
























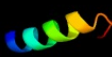


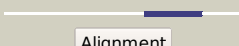

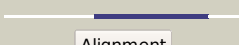
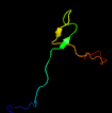
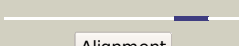



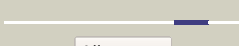
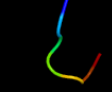


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2665 (-) _2982709_2982990
Date	Wed Aug 7 12:50:31 BST 2019
Unique Job ID	41417385491e61f7

Detailed template information

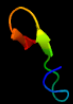
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4dq5B_	 Alignment		29.4	65	PDB header: membrane protein Chain: B: PDB Molecule: membrane protein phi6 p5wt; PDBTitle: structural investigation of bacteriophage phi6 lysin (wt)
2	c3ifuA_	 Alignment		26.3	56	PDB header: transcription Chain: A: PDB Molecule: non-structural protein; PDBTitle: the crystal structure of porcine reproductive and respiratory syndrome2 virus (prsv) leader protease nsp1
3	d1ubdc1_	 Alignment		14.3	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
4	c5mm2B_	 Alignment		13.1	39	PDB header: virus Chain: B: PDB Molecule: capsid protein vp4b; PDBTitle: nora virus structure
5	c6g4wr_	 Alignment		11.8	47	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s17; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a
6	c5cm2M_	 Alignment		11.1	33	PDB header: transferase Chain: M: PDB Molecule: trna methyltransferase activator subunit; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
7	c2j6aA_	 Alignment		10.7	27	PDB header: transferase Chain: A: PDB Molecule: protein trm112; PDBTitle: crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
8	d1k28a1_	 Alignment		8.2	25	Fold: OB-fold Superfamily: gp5 N-terminal domain-like Family: gp4 N-terminal domain-like
9	d1j75a_	 Alignment		6.6	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
10	c3a44D_	 Alignment		6.5	18	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
11	c2kdxA_	 Alignment		6.1	18	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein

12	c2elnA_	 Alignment		5.9	56	PDB header: transcription Chain: A; PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 11th c2h2 zinc finger of human2 zinc finger protein 406
13	c2l69A_	 Alignment		5.8	42	PDB header: de novo protein Chain: A; PDB Molecule: rossmann 2x3 fold protein; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
14	c4xb6D_	 Alignment		5.5	35	PDB header: transferase Chain: D; PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
15	c2mjca_	 Alignment		5.5	29	PDB header: metal binding protein Chain: A; PDB Molecule: eukaryotic translation initiation factor 3 subunit g; PDBTitle: zn-binding domain of eukaryotic translation initiation factor 3,2 subunit g
16	c3n40P_	 Alignment		5.5	25	PDB header: viral protein Chain: P; PDB Molecule: p62 envelope glycoprotein; PDBTitle: crystal structure of the immature envelope glycoprotein complex of2 chikungunya virus.
17	c2lnbA_	 Alignment		5.4	40	PDB header: immune system Chain: A; PDB Molecule: z-dna-binding protein 1; PDBTitle: solution nmr structure of n-terminal domain (6-74) of human zbp12 protein, northeast structural genomics consortium target hr8174a.
18	c4l3uA_	 Alignment		5.3	44	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf3571 family protein (abaye3784) from2 acinetobacter baumannii aye at 1.95 a resolution
19	c3hy4A_	 Alignment		5.2	86	PDB header: ligase Chain: A; PDB Molecule: 5-formyltetrahydrofolate cyclo-ligase; PDBTitle: structure of human mthfs with n5-iminium phosphate

20

[c1pg5B_](#)

Alignment



5.2

28

PDB header:transferase

Chain: B: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain;

PDBTitle: crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius