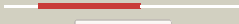


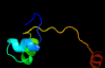
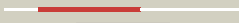










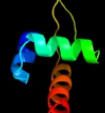








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2310 (-) _2583445_2583789
Date	Mon Aug 5 13:25:46 BST 2019
Unique Job ID	c78e3205e6f684a3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j2nA_	 Alignment		99.2	40	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
2	c4j2nB_	 Alignment		99.2	40	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
3	c6amaO_	 Alignment		98.8	30	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bidc-smea-ssfa complex to2 3.09 angstrom
4	c1z4hA_	 Alignment		98.6	20	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
5	c2zhhA_	 Alignment		98.2	17	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
6	c1y6uA_	 Alignment		98.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
7	c5c8eC_	 Alignment		97.7	16	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
8	c5i44E_	 Alignment		97.7	32	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
9	c2kfsA_	 Alignment		97.7	26	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
10	c4r24B_	 Alignment		97.6	16	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
11	c2vz4A_	 Alignment		97.6	18	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna

12	c4r4eA_	Alignment		97.5	19	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
13	c3ucsB_	Alignment		97.5	15	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
14	c3gpvA_	Alignment		97.4	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
15	d1r8da_	Alignment		97.3	14	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
16	d1q06a_	Alignment		97.3	9	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
17	c5af3A_	Alignment		97.2	19	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
18	c3gp4B_	Alignment		97.2	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
19	d1r8ea1	Alignment		97.2	12	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
20	c3qaoA_	Alignment		96.9	16	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
21	c3hh0C_	Alignment	not modelled	96.9	13	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
22	d1j9ia_	Alignment	not modelled	96.9	20	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
23	c2jmlA_	Alignment	not modelled	96.7	21	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
24	c5gpeB_	Alignment	not modelled	96.7	11	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, merr-family; PDBTitle: crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
25	c5xqlA_	Alignment	not modelled	96.5	18	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
26	c3d6zA_	Alignment	not modelled	96.5	12	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
27	c5cr1A_	Alignment	not modelled	96.4	20	PDB header: metal binding protein Chain: A: PDB Molecule: mercuric resistance operon regulatory protein; PDBTitle: crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
28	c6paxA_	Alignment	not modelled	94.9	14	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2

						complex reveals a general model for pax protein-dna3 interactions
29	c1u78A_	Alignment	not modelled	94.8	6	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
30	c6fkgC_	Alignment	not modelled	92.3	21	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
31	c1umqA_	Alignment	not modelled	92.2	20	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
32	d1umqa_	Alignment	not modelled	92.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
33	d1g2ha_	Alignment	not modelled	92.1	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
34	c1g2hA_	Alignment	not modelled	92.1	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
35	d1fipa_	Alignment	not modelled	92.1	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
36	c4lhfA_	Alignment	not modelled	92.0	29	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
37	d1etxa_	Alignment	not modelled	91.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
38	c3bd1B_	Alignment	not modelled	91.3	27	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
39	d1biaa1	Alignment	not modelled	90.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
40	c2m8gX_	Alignment	not modelled	90.2	28	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
41	d1j5ya1	Alignment	not modelled	90.1	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
42	d1ntca_	Alignment	not modelled	90.0	37	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
43	c3e7ID_	Alignment	not modelled	89.9	23	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
44	c6hn7A_	Alignment	not modelled	89.9	33	PDB header: dna binding protein Chain: A: PDB Molecule: redirecting phage packaging protein c (rppc); PDBTitle: hijacking the hijackers: escherichia coli pathogenicity islands2 redirect helper phage packaging for their own benefit.
45	c5m7nA_	Alignment	not modelled	89.8	24	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 crystaldirect automated mounting and cryo-cooling3 technology
46	d1etob_	Alignment	not modelled	89.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
47	c4r1hA_	Alignment	not modelled	89.7	16	PDB header: transcription regulator Chain: A: PDB Molecule: lmo0741 protein; PDBTitle: gntr family transcriptional regulator from listeria monocytogenes
48	c4l5eA_	Alignment	not modelled	89.5	21	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
49	d2jn6a1	Alignment	not modelled	89.4	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
50	d1pm6a_	Alignment	not modelled	89.3	21	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
51	c2fjrB_	Alignment	not modelled	89.1	11	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
52	c1ojlD_	Alignment	not modelled	89.0	27	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
53	c6j05B_	Alignment	not modelled	88.6	24	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	c2oqgA	Alignment	not modelled	88.4	19	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
55	c3eqxB	Alignment	not modelled	88.4	16	PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containing transcriptional regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
56	c3jthA	Alignment	not modelled	87.8	12	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
57	c2rn7A	Alignment	not modelled	87.7	18	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpε protein from shigella2 flexneri. northeast structural genomics target sfr125
58	c2kpiA	Alignment	not modelled	87.5	26	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
59	d1r1ta	Alignment	not modelled	87.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
60	d1r69a	Alignment	not modelled	87.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
61	c3hefB	Alignment	not modelled	87.1	18	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
62	c5j9iH	Alignment	not modelled	86.9	18	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
63	d1rh6a	Alignment	not modelled	86.9	20	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
64	c1r22B	Alignment	not modelled	86.8	22	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
65	c3omtA	Alignment	not modelled	86.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
66	c2lkpB	Alignment	not modelled	86.3	23	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr
67	d2d1ha1	Alignment	not modelled	86.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
68	c2gm4B	Alignment	not modelled	86.2	22	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
69	d2ppxa1	Alignment	not modelled	86.2	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
70	c2ppxA	Alignment	not modelled	86.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
71	c4omzG	Alignment	not modelled	86.1	15	PDB header: transcription Chain: G: PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii
72	c5jaaB	Alignment	not modelled	85.8	18	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
73	c4go1A	Alignment	not modelled	85.6	39	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
74	c6j0eB	Alignment	not modelled	85.6	26	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
75	d2ao9a1	Alignment	not modelled	85.5	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
76	c2ebyA	Alignment	not modelled	85.4	32	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
77	c2zkzC	Alignment	not modelled	85.2	18	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
78	c3ezfA	Alignment	not modelled	85.2	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
79	c3e6dA	Alignment	not modelled	85.1	24	PDB header: transcription regulation Chain: A: PDB Molecule: cyclic nucleotide-binding protein;

						PDBTitle: crystal structure of cprk c200s
80	c3gn5B_	Alignment	not modelled	85.0	22	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
81	c3bs3A_	Alignment	not modelled	84.9	21	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
82	c3f6vA_	Alignment	not modelled	84.7	21	PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: crystal structure of possible transcriptional regulator for arsenical2 resistance
83	c5dukA_	Alignment	not modelled	84.7	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
84	d1x57a1	Alignment	not modelled	84.4	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
85	c2w48D_	Alignment	not modelled	84.4	43	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
86	d1rzsa_	Alignment	not modelled	84.4	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
87	d1adra_	Alignment	not modelled	84.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
88	c3by6C_	Alignment	not modelled	84.0	10	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
89	c3m1fC_	Alignment	not modelled	83.8	29	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
90	c3cuoB_	Alignment	not modelled	83.5	18	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
91	c3vk0B_	Alignment	not modelled	83.5	18	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhf from2 heisseria
92	c2xcjB_	Alignment	not modelled	83.4	32	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
93	d1r1ua_	Alignment	not modelled	83.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
94	d1b0na2	Alignment	not modelled	83.3	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
95	d1llib_	Alignment	not modelled	83.2	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
96	c3iwfA_	Alignment	not modelled	83.2	32	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
97	d2lcta1	Alignment	not modelled	83.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
98	c2r0qF_	Alignment	not modelled	83.0	22	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
99	c3t76A_	Alignment	not modelled	83.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
100	d1i5za1	Alignment	not modelled	82.8	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
101	c3clcC_	Alignment	not modelled	82.8	11	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
102	d1y9qa1	Alignment	not modelled	82.8	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
103	c3pqkD_	Alignment	not modelled	82.7	14	PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
104	c3trbA_	Alignment	not modelled	82.7	14	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

105	d1utxa_	Alignment	not modelled	82.7	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
106	d1mkma1	Alignment	not modelled	82.6	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
107	c3fmyA_	Alignment	not modelled	82.6	22	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygjt/b3021)
108	c3f6wE_	Alignment	not modelled	82.4	20	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
109	c3i4pA_	Alignment	not modelled	82.3	25	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
110	d2a6ca1	Alignment	not modelled	82.1	50	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
111	c3neuA_	Alignment	not modelled	82.1	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
112	d1y7ya1	Alignment	not modelled	82.0	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
113	c2o3fC_	Alignment	not modelled	82.0	28	PDB header: transcription Chain: C: PDB Molecule: putative hth-type transcriptional regulator ybbh; PDBTitle: structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
114	c3f6oB_	Alignment	not modelled	81.9	17	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
115	d2o3fa1	Alignment	not modelled	81.7	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
116	c3op9A_	Alignment	not modelled	81.7	29	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
117	d2bjca1	Alignment	not modelled	81.6	32	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
118	d3e5ua1	Alignment	not modelled	81.6	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
119	d1ft9a1	Alignment	not modelled	81.6	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
120	c1b0nA_	Alignment	not modelled	81.5	11	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex