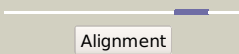
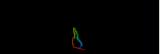
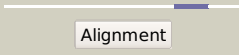

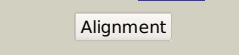
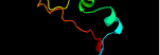
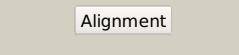

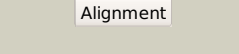

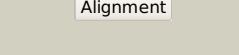
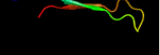
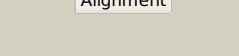
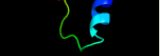
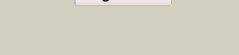


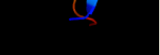


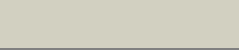



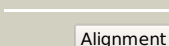
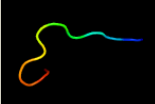
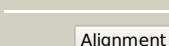
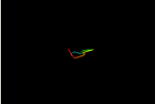


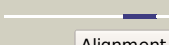
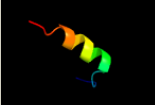
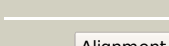
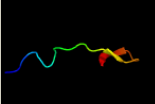





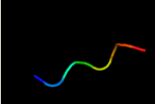
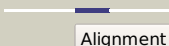



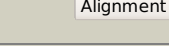
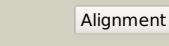
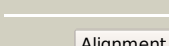



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0698 (-) _798836_799447
Date	Fri Jul 26 01:50:27 BST 2019
Unique Job ID	47027e204cd4d9c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c20xtC_	 Alignment		16.4	67	PDB header: viral protein Chain: C: PDB Molecule: nucleoside-2'-o-methyltransferase; PDBTitle: crystal structure of meaban virus nucleoside-2'-o-2 methyltransferase
2	c3elyA_	 Alignment		15.5	42	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: wesselsbron virus methyltransferase in complex with adohcy
3	c3nfgG_	 Alignment		9.7	29	PDB header: transcription Chain: G: PDB Molecule: dna-directed rna polymerase i subunit rpa49; PDBTitle: crystal structure of dimerization module of rna polymerase i2 subcomplex a49/a34.5
4	c5ccvH_	 Alignment		9.5	58	PDB header: transferase Chain: H: PDB Molecule: rna-directed rna polymerase ns5; PDBTitle: crystal structure of full-length ns5 from dengue virus type 3
5	d1ed7a_	 Alignment		9.5	42	Fold: WW domain-like Superfamily: Carbohydrate binding domain Family: Carbohydrate binding domain
6	c4f7oB_	 Alignment		9.3	38	PDB header: hydrolase Chain: B: PDB Molecule: cop9 signalosome complex subunit 5; PDBTitle: crystal structure of csn5
7	c2j8aA_	 Alignment		9.0	15	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-4 PDBTitle: x-ray structure of the n-terminus rrm domain of set1
8	c3u2aA_	 Alignment		9.0	58	PDB header: hydrolase Chain: A: PDB Molecule: ggdef family protein; PDBTitle: adaptor dependent degradation of a cell-cycle regulator reveals2 diversity in substrate architectures
9	d1yuaa1	 Alignment		8.9	50	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Prokaryotic DNA topoisomerase I, a C-terminal fragment
10	d1tffa_	 Alignment		8.4	24	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin thiolesterase protein OTUB2 (Otubain-2)
11	c6g4ww_	 Alignment		8.0	44	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s15a; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a

12	c5wwoB_	 Alignment		7.8	44	PDB header: rna binding protein Chain: B: PDB Molecule: essential nuclear protein 1; PDBTitle: crystal structure of enp1
13	c5tfrA_	 Alignment		7.7	67	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of zika virus ns5 protein
14	c4k6mA_	 Alignment		7.5	58	PDB header: transferase Chain: A: PDB Molecule: polyprotein; PDBTitle: crystal structure of the full-length japanese encephalitis virus ns5
15	c1yuaA_	 Alignment		7.4	50	PDB header: dna binding protein Chain: A: PDB Molecule: topoisomerase i; PDBTitle: c-terminal domain of escherichia coli topoisomerase i
16	c5o60b_	 Alignment		7.2	37	PDB header: ribosome Chain: B: PDB Molecule: 5s rrna; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
17	c5m8bB_	 Alignment		7.1	33	PDB header: hydrolase Chain: B: PDB Molecule: alpha-l-arabinofuranosidase ii; PDBTitle: crystal structure of alpha-l-arabinofuranosidase from lactobacillus2 brevis
18	c1oqeO_	 Alignment		7.0	63	PDB header: immune system Chain: O: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
19	c1oqeR_	 Alignment		7.0	63	PDB header: immune system Chain: R: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
20	c1oqeP_	 Alignment		7.0	63	PDB header: immune system Chain: P: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
21	c1oqeK_	 Alignment	not modelled	7.0	63	PDB header: immune system Chain: K: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
22	d1oqek_	 Alignment	not modelled	7.0	63	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: BAFF receptor-like
23	c1oqeM_	 Alignment	not modelled	7.0	63	PDB header: immune system Chain: M: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
24	c1oqeO_	 Alignment	not modelled	7.0	63	PDB header: immune system Chain: Q: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
25	c1oqeL_	 Alignment	not modelled	7.0	63	PDB header: immune system Chain: L: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
26	d1u2za_	 Alignment	not modelled	6.5	63	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Catalytic, N-terminal domain of histone methyltransferase Dot1l
27	c4wpbD_	 Alignment	not modelled	6.4	70	PDB header: protein binding Chain: D: PDB Molecule: alpha/beta-vegf-1; PDBTitle: vascular endothelial growth factor in complex with alpha/beta-vegf-1
28	c4d18E_	 Alignment	not modelled	6.4	43	PDB header: signaling protein Chain: E: PDB Molecule: cop9 signalosome complex subunit 5; PDBTitle: crystal structure of the cop9 signalosome

29	c4wpbC_	Alignment	not modelled	6.4	70	PDB header: protein binding Chain: C: PDB Molecule: alpha/beta-vegf-1; PDBTitle: vascular endothelial growth factor in complex with alpha/beta-vegf-1
30	c4v0qA_	Alignment	not modelled	6.3	42	PDB header: transferase Chain: A: PDB Molecule: ns5 polymerase; PDBTitle: dengue virus full length ns5 complexed with sah
31	c2lowA_	Alignment	not modelled	6.2	45	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfp
32	c5cw6A_	Alignment	not modelled	6.0	27	PDB header: metal binding protein Chain: A: PDB Molecule: drbrcc36; PDBTitle: structure of metal dependent enzyme drbrcc36
33	c4po6B_	Alignment	not modelled	6.0	71	PDB header: transferase Chain: B: PDB Molecule: interferon alpha/beta receptor 1; PDBTitle: crystal structure of the human tyk2 ferm and sh2 domains with an2 ifnar1 intracellular peptide
34	c4iikA_	Alignment	not modelled	5.8	67	PDB header: hydrolase Chain: A: PDB Molecule: adenosine monophosphate-protein hydrolase sidd; PDBTitle: legionella pneumophila effector
35	d1n26a1	Alignment	not modelled	5.7	83	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains