

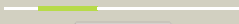




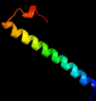



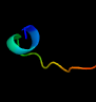

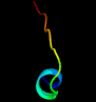



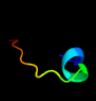

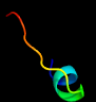




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2013 (-) _2260673_2261152
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	1addd0278fc39ccd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hjra_	 Alignment		68.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
2	c4ep5A_	 Alignment		62.2	32	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure
3	d2fi0a1	 Alignment		59.5	21	Fold: SP0561-like Superfamily: SP0561-like Family: SP0561-like
4	d2ozbb1	 Alignment		54.8	11	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
5	d1y81a1	 Alignment		53.2	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
6	c3ff4A_	 Alignment		47.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
7	c2duwA_	 Alignment		42.5	40	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of 2 klebsiella pneumoniae
8	d2d59a1	 Alignment		41.6	40	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
9	d1a9xa3	 Alignment		36.1	25	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
10	c5xavB_	 Alignment		35.2	27	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
11	c5t6oA_	 Alignment		31.2	40	PDB header: biosynthetic protein Chain: A: PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator

12	c5o9zH_	Alignment		26.4	11	PDB header: splicing Chain: H: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp31; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for 2 activation (b complex)
13	c5dotA_	Alignment		25.9	25	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1), 2 apo form
14	c5douC_	Alignment		23.6	25	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1), 2 ligand-bound form
15	c4as2D_	Alignment		22.9	50	PDB header: hydrolase Chain: D: PDB Molecule: phosphorylcholine phosphatase; PDBTitle: pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
16	d1iuka_	Alignment		22.2	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
17	c5axwA_	Alignment		20.9	18	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of staphylococcus aureus cas9 in complex with sgRNA2 and target DNA (ttgggt pam)
18	c4gxtA_	Alignment		19.9	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a conserved functionally unknown protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from anaerococcus prevotii DSM 20548
19	c3deeA_	Alignment		17.1	7	PDB header: transcription Chain: A: PDB Molecule: putative regulatory protein; PDBTitle: crystal structure of a putative regulatory protein involved in transcription (NGO1945) from Neisseria gonorrhoeae FA 1090 at 2.25 Å resolution
20	c4e17B_	Alignment		16.8	25	PDB header: cell adhesion Chain: B: PDB Molecule: catenin alpha-1; PDBTitle: alpha-e-catenin is an autoinhibited molecule that co-activates vinculin
21	c3icxB_	Alignment	not modelled	16.1	22	PDB header: RNA binding protein Chain: B: PDB Molecule: pre mRNA splicing protein; PDBTitle: crystal structure of Sulfolobus solfataricus Nop5 (135-380)
22	c2c9Iz_	Alignment	not modelled	14.6	17	PDB header: viral protein Chain: Z: PDB Molecule: bzfl1 trans-activator protein; PDBTitle: structure of the Epstein-Barr virus Zebra protein
23	c6cfzF_	Alignment	not modelled	12.0	12	PDB header: nuclear protein Chain: F: PDB Molecule: dad1, dad1; PDBTitle: structure of the Dash/Dam1 complex shows its role at the yeast 2 kinetochore-microtubule interface
24	c4i2nC_	Alignment	not modelled	11.5	19	PDB header: hydrolase Chain: C: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31 kDa heat shock protein, Vchsp31 from Vibrio cholerae
25	d1a9xa4	Alignment	not modelled	11.2	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
26	c5ig9H_	Alignment	not modelled	10.6	6	PDB header: ligase Chain: H: PDB Molecule: ATP grasp ligase; PDBTitle: crystal structure of macrocyclase MdnC bound with precursor peptide 2 mRNA from Microcystis aeruginosa MRC
27	c2rauA_	Alignment	not modelled	10.4	33	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from Sulfolobus solfataricus at 1.85 Å resolution
28	c3id6A_	Alignment	not modelled	10.1	22	PDB header: transferase Chain: A: PDB Molecule: pre mRNA splicing protein; PDBTitle: crystal structure of Sulfolobus solfataricus Nop5 (1-262) and 2 fibrillar complex
29	c5xr2D_	Alignment	not modelled	8.9	40	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase Hcha;

						PDBTitle: sav0551
30	c4e18B_	Alignment	not modelled	8.7	25	PDB header: cell adhesion Chain: B: PDB Molecule: catenin alpha-1; PDBTitle: alpha-e-catenin is an autoinhibited molecule that co-activates2 vinculin
31	c6nd4b_	Alignment	not modelled	8.7	16	PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
32	c2lyhA_	Alignment	not modelled	8.6	12	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
33	c6ewvA_	Alignment	not modelled	8.3	53	PDB header: peptide binding protein Chain: A: PDB Molecule: nrps kj12c-ndd, nrps kj12b-cdd; PDBTitle: solution structure of docking domain complex of rxp nrps: kj12c ndd -2 kj12b cdd
34	d2csua1	Alignment	not modelled	7.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
35	c2nnwC_	Alignment	not modelled	7.5	13	PDB header: transferase Chain: C: PDB Molecule: nop5/nop56 related protein; PDBTitle: alternative conformations of nop56/58-fibrillar complex and2 implication for induced-fit assenly of box c/d rnps
36	c3id5E_	Alignment	not modelled	7.5	22	PDB header: transferase/ribosomal protein/rna Chain: E: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillar, l7ae and a split half c/d rna
37	d1n57a_	Alignment	not modelled	6.8	27	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
38	d2aq0a1	Alignment	not modelled	6.6	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
39	c5ganF_	Alignment	not modelled	6.4	14	PDB header: transcription Chain: F: PDB Molecule: pre-mrna-processing factor 31; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
40	c5ig8A_	Alignment	not modelled	6.3	13	PDB header: ligase Chain: A: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnb from microcystis aeruginosa mrc
41	c5kstA_	Alignment	not modelled	6.2	44	PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase sure; PDBTitle: stationary phase survival protein e (sure) from xylella fastidiosa-2 xfsure-tsamp (tetramer smaller - crystallization with 3'amp).
42	c4qeaG_	Alignment	not modelled	6.2	19	PDB header: hydrolase Chain: G: PDB Molecule: 5'-nucleotidase sure; PDBTitle: crystal structure of stationary phase survival protein (sure) from2 brucella abortus
43	c1qgeD_	Alignment	not modelled	5.6	27	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
44	c3l3bA_	Alignment	not modelled	5.5	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
45	c3gr1A_	Alignment	not modelled	5.0	11	PDB header: membrane protein Chain: A: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-392)