








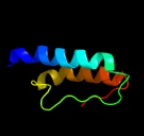


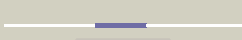









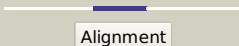

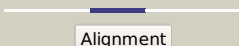



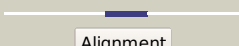
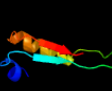
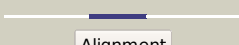

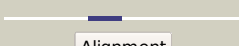
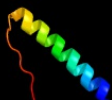
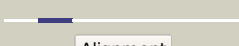
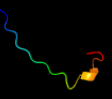






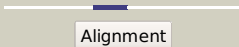


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2182c (-) _2444594_2445337
Date	Mon Aug 5 13:25:30 BST 2019
Unique Job ID	8897c6b8917ee15e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		100.0	29	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		99.6	14	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		99.5	13	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	19	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
5	c5vrhA_	 Alignment		23.9	14	PDB header: transferase Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
6	c3hxxA_	 Alignment		16.7	17	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from nesterenkonkia sp.
7	c4cyyA_	 Alignment		15.7	17	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
8	c1vj5B_	 Alignment		14.9	18	PDB header: transferase Chain: B: PDB Molecule: 5' polynucleotide kinase-3' phosphatase catalytic domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
9	c3zvmA_	 Alignment		13.3	18	PDB header: hydrolase/transferase/dna Chain: A: PDB Molecule: bifunctional polynucleotide phosphatase/kinase; PDBTitle: the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
10	d1to6a_	 Alignment		11.9	20	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
11	c2e11B_	 Alignment		9.7	14	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

12	c4chmB_	 Alignment		9.2	19	PDB header: cell cycle Chain: B; PDB Molecule: imc sub-compartment protein isp1; PDBTitle: structure of inner membrane complex (imc) sub-compartment protein 12 (isp1) from toxoplasma gondii
13	c2vhhA_	 Alignment		9.1	17	PDB header: hydrolase Chain: A; PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from drosophila melanogaster
14	c5khaA_	 Alignment		7.5	15	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)
15	c3cwcB_	 Alignment		7.5	24	PDB header: transferase Chain: B; PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
16	c4chjA_	 Alignment		7.3	13	PDB header: cell cycle Chain: A; PDB Molecule: imc sub-compartment protein isp3; PDBTitle: structure of inner membrane complex (imc) sub-compartment2 protein 3 (isp3) from toxoplasma gondii
17	c6ftqA_	 Alignment		6.5	13	PDB header: hydrolase Chain: A; PDB Molecule: beta-ureidopropionase; PDBTitle: crystal structure of human beta-ureidopropionase (beta-alanine2 synthase) - mutant t299c
18	c2zo7A_	 Alignment		6.3	28	PDB header: luminescent protein Chain: A; PDB Molecule: cyan/green-emitting gfp-like protein, kusabira-cyan mutant PDBTitle: crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein
19	c1emsB_	 Alignment		6.2	11	PDB header: antitumor protein Chain: B; PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
20	c3wuyA_	 Alignment		5.9	17	PDB header: hydrolase Chain: A; PDB Molecule: nitrilase; PDBTitle: crystal structure of nit6803
21	d1v7za_	 Alignment	not modelled	5.7	19	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
22	c2zo6A_	 Alignment	not modelled	5.4	28	PDB header: luminescent protein Chain: A; PDB Molecule: cyan-emitting gfp-like protein, kusabira-cyan (kcy); PDBTitle: crystal structure of kusabira-cyan (kcy), a cyan-emitting gfp-like2 protein
23	c4hg3C_	 Alignment	not modelled	5.4	8	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