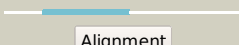



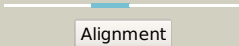


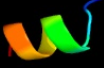
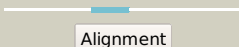

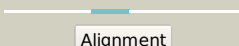

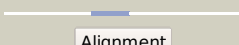

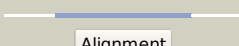

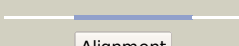
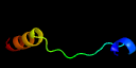
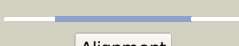


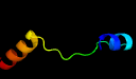

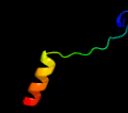

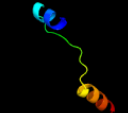
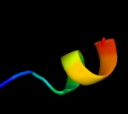


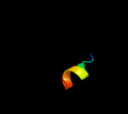



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2309Xc_(RVBD2309Xc)_2582487_2582654
 Date Mon Aug 5 13:25:45 BST 2019
 Unique Job ID 068321a7df129846

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6amaO_	 Alignment		35.3	20	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
2	c2jmlA_	 Alignment		32.9	60	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
3	d1r8da_	 Alignment		31.5	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
4	c4r4eA_	 Alignment		31.2	27	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
5	c4r24B_	 Alignment		30.9	50	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator trna; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
6	c2vz4A_	 Alignment		30.6	30	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
7	d1q06a_	 Alignment		29.9	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
8	c4jjiA_	 Alignment		29.7	28	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of t. fusca gh48 d224n mutant
9	d1l1ya_	 Alignment		29.2	25	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
10	c4fusA_	 Alignment		28.6	31	PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related ca2+-binding protein; PDBTitle: the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
11	c4el8A_	 Alignment		27.7	42	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.bescii cela gh48 module

12	d2coba1	Alignment		27.6	56	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
13	c1l2aD	Alignment		26.1	25	PDB header: hydrolase Chain: D: PDB Molecule: cellobiohydrolase; PDBTitle: the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
14	c5c8eC	Alignment		22.7	50	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
15	d1g9ga	Alignment		22.0	25	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
16	c2zhhA	Alignment		21.7	30	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
17	c3gp4B	Alignment		21.3	40	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
18	d1r8ea1	Alignment		19.7	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
19	c5i44E	Alignment		18.7	30	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
20	c3qaoA	Alignment		17.3	30	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
21	c1hlvA	Alignment	not modelled	16.8	29	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
22	c4kkkA	Alignment	not modelled	14.9	22	PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
23	c3gpvA	Alignment	not modelled	14.5	40	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
24	c5gpeB	Alignment	not modelled	14.3	20	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, merr-family; PDBTitle: crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
25	c3hh0C	Alignment	not modelled	12.1	30	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
26	c5crIA	Alignment	not modelled	12.1	30	PDB header: metal binding protein Chain: A: PDB Molecule: mercuric resistance operon regulatory protein; PDBTitle: crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
27	d1bw6a	Alignment	not modelled	11.6	40	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
28	c6itwA	Alignment	not modelled	11.3	25	PDB header: antitoxin Chain: A: PDB Molecule: type vi immunity protein atu4351; PDBTitle: crystal structure of atu4351 from agrobacterium tumefaciens

29	c5bv9A_	Alignment	not modelled	10.6	32	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of bacillus pumilus gh48 in complex with cellobiose
30	d1hlva1	Alignment	not modelled	10.2	40	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
31	c5af3A_	Alignment	not modelled	9.7	37	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
32	c2nvjA_	Alignment	not modelled	8.1	33	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
33	d2enda_	Alignment	not modelled	7.9	21	Fold: T4 endonuclease V Superfamily: T4 endonuclease V Family: T4 endonuclease V
34	d1jfla1	Alignment	not modelled	7.8	46	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
35	c2ruhA_	Alignment	not modelled	7.7	67	PDB header: peptide binding protein Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mdm2; PDBTitle: chemical shift assignments for mip and mdm2 in bound state
36	c2dx7B_	Alignment	not modelled	6.7	46	PDB header: isomerase Chain: B: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
37	c2ky4A_	Alignment	not modelled	6.4	32	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
38	c6nmiB_	Alignment	not modelled	6.3	37	PDB header: transcription Chain: B: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: cryo-em structure of the human tfiih core complex
39	d1gtra2	Alignment	not modelled	6.2	50	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
40	c2zskA_	Alignment	not modelled	5.8	62	PDB header: unknown function Chain: A: PDB Molecule: 226aa long hypothetical aspartate racemase; PDBTitle: crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
41	c2elhA_	Alignment	not modelled	5.7	80	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
42	c4j2nA_	Alignment	not modelled	5.7	29	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
43	c4j2nB_	Alignment	not modelled	5.7	29	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
44	c5wxzA_	Alignment	not modelled	5.6	38	PDB header: isomerase Chain: A: PDB Molecule: mcyf; PDBTitle: crystal structure of microcystis aeruginosa pcc 7806 aspartate2 racemase in complex with d-aspartate
45	c3al0C_	Alignment	not modelled	5.3	50	PDB header: ligase/rna Chain: C: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit c,linker, PDBTitle: crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
46	c2ja2A_	Alignment	not modelled	5.2	63	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: mycobacterium tuberculosis glutamyl-trna synthetase