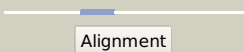

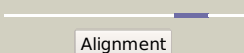


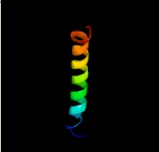
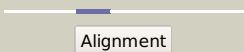

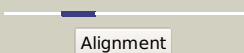





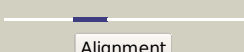

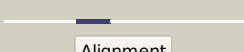
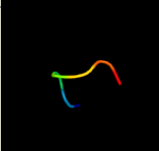
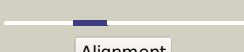








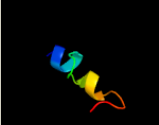
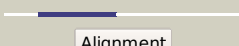
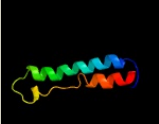
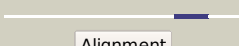

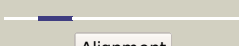


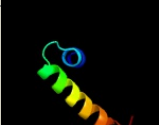




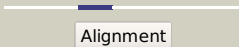


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2617c (-)_2945857_2946297
Date	Wed Aug 7 12:50:26 BST 2019
Unique Job ID	60b2dce301502818

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5e9oC_	 Alignment		20.1	36	PDB header: hydrolase Chain: C: PDB Molecule: cellulase, glycosyl hydrolase family 5, tps linker, domain PDBTitle: spirochaeta thermophila x module - cbm64 - mutant g504a
2	d2fd5a2	 Alignment		16.9	45	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
3	c2mpnB_	 Alignment		12.4	23	PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
4	c1cfgA_	 Alignment		11.4	50	PDB header: coagulation factor Chain: A: PDB Molecule: coagulation factor viii; PDBTitle: membrane-binding peptide from the c2 domain of factor viii2 forms an amphipathic structure as determined by nmr3 spectroscopy
5	c6n0tA_	 Alignment		8.5	75	PDB header: ligase Chain: A: PDB Molecule: trna ligase; PDBTitle: trna ligase
6	c2mpnA_	 Alignment		7.9	24	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
7	c2n5nA_	 Alignment		7.5	20	PDB header: dna binding protein Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 4; PDBTitle: structure of an n-terminal domain of chd4
8	d1q0qa3	 Alignment		7.3	50	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydropicolinate reductase-like
9	c4uznA_	 Alignment		6.9	43	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-glucanase (celulase b); PDBTitle: the native structure of the family 46 carbohydrate-binding2 module (cbm46) of endo-beta-1,4-glucanase b (cel5b) from3 bacillus halodurans
10	c5kqoA_	 Alignment		6.6	50	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from vibrio vulnificus
11	d2o3bb1	 Alignment		6.6	50	Fold: Nuclease A inhibitor (NuiA) Superfamily: Nuclease A inhibitor (NuiA) Family: Nuclease A inhibitor (NuiA)

12	c3au9A_	 Alignment		6.4	63	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of the quaternary complex-1 of an isomerase
13	c2eghA_	 Alignment		6.1	50	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
14	d1a5ta1	 Alignment		5.9	24	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
15	c2mpkA_	 Alignment		5.9	25	PDB header: transferase Chain: A: PDB Molecule: chitin synthase 1; PDBTitle: characterization and structure of the mit1 domain of a chitin synthase2 from the oomycete saprolegnia monoica
16	c1ry3A_	 Alignment		5.7	47	PDB header: antibiotic Chain: A: PDB Molecule: bacteriocin carnobacteriocin b2; PDBTitle: nmr solution structure of the precursor for2 carnobacteriocin b2, an antimicrobial peptide from3 carnobacterium piscicola
17	c6b3yA_	 Alignment		5.7	54	PDB header: transport protein Chain: A: PDB Molecule: denn domain-containing protein 3; PDBTitle: crystal structure of the ph-like domain from denn3
18	c3zfiB_	 Alignment		5.6	12	PDB header: transport protein Chain: B: PDB Molecule: rap1a protein; PDBTitle: rap1a protein (sma2260) from serratia marcescens
19	d2lisa_	 Alignment		5.6	25	Fold: Fertilization protein Superfamily: Fertilization protein Family: Fertilization protein
20	c2jo1A_	 Alignment		5.5	27	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
21	d2es7a1	 Alignment	not modelled	5.4	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like