
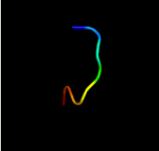

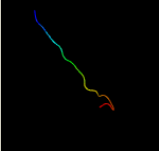
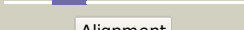






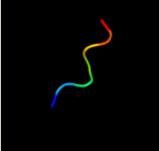

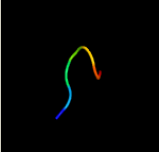

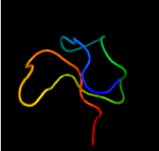
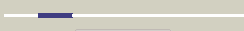


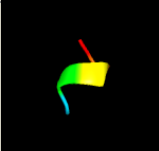

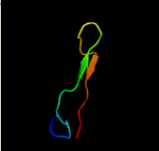

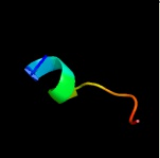
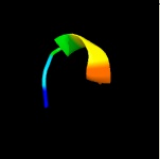
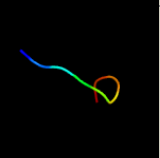
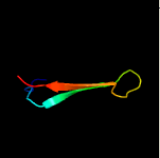
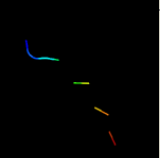

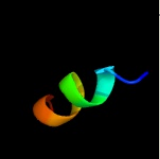
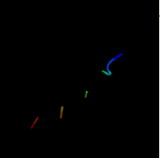


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2730_(-)_3042552_3043028
Date	Wed Aug 7 12:50:38 BST 2019
Unique Job ID	92283dd698846a76

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2knuA_	 Alignment		50.4	75	PDB header: membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of the transmembrane proximal region of2 the hepatitis c virus e1 glycoprotein
2	c6atkE_	 Alignment		20.8	33	PDB header: hydrolase/viral protein Chain: E: PDB Molecule: spike glycoprotein; PDBTitle: crystal structure of the human coronavirus 229e spike protein receptor2 binding domain in complex with human aminopeptidase n
3	c1vw4G_	 Alignment		14.1	67	PDB header: ribosome Chain: G: PDB Molecule: 54s ribosomal protein l50, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
4	c3kk4B_	 Alignment		13.2	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
5	c2m7tA_	 Alignment		11.9	67	PDB header: protein binding Chain: A: PDB Molecule: cystine knot protein 2.5d; PDBTitle: solution nmr structure of engineered cystine knot protein 2.5d
6	c5a4hA_	 Alignment		8.6	71	PDB header: transferase Chain: A: PDB Molecule: 1-acylglycerol-3-phosphate o-acyltransferase abhd5; PDBTitle: solution structure of the lipid droplet anchoring peptide2 of cgi-58 bound to dpc micelles
7	c2ahqA_	 Alignment		8.2	57	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
8	c1koza_	 Alignment		7.9	35	PDB header: toxin Chain: A: PDB Molecule: voltage-dependent channel inhibitor; PDBTitle: solution structure of omega-grammotoxin sia
9	c3nctC_	 Alignment		7.7	71	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
10	c1sb7A_	 Alignment		7.2	67	PDB header: lyase Chain: A: PDB Molecule: trna pseudouridine synthase d; PDBTitle: crystal structure of the e.coli pseudouridine synthase trud
11	c2kzkA_	 Alignment		7.2	21	PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein yol083w; PDBTitle: solution structure of alpha-mannosidase binding domain of atg34

12	c2vqzB_	Alignment		6.8	14	PDB header: transcription Chain: B; PDB Molecule: polymerase basic protein 2; PDBTitle: structure of the cap-binding domain of influenza virus2 polymerase subunit pb2 with bound m7gtp
13	c6cfzj_	Alignment		6.4	25	PDB header: nuclear protein Chain: J; PDB Molecule: spc34; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
14	d1szwa_	Alignment		6.0	67	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: tRNA pseudouridine synthase TruD
15	c4gu8G_	Alignment		6.0	78	PDB header: sugar binding protein Chain: G; PDB Molecule: burkholderia oklahomensis agglutinin (boa); PDBTitle: crystal structure of burkholderia oklahomensis agglutinin (boa)
16	c2kzba_	Alignment		6.0	29	PDB header: protein transport Chain: A; PDB Molecule: autophagy-related protein 19; PDBTitle: solution structure of alpha-mannosidase binding domain of atg19
17	c1bkvA_	Alignment		5.8	70	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
18	c2lr3A_	Alignment		5.8	42	PDB header: antifungal protein Chain: A; PDB Molecule: defensin; PDBTitle: solution structure of the anti-fungal defensin def4 (mtr_8g070770)2 from medicago truncatula (barrel clover)
19	c5zghl_	Alignment		5.5	67	PDB header: photosynthesis Chain: I; PDB Molecule: psai; PDBTitle: cryo-em structure of the red algal psi-lhcr
20	c1bkvB_	Alignment		5.3	70	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
21	c1bkvC_	Alignment	not modelled	5.3	70	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
22	c1wbiD_	Alignment	not modelled	5.3	21	PDB header: avidin-related protein Chain: D; PDB Molecule: avidin-related protein 2; PDBTitle: avr2
23	c5un7A_	Alignment	not modelled	5.2	31	PDB header: protein binding Chain: A; PDB Molecule: protection of telomeres protein 1; PDBTitle: structure of the human pot1-tpp1 telomeric complex
24	c5nceA_	Alignment	not modelled	5.2	36	PDB header: plant protein Chain: A; PDB Molecule: defensin-1; PDBTitle: structure of psdef1 defensin from pinus sylvestris