
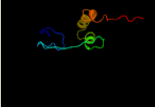
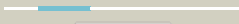
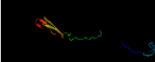



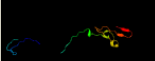

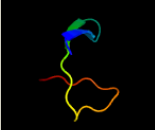

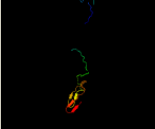
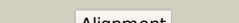
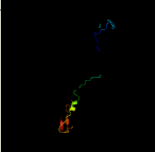

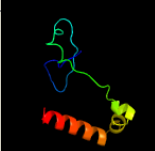



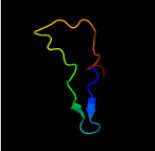
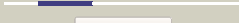
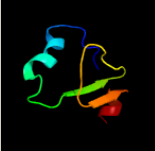


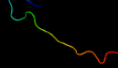

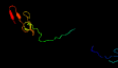

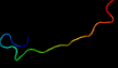




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0381c (-)_456916_457824
Date	Tue Jul 23 14:50:45 BST 2019
Unique Job ID	a5bb6cec7239be27

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3c0na2	 Alignment		46.5	25	Fold: Aerolisin/ETX pore-forming domain Superfamily: Aerolisin/ETX pore-forming domain Family: (Pro)aerolysin, pore-forming lobe
2	c1urzC_	 Alignment		32.5	18	PDB header: virus/viral protein Chain: C: PDB Molecule: envelope protein; PDBTitle: low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus
3	c4iaoB_	 Alignment		24.7	37	PDB header: hydrolase/transcription Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of sir2 c543s mutant in complex with sid domain of2 sir4
4	d1ok8a2	 Alignment		14.8	20	Fold: Viral glycoprotein, central and dimerisation domains Superfamily: Viral glycoprotein, central and dimerisation domains Family: Viral glycoprotein, central and dimerisation domains
5	d1qcsa1	 Alignment		13.3	27	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
6	d1svba2	 Alignment		11.7	21	Fold: Viral glycoprotein, central and dimerisation domains Superfamily: Viral glycoprotein, central and dimerisation domains Family: Viral glycoprotein, central and dimerisation domains
7	c5ireA_	 Alignment		11.5	22	PDB header: virus Chain: A: PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus
8	c6bi6A_	 Alignment		8.4	24	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yejg; PDBTitle: solution nmr structure of uncharacterized protein yejg
9	d1i40a_	 Alignment		7.3	29	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
10	c4o4dA_	 Alignment		7.0	23	PDB header: transferase Chain: A: PDB Molecule: inositol hexakisphosphate kinase; PDBTitle: crystal structure of an inositol hexakisphosphate kinase ehip6ka in2 complexed with atp and ins(1,4,5)p3
11	c2hjhB_	 Alignment		7.0	32	PDB header: hydrolase Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of the sir2 deacetylase

12	d2erla_	Alignment		7.0	86	Fold: Protozoan pheromone-like Superfamily: Protozoan pheromone proteins Family: Protozoan pheromone proteins
13	d2cu9a1	Alignment		6.8	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
14	d1roca_	Alignment		6.6	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
15	c4drbC_	Alignment		6.5	20	PDB header: dna binding protein/protein binding Chain: C: PDB Molecule: fanconi anemia group m protein; PDBTitle: the crystal structure of fancm bound mhf complex
16	c3uaja_	Alignment		6.5	21	PDB header: viral protein/immune system Chain: A: PDB Molecule: envelope protein; PDBTitle: crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
17	d2z1ca1	Alignment		6.2	33	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
18	c2idcA_	Alignment		6.1	23	PDB header: replication/chaperone Chain: A: PDB Molecule: anti-silencing protein 1 and histone h3 chimera; PDBTitle: structure of the histone h3-asf1 chaperone interaction
19	c3j21R_	Alignment		5.9	36	PDB header: ribosome Chain: R: PDB Molecule: 50s ribosomal protein l21e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
20	c5vqjA_	Alignment		5.9	28	PDB header: hydrolase Chain: A: PDB Molecule: exo-beta-1,4-xylanase; PDBTitle: discovery of a first gh11 exo-1,4-beta-xylanase from a diverse2 microbial sugar cane bagasse composting community
21	c3lmaC_	Alignment	not modelled	5.9	37	PDB header: membrane protein Chain: C: PDB Molecule: stage v sporulation protein ad (spovad); PDBTitle: crystal structure of the stage v sporulation protein ad (spovad) from2 bacillus licheniformis. northeast structural genomics consortium3 target bir6.
22	d2ot2a1	Alignment	not modelled	5.7	44	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
23	c2i32A_	Alignment	not modelled	5.7	27	PDB header: replication chaperone Chain: A: PDB Molecule: anti-silencing factor 1 paralog a; PDBTitle: structure of a human asf1a-hira complex and insights into specificity2 of histone chaperone complex assembly
24	d2i32a1	Alignment	not modelled	5.7	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
25	d1vmba_	Alignment	not modelled	5.6	25	Fold: Ferredoxin-like Superfamily: Ribosomal protein S6 Family: Ribosomal protein S6
26	c1vmbA_	Alignment	not modelled	5.6	25	PDB header: translation Chain: A: PDB Molecule: 30s ribosomal protein s6; PDBTitle: crystal structure of 30s ribosomal protein s6 (tm0603) from thermotoga2 maritima at 1.70 a resolution
27	d1loua_	Alignment	not modelled	5.6	13	Fold: Ferredoxin-like Superfamily: Ribosomal protein S6 Family: Ribosomal protein S6
28	c3ld3A_	Alignment	not modelled	5.4	33	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic phosphatase from anaplasma2 phagocytophilum at 1.75a resolution

29	d1pz8a_	Alignment	not modelled	5.4	38	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
30	d1j8fa_	Alignment	not modelled	5.3	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
31	d1v3ea_	Alignment	not modelled	5.2	18	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
32	c4bg7A_	Alignment	not modelled	5.2	39	PDB header: replication Chain: A: PDB Molecule: putative transcriptional coactivator p15; PDBTitle: bacteriophage t5 homolog of the eukaryotic transcription coactivator2 pc4 implicated in recombination-dependent dna replication
33	d3d3ra1	Alignment	not modelled	5.1	67	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like