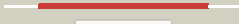



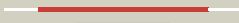


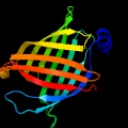





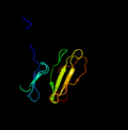

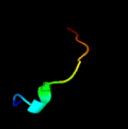

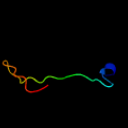



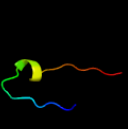
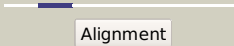
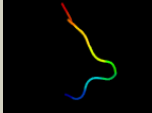
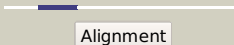

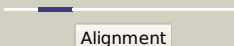


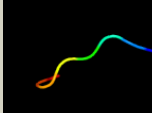
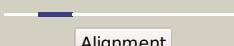
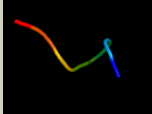
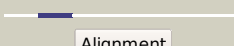
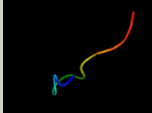
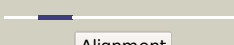






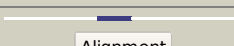
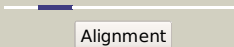


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2717c_(-)_3029877_3030371
Date	Wed Aug 7 12:50:37 BST 2019
Unique Job ID	8853971f46842064

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fr2a1	 Alignment		100.0	100	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717c-like
2	d2a13a1	 Alignment		100.0	41	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717c-like
3	c2fvva_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein mtubf_01000852; PDBTitle: crystal structure of rv0813
4	c3ia8A_	 Alignment		100.0	32	PDB header: metal binding protein Chain: A; PDB Molecule: thap domain-containing protein 4; PDBTitle: the structure of the c-terminal heme nitrobindin domain of thap2 domain-containing protein 4 from homo sapiens
5	d2o62a1	 Alignment		73.5	32	Fold: Lipocalins Superfamily: Lipocalins Family: All1756-like
6	d1jvaa2	 Alignment		45.7	33	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
7	c5yznA_	 Alignment		37.9	11	PDB header: hydrolase Chain: A; PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
8	c4mveB_	 Alignment		27.4	29	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcur_1030 protein from thermomonospora curvata
9	c5yvfD_	 Alignment		17.6	31	PDB header: plant protein Chain: D; PDB Molecule: bfa1; PDBTitle: crystal structure of bfa1
10	d2d8za1	 Alignment		8.7	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
11	c4kkaA_	 Alignment		8.1	30	PDB header: structural protein Chain: A; PDB Molecule: rbma protein; PDBTitle: crystal structure of vibrio cholerae rbma (crystal form 2)

12	c3fqmA_	 Alignment		7.1	40	PDB header: metal binding protein Chain: A; PDB Molecule: non-structural protein 5a; PDBTitle: crystal structure of a novel dimeric form of hcv ns5a domain i protein
13	c1b24A_	 Alignment		6.8	23	PDB header: intron-encoded Chain: A; PDB Molecule: protein (i-dmoi); PDBTitle: i-dmoi, intron-encoded endonuclease
14	c6dzpg_	 Alignment		6.4	13	PDB header: ribosome Chain: G; PDB Molecule: 50s ribosomal protein l6; PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit
15	d2cura2	 Alignment		6.2	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
16	c4i0xA_	 Alignment		6.1	57	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	d1vs6z1	 Alignment		5.6	23	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
18	c2b664_	 Alignment		5.6	27	PDB header: ribosome Chain: 4; PDB Molecule: 50s ribosomal protein l31; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
19	c2j034_	 Alignment		5.3	25	PDB header: ribosome Chain: 4; PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
20	d2j0141	 Alignment		5.3	25	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
21	c2mobA_	 Alignment	not modelled	5.2	23	PDB header: oxidoreductase Chain: A; PDB Molecule: protein (methane monooxygenase regulatory PDBTitle: methane monooxygenase component b
22	d2moba_	 Alignment	not modelled	5.2	23	Fold: Monooxygenase (hydroxylase) regulatory protein Superfamily: Monooxygenase (hydroxylase) regulatory protein Family: Monooxygenase (hydroxylase) regulatory protein
23	c5o60g_	 Alignment	not modelled	5.1	17	PDB header: ribosome Chain: G; PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis