header: transcription Chain: B: PDB Molecule: transcription factor pf0095; PDBTitle: crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
90	d1ub9a_	Alignment	not modelled	99.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
91	c5dukA_	Alignment	not modelled	99.1	16	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
92	c4gcvD_	Alignment	not modelled	98.7	18	PDB header: transcription Chain: D: PDB Molecule: putative transcription protein; PDBTitle: structure of a putative transcription factor (pa1374)from pseudomonas2 aeruginosa
93	c4a5mH_	Alignment	not modelled	98.5	9	PDB header: transcription Chain: H: PDB Molecule: uncharacterized hth-type transcriptional regulator yybr; PDBTitle: redox regulator hypr in its oxidized form
94	d2f2ea1	Alignment	not modelled	98.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
95	c4nb5D_	Alignment	not modelled	98.5	19	PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator
96	c3r0aB_	Alignment	not modelled	98.5	12	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazeri go1 (gi2 21227196)
97	d2fswa1	Alignment	not modelled	98.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
98	d1z7ua1	Alignment	not modelled	98.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
99	c5hs9A_	Alignment	not modelled	98.4	18	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator yodb; PDBTitle: crystal structure of the quinone-bound yodb from b. subtilis
100	c4hqeB_	Alignment	not modelled	98.4	15	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional regulator qsrr; PDBTitle: the crystal structure of qsrr-dna complex
101	c6cmvA_	Alignment	not modelled	98.4	20	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator Irs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from2 sulfolobus acidocaldarius
102	d1y0ua_	Alignment	not modelled	98.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
103	d1sfxa_	Alignment	not modelled	98.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
104	c3df8A_	Alignment	not modelled	98.2	24	PDB header: transcription Chain: A: PDB Molecule: possible hxlr family transcriptional factor; PDBTitle: the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1

105	c3ctaA_	Alignment	not modelled	98.2	14	PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma acidophilum
106	c5jlsA_	Alignment	not modelled	98.2	13	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)
107	d1ku9a_	Alignment	not modelled	98.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding protein Mj223
108	d3ctaa1	Alignment	not modelled	98.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
109	c2gxgA_	Alignment	not modelled	98.2	16	PDB header: transcription Chain: A: PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfobus tokodaii strain7
110	d1yyva1	Alignment	not modelled	98.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
111	c5jbrA_	Alignment	not modelled	98.1	15	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
112	d2etha1	Alignment	not modelled	98.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
113	c3k0IA_	Alignment	not modelled	98.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
114	c2rdpA_	Alignment	not modelled	98.0	17	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus
115	c3zmdD_	Alignment	not modelled	97.9	16	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor
116	c3cjnA_	Alignment	not modelled	97.9	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
117	c4xrfA_	Alignment	not modelled	97.9	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of mepr like protein complexed with pseudoligands
118	c3bpxB_	Alignment	not modelled	97.9	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr
119	d1okra_	Alignment	not modelled	97.9	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
120	d2a61a1	Alignment	not modelled	97.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators