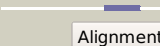

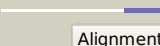

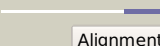
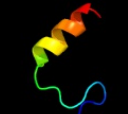
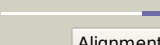
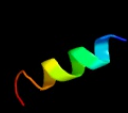
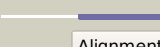

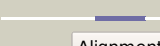


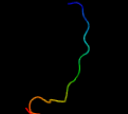





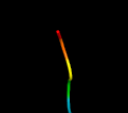

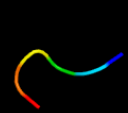


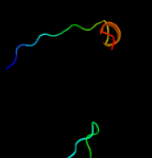
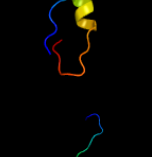

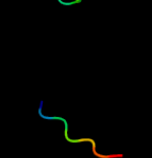
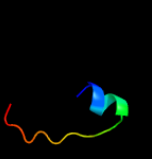
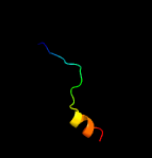
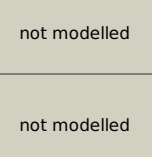


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2960c (-)_3312963_3313211
Date	Thu Aug 8 16:20:12 BST 2019
Unique Job ID	79abd7d2868ae42a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uwva2	 Alignment		19.6	50	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: (Uracil-5-)-methyltransferase
2	c5xs1A_	 Alignment		19.4	24	PDB header: hormone Chain: A: PDB Molecule: hyperglycemic hormone-like peptide; PDBTitle: solution structure of crustacean hyperglycemic hormone-like (chh-l)2 from the scylla olivacea
3	c5b5iB_	 Alignment		16.7	48	PDB header: hormone Chain: B: PDB Molecule: crustacean hyperglycemic hormones 1; PDBTitle: the crystal structure of a crustacean hyperglycemic hormone precursor2 from the kuruma prawn
4	c5x3iA_	 Alignment		12.5	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: pilosulin-1; PDBTitle: solution structure of a novel antimicrobial peptide, p1, from jumper2 ant myrmecia pilosula
5	c1vbkA_	 Alignment		11.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
6	c2xfyA_	 Alignment		10.9	44	PDB header: hydrolase Chain: A: PDB Molecule: beta-amylase; PDBTitle: crystal structure of barley beta-amylase complexed with alpha-2 cyclodextrin
7	d1wdpa1	 Alignment		10.5	44	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
8	d1fa2a_	 Alignment		10.1	44	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
9	d3b7sa1	 Alignment		9.9	38	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Leukotriene A4 hydrolase C-terminal domain
10	c4v1af_	 Alignment		9.8	83	PDB header: ribosome Chain: F: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
11	d2dloa1	 Alignment		9.1	67	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain

12	c5xj2C_	Alignment		8.9	14	PDB header: transferase/rna Chain: C: PDB Molecule: uncharacterized rna methyltransferase sp_1029; PDBTitle: structure of sprlmcid with u747 rna
13	c2yurA_	Alignment		8.9	25	PDB header: protein binding Chain: A: PDB Molecule: retinoblastoma-binding protein 6; PDBTitle: solution structure of the ring finger of human2 retinoblastoma-binding protein 6
14	d1b1ya_	Alignment		8.6	47	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
15	c4hrvB_	Alignment		8.1	23	PDB header: lipid binding protein Chain: B: PDB Molecule: putative lipoprotein gna1162; PDBTitle: crystal structure of lipoprotein gna1162 from neisseria meningitidis
16	c5j9hA_	Alignment		7.8	24	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: crystal structure of glycoprotein c from puumala virus in the post-2 fusion conformation (ph 8.0)
17	c1uwvA_	Alignment		7.3	50	PDB header: transferase Chain: A: PDB Molecule: 23s rna (uracil-5-)-methyltransferase ruma; PDBTitle: crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
18	c5ooma_	Alignment		7.2	71	PDB header: ribosome Chain: A: PDB Molecule: 16s ribosomal rna; PDBTitle: structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rna
19	d1xmta_	Alignment		6.5	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
20	c5ljya_	Alignment		6.5	33	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: structure of hantavirus envelope glycoprotein gc in complex with scfv2 a5
21	c4indR_	Alignment	not modelled	5.9	60	PDB header: viral protein Chain: R: PDB Molecule: c381 turret protein; PDBTitle: the triple jelly roll fold and turret assembly in an archaeal virus
22	c5y7IA_	Alignment	not modelled	5.8	50	PDB header: metal binding protein Chain: A: PDB Molecule: calcium-activated potassium channel subunit beta-4; PDBTitle: solution structure of hbeta4 extracellular loop of bk potassium2 channel
23	d3blhb1	Alignment	not modelled	5.6	21	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
24	c5lk1A_	Alignment	not modelled	5.4	33	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: structure of hantavirus envelope glycoprotein gc in postfusion2 conformation in presence of 200 mm kcl
25	d1sq4a_	Alignment	not modelled	5.2	57	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Ylba-like
26	c2k2tA_	Alignment	not modelled	5.2	47	PDB header: cell adhesion Chain: A: PDB Molecule: micronemal protein 6; PDBTitle: epidermal growth factor-like domain 2 from toxoplasma2 gondii microneme protein 6
27	d2fp1a1	Alignment	not modelled	5.1	29	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Secreted chorismate mutase-like
28	c1j0tA_	Alignment	not modelled	5.1	29	PDB header: hormone/growth factor Chain: A: PDB Molecule: molt-inhibiting hormone; PDBTitle: the solution structure of molt-inhibiting hormone from the2 kuruma prawn