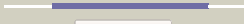
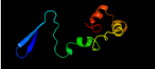





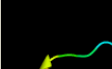



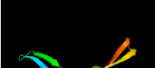



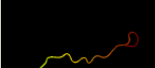




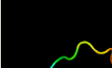
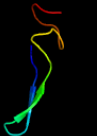
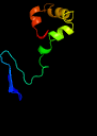



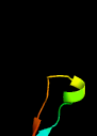

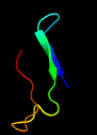
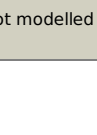


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2644c (-) _2968543_2968860
Date	Wed Aug 7 12:50:29 BST 2019
Unique Job ID	1445abea3b79bea1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ee8A_	 Alignment		16.3	41	PDB header: dna binding protein Chain: A; PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermophilus hb8
2	c5zqvG_	 Alignment		14.8	70	PDB header: hydrolase Chain: G; PDB Molecule: protein phosphatase 1 regulatory subunit 3a; PDBTitle: crystal structure of protein phosphatase 1 complexed with pp1 binding2 domain of gm
3	c5zqvH_	 Alignment		14.0	70	PDB header: hydrolase Chain: H; PDB Molecule: protein phosphatase 1 regulatory subunit 3a; PDBTitle: crystal structure of protein phosphatase 1 complexed with pp1 binding2 domain of gm
4	c5zqvF_	 Alignment		13.9	70	PDB header: hydrolase Chain: F; PDB Molecule: protein phosphatase 1 regulatory subunit 3a; PDBTitle: crystal structure of protein phosphatase 1 complexed with pp1 binding2 domain of gm
5	c6dnoB_	 Alignment		13.7	70	PDB header: signaling protein Chain: B; PDB Molecule: protein phosphatase 1 regulatory subunit 3a; PDBTitle: crystal structure of protein phosphatase 1 (pp1) bound to the muscle2 glycogen-targeting subunit (gm)
6	c3fveA_	 Alignment		12.5	24	PDB header: isomerase Chain: A; PDB Molecule: diaminopimelate epimerase; PDBTitle: crystal structure of diaminopimelate epimerase mycobacterium2 tuberculosis dapf
7	c5zqvE_	 Alignment		10.7	70	PDB header: hydrolase Chain: E; PDB Molecule: protein phosphatase 1 regulatory subunit 3a; PDBTitle: crystal structure of protein phosphatase 1 complexed with pp1 binding2 domain of gm
8	d1l4zb_	 Alignment		9.9	36	Fold: beta-Grasp (ubiquitin-like) Superfamily: Staphylokinase/streptokinase Family: Staphylokinase/streptokinase
9	d2b8ea1	 Alignment		9.7	35	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
10	c2k87A_	 Alignment		7.2	21	PDB header: viral protein, rna binding protein Chain: A; PDB Molecule: non-structural protein 3 of replicase polyprotein 1a; PDBTitle: nmr structure of a putative rna binding protein (sars1) from sars2 coronavirus
11	d1t1ra3	 Alignment		7.2	50	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

12	d1saza2	Alignment		7.2	31	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
13	c3twkB_	Alignment		7.0	21	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
14	c5xivA_	Alignment		6.8	40	PDB header: unknown function Chain: A: PDB Molecule: beta-ginkgotide, beta-gb1; PDBTitle: beta-ginkgotides: hyperdisulfide-constrained peptides from ginkgo2 biloba
15	c5ldwC_	Alignment		6.8	47	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, PDBTitle: structure of mammalian respiratory complex i, class1
16	c6musK_	Alignment		6.0	55	PDB header: rna binding protein/rna Chain: K: PDB Molecule: uncharacterized protein csm3; PDBTitle: cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system
17	c3fhkF_	Alignment		5.8	60	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
18	c3opyL_	Alignment		5.2	59	PDB header: transferase Chain: L: PDB Molecule: 6-phosphofructo-1-kinase gamma-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
19	d1g6ea_	Alignment		5.2	60	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Antifungal protein AFP1
20	d1bu8a2	Alignment		5.1	32	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
21	c2eouA_	Alignment	not modelled	5.0	86	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 473; PDBTitle: solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473