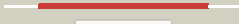


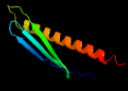





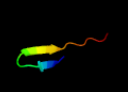

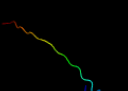







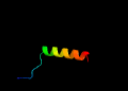




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1738 (-) _1965664_1965948
Date	Fri Aug 2 13:30:34 BST 2019
Unique Job ID	9d65d6b53c859f81

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wpyA_	 Alignment		100.0	100	PDB header: de novo protein Chain: A: PDB Molecule: protein dl-rv1738; PDBTitle: racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
2	d2fgga1	 Alignment		100.0	56	Fold: dsRBD-like Superfamily: Rv2632c-like Family: Rv2632c-like
3	c6j9mA_	 Alignment		54.8	36	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: nmebh+acriic2
4	c6j9mF_	 Alignment		52.2	38	PDB header: hydrolase/hydrolase inhibitor Chain: F: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: nmebh+acriic2
5	c3bcyA_	 Alignment		20.8	11	PDB header: unknown function Chain: A: PDB Molecule: protein yer067w; PDBTitle: crystal structure of yer067w
6	d2ibaa1	 Alignment		20.6	10	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
7	c5mhjA_	 Alignment		17.5	29	PDB header: transcription Chain: A: PDB Molecule: major viral transcription factor icp4; PDBTitle: icp4 dna-binding domain, lacking intrinsically disordered region, in2 complex with 12mer dna duplex from its own promoter
8	d1grja1	 Alignment		15.3	41	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
9	c2hjdA_	 Alignment		15.1	22	PDB header: signaling protein Chain: A: PDB Molecule: quorum-sensing antiactivator; PDBTitle: crystal structure of a second quorum sensing antiactivator tram2 from2 a. tumefaciens strain a6
10	c6jdxC_	 Alignment		14.2	33	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of acriic2 dimer in complex with partial nme1cas92 preprocessed with protease alpha-chymotrypsin
11	c4q0pA_	 Alignment		13.3	36	PDB header: isomerase Chain: A: PDB Molecule: l-ribose isomerase; PDBTitle: crystal structure of acinetobacter sp. d128 l-ribose isomerase in2 complex with l-ribose

12	c5my7A_	Alignment		12.1	16	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin; PDBTitle: adhesin complex protein from neisseria meningitidis
13	d2f23a1	Alignment		10.9	24	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
14	c1r56H_	Alignment		9.6	10	PDB header: oxidoreductase Chain: H: PDB Molecule: uricase; PDBTitle: uncomplexed urate oxidase from aspergillus flavus
15	d1j2ga1	Alignment		6.7	29	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
16	d2yzca1	Alignment		6.5	16	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
17	d1ci4a_	Alignment		5.9	27	Fold: SAM domain-like Superfamily: Barrier-to-autointegration factor, BAF Family: Barrier-to-autointegration factor, BAF
18	c4kzsA_	Alignment		5.6	40	PDB header: unknown function Chain: A: PDB Molecule: lpp20 lipofamily protein; PDBTitle: crystal structure of the secreted protein hp1454 from the human2 pathogen helicobacter pylori
19	c4fy1B_	Alignment		5.5	17	PDB header: translation Chain: B: PDB Molecule: ribosome hibernation protein yhbh; PDBTitle: high-resolution x-ray structure of hpf from vibrio cholerae
20	c4lg3B_	Alignment		5.3	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf487 family protein (despig_00776) from2 desulfovibrio piger atcc 29098 at 2.49 a resolution
21	d3ctda1	Alignment	not modelled	5.2	29	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
22	d2hkja2	Alignment	not modelled	5.1	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
23	d2rcda1	Alignment	not modelled	5.1	25	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
24	c2voiB_	Alignment	not modelled	5.0	50	PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist p13; PDBTitle: structure of mouse a1 bound to the bid bh3-domain