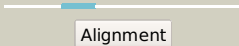


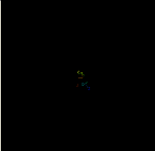

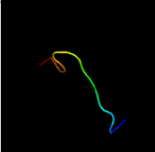
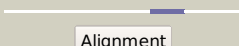

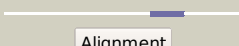
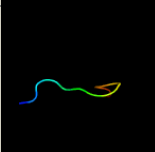
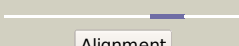
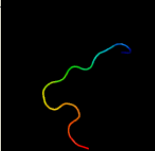
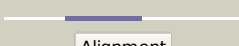
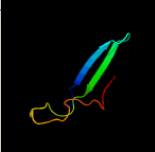

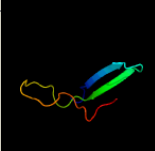

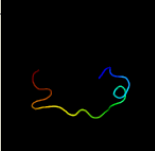

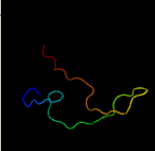





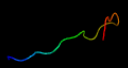
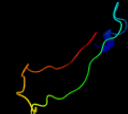

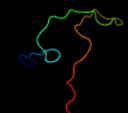




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2451_(-)_2752272_2752670
Date	Wed Aug 7 12:50:07 BST 2019
Unique Job ID	8f865e70b854768f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5muuC_	 Alignment		35.2	75	PDB header: virus Chain: C: PDB Molecule: packaging enzyme p4; PDBTitle: dsrna bacteriophage phi6 nucleocapsid
2	c6escA_	 Alignment		25.6	24	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of pseudorabies virus glycoprotein b
3	c3vbaE_	 Alignment		17.7	44	PDB header: lyase Chain: E: PDB Molecule: isopropylmalate/citramalate isomerase small subunit; PDBTitle: crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit
4	c3h5jA_	 Alignment		15.7	44	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from <i>Mycobacterium tuberculosis</i>
5	c3q3wB_	 Alignment		15.5	31	PDB header: transferase Chain: B: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from <i>Campylobacter jejuni</i> .
6	c2pkpA_	 Alignment		15.0	44	PDB header: lyase Chain: A: PDB Molecule: homoaconitase small subunit; PDBTitle: crystal structure of 3-isopropylmalate dehydratase (leud)2 from <i>Methanocaldococcus jannaschii</i> dsm2661 (mj1271)
7	c2giaB_	 Alignment		14.7	39	PDB header: translation Chain: B: PDB Molecule: mitochondrial rna-binding protein 1; PDBTitle: crystal structures of <i>Trypanosoma brucei</i> mrp1/mrp2
8	d2giab1	 Alignment		14.7	39	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Guide RNA binding protein gBP
9	c2hcuA_	 Alignment		14.3	27	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from <i>Streptococcus mutans</i>
10	d2guma1	 Alignment		14.0	17	Fold: Viral glycoprotein ectodomain-like Superfamily: Viral glycoprotein ectodomain-like Family: Glycoprotein B-like
11	d1v7la_	 Alignment		13.7	56	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: LeuD-like

12	c5v2sA_	Alignment		12.7	17	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
13	c6adqP_	Alignment		10.9	26	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
14	d1ppya_	Alignment		10.4	40	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Pyruvoyl dependent aspartate decarboxylase, ADC
15	d2akja4	Alignment		9.6	30	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
16	c3hfkB_	Alignment		9.2	27	PDB header: isomerase Chain: B: PDB Molecule: 4-methylmuconolactone methylisomerase; PDBTitle: crystal structure of 4-methylmuconolactone methylisomerase (h52a) in2 complex with 4-methylmuconolactone
17	c3fvcA_	Alignment		8.7	15	PDB header: viral protein Chain: A: PDB Molecule: glycoprotein gp110; PDBTitle: crystal structure of a trimeric variant of the epstein-barr virus2 glycoprotein b
18	c3nw8B_	Alignment		7.7	17	PDB header: viral protein Chain: B: PDB Molecule: envelope glycoprotein b; PDBTitle: glycoprotein b from herpes simplex virus type 1, y179s mutant, high-ph
19	c5t7eD_	Alignment		7.2	16	PDB header: transferase Chain: D: PDB Molecule: phosphinothricin n-acetyltransferase; PDBTitle: crystal structure of streptomyces hygrosopicus bialaphos resistance2 (bar) protein in complex with coenzyme a and l-phosphinothricin
20	c2m05A_	Alignment		7.2	63	PDB header: unknown function Chain: A: PDB Molecule: beta-amyloid-like protein; PDBTitle: structure of module 2 from the e1 domain of c. elegans apl-1
21	d1f0la2	Alignment	not modelled	6.6	46	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins
22	d1fasa_	Alignment	not modelled	6.5	38	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
23	c3zqbB_	Alignment	not modelled	6.4	33	PDB header: cell invasion Chain: B: PDB Molecule: protein prgi, cell invasion protein sipd; PDBTitle: prgi-sipd from salmonella typhimurium
24	c6bm8A_	Alignment	not modelled	6.2	17	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
25	c3ktmB_	Alignment	not modelled	5.5	43	PDB header: cell adhesion, signaling protein Chain: B: PDB Molecule: amyloid beta a4 protein; PDBTitle: structure of the heparin-induced e1-dimer of the amyloid precursor2 protein (app)
26	d2fklA1	Alignment	not modelled	5.5	71	Fold: Dodecin subunit-like Superfamily: Amyloid beta a4 protein copper binding domain (domain 2) Family: Amyloid beta a4 protein copper binding domain (domain 2)
27	c2dnaA_	Alignment	not modelled	5.4	67	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
28	c2lnkC_	Alignment	not modelled	5.3	50	PDB header: calcium binding protein Chain: C: PDB Molecule: myosin heavy chain, non-muscle iia; PDBTitle: solution structure of ca-bound s100a4 in complex with non-muscle2 myosin iia