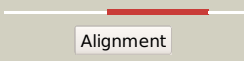

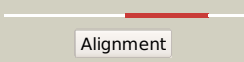

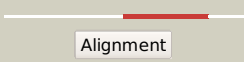

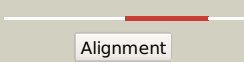

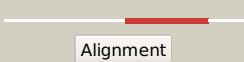

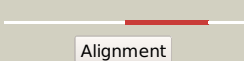

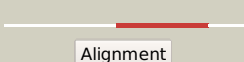

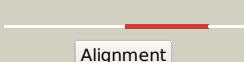

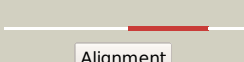





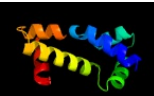










# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1931c (- )_2182467_2183246
Date	Fri Aug 2 13:30:55 BST 2019
Unique Job ID	6be61b4d11e34a9a

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gbgA_</a>	 Alignment		100.0	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tcp pilus virulence regulatory protein; <b>PDBTitle:</b> crystal structure of toxT from vibrio cholerae o395
2	<a href="#">c5chhA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arac family transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
3	<a href="#">c3oioA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (arac-type dna-binding domain- <b>PDBTitle:</b> crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
4	<a href="#">c1d5yD_</a>	 Alignment		100.0	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> rob transcription factor; <b>PDBTitle:</b> crystal structure of the e. coli rob transcription factor2 in complex with dna
5	<a href="#">c3oouA_</a>	 Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2118 protein; <b>PDBTitle:</b> the structure of a protein with unkown function from listeria innocua
6	<a href="#">c3w6vA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transcription activator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> adpa; <b>PDBTitle:</b> crystal structure of the dna-binding domain of adpa, the global2 transcriptional factor, in complex with a target dna
7	<a href="#">c4fe4C_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> xylose operon regulatory protein; <b>PDBTitle:</b> crystal structure of apo e. coli xylr
8	<a href="#">c2k9sA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose operon regulatory protein; <b>PDBTitle:</b> solution structure of dna binding domain of e. coli arac
9	<a href="#">c1b10A_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (multiple antibiotic resistance protein); <b>PDBTitle:</b> multiple antibiotic resistance protein (mara)/dna complex
10	<a href="#">c3mn2B_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable arac family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
11	<a href="#">c3mk1B_</a>	 Alignment		99.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator gadx; <b>PDBTitle:</b> crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12

12	<a href="#">c3lsgD</a>	Alignment		99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> two-component response regulator yesn; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
13	<a href="#">d1d5ya2</a>	Alignment		99.6	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
14	<a href="#">d1bl0a2</a>	Alignment		99.6	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
15	<a href="#">c3nooB</a>	Alignment		99.5	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
16	<a href="#">c5nlaA</a>	Alignment		99.5	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator transcription regulator <b>PDBTitle:</b> crystal structure of the arac-like transcriptional activator curx
17	<a href="#">d1d5ya1</a>	Alignment		99.2	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
18	<a href="#">c3bhnA</a>	Alignment		99.2	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi domain protein; <b>PDBTitle:</b> crystal structure of a dj-1/pfpi-like protein (shew_2856) from2 shewanella loihica pv-4 at 1.76 a resolution
19	<a href="#">c1zgwA</a>	Alignment		99.1	24	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ada polyprotein; <b>PDBTitle:</b> nmr structure of e. coli ada protein in complex with dna
20	<a href="#">d1bl0a1</a>	Alignment		99.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
21	<a href="#">c3ewnA</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> crystal structure of a thij/pfpi family protein from pseudomonas2 syringae
22	<a href="#">c3mgkA</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> intracellular protease/amidase related enzyme (thij) <b>PDBTitle:</b> crystal structure of probable protease/amidase from clostridium2 acetobutylicum atcc 824
23	<a href="#">c3ot1B</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate <b>PDBTitle:</b> crystal structure of vc2308 protein
24	<a href="#">c3cneD</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative protease i; <b>PDBTitle:</b> crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
25	<a href="#">d1p5fa</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
26	<a href="#">d1g2ia</a>	Alignment	not modelled	98.8	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
27	<a href="#">c3er6D</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator protein; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator protein from2 vibrio parahaemolyticus
28	<a href="#">c4hcgA</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi domain protein; <b>PDBTitle:</b> crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
						<b>PDB header:</b> motor protein

29	<a href="#">c4e08B_</a>	Alignment	not modelled	98.7	13	<b>Chain:</b> B: <b>PDB Molecule:</b> dj-1 beta; <b>PDBTitle:</b> crystal structure of drosophila melanogaster dj-1beta
30	<a href="#">c3graA_</a>	Alignment	not modelled	98.7	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, arac family; <b>PDBTitle:</b> crystal structure of arac family transcriptional regulator from2 pseudomonas putida
31	<a href="#">c3efeC_</a>	Alignment	not modelled	98.7	14	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
32	<a href="#">c4xllB_</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dj-1 family protein; <b>PDBTitle:</b> toxoplasma gondii dj-1, oxidized
33	<a href="#">c3uk7B_</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> class i glutamine amidotransferase-like domain-containing <b>PDBTitle:</b> crystal structure of arabidopsis thaliana dj-1d
34	<a href="#">d1oi4a1</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
35	<a href="#">c3f5dA_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein ydea; <b>PDBTitle:</b> crystal structure of a protein of unknown function from bacillus2 subtilis
36	<a href="#">c3fseB_</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> two-domain protein containing dj-1/thij/pfpi-like and <b>PDBTitle:</b> crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
37	<a href="#">c4y0nB_</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein sav1875; <b>PDBTitle:</b> sav1875
38	<a href="#">d2ab0a1</a>	Alignment	not modelled	98.5	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
39	<a href="#">d1sy7a1</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
40	<a href="#">d2fexa1</a>	Alignment	not modelled	98.4	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
41	<a href="#">c4k2hG_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> intracellular protease/amidase; <b>PDBTitle:</b> crystal structure of c103a mutant of dj-1 superfamily protein stm19312 from salmonella typhimurium
42	<a href="#">c1sy7B_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase 1; <b>PDBTitle:</b> crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
43	<a href="#">c4ge0C_</a>	Alignment	not modelled	98.0	11	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein c22e12.03c; <b>PDBTitle:</b> schizosaccharomyces pombe dj-1 t114p mutant
44	<a href="#">c2vrnA_</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease i; <b>PDBTitle:</b> the structure of the stress response protein dr1199 from deinococcus2 radiodurans: a member of the dj-1 superfamily
45	<a href="#">d1p80a1</a>	Alignment	not modelled	98.0	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
46	<a href="#">c3n7tA_</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage binding protein; <b>PDBTitle:</b> crystal structure of a macrophage binding protein from coccidioides2 immitis
47	<a href="#">c3kkIA_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable chaperone protein hsp33; <b>PDBTitle:</b> crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
48	<a href="#">c4lruA_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase iii (glutathione-independent); <b>PDBTitle:</b> crystal structure of glyoxalase iii (orf 19.251) from candida albicans
49	<a href="#">d1u9ca_</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
50	<a href="#">c3l3bA_</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> es1 family protein; <b>PDBTitle:</b> crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
51	<a href="#">d1qvwa_</a>	Alignment	not modelled	97.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
52	<a href="#">d1vhqa_</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
53	<a href="#">c4p5pA_</a>	Alignment	not modelled	97.4	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
54	<a href="#">c4i2nC_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> intracellular protease/amidase; <b>PDBTitle:</b> crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
						<b>PDB header:</b> chaperone

55	<a href="#">c5xr2D_</a>	Alignment	not modelled	97.1	23	<b>Chain:</b> D: <b>PDB Molecule:</b> protein/nucleic acid deglycase hcha; <b>PDBTitle:</b> sav0551
56	<a href="#">d1n57a_</a>	Alignment	not modelled	96.9	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
57	<a href="#">d2hsqa1</a>	Alignment	not modelled	95.6	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
58	<a href="#">d1sgma1</a>	Alignment	not modelled	95.4	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
59	<a href="#">c2o3fC_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybbh; <b>PDBTitle:</b> structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
60	<a href="#">d2o3fa1</a>	Alignment	not modelled	95.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> RpiR-like
61	<a href="#">c5fglA_</a>	Alignment	not modelled	95.2	6	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> nicr; <b>PDBTitle:</b> co-crystal structure of nicr2_hsp
62	<a href="#">d1qpza1</a>	Alignment	not modelled	95.1	30	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
63	<a href="#">d1efaa1</a>	Alignment	not modelled	95.1	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
64	<a href="#">d2bjca1</a>	Alignment	not modelled	95.1	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
65	<a href="#">c4ivnB_</a>	Alignment	not modelled	94.9	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the vibrio vulnificus nanr protein complexed with mannac-6p
66	<a href="#">c2gfnA_</a>	Alignment	not modelled	94.8	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator pksa related protein; <b>PDBTitle:</b> crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
67	<a href="#">c1sgmA_</a>	Alignment	not modelled	94.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator yxaf; <b>PDBTitle:</b> crystal structure of hypothetical protein yxaf
68	<a href="#">c1p81A_</a>	Alignment	not modelled	94.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catalase hpii; <b>PDBTitle:</b> crystal structure of the d181e variant of catalase hpii2 from e. coli
69	<a href="#">d1j5ya1</a>	Alignment	not modelled	94.7	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
70	<a href="#">d2fbqa1</a>	Alignment	not modelled	94.5	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
71	<a href="#">c2qtqB_</a>	Alignment	not modelled	94.4	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
72	<a href="#">c2genA_</a>	Alignment	not modelled	94.4	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1
73	<a href="#">c3iwfA_</a>	Alignment	not modelled	94.2	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
74	<a href="#">c2m8gX_</a>	Alignment	not modelled	94.2	7	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> structure, function, and tethering of dna-binding domains in 542 transcriptional activators
75	<a href="#">c2hytA_</a>	Alignment	not modelled	94.0	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator (eca1819)2 from pectobacterium atrosepticum at 1.64 a resolution
76	<a href="#">c3rd3B_</a>	Alignment	not modelled	93.9	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> structure of pseudomonas aeruginosa transcriptional regulator pa2196
77	<a href="#">c1vi0B_</a>	Alignment	not modelled	93.8	7	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
78	<a href="#">c2dg7A_</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
79	<a href="#">c2ibdB_</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulatory protein2 rha5900
80	<a href="#">d2gfna1</a>	Alignment	not modelled	93.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain

81	<a href="#">d1biaa1</a>	Alignment	not modelled	93.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
82	<a href="#">d2i10a1</a>	Alignment	not modelled	93.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
83	<a href="#">d1jt6a1</a>	Alignment	not modelled	93.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
84	<a href="#">d1o1ya_</a>	Alignment	not modelled	93.7	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
85	<a href="#">c3on4D_</a>	Alignment	not modelled	93.7	6	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of tetr transcriptional regulator from legionella2 pneumophila
86	<a href="#">c3bruA_</a>	Alignment	not modelled	93.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein, tetr family; <b>PDBTitle:</b> crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
87	<a href="#">c3b6aC_</a>	Alignment	not modelled	93.7	13	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> actr protein; <b>PDBTitle:</b> crystal structure of the streptomyces coelicolor tetr family protein2 actr in complex with actinorhodin
88	<a href="#">c1lbgB_</a>	Alignment	not modelled	93.6	16	<b>PDB header:</b> <b>PDB COMPND:</b>
89	<a href="#">c1zvva_</a>	Alignment	not modelled	93.6	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
90	<a href="#">d2cg4a1</a>	Alignment	not modelled	93.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
91	<a href="#">c3geuC_</a>	Alignment	not modelled	93.5	5	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> intercellular adhesion protein r; <b>PDBTitle:</b> crystal structure of icar from staphylococcus aureus, a member of the2 tetracycline repressor protein family
92	<a href="#">d2fq4a1</a>	Alignment	not modelled	93.5	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
93	<a href="#">c5dajB_</a>	Alignment	not modelled	93.5	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> nald; <b>PDBTitle:</b> crystal structure of nald, the secondary repressor of mexab-oprm2 multidrug efflux pump in pseudomonas aeruginosa
94	<a href="#">c5ydpC_</a>	Alignment	not modelled	93.5	15	<b>PDB header:</b> gene regulation <b>Chain:</b> C: <b>PDB Molecule:</b> tetr transcriptional regulatory protein; <b>PDBTitle:</b> crystal structure of tetr family repressor alkx from dietzia sp.2 strain dq12-45-1b implicated in biodegradation of n-alkanes
95	<a href="#">c3vprA_</a>	Alignment	not modelled	93.4	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator pfmr from2 thermus thermophilus hb8
96	<a href="#">c5d19A_</a>	Alignment	not modelled	93.4	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv0302, form ii
97	<a href="#">c1jumB_</a>	Alignment	not modelled	93.4	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical transcriptional regulator in qaca 5' region; <b>PDBTitle:</b> crystal structure of the multidrug binding transcriptional repressor2 qacr bound to the natural drug berberine
98	<a href="#">c2nx4A_</a>	Alignment	not modelled	93.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family protein; <b>PDBTitle:</b> the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
99	<a href="#">d3c07a1</a>	Alignment	not modelled	93.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
100	<a href="#">c3kxD_</a>	Alignment	not modelled	93.3	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
101	<a href="#">d2o7ta1</a>	Alignment	not modelled	93.3	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
102	<a href="#">c1u78A_</a>	Alignment	not modelled	93.2	10	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
103	<a href="#">c3f1bA_</a>	Alignment	not modelled	93.2	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
104	<a href="#">c2fq4A_</a>	Alignment	not modelled	93.2	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus
105	<a href="#">c3iuvA_</a>	Alignment	not modelled	93.2	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized tetr family protein; <b>PDBTitle:</b> the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
106	<a href="#">c3cwrA_</a>	Alignment	not modelled	93.2	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of tetr family2 (yp_425770.1) from rhodospirillum rubrum atcc 11170 at

						1.50 a3 resolution
107	<a href="#">c2f07A_</a>	Alignment	not modelled	93.2	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yvdt; <b>PDBTitle:</b> crystal structure of yvdt from bacillus subtilis
108	<a href="#">c6j05B_</a>	Alignment	not modelled	93.2	5	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
109	<a href="#">c3dpjB_</a>	Alignment	not modelled	93.2	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator, tetr family; <b>PDBTitle:</b> the crystal structure of a tetr transcription regulator2 from silicibacter pomeroyi dss
110	<a href="#">d1v7ba1</a>	Alignment	not modelled	93.2	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
111	<a href="#">c2i10A_</a>	Alignment	not modelled	93.1	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr transcriptional regulator; <b>PDBTitle:</b> putative tetr transcriptional regulator from rhodococcus sp. rha1
112	<a href="#">c3bniA_</a>	Alignment	not modelled	93.1	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
113	<a href="#">c2yvha_</a>	Alignment	not modelled	93.1	9	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of the operator-binding form of the multi-drug2 binding transcriptional repressor cgmr
114	<a href="#">c3h5tA_</a>	Alignment	not modelled	93.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
115	<a href="#">c2of7A_</a>	Alignment	not modelled	93.1	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
116	<a href="#">c3bhqB_</a>	Alignment	not modelled	93.1	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution
117	<a href="#">c2g3bB_</a>	Alignment	not modelled	93.1	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
118	<a href="#">c5k7fA_</a>	Alignment	not modelled	93.1	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of apo aibr
119	<a href="#">d1pb6a1</a>	Alignment	not modelled	93.1	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
120	<a href="#">c3dcfB_</a>	Alignment	not modelled	93.0	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator of the tetr/acrr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of the tetr/acrr family2 (yp_290855.1) from thermobifida fusca yx-er1 at 2.50 a resolution