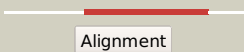

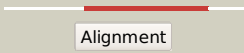

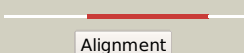

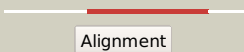

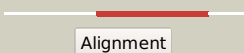
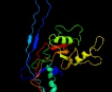
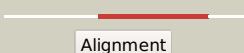




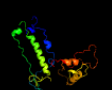


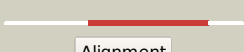



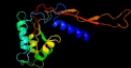





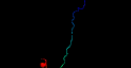
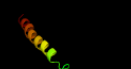
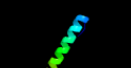


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1576c_(-)_1780650_1782071
Date	Fri Aug 2 13:30:16 BST 2019
Unique Job ID	255bf0a26398771e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5tjtA_	 Alignment		100.0	17	PDB header: viral protein Chain: A; PDB Molecule: major capsid protein; PDBTitle: t5 bacteriophage major capsid protein - one pb8 hexon
2	d2ft1a1	 Alignment		100.0	15	Fold: Major capsid protein gp5 Superfamily: Major capsid protein gp5 Family: Major capsid protein gp5
3	c3jb5C_	 Alignment		100.0	13	PDB header: virus Chain: C; PDB Molecule: major capsid protein; PDBTitle: capsid structure of the propionibacterium acnes bacteriophage2 atcc_clear
4	c6b0xG_	 Alignment		100.0	14	PDB header: virus Chain: G; PDB Molecule: major head protein; PDBTitle: capsid protein and c-terminal part of scaffolding protein in the2 staphylococcus aureus phage 80alpha procapsid
5	c1if0A_	 Alignment		100.0	14	PDB header: virus Chain: A; PDB Molecule: protein (major capsid protein gp5); PDBTitle: pseudo-atomic model of bacteriophage hk97 procapsid2 (prohead ii)
6	c3p8qF_	 Alignment		100.0	15	PDB header: virus Chain: F; PDB Molecule: gp5, head protein; PDBTitle: hk97 prohead i encapsidating inactive virally encoded protease
7	c3j1aE_	 Alignment		99.5	24	PDB header: virus Chain: E; PDB Molecule: capsid protein; PDBTitle: hk97-like fold fitted into 3d reconstruction of bacteriophage cw02
8	c3j4uA_	 Alignment		98.7	18	PDB header: virus Chain: A; PDB Molecule: major capsid protein; PDBTitle: a new topology of the hk97-like fold revealed in bordetella2 bacteriophage: non-covalent chainmail secured by jellyrolls
9	c3j7wF_	 Alignment		98.4	14	PDB header: virus Chain: F; PDB Molecule: major capsid protein 10a; PDBTitle: capsid expansion mechanism of bacteriophage t7 revealed by multi-state2 atomic models derived from cryo-em reconstructions
10	c4bmlA_	 Alignment		98.2	12	PDB header: virus Chain: A; PDB Molecule: major capsid protein; PDBTitle: c-alpha backbone trace of major capsid protein gp39 found in marine2 virus syn5.
11	c2e0zA_	 Alignment		98.1	10	PDB header: virus like particle Chain: A; PDB Molecule: virus-like particle; PDBTitle: crystal structure of virus-like particle from pyrococcus2 furiosus

12	c4pt2B_	Alignment		98.1	10	PDB header: virus like particle Chain: B: PDB Molecule: encapsulin protein; PDBTitle: myxococcus xanthus encapsulin protein (enca)
13	c3dktD_	Alignment		97.9	12	PDB header: structural protein/virus like particle Chain: D: PDB Molecule: maritimacin; PDBTitle: crystal structure of thermotoga maritima encapsulin
14	c3c5bF_	Alignment		97.7	16	PDB header: virus Chain: F: PDB Molecule: putative uncharacterized protein; PDBTitle: de novo model of bacteriophage epsilon 15 major capsid protein gp7
15	c4an5F_	Alignment		97.2	12	PDB header: virus Chain: F: PDB Molecule: coat protein; PDBTitle: capsid structure and its stability at the late stages of bacteriophage2 spp1 assembly
16	c2xd8F_	Alignment		95.1	13	PDB header: virus Chain: F: PDB Molecule: t7-like capsid protein; PDBTitle: capsid structure of the infectious prochlorococcus cyanophage p-ssp7
17	c1yueA_	Alignment		91.7	13	PDB header: viral protein Chain: A: PDB Molecule: head vertex protein gp24; PDBTitle: bacteriophage t4 capsid vertex protein gp24
18	c5vf3H_	Alignment		87.7	20	PDB header: virus Chain: H: PDB Molecule: major capsid protein; PDBTitle: bacteriophage t4 isometric capsid
19	c1j1eB_	Alignment		60.6	20	PDB header: contractile protein Chain: B: PDB Molecule: troponin t; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
20	c1j1dF_	Alignment		37.5	17	PDB header: contractile protein Chain: F: PDB Molecule: troponin i; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
21	c5liiP_	Alignment	not modelled	34.2	12	PDB header: virus like particle Chain: P: PDB Molecule: major capsid protein; PDBTitle: bacteriophage phi812k1-420 major capsid protein
22	c5eonA_	Alignment	not modelled	28.6	18	PDB header: de novo protein Chain: A: PDB Molecule: acc-hex; PDBTitle: crystal structure of a de novo antiparallel coiled-coil hexamer - acc-2 hex
23	c5eonB_	Alignment	not modelled	28.6	18	PDB header: de novo protein Chain: B: PDB Molecule: acc-hex; PDBTitle: crystal structure of a de novo antiparallel coiled-coil hexamer - acc-2 hex
24	c5eonC_	Alignment	not modelled	28.6	18	PDB header: de novo protein Chain: C: PDB Molecule: acc-hex; PDBTitle: crystal structure of a de novo antiparallel coiled-coil hexamer - acc-2 hex
25	c1yv0T_	Alignment	not modelled	28.0	21	PDB header: contractile protein Chain: T: PDB Molecule: troponin t, fast skeletal muscle isoforms; PDBTitle: crystal structure of skeletal muscle troponin in the ca2+-free state
26	c1j1eF_	Alignment	not modelled	23.0	17	PDB header: contractile protein Chain: F: PDB Molecule: troponin i; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
27	c5I35D_	Alignment	not modelled	17.6	10	PDB header: virus Chain: D: PDB Molecule: gene 5 protein; PDBTitle: cryo-em structure of bacteriophage sf6 at 2.9 angstrom resolution
28	c1j1eC_	Alignment	not modelled	16.7	17	PDB header: contractile protein Chain: C: PDB Molecule: troponin i; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form

29	d1vqov1	Alignment	not modelled	16.2	14	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
30	c3izgG	Alignment	not modelled	15.9	19	PDB header: virus Chain: G: PDB Molecule: major capsid protein 10a; PDBTitle: bacteriophage t7 prohead shell em-derived atomic model
31	d1jeia	Alignment	not modelled	12.1	22	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
32	c4l6rA	Alignment	not modelled	11.8	15	PDB header: membrane protein Chain: A: PDB Molecule: soluble cytochrome b562 and glucagon receptor chimera; PDBTitle: structure of the class b human glucagon g protein coupled receptor
33	c3uotB	Alignment	not modelled	11.7	8	PDB header: cell cycle Chain: B: PDB Molecule: mediator of dna damage checkpoint protein 1; PDBTitle: crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
34	c3d55A	Alignment	not modelled	9.8	27	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
35	c4bjsC	Alignment	not modelled	9.7	35	PDB header: cell cycle Chain: C: PDB Molecule: telomere length regulator protein rif1; PDBTitle: crystal structure of the rif1 c-terminal domain (rif1-ctd)2 from saccharomyces cerevisiae
36	d1s35a1	Alignment	not modelled	9.3	13	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
37	c3jcuw	Alignment	not modelled	9.1	33	PDB header: membrane protein Chain: W: PDB Molecule: photosystem ii reaction center w protein, chloroplastic; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
38	c3bqwA	Alignment	not modelled	8.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative capsid protein of prophage; PDBTitle: crystal structure of the putative capsid protein of prophage (e.coli2 cft073)
39	d2hgq11	Alignment	not modelled	8.0	14	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
40	c2myvA	Alignment	not modelled	7.8	6	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of m. oryzae protein avr1-co39
41	c2krxA	Alignment	not modelled	7.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: asl3597 protein; PDBTitle: solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
42	c3jtzA	Alignment	not modelled	7.6	29	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: structure of the arm-type binding domain of hpi integrase
43	c1ytzl	Alignment	not modelled	7.1	16	PDB header: contractile protein Chain: I: PDB Molecule: troponin i; PDBTitle: crystal structure of skeletal muscle troponin in the ca2+-activated state
44	d1tdha3	Alignment	not modelled	7.0	13	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
45	d1gija2	Alignment	not modelled	6.8	18	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
46	d2ho2a1	Alignment	not modelled	6.6	8	Fold: WW domain-like Superfamily: WW domain Family: WW domain
47	d1dd3a1	Alignment	not modelled	6.4	21	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
48	d2vo1a1	Alignment	not modelled	6.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
49	c3bboZ	Alignment	not modelled	6.2	14	PDB header: ribosome Chain: Z: PDB Molecule: ribosomal protein l29; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
50	c3m8jA	Alignment	not modelled	5.8	8	PDB header: transcription Chain: A: PDB Molecule: focb protein; PDBTitle: crystal structure of e.coli focb at 1.4 a resolution
51	c5mlcZ	Alignment	not modelled	5.6	14	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l29, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
52	c6cc4A	Alignment	not modelled	5.6	8	PDB header: transport protein Chain: A: PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
53	d1h9fa	Alignment	not modelled	5.5	14	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
						PDB header: transport protein

