



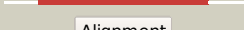

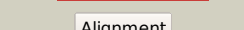

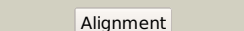


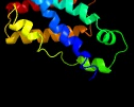






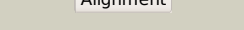

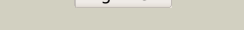



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0258c_(-)_310294_310749
Date	Tue Jul 23 14:50:32 BST 2019
Unique Job ID	37f8e8713aa8f635

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2np3A_	 Alignment		100.0	23	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family regulator; PDBTitle: crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
2	d2np3a2	 Alignment		100.0	24	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
3	c2guhA_	 Alignment		99.0	15	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
4	d2fq4a2	 Alignment		96.8	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
5	d2id3a2	 Alignment		95.4	14	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
6	c5d1wD_	 Alignment		93.6	12	PDB header: transcription Chain: D: PDB Molecule: rv3249c transcriptional regulator; PDBTitle: crystal structure of mycobacterium tuberculosis rv3249c2 transcriptional regulator.
7	c5ydpC_	 Alignment		91.7	14	PDB header: gene regulation Chain: C: PDB Molecule: tetr transcriptional regulatory protein; PDBTitle: crystal structure of tetr family repressor alkx from dietzia sp.2 strain dq12-45-1b implicated in biodegradation of n-alkanes
8	d2np5a2	 Alignment		91.2	22	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
9	c5x5iC_	 Alignment		90.0	8	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator rcda; PDBTitle: the x-ray crystal structure of a tetr family transcription regulator2 rcda involved in the regulation of biofilm formation in escherichia3 coli
10	d1t56a2	 Alignment		87.6	10	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
11	c3g56A_	 Alignment		82.3	7	PDB header: dna binding protein Chain: A: PDB Molecule: regulator of macrolide 2'-phosphotransferase i; PDBTitle: structure of the macrolide biosensor protein, mphr(a)

12	c2zb9A_	Alignment		68.3	20	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of tetr family transcription regulator2 sco332
13	c6g8hC_	Alignment		67.5	12	PDB header: transcription Chain: C: PDB Molecule: tetr/acrr family transcriptional regulator; PDBTitle: flavonoid-responsive regulator frfa in complex with naringenin
14	c2id3A_	Alignment		55.5	13	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
15	d2gena2	Alignment		52.0	8	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
16	d1t33a2	Alignment		51.7	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
17	c2qibA_	Alignment		50.1	12	PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
18	c5mruA_	Alignment		42.1	11	PDB header: transcription Chain: A: PDB Molecule: tetracycline repressor, class a; PDBTitle: tetr(class a) in complex with 5a,6-anhydrotetracycline and magnesium
19	c1t33B_	Alignment		40.4	7	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional repressor (tetr/acrr family); PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional repressor (tetr/acrr family) from salmonella3 typhimurim lt2
20	c2fq4A_	Alignment		35.9	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus
21	c3nxC_	Alignment	not modelled	35.0	11	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type protein slma; PDBTitle: molecular mechanism by which the escherichia coli nucleoid occlusion2 factor, slma, keeps cytokinesis in check
22	c2dg8D_	Alignment	not modelled	33.8	8	PDB header: gene regulation Chain: D: PDB Molecule: putative tetr-family transcriptional regulatory protein; PDBTitle: crystal structure of the putative trasncriptional regulator sco75182 from streptomyces coelicolor a3(2)
23	c2np5A_	Alignment	not modelled	33.2	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
24	d1rkt2	Alignment	not modelled	30.5	10	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
25	c5zghK_	Alignment	not modelled	30.3	29	PDB header: photosynthesis Chain: K: PDB Molecule: psak; PDBTitle: cryo-em structure of the red algal psi-lhcr
26	c3npiB_	Alignment	not modelled	23.9	11	PDB header: gene regulation Chain: B: PDB Molecule: tetr family regulatory protein; PDBTitle: crystal structure of a tetr family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution
27	c4jl3B_	Alignment	not modelled	23.6	17	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of ms6564-dna complex
28	d1axna_	Alignment	not modelled	23.4	15	Fold: Annexin Superfamily: Annexin Family: Annexin

29	d2gfna2	Alignment	not modelled	23.2	10	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
30	c2m0nA	Alignment	not modelled	22.9	19	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
31	c4nn1A	Alignment	not modelled	22.4	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator rv1219c of2 mycobacterium tuberculosis
32	c2fmmE	Alignment	not modelled	21.3	2	PDB header: transcription Chain: E: PDB Molecule: protein emsy; PDBTitle: crystal structure of emsy-hp1 complex
33	d2fmme1	Alignment	not modelled	18.3	2	Fold: ENT-like Superfamily: ENT-like Family: Emsy N terminal (ENT) domain-like
34	d1avca1	Alignment	not modelled	17.0	13	Fold: Annexin Superfamily: Annexin Family: Annexin
35	c2oerA	Alignment	not modelled	16.0	14	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: probable transcriptional regulator from pseudomonas aeruginosa
36	c3o14B	Alignment	not modelled	15.4	8	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
37	c2of7A	Alignment	not modelled	15.3	13	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
38	c3mn1A	Alignment	not modelled	15.0	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein (probably tetr-family); PDBTitle: the crystal structure of kstr (rv3574) from mycobacterium tuberculosis2 h37rv
39	c5vl9D	Alignment	not modelled	14.9	9	PDB header: transcription/dna Chain: D: PDB Molecule: regulatory protein tetr; PDBTitle: crystal structure of eilr in complex with eilo dna element
40	c6fosK	Alignment	not modelled	14.5	29	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x; PDBTitle: cyanidioschyzon merolae photosystem i
41	c3s5rA	Alignment	not modelled	14.2	9	PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator tetr family; PDBTitle: crystal structure of a putative transcriptional regulator of the tetr2 family (syn_02108) from syntrophus aciditrophicus at 2.60 a3 resolution
42	c3cwrA	Alignment	not modelled	13.4	8	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of transcriptional regulator of tetr family2 (yp_425770.1) from rhodospirillum rubrum atcc 11170 at 1.50 a3 resolution
43	c2lkyA	Alignment	not modelled	13.3	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeq_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
44	c3cjdB	Alignment	not modelled	12.3	4	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution
45	c2dg7A	Alignment	not modelled	12.2	10	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
46	d2fd5a2	Alignment	not modelled	12.2	10	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
47	c3l9vE	Alignment	not modelled	11.9	23	PDB header: oxidoreductase Chain: E: PDB Molecule: putative thiol-disulfide isomerase or thioredoxin; PDBTitle: crystal structure of salmonella enterica serovar typhimurium srga
48	d1uz3a1	Alignment	not modelled	11.1	2	Fold: ENT-like Superfamily: ENT-like Family: Emsy N terminal (ENT) domain-like
49	c2kvcA	Alignment	not modelled	11.1	4	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
50	c2wmmA	Alignment	not modelled	10.9	15	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein mukb; PDBTitle: crystal structure of the hinge domain of mukb
51	c3cd1A	Alignment	not modelled	10.7	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator aefr; PDBTitle: crystal structure of a tetr family transcriptional regulator from2 pseudomonas syringae pv. tomato str. dc3000
52	c3iuvA	Alignment	not modelled	10.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized tetr family protein; PDBTitle: the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3

53	c3c2bA_	Alignment	not modelled	10.2	8	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
54	c2yvvhA_	Alignment	not modelled	9.1	12	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the operator-binding form of the multi-drug2 binding transcriptional repressor cgmr
55	d2g3ba2	Alignment	not modelled	8.7	12	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
56	c3ibpA_	Alignment	not modelled	8.4	15	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein mukb; PDBTitle: the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
57	c5yq7H_	Alignment	not modelled	8.1	25	PDB header: photosynthesis Chain: H: PDB Molecule: alpha subunit of light-harvesting 1; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
58	d1ycna_	Alignment	not modelled	7.9	10	Fold: Annexin Superfamily: Annexin Family: Annexin
59	c1q90M_	Alignment	not modelled	7.8	33	PDB header: photosynthesis Chain: M: PDB Molecule: cytochrome b6f complex subunit petm; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
60	d1q90m_	Alignment	not modelled	7.8	33	Fold: Single transmembrane helix Superfamily: PetM subunit of the cytochrome b6f complex Family: PetM subunit of the cytochrome b6f complex
61	c3bniA_	Alignment	not modelled	7.7	12	PDB header: transcription regulator Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
62	d1w7ba_	Alignment	not modelled	7.7	13	Fold: Annexin Superfamily: Annexin Family: Annexin
63	c3bhqB_	Alignment	not modelled	7.4	12	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution
64	c2eh3A_	Alignment	not modelled	7.2	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
65	c3jsjC_	Alignment	not modelled	6.6	12	PDB header: transcription Chain: C: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of a putative tetr-transcriptional regulator2 (sav143) from streptomyces avermitilis ma-4680 at 2.10 a resolution
66	c6c4rA_	Alignment	not modelled	6.3	6	PDB header: oxidoreductase Chain: A: PDB Molecule: staphylopine dehydrogenase; PDBTitle: staphylopine dehydrogenase (saodh) - apo
67	c3bjbE_	Alignment	not modelled	6.2	12	PDB header: transcription regulator Chain: E: PDB Molecule: probable transcriptional regulator, tetr family protein; PDBTitle: crystal structure of a tetr transcriptional regulator from rhodococcus2 sp. rha1
68	d1i4aa_	Alignment	not modelled	6.1	11	Fold: Annexin Superfamily: Annexin Family: Annexin
69	d1v7ba2	Alignment	not modelled	5.8	13	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
70	d2aq0a1	Alignment	not modelled	5.4	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like