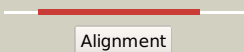

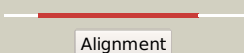

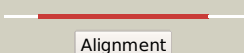

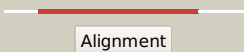

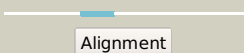
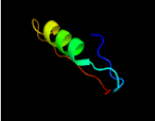
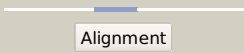

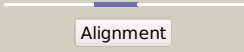
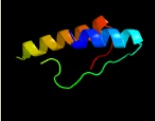
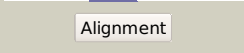



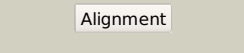

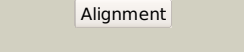
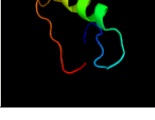

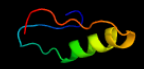




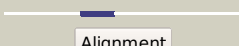

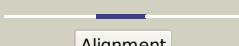
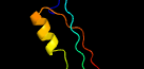
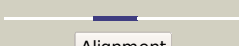


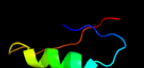







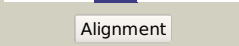
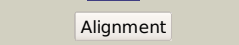
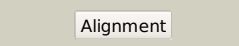


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3816c (-) _4280970_4281749
Date	Fri Aug 9 18:20:52 BST 2019
Unique Job ID	195f5ed8fb1aaa8b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		100.0	22	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		99.7	17	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		99.6	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		99.2	17	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
5	c4mxB_	 Alignment		37.1	11	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative glycosyl hydrolase (parmer_00599) from2 parabacteroides merdae atcc 43184 at 1.95 a resolution
6	c4cyyA_	 Alignment		25.6	18	PDB header: hydrolase Chain: A: PDB Molecule: pantetheinase; PDBTitle: the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
7	c3hxA_	 Alignment		18.6	22	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from nesterenkonia sp.
8	c2e11B_	 Alignment		18.2	20	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
9	c5vrhA_	 Alignment		15.2	18	PDB header: transferase Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
10	c3jurA_	 Alignment		14.7	27	PDB header: hydrolase Chain: A: PDB Molecule: exo-poly-alpha-d-galacturonidase; PDBTitle: the crystal structure of a hyperthermoactive exopolygalacturonase from2 thermotoga maritima
11	c3zppA_	 Alignment		14.1	16	PDB header: cell adhesion Chain: A: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structure of the streptococcus pneumoniae surface protein2 and adhesin pfba

12	c5olpB_	 Alignment		12.7	24	PDB header: hydrolase Chain: B: PDB Molecule: pectate lyase; PDBTitle: galacturonidase
13	c5khaA_	 Alignment		12.1	16	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad+ synthetase; PDBTitle: structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
14	c3eqnB_	 Alignment		9.7	16	PDB header: hydrolase Chain: B: PDB Molecule: glucan 1,3-beta-glucosidase; PDBTitle: crystal structure of beta-1,3-glucanase from phanerochaete2 chrysosporium (lam55a)
15	c2pyhB_	 Alignment		8.0	22	PDB header: isomerase Chain: B: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
16	d1v7za_	 Alignment		6.9	17	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
17	c1emsB_	 Alignment		6.9	14	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
18	d1bhea_	 Alignment		6.8	13	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Galacturonase
19	d1hrua_	 Alignment		6.8	26	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
20	d2csua1	 Alignment		6.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
21	c4hg3C_	 Alignment	not modelled	6.3	15	PDB header: hydrolase Chain: C: PDB Molecule: probable hydrolase nit2; PDBTitle: structural insights into yeast nit2: wild-type yeast nit2 in complex2 with alpha-ketoglutarate
22	c1r0lD_	 Alignment	not modelled	6.3	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
23	c3uwsA_	 Alignment	not modelled	6.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a clostripain (parmer_00083) from parabacteroides2 merdae atcc 43184 at 1.70 a resolution
24	d1uf5a_	 Alignment	not modelled	6.0	18	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamilase
25	c3a14B_	 Alignment	not modelled	5.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph
26	d1o59a2	 Alignment	not modelled	5.1	18	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Allantoicase repeat