

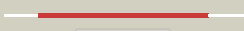




















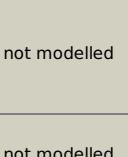


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1930c (- )_2181925_2182449
Date	Fri Aug 2 13:30:55 BST 2019
Unique Job ID	6a18e826e278baab

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ewnA</a>	 Alignment		100.0	43	<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
2	<a href="#">c3nooB</a>	 Alignment		100.0	45	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> crystal structure of a c101a isocyanide hydratase from pseudomonas2 fluorescens
3	<a href="#">c3bhnA</a>	 Alignment		99.9	24	<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
4	<a href="#">c3mgkA</a>	 Alignment		99.9	38	<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
5	<a href="#">c3ot1B</a>	 Alignment		99.9	24	<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
6	<a href="#">c3graA</a>	 Alignment		99.9	17	<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
7	<a href="#">d1p5fa</a>	 Alignment		99.9	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
8	<a href="#">c4ge0C</a>	 Alignment		99.9	24	<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
9	<a href="#">c3er6D</a>	 Alignment		99.9	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
10	<a href="#">c4e08B</a>	 Alignment		99.9	29	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dj-1 beta; <b>PDBTitle:</b> crystal structure of drosophila melanogaster dj-1beta
11	<a href="#">c4k2hG</a>	 Alignment		99.9	35	<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

12	<a href="#">d2ab0a1</a>	Alignment		99.8	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
13	<a href="#">c4xllB</a>	Alignment		99.8	31	<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
14	<a href="#">c4y0nB</a>	Alignment		99.8	34	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein sav1875; <b>PDBTitle:</b> sav1875
15	<a href="#">c2vrnA</a>	Alignment		99.8	27	<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
16	<a href="#">c3f5dA</a>	Alignment		99.8	19	<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
17	<a href="#">d1oi4a1</a>	Alignment		99.8	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
18	<a href="#">d2fexa1</a>	Alignment		99.8	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
19	<a href="#">d1g2ia</a>	Alignment		99.8	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
20	<a href="#">c3efeC</a>	Alignment		99.7	17	<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
21	<a href="#">c3fseB</a>	Alignment	not modelled	99.7	23	<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
22	<a href="#">c4hclA</a>	Alignment	not modelled	99.6	24	<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
23	<a href="#">c3cneD</a>	Alignment	not modelled	99.6	28	<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
24	<a href="#">c3uk7B</a>	Alignment	not modelled	99.6	28	<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
25	<a href="#">d1u9ca</a>	Alignment	not modelled	99.3	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
26	<a href="#">c4p5pA</a>	Alignment	not modelled	99.1	24	<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
27	<a href="#">c3kklA</a>	Alignment	not modelled	99.1	19	<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
28	<a href="#">d1sy7a1</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like

						<b>Family:</b> Catalase, C-terminal domain
29	<a href="#">c4lrUA</a>	Alignment	not modelled	98.9	28	<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
30	<a href="#">d1qvwa</a>	Alignment	not modelled	98.8	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
31	<a href="#">c3n7tA</a>	Alignment	not modelled	98.6	24	<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
32	<a href="#">d1bl0a1</a>	Alignment	not modelled	98.4	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
33	<a href="#">d1d5ya1</a>	Alignment	not modelled	98.4	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
34	<a href="#">c3oioA</a>	Alignment	not modelled	98.4	16	<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
35	<a href="#">c4fe4C</a>	Alignment	not modelled	98.3	13	<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
36	<a href="#">d1vhqa</a>	Alignment	not modelled	98.3	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
37	<a href="#">c1zgwA</a>	Alignment	not modelled	98.2	11	<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
38	<a href="#">c1sy7B</a>	Alignment	not modelled	98.2	14	<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.
39	<a href="#">c3w6vA</a>	Alignment	not modelled	98.2	13	<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
40	<a href="#">c3mn2B</a>	Alignment	not modelled	98.2	9	<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
41	<a href="#">c3oouA</a>	Alignment	not modelled	98.1	13	<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
42	<a href="#">c1bl0A</a>	Alignment	not modelled	98.0	7	<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
43	<a href="#">c2k9sA</a>	Alignment	not modelled	98.0	15	<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
44	<a href="#">c5xr2D</a>	Alignment	not modelled	97.9	26	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein/nucleic acid deglycase hcha; <b>PDBTitle:</b> sav0551
45	<a href="#">c3mk1B</a>	Alignment	not modelled	97.9	12	<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
46	<a href="#">c3gbgA</a>	Alignment	not modelled	97.7	7	<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
47	<a href="#">c3lsgD</a>	Alignment	not modelled	97.7	7	<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
48	<a href="#">c5chhA</a>	Alignment	not modelled	97.6	13	<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
49	<a href="#">c5nlaA</a>	Alignment	not modelled	97.5	5	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator <b>PDBTitle:</b> crystal structure of the arac-like transcriptional activator cuxr
50	<a href="#">c3l3bA</a>	Alignment	not modelled	97.5	25	<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="#">d1n57a</a>	Alignment	not modelled	97.4	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
52	<a href="#">c4i2nC</a>	Alignment	not modelled	97.2	21	<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
53	<a href="#">d1p80a1</a>	Alignment	not modelled	96.5	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like

						<b>Family:</b> Catalase, C-terminal domain
54	<a href="#">d1bl0a2</a>	Alignment	not modelled	93.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
55	<a href="#">d1d5ya2</a>	Alignment	not modelled	88.2	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
56	<a href="#">c2y31A</a>	Alignment	not modelled	81.8	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor simreg2; <b>PDBTitle:</b> simocyclinone c4 bound form of tetr-like repressor simr
57	<a href="#">d1biaa1</a>	Alignment	not modelled	76.0	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
58	<a href="#">c2dg7A</a>	Alignment	not modelled	75.5	15	<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)
59	<a href="#">c1d5yD</a>	Alignment	not modelled	75.4	11	<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
60	<a href="#">d2fq4a1</a>	Alignment	not modelled	75.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
61	<a href="#">d3c07a1</a>	Alignment	not modelled	73.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
62	<a href="#">c2m8gX</a>	Alignment	not modelled	73.1	13	<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
63	<a href="#">d1j5ya1</a>	Alignment	not modelled	73.0	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
64	<a href="#">c3gziA</a>	Alignment	not modelled	72.1	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
65	<a href="#">d2fbqa1</a>	Alignment	not modelled	69.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
66	<a href="#">d2obpa1</a>	Alignment	not modelled	69.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ReutB4095-like
67	<a href="#">d2i10a1</a>	Alignment	not modelled	69.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
68	<a href="#">c2e1cA</a>	Alignment	not modelled	68.9	10	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
69	<a href="#">c3t8tA</a>	Alignment	not modelled	68.2	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcus aureus cymr (oxidized form); <b>PDBTitle:</b> crystal structure of staphylococcus aureus cymr oxidized form
70	<a href="#">d2id3a1</a>	Alignment	not modelled	68.1	15	<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="#">d2vkea1</a>	Alignment	not modelled	67.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
72	<a href="#">d2g3ba1</a>	Alignment	not modelled	66.8	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
73	<a href="#">d1t56a1</a>	Alignment	not modelled	66.4	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
74	<a href="#">d2iu5a1</a>	Alignment	not modelled	66.2	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
75	<a href="#">c2iaia</a>	Alignment	not modelled	65.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator sco3833; <b>PDBTitle:</b> crystal structure of sco3833, a member of the tetr transcriptional2 regulator family from streptomyces coelicolor a3
76	<a href="#">d1pb6a1</a>	Alignment	not modelled	65.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
77	<a href="#">d2gfna1</a>	Alignment	not modelled	65.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
78	<a href="#">d1jt6a1</a>	Alignment	not modelled	65.1	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
79	<a href="#">d1vi0a1</a>	Alignment	not modelled	64.6	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain

80	<a href="#">d2fd5a1</a>	Alignment	not modelled	64.6	8	<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="#">d2np5a1</a>	Alignment	not modelled	63.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
82	<a href="#">d2hya1</a>	Alignment	not modelled	63.2	11	<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="#">c2nx4A_</a>	Alignment	not modelled	62.7	10	<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 the putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
84	<a href="#">d2cg4a1</a>	Alignment	not modelled	62.1	18	<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
85	<a href="#">d1rka1</a>	Alignment	not modelled	61.9	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
86	<a href="#">c3nrgA_</a>	Alignment	not modelled	61.5	8	<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 regulator2 (caur_2714) from chloroflexus aurantiacus j-10-fl at 2.56 a3 resolution
87	<a href="#">d2fx0a1</a>	Alignment	not modelled	61.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
88	<a href="#">c5d1wD_</a>	Alignment	not modelled	59.4	5	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> rv3249c transcriptional regulator; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv3249c2 transcriptional regulator.
89	<a href="#">c2f07A_</a>	Alignment	not modelled	59.1	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> syvdt; <b>PDBTitle:</b> crystal structure of yvdt from bacillus subtilis
90	<a href="#">c3e7qB_</a>	Alignment	not modelled	58.2	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
91	<a href="#">d2gena1</a>	Alignment	not modelled	57.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
92	<a href="#">d2d6ya1</a>	Alignment	not modelled	57.3	8	<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="#">c3on2C_</a>	Alignment	not modelled	57.1	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> structure of a protein with unknown function from rhodococcus sp. rha1
94	<a href="#">d2g7sa1</a>	Alignment	not modelled	56.9	3	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
95	<a href="#">c2gfnA_</a>	Alignment	not modelled	56.7	15	<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
96	<a href="#">d1sgma1</a>	Alignment	not modelled	56.4	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
97	<a href="#">d2id6a1</a>	Alignment	not modelled	56.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
98	<a href="#">d2vkva1</a>	Alignment	not modelled	56.2	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
99	<a href="#">c3kkcB_</a>	Alignment	not modelled	56.2	6	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
100	<a href="#">d1ui5a1</a>	Alignment	not modelled	56.1	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
101	<a href="#">c3cwrA_</a>	Alignment	not modelled	56.1	18	<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
102	<a href="#">c2l4aA_</a>	Alignment	not modelled	55.7	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
103	<a href="#">c2id3A_</a>	Alignment	not modelled	55.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
104	<a href="#">c3f1bA_</a>	Alignment	not modelled	54.5	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.
105	<a href="#">c2iu5A_</a>	Alignment	not modelled	54.4	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type dhaklm operon transcriptional activator dhas; <b>PDBTitle:</b> dihydroxyacetone kinase operon activator dhas

106	<a href="#">d1v7ba1</a>	Alignment	not modelled	54.2	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
107	<a href="#">d2g7ga1</a>	Alignment	not modelled	53.2	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
108	<a href="#">c1i1gA_</a>	Alignment	not modelled	53.2	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
109	<a href="#">c2of7A_</a>	Alignment	not modelled	53.1	13	<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
110	<a href="#">c3mn1A_</a>	Alignment	not modelled	53.1	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein (probably tetr-family); <b>PDBTitle:</b> the crystal structure of kstr (rv3574) from mycobacterium tuberculosis2 h37rv
111	<a href="#">c3bhqB_</a>	Alignment	not modelled	53.0	11	<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
112	<a href="#">c2rasB_</a>	Alignment	not modelled	52.0	8	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a putative tetr/acrr family transcriptional2 regulator (saro_0558) from novosphingobium aromaticivorans dsm at3 1.80 a resolution
113	<a href="#">c2fd5A_</a>	Alignment	not modelled	51.0	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a transcriptional regulator from pseudomonas2 aeruginosa pao1
114	<a href="#">c4w97A_</a>	Alignment	not modelled	50.5	4	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor kstr2; <b>PDBTitle:</b> structure of ketosteroid transcriptional regulator kstr2 of2 mycobacterium tuberculosis
115	<a href="#">c1rktA_</a>	Alignment	not modelled	50.2	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein yfir; <b>PDBTitle:</b> crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis
116	<a href="#">c4mk6A_</a>	Alignment	not modelled	49.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> probable dihydroxyacetone kinase regulator dhsk_reg; <b>PDBTitle:</b> crystal structure of probable dihydroxyacetone kinase regulator2 dhsk_reg from listeria monocytogenes egd-e
117	<a href="#">c3k69A_</a>	Alignment	not modelled	49.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
118	<a href="#">c2qcoA_</a>	Alignment	not modelled	49.7	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cmer; <b>PDBTitle:</b> crystal structure of the transcriptional regulator cmer from2 campylobacter jejuni
119	<a href="#">d2g7la1</a>	Alignment	not modelled	49.3	10	<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="#">d1tw3a1</a>	Alignment	not modelled	49.3	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain