



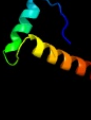






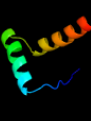









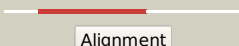

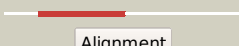

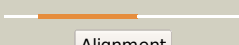

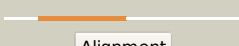


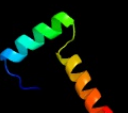

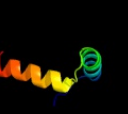

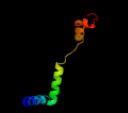
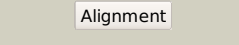
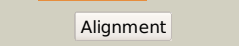
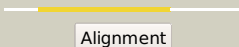
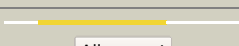
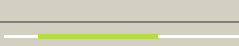
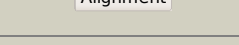




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1991A_(RVBD1991A)_2234651_2234899
Date	Mon Aug 5 13:25:09 BST 2019
Unique Job ID	676102d57e476eca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bj3D_	 Alignment		97.9	18	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
2	c4me7E_	 Alignment		97.9	22	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
3	c2ca9B_	 Alignment		97.8	24	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
4	d2bj7a1	 Alignment		97.5	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
5	c1q5vB_	 Alignment		97.5	19	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
6	c4p7dA_	 Alignment		97.5	13	PDB header: toxin Chain: A: PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
7	c2k5jB_	 Alignment		97.5	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
8	c6g1nB_	 Alignment		97.3	21	PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
9	c1ea4K_	 Alignment		96.8	23	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
10	d2cpga_	 Alignment		96.8	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
11	d2hzaa1	 Alignment		96.7	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like

12	c5yrzC_	 Alignment		96.4	22	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
13	d2hzab1	 Alignment		96.3	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
14	c2k9iB_	 Alignment		95.2	30	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus
15	c2mdvB_	 Alignment		90.9	35	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
16	c2k29A_	 Alignment		89.8	15	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
17	c6qeqD_	 Alignment		89.0	14	PDB header: dna binding protein Chain: D: PDB Molecule: pcf;f; PDBTitle: pcf from enterococcus faecalis pcf10
18	c4fxeB_	 Alignment		88.7	15	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
19	c4q2uM_	 Alignment		85.5	8	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
20	c3h87D_	 Alignment		84.9	19	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
21	c2rbfB_	 Alignment	not modelled	83.9	22	PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
22	c6iyaD_	 Alignment	not modelled	83.2	16	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
23	c3kk4B_	 Alignment	not modelled	78.0	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
24	c6noyB_	 Alignment	not modelled	76.9	10	PDB header: structural protein Chain: B: PDB Molecule: maintenance of carboxysome positioning b protein, mcsb; PDBTitle: structure of cyanothecce mcdb
25	c6a7vU_	 Alignment	not modelled	66.9	19	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
26	c4hv0B_	 Alignment	not modelled	66.7	21	PDB header: transcription, viral protein Chain: B: PDB Molecule: avtr; PDBTitle: structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
27	c2kelB_	 Alignment	not modelled	64.7	13	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
28	c6bwqB_	 Alignment	not modelled	63.9	7	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in

						complex with3 mnctp
29	d2ay0a1	Alignment	not modelled	54.7	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: PutA pre-N-terminal region-like
30	c4l5eA	Alignment	not modelled	53.5	11	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
31	c5x3tA	Alignment	not modelled	51.5	30	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapb26; PDBTitle: vapbc from mycobacterium tuberculosis
32	c1umqA	Alignment	not modelled	51.4	33	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
33	d1umqa	Alignment	not modelled	51.4	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
34	c3clcC	Alignment	not modelled	49.3	17	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c. esp1396i tetramer in complex with its natural 35 base-pair operator
35	c2m8gX	Alignment	not modelled	48.4	28	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
36	c3e7lD	Alignment	not modelled	48.2	33	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
37	c3c19A	Alignment	not modelled	47.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
38	d1ntca	Alignment	not modelled	46.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
39	c3f52A	Alignment	not modelled	45.8	19	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
40	c4d8jD	Alignment	not modelled	44.2	17	PDB header: dna binding protein Chain: D: PDB Molecule: macrodmain ter protein; PDBTitle: structure of e. coli matp-mats complex
41	c6ajnF	Alignment	not modelled	44.2	21	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa
42	d1zk8a1	Alignment	not modelled	42.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
43	c5m7nA	Alignment	not modelled	41.9	44	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystal direct automated mounting and cryo-cooling3 technology
44	d2fq4a1	Alignment	not modelled	41.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
45	c3fmtF	Alignment	not modelled	41.4	24	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
46	c4go1A	Alignment	not modelled	41.0	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
47	c5ytpA	Alignment	not modelled	40.6	18	PDB header: dna binding protein Chain: A: PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 l34a from thermus thermophilus hb8
48	d1etxa	Alignment	not modelled	39.6	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
49	c6gcsH	Alignment	not modelled	39.5	19	PDB header: oxidoreductase Chain: H: PDB Molecule: 24-kda subunit (nuhm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
50	c2g8yB	Alignment	not modelled	39.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
51	c2qsfX	Alignment	not modelled	39.2	23	PDB header: dna binding protein Chain: X: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of the rad4-rad23 complex
52	d1fipa	Alignment	not modelled	38.9	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
53	c6gtsC	Alignment	not modelled	38.8	21	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
54	d1etob	Alignment	not modelled	38.6	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like

						Family: FIS-like
55	d1g2ha_	Alignment	not modelled	38.5	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
56	c1g2hA_	Alignment	not modelled	38.5	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
57	d1bl0a1	Alignment	not modelled	36.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
58	c6hl2C_	Alignment	not modelled	36.3	10	PDB header: electron transport Chain: C: PDB Molecule: nadh-quinone oxidoreductase subunit e; PDBTitle: wild-type nuof from aquifex aeolicus - oxidized form
59	c3r23B_	Alignment	not modelled	36.2	13	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
60	c2k9qB_	Alignment	not modelled	36.2	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
61	d2g3ba1	Alignment	not modelled	35.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
62	c1ojlD_	Alignment	not modelled	35.7	28	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
63	c5lc5E_	Alignment	not modelled	33.2	14	PDB header: oxidoreductase Chain: E: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: structure of mammalian respiratory complex i, class2
64	c2w48D_	Alignment	not modelled	33.0	29	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
65	c5vntA_	Alignment	not modelled	32.9	19	PDB header: protein binding Chain: A: PDB Molecule: villin-4; PDBTitle: solution nmr structure of the c-terminal headpiece domain of villin 42 from a.thaliana, the first non-vertebrate headpiece structure
66	d1d5ya1	Alignment	not modelled	32.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
67	d2b0la1	Alignment	not modelled	32.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cody HTH domain
68	c5woqA_	Alignment	not modelled	32.7	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
69	c5d4zF_	Alignment	not modelled	32.4	12	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
70	d2fug21	Alignment	not modelled	32.4	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
71	c3b7hA_	Alignment	not modelled	32.3	26	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
72	c3w6vA_	Alignment	not modelled	32.3	21	PDB header: transcription activator/dna Chain: A: PDB Molecule: adpa; PDBTitle: crystal structure of the dna-binding domain of adpa, the global2 transcriptional factor, in complex with a target dna
73	d2vkva1	Alignment	not modelled	31.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
74	d1mkma1	Alignment	not modelled	31.4	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
75	d1qzpa_	Alignment	not modelled	31.2	25	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
76	d1y9ba1	Alignment	not modelled	31.0	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
77	d2g7sa1	Alignment	not modelled	30.9	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
78	d1rfma_	Alignment	not modelled	30.8	14	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
79	c3trbA_	Alignment	not modelled	30.7	11	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
						PDB header: transcription Chain: A: PDB Molecule: putative tet-family transcriptional

80	c2guhA	Alignment	not modelled	30.6	18	regulator; PDBTitle: crystal structure of the putative tet-family transcriptional2 regulator from rhodococcus sp. rha1
81	c3mkyP	Alignment	not modelled	30.5	23	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
82	d1jt6a1	Alignment	not modelled	30.3	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
83	d1pb6a1	Alignment	not modelled	30.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
84	c3lw9B	Alignment	not modelled	29.8	5	PDB header: protein transport Chain: B: PDB Molecule: invasion protein inva; PDBTitle: structure of a cytoplasmic domain of salmonella inva
85	d1unda	Alignment	not modelled	29.6	25	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
86	c2l3xA	Alignment	not modelled	29.4	31	PDB header: protein binding Chain: A: PDB Molecule: ablm2 protein; PDBTitle: villin head piece domain of human ablm2
87	d1au7a1	Alignment	not modelled	29.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
88	c5ey0A	Alignment	not modelled	29.1	27	PDB header: transcription Chain: A: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: crystal structure of cody from staphylococcus aureus with gtp and ile
89	d2i10a1	Alignment	not modelled	28.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
90	c1z4hA	Alignment	not modelled	27.9	5	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
91	d2id6a1	Alignment	not modelled	27.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
92	d1gt0c1	Alignment	not modelled	27.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
93	c5lnk2	Alignment	not modelled	27.2	14	PDB header: oxidoreductase Chain: 2: PDB Molecule: mitochondrial complex i, 24 kda subunit; PDBTitle: entire ovine respiratory complex i
94	c2ph0A	Alignment	not modelled	27.2	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia carotovora.2 nesg target ewr41.
95	d1af7a1	Alignment	not modelled	27.0	13	Fold: Chemotaxis receptor methyltransferase CheR, N-terminal domain Superfamily: Chemotaxis receptor methyltransferase CheR, N-terminal domain Family: Chemotaxis receptor methyltransferase CheR, N-terminal domain
96	d1l5aa2	Alignment	not modelled	26.5	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
97	d1t56a1	Alignment	not modelled	26.4	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
98	c2gm4B	Alignment	not modelled	26.3	17	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
99	d1unca	Alignment	not modelled	26.2	19	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
100	d1yu5x1	Alignment	not modelled	25.8	31	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
101	c5hodD	Alignment	not modelled	25.5	18	PDB header: transcription Chain: D: PDB Molecule: lim/homeobox protein lhx4; PDBTitle: structure of lhx4 transcription factor complexed with dna
102	d1z67a1	Alignment	not modelled	25.4	26	Fold: YidB-like Superfamily: YidB-like Family: YidB-like
103	d1yu8x1	Alignment	not modelled	25.4	31	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
104	d1wh5a	Alignment	not modelled	25.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
105	c2axzC	Alignment	not modelled	25.1	19	PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
106	c2qcxA	Alignment	not modelled	25.1	23	PDB header: hydrolase Chain: A: PDB Molecule: transcriptional activator tena; PDBTitle: crystal structure of bacillus subtilis tena y112f mutant

						complexed2 with formyl aminomethyl pyrimidine
107	c1z2IA_	Alignment	not modelled	24.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
108	d1i1ga1	Alignment	not modelled	24.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
109	c2k6nA_	Alignment	not modelled	24.5	25	PDB header: structural protein Chain: A: PDB Molecule: supervillin; PDBTitle: solution structure of human supervillin headpiece, minimized2 average
110	c3mkzU_	Alignment	not modelled	24.5	23	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
111	d1utxa_	Alignment	not modelled	24.4	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
112	d1k61a_	Alignment	not modelled	24.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
113	c2mqkA_	Alignment	not modelled	24.3	25	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
114	c2da4A_	Alignment	not modelled	24.2	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dkfzp686k21156; PDBTitle: solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
115	d2cyva1	Alignment	not modelled	23.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
116	d1x2ma1	Alignment	not modelled	23.8	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
117	c5mnwA_	Alignment	not modelled	23.6	15	PDB header: lyase Chain: A: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: solution structure of the cinaciguat bound human beta1 h-nox.
118	d2jn6a1	Alignment	not modelled	23.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
119	d2ao9a1	Alignment	not modelled	23.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
120	d1bw5a_	Alignment	not modelled	23.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain