

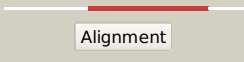
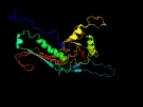
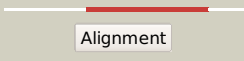

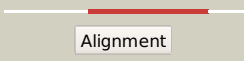

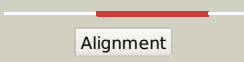

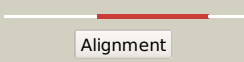

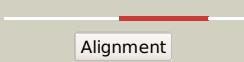

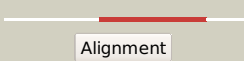
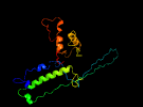
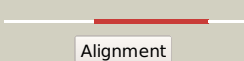

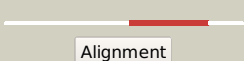

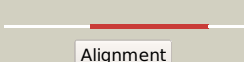
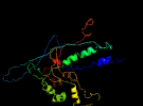



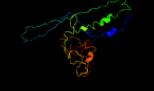
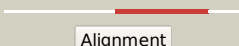

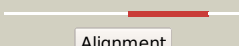

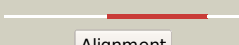

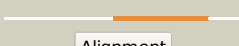


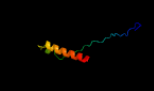
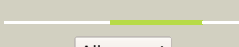


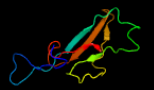


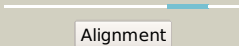
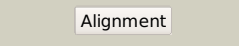


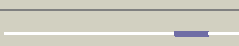



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2650c (-) _2973805_2975244
Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	3560099d1ae3225b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5tjtA_	 Alignment		100.0	15	PDB header: viral protein Chain: A; PDB Molecule: major capsid protein; PDBTitle: t5 bacteriophage major capsid protein - one pb8 hexon
2	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
3	d2ft1a1	 Alignment		100.0	15	Fold: Major capsid protein gp5 Superfamily: Major capsid protein gp5 Family: Major capsid protein gp5
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	16	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		98.3	13	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	c4pt2B_	 Alignment		98.0	11	PDB header: virus like particle Chain: B; PDB Molecule: encapsulin protein; PDBTitle: myxococcus xanthus encapsulin protein (enca)
11	c4bmlA_	 Alignment		97.8	11	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.

12	c2e0zA_	 Alignment		97.8	10	PDB header: virus like particle Chain: A; PDB Molecule: virus-like particle; PDBTitle: crystal structure of virus-like particle from pyrococcus2 furiosus
13	c3c5bF_	 Alignment		97.7	18	PDB header: virus Chain: F; PDB Molecule: putative uncharacterized protein; PDBTitle: de novo model of bacteriophage epsilon 15 major capsid protein gp7
14	c3dktD_	 Alignment		97.7	13	PDB header: structural protein/virus like particle Chain: D; PDB Molecule: maritimacin; PDBTitle: crystal structure of thermotoga maritima encapsulin
15	c4an5F_	 Alignment		97.5	11	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		94.3	13	PDB header: virus Chain: F; PDB Molecule: t7-like capsid protein; PDBTitle: capsid structure of the infectious prochlorococcus cyanophage p-ssp7
17	c5vf3H_	 Alignment		89.6	12	PDB header: virus Chain: H; PDB Molecule: major capsid protein; PDBTitle: bacteriophage t4 isometric capsid
18	c1yueA_	 Alignment		83.3	10	PDB header: viral protein Chain: A; PDB Molecule: head vertex protein gp24; PDBTitle: bacteriophage t4 capsid vertex protein gp24
19	c5liiP_	 Alignment		68.8	10	PDB header: virus like particle Chain: P; PDB Molecule: major capsid protein; PDBTitle: bacteriophage phi812k1-420 major capsid protein
20	c6h3jC_	 Alignment		51.8	9	PDB header: protein transport Chain: C; PDB Molecule: plug; PDBTitle: structural snapshots of the type 9 protein translocon plug-complex
21	c3layF_	 Alignment	not modelled	42.2	18	PDB header: metal binding protein Chain: F; PDB Molecule: zinc resistance-associated protein; PDBTitle: alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
22	c4l6rA_	 Alignment	not modelled	31.5	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
23	c3izgG_	 Alignment	not modelled	31.5	14	PDB header: virus Chain: G; PDB Molecule: major capsid protein 10a; PDBTitle: bacteriophage t7 prohead shell em-derived atomic model
24	c3jtzA_	 Alignment	not modelled	26.2	31	PDB header: dna binding protein Chain: A; PDB Molecule: integrase; PDBTitle: structure of the arm-type binding domain of hpi integrase
25	c3ju0A_	 Alignment	not modelled	24.6	25	PDB header: dna binding protein Chain: A; PDB Molecule: phage integrase; PDBTitle: structure of the arm-type binding domain of hai7 integrase
26	c1m1zB_	 Alignment	not modelled	18.4	9	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
27	c3uotB_	 Alignment	not modelled	16.9	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
28	d1tdha3	 Alignment	not modelled	16.3	13	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain)

28	d1tunb3	Alignment	not modelled	10.5	13	Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
29	d2ho2a1	Alignment	not modelled	14.5	8	Fold: WW domain-like Superfamily: WW domain Family: WW domain
30	d16pka	Alignment	not modelled	13.8	25	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
31	c4bjsC	Alignment	not modelled	13.2	40	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 <i>saccharomyces cerevisiae</i>
32	d1phpa	Alignment	not modelled	11.7	10	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
33	c4r7fA	Alignment	not modelled	11.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein (parmer_01801) from <i>2 parabacteroides merdae</i> atcc 43184 at 2.30 a resolution
34	c3jcuw	Alignment	not modelled	10.5	42	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
35	c3bqwA	Alignment	not modelled	9.9	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)
36	d1zpya1	Alignment	not modelled	8.9	16	Fold: Ferritin-like Superfamily: Ferritin-like Family: half-ferritin
37	d2dsya1	Alignment	not modelled	8.5	25	Fold: TTHA1013/TTHA0281-like Superfamily: TTHA1013/TTHA0281-like Family: TTHA0281-like
38	d2ysca1	Alignment	not modelled	8.1	25	Fold: WW domain-like Superfamily: WW domain Family: WW domain
39	c3q3vA	Alignment	not modelled	8.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from <i>campylobacter2 jejuni</i> .
40	c5wk1C	Alignment	not modelled	7.9	15	PDB header: virus Chain: C: PDB Molecule: major capsid protein; PDBTitle: structure of the major capsid protein and the capsid stabilizing2 protein of the marine siphovirus tw1
41	c3dwkC	Alignment	not modelled	7.6	12	PDB header: transferase Chain: C: PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
42	c4or2A	Alignment	not modelled	7.5	15	PDB header: signaling protein Chain: A: PDB Molecule: soluble cytochrome b562, metabotropic glutamate receptor 1; PDBTitle: human class c g protein-coupled metabotropic glutamate receptor 1 in2 complex with a negative allosteric modulator
43	d1vj1a1	Alignment	not modelled	7.3	17	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
44	c3m8jA	Alignment	not modelled	7.3	8	PDB header: transcription Chain: A: PDB Molecule: focb protein; PDBTitle: crystal structure of e.coli focb at 1.4 a resolution
45	c3he5D	Alignment	not modelled	7.2	16	PDB header: de novo protein Chain: D: PDB Molecule: synzip2; PDBTitle: heterospecific coiled-coil pair synzip2:synzip1
46	d1kska3	Alignment	not modelled	7.2	29	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
47	d1vpea	Alignment	not modelled	6.7	25	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
48	c2lf0A	Alignment	not modelled	6.6	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yib1; PDBTitle: solution structure of sf3636, a two-domain unknown function protein2 from <i>shigella flexneri</i> 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scattering, nesg4 target sfr339/ocsp target sf3636
49	d1ltkA	Alignment	not modelled	6.6	15	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
50	c2pqqD	Alignment	not modelled	6.5	10	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: structural genomics, the crystal structure of the n-terminal domain of2 a transcriptional regulator from <i>streptomyces coelicolor</i> a3(2)
51	d1hywa	Alignment	not modelled	6.4	29	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
52	c3kyaA	Alignment	not modelled	6.3	14	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: crystal structure of putative phosphatase (np_812416.1) from2 <i>bacteroides thetaiotaomicron</i> vpi-5482 at 1.77 a resolution
53	c2cunA	Alignment	not modelled	6.2	10	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from

						pyrococcus2 horikoshii ot3
54	c4bryB_	Alignment	not modelled	6.2	21	PDB header: cell cycle Chain: B: PDB Molecule: multicilin; PDBTitle: the idas:geminin heterodimeric parallel coiled-coil
55	c2qeyA_	Alignment	not modelled	6.0	25	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxykinase, cytosolic [gtp]; PDBTitle: rat cytosolic pepck in complex with gtp
56	c5b7iC_	Alignment	not modelled	5.9	35	PDB header: hydrolase/unknown function Chain: C: PDB Molecule: uncharacterized protein acrf3; PDBTitle: cas3-acrf3 complex
57	d1khba1	Alignment	not modelled	5.8	17	Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: PEP carboxykinase C-terminal domain
58	c4hwmA_	Alignment	not modelled	5.7	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yedd; PDBTitle: crystal structure of a lipoprotein yedd (kpn_02420) from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 at 1.38 a resolution
59	c2lwxA_	Alignment	not modelled	5.5	22	PDB header: chaperone Chain: A: PDB Molecule: zuotin; PDBTitle: solution structure of the c-terminal pdr1-activating domain of the j-2 protein zuo1
60	c3i31A_	Alignment	not modelled	5.4	23	PDB header: rna binding protein,hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: hera helicase rna binding domain is an rrm fold
61	d1ybza1	Alignment	not modelled	5.4	11	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase
62	d1s35a1	Alignment	not modelled	5.4	14	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
63	c3k5bB_	Alignment	not modelled	5.3	11	PDB header: hydrolase Chain: B: PDB Molecule: v-type atp synthase, subunit (vapc-therm); PDBTitle: crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
64	d2pwwa1	Alignment	not modelled	5.3	16	Fold: TBP-like Superfamily: YugN-like Family: YugN-like
65	c5i35D_	Alignment	not modelled	5.2	10	PDB header: virus Chain: D: PDB Molecule: gene 5 protein; PDBTitle: cryo-em structure of bacteriophage sf6 at 2.9 angstrom resolution
66	c1yd6A_	Alignment	not modelled	5.1	14	PDB header: dna binding protein Chain: A: PDB Molecule: uvrc; PDBTitle: crystal structure of the gjy-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
67	d1xs8a_	Alignment	not modelled	5.0	9	Fold: YggX-like Superfamily: YggX-like Family: YggX-like