
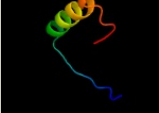



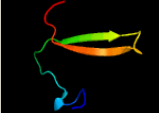





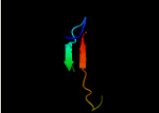

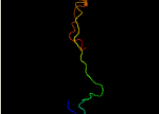

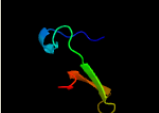

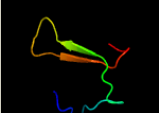

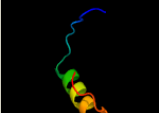


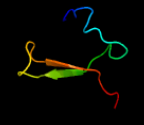

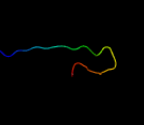
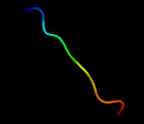
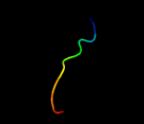

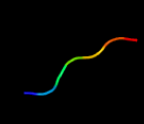
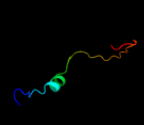


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2472_(-)_2775282_2775575
Date	Wed Aug 7 12:50:10 BST 2019
Unique Job ID	bda4a3a1cd30a04d

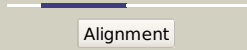
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bj7a1	 Alignment		26.1	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
2	c2ca9B_	 Alignment		17.3	21	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
3	c5l6mA_	 Alignment		16.2	33	PDB header: hydrolase Chain: A: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
4	d1r53a_	 Alignment		15.3	42	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
5	c6nklD_	 Alignment		13.4	35	PDB header: antitoxin Chain: D: PDB Molecule: antitoxin vapb1; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
6	d1v8ca2	 Alignment		13.2	46	Fold: TBP-like Superfamily: MoaD-related protein, C-terminal domain Family: MoaD-related protein, C-terminal domain
7	c4lj2A_	 Alignment		12.7	29	PDB header: lyase Chain: A: PDB Molecule: chorismate synthase; PDBTitle: crystal structure of chorismate synthase from acinetobacter baumannii2 at 3.15a resolution
8	c5l6lD_	 Alignment		12.7	36	PDB header: hydrolase Chain: D: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 bound to operator dna
9	c3tndF_	 Alignment		12.2	24	PDB header: translation, toxin Chain: F: PDB Molecule: antitoxin vapb; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
10	c1q5vB_	 Alignment		10.8	21	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
11	c2bj3D_	 Alignment		10.3	18	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo

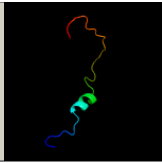
12	c3zvkg_	Alignment		8.8	44	PDB header: antitoxin/toxin/dna Chain: G: PDB Molecule: antitoxin of toxin-antitoxin system vapb; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
13	c3ms6a_	Alignment		8.5	47	PDB header: protein binding Chain: A: PDB Molecule: hepatitis b virus x-interacting protein; PDBTitle: crystal structure of hepatitis b x-interacting protein (hbxi)
14	d1sq1a_	Alignment		8.1	26	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
15	d1p9qc3	Alignment		8.0	50	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain
16	d1rdua_	Alignment		7.7	36	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
17	c2wfbA_	Alignment		6.8	83	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
18	c5z2fa_	Alignment		6.1	57	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14
19	d4ubpb_	Alignment		5.8	36	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit

20

[d1ejxb_](#)



Alignment



5.7

30

Fold:beta-clip
Superfamily:Urease, beta-subunit
Family:Urease, beta-subunit