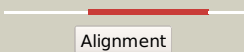

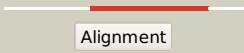



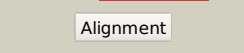



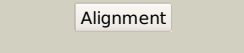
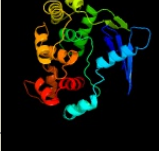
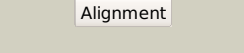



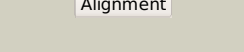
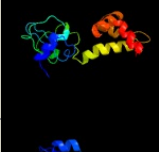
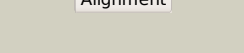

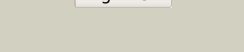



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1317c_alkA_1477634_1479124
Date	Wed Jul 31 22:05:41 BST 2019
Unique Job ID	68cddb1b629cfe3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1mpgB_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyladenine dna glycosylase ii; <b>PDBTitle:</b> 3-methyladenine dna glycosylase ii from escherichia coli
2	<a href="#">c2jhnB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyladenine dna-glycosylase; <b>PDBTitle:</b> 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
3	<a href="#">c4ejyA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> 3-methyladenine dna glycosylase; <b>PDBTitle:</b> structure of mbogg1 in complex with high affinity dna ligand
4	<a href="#">c1yqmA_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> n-glycosylase/dna lyase; <b>PDBTitle:</b> catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna
5	<a href="#">c3f10A_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-oxoguanine-dna-glycosylase; <b>PDBTitle:</b> crystal structure of clostridium acetobutylicum 8-oxoguanine dna2 glycosylase in complex with 8-oxoguanosine
6	<a href="#">c1ko9A_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-oxoguanine dna glycosylase; <b>PDBTitle:</b> native structure of the human 8-oxoguanine dna glycosylase2 hogg1
7	<a href="#">d1mpga1</a>	 Alignment		100.0	32	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> DNA repair glycosylase, 2 C-terminal domains
8	<a href="#">c2yg8B_</a>	 Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna-3-methyladenine glycosidase ii, putative; <b>PDBTitle:</b> structure of an unusual 3-methyladenine dna glycosylase ii (alka) from2 deinococcus radiodurans
9	<a href="#">c1zgwA_</a>	 Alignment		100.0	35	<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
10	<a href="#">c4b24A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> probable dna-3-methyladenine glycosylase 2; <b>PDBTitle:</b> unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
11	<a href="#">c2h56C_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dna-3-methyladenine glycosidase; <b>PDBTitle:</b> crystal structure of dna-3-methyladenine glycosidase (10174367) from2 bacillus halodurans at 2.55 a resolution

12	<a href="#">c3s6iA_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna-3-methyladenine glycosylase 1; <b>PDBTitle:</b> schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
13	<a href="#">d2noha1</a>	Alignment		100.0	22	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> DNA repair glycosylase, 2 C-terminal domains
14	<a href="#">d1eyfa_</a>	Alignment		100.0	38	<b>Fold:</b> Ada DNA repair protein, N-terminal domain (N-Ada 10) <b>Superfamily:</b> Ada DNA repair protein, N-terminal domain (N-Ada 10) <b>Family:</b> Ada DNA repair protein, N-terminal domain (N-Ada 10)
15	<a href="#">c3fhgA_</a>	Alignment		99.9	15	<b>PDB header:</b> dna repair, hydrolase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-glycosylase/dna lyase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
16	<a href="#">d1mpga2</a>	Alignment		99.9	29	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> DNA repair glycosylase, N-terminal domain
17	<a href="#">c3gbgA_</a>	Alignment		99.9	15	<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
18	<a href="#">c3kntC</a>	Alignment		99.9	11	<b>PDB header:</b> hydrolase, lyase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> n-glycosylase/dna lyase; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii 8-oxoguanine2 glycosylase/lyase in complex with 15mer dna containing 8-oxoguanine
19	<a href="#">c4unfA_</a>	Alignment		99.9	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease iii-1; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans endonuclease iii-1
20	<a href="#">d1orna_</a>	Alignment		99.9	21	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
21	<a href="#">c1d5yD_</a>	Alignment	not modelled	99.9	22	<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
22	<a href="#">d1pu6a_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> 3-Methyladenine DNA glycosylase III (MagIII)
23	<a href="#">d2abka_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
24	<a href="#">c5chhA_</a>	Alignment	not modelled	99.9	22	<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
25	<a href="#">c4uobA_</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease iii-3; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans endonuclease iii-3
26	<a href="#">c3oioA_</a>	Alignment	not modelled	99.9	27	<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
27	<a href="#">c3w6vA_</a>	Alignment	not modelled	99.9	27	<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
28	<a href="#">c3n0uB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> probable n-glycosylase/dna lyase; <b>PDBTitle:</b> crystal structure of tm1821, the 8-oxoguanine dna

						glycosylase of2 thermotoga maritima <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
29	<a href="#">c1bl0A_</a>	Alignment	not modelled	99.9	17	
30	<a href="#">c3oouA_</a>	Alignment	not modelled	99.9	15	<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
31	<a href="#">c3mn2B_</a>	Alignment	not modelled	99.9	25	<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
32	<a href="#">d1keaa_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
33	<a href="#">c3mkIB_</a>	Alignment	not modelled	99.9	23	<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
34	<a href="#">c2k9sA_</a>	Alignment	not modelled	99.9	23	<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
35	<a href="#">c4fe4C_</a>	Alignment	not modelled	99.9	23	<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="#">d1ngna_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
37	<a href="#">d1rrqa1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
38	<a href="#">d1kg2a_</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
39	<a href="#">c3n5nX_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> a/g-specific adenine dna glycosylase; <b>PDBTitle:</b> crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
40	<a href="#">c3lsgD_</a>	Alignment	not modelled	99.8	19	<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
41	<a href="#">c1rrqA_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> muty; <b>PDBTitle:</b> muty adenine glycosylase in complex with dna containing an2 a:oxog pair
42	<a href="#">d1d5ya2</a>	Alignment	not modelled	99.3	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
43	<a href="#">d1bl0a2</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
44	<a href="#">c5nlaA_</a>	Alignment	not modelled	99.2	22	<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 cuxr
45	<a href="#">d1d5ya1</a>	Alignment	not modelled	98.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
46	<a href="#">d1bl0a1</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
47	<a href="#">d2noha2</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> DNA repair glycosylase, N-terminal domain
48	<a href="#">d1sgma1</a>	Alignment	not modelled	94.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
49	<a href="#">c5fgIA_</a>	Alignment	not modelled	94.1	6	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> nicr; <b>PDBTitle:</b> co-crystal structure of nicr2_hsp
50	<a href="#">c3cwrA_</a>	Alignment	not modelled	93.5	29	<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
51	<a href="#">c1sgmA_</a>	Alignment	not modelled	93.4	11	<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
52	<a href="#">c2gfnA_</a>	Alignment	not modelled	93.3	12	<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
53	<a href="#">d1vdda_</a>	Alignment	not modelled	92.9	29	<b>Fold:</b> Recombination protein RecR <b>Superfamily:</b> Recombination protein RecR <b>Family:</b> Recombination protein RecR
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

54	<a href="#">d1jt6a1</a>	Alignment	not modelled	92.8	9	<b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
55	<a href="#">c3rd3B</a>	Alignment	not modelled	92.8	11	<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
56	<a href="#">c2h5xA</a>	Alignment	not modelled	92.8	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruva; <b>PDBTitle:</b> ruva from mycobacterium tuberculosis
57	<a href="#">c2csdB</a>	Alignment	not modelled	92.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> topoisomerase v; <b>PDBTitle:</b> crystal structure of topoisomerase v (61 kda fragment)
58	<a href="#">c1vddC</a>	Alignment	not modelled	92.6	29	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recombinational repair protein recr
59	<a href="#">d2fbga1</a>	Alignment	not modelled	92.5	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
60	<a href="#">c5dxzA</a>	Alignment	not modelled	92.4	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> crystal of amtr from corynebacterium glutamicum
61	<a href="#">c3on4D</a>	Alignment	not modelled	92.4	10	<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
62	<a href="#">c2ibdB</a>	Alignment	not modelled	92.3	13	<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
63	<a href="#">c6gh5M</a>	Alignment	not modelled	92.3	12	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor,rna polymerase sigma-54 <b>PDBTitle:</b> cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
64	<a href="#">c2dg7A</a>	Alignment	not modelled	92.2	20	<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)
65	<a href="#">c2d6yA</a>	Alignment	not modelled	92.1	7	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr family regulatory protein; <b>PDBTitle:</b> crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
66	<a href="#">d2fq4a1</a>	Alignment	not modelled	91.8	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
67	<a href="#">c5byhM</a>	Alignment	not modelled	91.8	15	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor; <b>PDBTitle:</b> crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
68	<a href="#">c2qtqB</a>	Alignment	not modelled	91.7	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
69	<a href="#">c1u78A</a>	Alignment	not modelled	91.6	9	<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
70	<a href="#">d2i10a1</a>	Alignment	not modelled	91.6	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="#">c1jumB</a>	Alignment	not modelled	91.5	9	<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
72	<a href="#">c1d8IA</a>	Alignment	not modelled	91.5	34	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> protein (holliday junction dna helicase ruva); <b>PDBTitle:</b> e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
73	<a href="#">c1ixrB</a>	Alignment	not modelled	91.4	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction dna helicase ruva; <b>PDBTitle:</b> ruva-ruvb complex
74	<a href="#">c2f07A</a>	Alignment	not modelled	91.3	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
75	<a href="#">c3f1bA</a>	Alignment	not modelled	91.3	13	<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.
76	<a href="#">c4ichA</a>	Alignment	not modelled	91.3	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative tetr family transcriptional regulator2 from saccharomonospora viridis dsm 43017
77	<a href="#">d2g3ba1</a>	Alignment	not modelled	91.3	18	<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="#">c3vibD</a>	Alignment	not modelled	91.2	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> mtrr; <b>PDBTitle:</b> structural basis for multidrug recognition and antimicrobial2 resistance by mtrr, an efflux pump regulator from neisseria3 gonorrhoeae
79	<a href="#">c2ggaA</a>	Alignment	not modelled	91.2	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator;

79	<a href="#">c2genaA</a>	Alignment	not modelled	91.2	11	<b>PDBTitle:</b> structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator;
80	<a href="#">c3bhqB</a>	Alignment	not modelled	91.1	10	<b>PDBTitle:</b> crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family protein;
81	<a href="#">c5dajB</a>	Alignment	not modelled	91.1	20	<b>PDBTitle:</b> crystal structure of nald, the secondary repressor of mexab-oprm2 multidrug efflux pump in pseudomonas aeruginosa <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acr family protein;
82	<a href="#">c2raeA</a>	Alignment	not modelled	91.1	19	<b>PDBTitle:</b> crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acr family protein;
83	<a href="#">c1ixrA</a>	Alignment	not modelled	91.1	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruva; <b>PDBTitle:</b> ruva-ruvb complex
84	<a href="#">c3iuvA</a>	Alignment	not modelled	91.0	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
85	<a href="#">c3qbmA</a>	Alignment	not modelled	91.0	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr transcriptional regulator (caur_2221) from2 chloroflexus aurantiacus j-10-fl at 1.80 a resolution
86	<a href="#">c5d19A</a>	Alignment	not modelled	91.0	15	<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
87	<a href="#">c5k7fA</a>	Alignment	not modelled	91.0	24	<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
88	<a href="#">c5zvqA</a>	Alignment	not modelled	91.0	36	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recombination mediator protein recr
89	<a href="#">c2wuia</a>	Alignment	not modelled	90.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
90	<a href="#">c2yvha</a>	Alignment	not modelled	90.9	14	<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
91	<a href="#">c2y31A</a>	Alignment	not modelled	90.8	19	<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
92	<a href="#">d1ui5a1</a>	Alignment	not modelled	90.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
93	<a href="#">c1vi0B</a>	Alignment	not modelled	90.8	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
94	<a href="#">d1pb6a1</a>	Alignment	not modelled	90.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
95	<a href="#">d2fx0a1</a>	Alignment	not modelled	90.8	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
96	<a href="#">c2of7A</a>	Alignment	not modelled	90.8	17	<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
97	<a href="#">c2bcuA</a>	Alignment	not modelled	90.7	20	<b>PDB header:</b> transferase, lyase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase lambda; <b>PDBTitle:</b> dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
98	<a href="#">d2np5a1</a>	Alignment	not modelled	90.7	13	<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="#">c3dewA</a>	Alignment	not modelled	90.7	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the structure of a putative tetr family transcriptional regulator from2 geobacter sulfurreducens pca.
100	<a href="#">c6g8hC</a>	Alignment	not modelled	90.7	14	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> tetr/acrr family transcriptional regulator; <b>PDBTitle:</b> flavonoid-responsive regulator frra in complex with naringenin
101	<a href="#">c3vprA</a>	Alignment	not modelled	90.7	21	<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
102	<a href="#">c2nx4A</a>	Alignment	not modelled	90.7	29	<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.
103	<a href="#">d2gena1</a>	Alignment	not modelled	90.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
104	<a href="#">c5z2vB</a>	Alignment	not modelled	90.6	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recr from pseudomonas aeruginosa



						pao1
105	<a href="#">d2vkea1</a>	Alignment	not modelled	90.6	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
106	<a href="#">c4gctA</a>	Alignment	not modelled	90.6	14	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoid occlusion factor slma; <b>PDBTitle:</b> structure of no factor protein-dna complex
107	<a href="#">c2g3bB</a>	Alignment	not modelled	90.5	16	<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.
108	<a href="#">c2hytA</a>	Alignment	not modelled	90.5	14	<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
109	<a href="#">c2guhA</a>	Alignment	not modelled	90.5	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
110	<a href="#">c2i10A</a>	Alignment	not modelled	90.5	15	<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
111	<a href="#">c2eh3A</a>	Alignment	not modelled	90.5	5	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
112	<a href="#">c2fbqA</a>	Alignment	not modelled	90.4	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> the crystal structure of transcriptional regulator pa3006
113	<a href="#">c3ppbB</a>	Alignment	not modelled	90.4	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr family transcription regulator; <b>PDBTitle:</b> crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
114	<a href="#">c3g7rB</a>	Alignment	not modelled	90.4	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of sco4454, a tetr-family transcriptional regulator2 from streptomyces coelicolor
115	<a href="#">d2d6ya1</a>	Alignment	not modelled	90.4	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
116	<a href="#">c3dcfB</a>	Alignment	not modelled	90.4	14	<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
117	<a href="#">d2o7ta1</a>	Alignment	not modelled	90.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
118	<a href="#">c3b6aC</a>	Alignment	not modelled	90.3	18	<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
119	<a href="#">c2fq4A</a>	Alignment	not modelled	90.3	8	<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
120	<a href="#">c2hxiA</a>	Alignment	not modelled	90.3	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator from streptomyces coelicolor a3(2)