



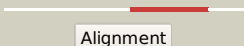
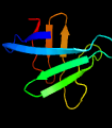

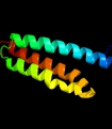


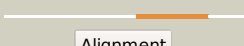
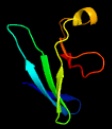
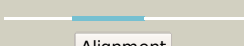
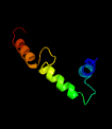



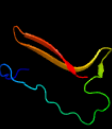

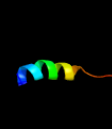

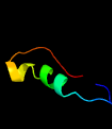
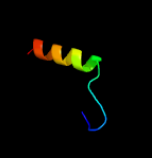

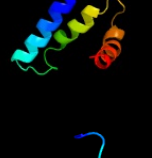
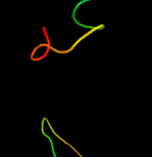
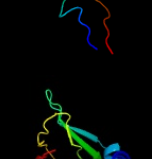
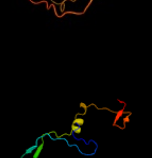

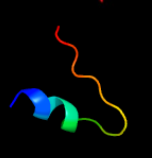
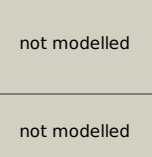


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1541c_(lprl)_1743784_1744377
 Date Fri Aug 2 13:30:13 BST 2019
 Unique Job ID 739b369241f09dff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f6zB_	 Alignment		99.6	23	PDB header: hydrolase Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pseudomonas aeruginosa mlc in complex2 with hen egg white lysozyme
2	d2f09a1	 Alignment		99.5	22	Fold: Streptavidin-like Superfamily: YdhA-like Family: YdhA-like
3	c3oe3B_	 Alignment		99.4	9	PDB header: hydrolase inhibitor Chain: B; PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of plic-st, periplasmic lysozyme inhibitor of c-type2 lysozyme from salmonella typhimurium
4	c6ar7C_	 Alignment		99.3	19	PDB header: unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia thailandensis
5	c3gi7A_	 Alignment		99.1	25	PDB header: unknown function Chain: A; PDB Molecule: secreted protein of unknown function duf1311; PDBTitle: crystal structure of a duf1311 family protein (pp0307) from2 pseudomonas putida kt2440 at 1.85 a resolution
6	c5my7A_	 Alignment		81.2	21	PDB header: cell adhesion Chain: A; PDB Molecule: adhesin; PDBTitle: adhesin complex protein from neisseria meningitidis
7	c4rg8A_	 Alignment		32.7	18	PDB header: hydrolase Chain: A; PDB Molecule: exonuclease i; PDBTitle: structural and biochemical studies of a moderately thermophilic2 exonuclease i from methylocaldum szegediense
8	d1dn0b2	 Alignment		19.2	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
9	c2n59A_	 Alignment		12.0	21	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein csgh; PDBTitle: solution structure of r. palustris csgh
10	c1yybA_	 Alignment		12.0	15	PDB header: apoptosis Chain: A; PDB Molecule: programmed cell death protein 5; PDBTitle: solution structure of 1-26 fragment of human programmed2 cell death 5 protein
11	c4r8aF_	 Alignment		10.7	14	PDB header: hydrolase/dna Chain: F; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pafan1 - 5' flap dna complex

12	c4ribA	Alignment		10.7	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: fanconi-associated nuclease 1; PDBTitle: fan1 nuclease bound to 5' phosphorylated p(dt) single flap dna
13	c1ny9A	Alignment		10.0	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator tipa-s; PDBTitle: antibiotic binding domain of a tipa-class multidrug2 resistance transcriptional regulator
14	d1ny9a	Alignment		10.0	13	Fold: Antibiotic binding domain of TipA-like multidrug resistance regulators Superfamily: Antibiotic binding domain of TipA-like multidrug resistance regulators Family: Antibiotic binding domain of TipA-like multidrug resistance regulators
15	c5e9fD	Alignment		9.5	13	PDB header: lyase Chain: D: PDB Molecule: isocitrate lyase; PDBTitle: structural insights of isocitrate lyases from magnaporthe oryzae
16	c6d2cB	Alignment		8.9	24	PDB header: lyase Chain: B: PDB Molecule: ulvan lyase; PDBTitle: structure of ulvan lyase from nonlaben ulvanivorans-nlr48
17	c1ea9D	Alignment		8.6	11	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltodextrinase; PDBTitle: cyclomaltodextrinase
18	c5ljyA	Alignment		6.9	12	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: structure of hantavirus envelope glycoprotein gc in complex with scfv2 a5
19	c6hc2L	Alignment		6.8	20	PDB header: cell cycle Chain: L: PDB Molecule: nuclear mitotic apparatus protein 1; PDBTitle: crystal structure of numa/lgn hetero-hexamers
20	c3f0nB	Alignment		6.8	33	PDB header: lyase Chain: B: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: mus musculus mevalonate pyrophosphate decarboxylase
21	c6n10A	Alignment	not modelled	5.8	33	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase mvd1, peroxisomal; PDBTitle: crystal structure of arabidopsis thaliana mevalonate 5-diphosphate2 decarboxylase 1 complexed with (r)-mvapp
22	d2qxfa1	Alignment	not modelled	5.7	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
23	d1osph2	Alignment	not modelled	5.7	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
24	c4qboA	Alignment	not modelled	5.7	5	PDB header: hydrolase Chain: A: PDB Molecule: nuclease; PDBTitle: vrr_nuc domain
25	c2hkeB	Alignment	not modelled	5.7	33	PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from trypanosoma brucei
26	c5lk1A	Alignment	not modelled	5.6	12	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: structure of hantavirus envelope glycoprotein gc in postfusion2 conformation in presence of 200 mm kcl
27	c4bg7A	Alignment	not modelled	5.4	47	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
						PDB header: immune system Chain: A: PDB Molecule: m protein, serotype 49;

28	c5hzpA_	Alignment	not modelled	5.4	30	PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m493 protein.
29	c6c6IN_	Alignment	not modelled	5.3	16	PDB header: membrane protein Chain: N: PDB Molecule: v0 assembly protein 1; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc