






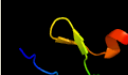

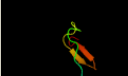

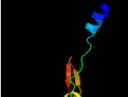

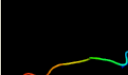

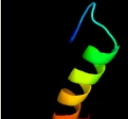

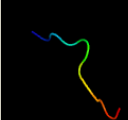

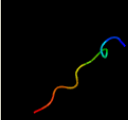




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2474c (-)_2776326_2776979
Date	Wed Aug 7 12:50:10 BST 2019
Unique Job ID	af88821577a8e22a

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1avyA_	 Alignment		45.9	26	PDB header: coiled coil Chain: A: PDB Molecule: fibritin; PDBTitle: fibritin deletion mutant m (bacteriophage t4)
2	c3g80B_	 Alignment		25.3	32	PDB header: viral protein Chain: B: PDB Molecule: protein b2; PDBTitle: nodamura virus protein b2, rna-binding domain
3	c1rfoC_	 Alignment		22.9	24	PDB header: viral protein Chain: C: PDB Molecule: whisker antigen control protein; PDBTitle: trimeric foldon of the t4 phagehead fibritin
4	c2lp7C_	 Alignment		17.6	28	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein; PDBTitle: structure of gp41-m-mat, a membrane associated mper trimer from hiv-12 gp41.
5	c1aa0A_	 Alignment		17.4	26	PDB header: attachment protein Chain: A: PDB Molecule: fibritin; PDBTitle: fibritin deletion mutant e (bacteriophage t4)
6	c1ox3A_	 Alignment		13.7	17	PDB header: chaperone Chain: A: PDB Molecule: fibritin; PDBTitle: crystal structure of mini-fibritin
7	d1k4na_	 Alignment		11.6	25	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Hypothetical protein YecM (EC4020)
8	c2knrA_	 Alignment		10.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atc0905; PDBTitle: solution structure of protein atu0922 from a. tumefaciens. northeast2 structural genomics consortium target att13. ontario center for3 structural proteomics target atc0905
9	c5o31Z_	 Alignment		9.8	33	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: mitochondrial complex i in the deactive state
10	c6gcsW_	 Alignment		9.1	36	PDB header: oxidoreductase Chain: W: PDB Molecule: nb6m subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
11	c2mckA_	 Alignment		8.9	75	PDB header: hydrolase Chain: A: PDB Molecule: polyprotein; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus cr6 ns1/2 protein

12	c5lnkq_	Alignment		7.7	36	PDB header: oxidoreductase Chain: Q: PDB Molecule: PDBTitle: entire ovine respiratory complex i
13	d1gsma1	Alignment		7.3	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
14	d1kbla2	Alignment		6.7	20	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
15	c2gqcA_	Alignment		6.6	21	PDB header: hydrolase Chain: A: PDB Molecule: rhomboid intramembrane protease; PDBTitle: solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa
16	c1v1cA_	Alignment		6.6	25	PDB header: sh3-domain Chain: A: PDB Molecule: obscurin; PDBTitle: solution structure of the sh3 domain of obscurin
17	c3mwzA_	Alignment		6.3	15	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: sialostatin I2; PDBTitle: crystal structure of the selenomethionine derivative of the I 22,47,2 100 m mutant of sialostatin I2
18	c1r7cA_	Alignment		5.6	67	PDB header: membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 50% tfe)
19	c1r7gA_	Alignment		5.6	67	PDB header: membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)
20	c4goqD_	Alignment		5.5	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1491 family protein (cc_1065) from2 caulobacter crescentus cb15 at 1.87 a resolution
21	d2pstx1	Alignment	not modelled	5.5	17	Fold: MbtH/L9 domain-like Superfamily: MbtH-like Family: MbtH-like
22	d3ci0k1	Alignment	not modelled	5.4	30	Fold: SAM domain-like Superfamily: GspK insert domain-like Family: GspK insert domain-like
23	c5xtbW_	Alignment	not modelled	5.1	33	PDB header: oxidoreductase/electron transport Chain: W: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: cryo-em structure of human respiratory complex i matrix arm