
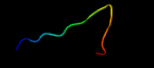





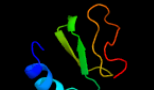

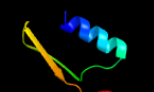











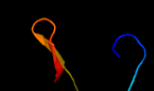









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1499_(-)_1690413_1690811
Date	Fri Aug 2 13:30:08 BST 2019
Unique Job ID	be542fec4fed7f83

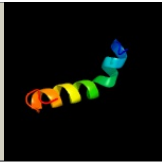
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qc2A_	 Alignment		25.0	53	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase; PDBTitle: crystal structure of a glycosyl hydrolase (bacova_03624) from <i>Bacteroides ovatus</i> at 2.30 Å resolution
2	d2a2ja1	 Alignment		18.6	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
3	d1k8ib2	 Alignment		18.4	36	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
4	d1r89a1	 Alignment		14.9	16	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: Archaeal tRNA CCA-adding enzyme substrate-binding domain
5	c4lowA_	 Alignment		14.3	20	PDB header: unknown function Chain: A: PDB Molecule: acraf; PDBTitle: structure and identification of a pterin dehydratase-like protein as α2 rubisco assembly factor in the α-carboxysome
6	c3kb4D_	 Alignment		13.8	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr8543 protein; PDBTitle: crystal structure of the alr8543 protein in complex with 2 geranylgeranyl monophosphate and magnesium ion from <i>Nostoc</i> sp. pcc 37120, northeast structural genomics consortium target nsr141
7	c2e6xD_	 Alignment		12.2	43	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ttha1281; PDBTitle: x-ray structure of tt1592 from <i>Thermus thermophilus</i> hb8
8	c3msqC_	 Alignment		12.1	31	PDB header: biosynthetic protein Chain: C: PDB Molecule: putative ubiquinone biosynthesis protein; PDBTitle: crystal structure of a putative ubiquinone biosynthesis protein 2 (npun02000094) from <i>Nostoc punctiforme</i> pcc 73102 at 2.85 Å resolution
9	c1zvbC_	 Alignment		9.6	78	PDB header: viral protein Chain: C: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of SARS virus membrane fusion
10	c2e76G_	 Alignment		9.5	86	PDB header: photosynthesis Chain: G: PDB Molecule: cytochrome b6-f complex subunit 5; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from <i>M. lamosus</i>
11	c6f37B_	 Alignment		9.1	9	PDB header: sugar binding protein Chain: B: PDB Molecule: nano3, fucose-binding lectin protein; PDBTitle: fusion protein of rsl and trimeric coiled coil

12	d2e74g1	Alignment		9.0	86	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
13	d1jw2a_	Alignment		8.7	46	Fold: Open three-helical up-and-down bundle Superfamily: Hemolysin expression modulating protein HHA Family: Hemolysin expression modulating protein HHA
14	c3m06F_	Alignment		8.2	45	PDB header: protein binding Chain: F; PDB Molecule: tnf receptor-associated factor 2; PDBTitle: crystal structure of traf2
15	d1soua_	Alignment		8.1	29	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase
16	d1ty9a_	Alignment		7.4	24	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
17	d1t1ja_	Alignment		6.4	26	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: Hypothetical protein PA1492
18	c3m0dC_	Alignment		6.2	56	PDB header: signaling protein Chain: C; PDB Molecule: tnf receptor-associated factor 1; PDBTitle: crystal structure of the traf1:traf2:ciap2 complex

19 [d2cx6a1](#)

Alignment



5.9

21

Fold:Barstar-like
Superfamily:Barstar-related
Family:Barstar-related