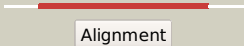

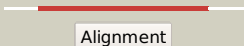

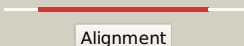







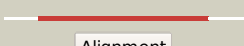










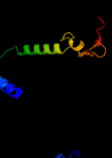






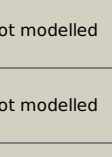


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2317_(uspB)_2589707_2590531
Date	Mon Aug 5 13:25:46 BST 2019
Unique Job ID	fc0dba08204a4d38

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r6gg1	 Alignment		100.0	21	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
2	c4tqvj_	 Alignment		100.0	25	PDB header: transport protein Chain: J; PDB Molecule: algm2; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
3	c3fh6F_	 Alignment		100.0	18	PDB header: transport protein Chain: F; PDB Molecule: maltose transport system permease protein malF; PDBTitle: crystal structure of the resting state maltose transporter from e.2 coli
4	c4tqvj_	 Alignment		100.0	12	PDB header: transport protein Chain: I; PDB Molecule: algm1; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
5	c2r6gF_	 Alignment		100.0	20	PDB header: hydrolase/transport protein Chain: F; PDB Molecule: maltose transport system permease protein malF; PDBTitle: the crystal structure of the e. coli maltose transporter
6	c2onkC_	 Alignment		100.0	19	PDB header: membrane protein Chain: C; PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
7	d2onkc1	 Alignment		100.0	19	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	c3d31D_	 Alignment		100.0	16	PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
9	d3d31c1	 Alignment		100.0	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	d2r6gf2	 Alignment		100.0	20	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
11	c4ymuC_	 Alignment		99.9	13	PDB header: protein binding/transport protein Chain: C; PDB Molecule: abc-type amino acid transport system, permease component; PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps

12	d3dhwa1	Alignment		99.8	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	c5kbuA	Alignment		79.7	6	PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor 2,voltage-dependent calcium channel PDBTitle: cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution
14	d2r6gf1	Alignment		77.8	16	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
15	c2m8gX	Alignment		50.5	16	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
16	c4l5eA	Alignment		46.1	6	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
17	d1umqa	Alignment		42.0	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
18	c1umqA	Alignment		42.0	6	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
19	d1fipa	Alignment		39.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
20	c3e7lD	Alignment		37.9	19	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
21	d1ntca	Alignment	not modelled	37.3	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
22	d1etob	Alignment	not modelled	36.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
23	d1etxa	Alignment	not modelled	33.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
24	c2hx6A	Alignment	not modelled	28.7	19	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
25	c1g2hA	Alignment	not modelled	27.4	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
26	d1g2ha	Alignment	not modelled	27.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
27	c5m7nA	Alignment	not modelled	22.3	10	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
28	c1ojlD	Alignment	not modelled	17.3	13	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54

						binding
29	c1bctA	Alignment	not modelled	8.0	11	PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution
30	c2cw1A	Alignment	not modelled	8.0	27	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
31	d1cf7a	Alignment	not modelled	7.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp
32	c4j2nA	Alignment	not modelled	7.5	20	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
33	c4j2nB	Alignment	not modelled	7.5	20	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
34	c4cvoA	Alignment	not modelled	7.3	14	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-6; PDBTitle: crystal structure of the n-terminal colied-coil domain of human dna2 excision repair protein ercc-6
35	c4v1ad	Alignment	not modelled	7.2	33	PDB header: ribosome Chain: D: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
36	c3wg7T	Alignment	not modelled	7.1	15	PDB header: oxidoreductase Chain: T: PDB Molecule: cytochrome c oxidase subunit 6a2, mitochondrial; PDBTitle: a 1.9 angstrom radiation damage free x-ray structure of large (420kda)2 protein by femtosecond crystallography
37	c1pyuD	Alignment	not modelled	6.9	31	PDB header: lyase Chain: D: PDB Molecule: aspartate 1-decarboxylase alfa chain; PDBTitle: processed aspartate decarboxylase mutant with ser25 mutated to cys
38	d1v54g	Alignment	not modelled	6.8	15	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIa Family: Mitochondrial cytochrome c oxidase subunit VIa
39	d2ns0a1	Alignment	not modelled	6.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
40	c4qiwT	Alignment	not modelled	5.9	36	PDB header: transcription Chain: T: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
41	d1brwa3	Alignment	not modelled	5.9	35	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
42	d2diia1	Alignment	not modelled	5.9	17	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
43	d2tpta3	Alignment	not modelled	5.8	18	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
44	c1vc3B	Alignment	not modelled	5.8	31	PDB header: lyase Chain: B: PDB Molecule: l-aspartate-alpha-decarboxylase heavy chain; PDBTitle: crystal structure of l-aspartate-alpha-decarboxylase
45	c1uheA	Alignment	not modelled	5.6	38	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase alpha chain; PDBTitle: crystal structure of aspartate decarboxylase, isoasparagine complex
46	d2jdih2	Alignment	not modelled	5.5	37	Fold: Epsilon subunit of F1F0-ATP synthase N-terminal domain Superfamily: Epsilon subunit of F1F0-ATP synthase N-terminal domain Family: Epsilon subunit of F1F0-ATP synthase N-terminal domain
47	c2diiA	Alignment	not modelled	5.5	17	PDB header: transcription Chain: A: PDB Molecule: tfiih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
48	c1vw42	Alignment	not modelled	5.5	25	PDB header: ribosome Chain: 2: PDB Molecule: 54s ribosomal protein l28, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
49	c2w6jH	Alignment	not modelled	5.4	35	PDB header: hydrolase Chain: H: PDB Molecule: f1-atpase delta subunit; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 5.
50	c2i5gB	Alignment	not modelled	5.4	20	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal strcuture of amidohydrolase from pseudomonas aeruginosa
51	c3plxB	Alignment	not modelled	5.3	23	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
52	c1twcF	Alignment	not modelled	5.3	29	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii 23 PDBTitle: rna polymerase ii complexed with gtp
53	d1twff	Alignment	not modelled	5.3	29	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6