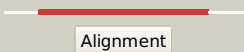

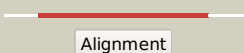

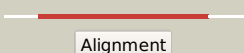

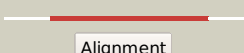

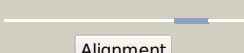
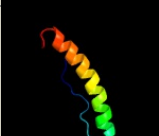
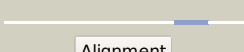


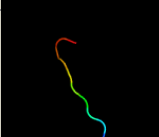
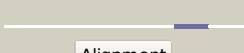
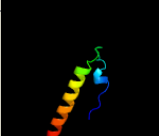








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1428c_(-)_1603938_1604765
Date	Wed Jul 31 22:05:53 BST 2019
Unique Job ID	0e6e77154ad7bac9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: 1-acyl-sn-glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima
2	c5f34A_	 Alignment		99.1	15	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
3	c5knkB_	 Alignment		98.8	12	PDB header: transferase Chain: B: PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
4	d1iuga_	 Alignment		97.5	16	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
5	c1zggA_	 Alignment		27.4	13	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine- PDBTitle: solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
6	c4etiA_	 Alignment		27.4	13	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine-phosphatase ywle; PDBTitle: crystal structure of ywle from bacillus subtilis
7	c2qlcC_	 Alignment		13.7	36	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein radc homolog; PDBTitle: the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s
8	d1dqwa_	 Alignment		13.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
9	c2akfC_	 Alignment		12.7	29	PDB header: protein binding Chain: C: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
10	c2akfB_	 Alignment		12.7	29	PDB header: protein binding Chain: B: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
11	c2akfA_	 Alignment		12.7	29	PDB header: protein binding Chain: A: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1

12	c3zbeA_	Alignment		10.8	15	PDB header: toxin-antitoxin Chain: A; PDB Molecule: paaa2; PDBTitle: e. coli o157 pare2-associated antitoxin 2 (paaa2)
13	c6adqP_	Alignment		10.4	17	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciiv2civ2sod2 from mycobacterium smegmatis
14	c3tqmD_	Alignment		9.0	13	PDB header: protein binding Chain: D; PDB Molecule: ribosome-associated factor y; PDBTitle: structure of an ribosomal subunit interface protein from coxiella2 burnetii
15	c5ctiC_	Alignment		8.9	23	PDB header: structural protein Chain: C; PDB Molecule: collagen alpha-1(i) chain,collagen alpha-3(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
16	c5b0oG_	Alignment		8.5	26	PDB header: hydrolase/motor protein Chain: G; PDB Molecule: flagellar assembly protein flih; PDBTitle: structure of the flih-flii complex
17	c5b0oH_	Alignment		8.5	26	PDB header: hydrolase/motor protein Chain: H; PDB Molecule: flagellar assembly protein flih; PDBTitle: structure of the flih-flii complex
18	c2fekA_	Alignment		8.4	13	PDB header: hydrolase Chain: A; PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
19	d1owla2	Alignment		8.0	17	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
20	c2zy4F_	Alignment		6.5	21	PDB header: lyase Chain: F; PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
21	d1np7a2	Alignment	not modelled	6.3	22	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
22	d1gtda_	Alignment	not modelled	6.0	17	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
23	d1j3ma_	Alignment	not modelled	5.7	19	Fold: TBP-like Superfamily: TT1751-like Family: TT1751-like
24	c2kelB_	Alignment	not modelled	5.6	18	PDB header: transcription repressor Chain: B; PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1