

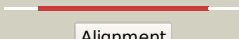

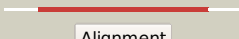


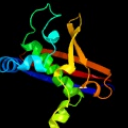














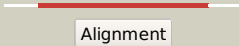

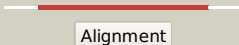

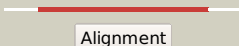



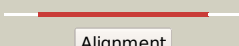

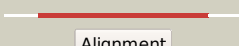
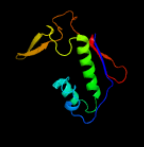
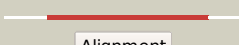






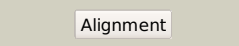
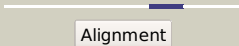
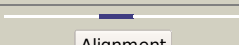

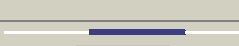

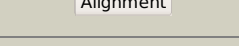



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2523c_acpS_2839548_2839940
Date	Wed Aug 7 12:50:15 BST 2019
Unique Job ID	94a4f0679a582d8e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5vbxB_	 Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of holo-[acyl-carrier-protein] synthase (acps) from2 escherichia coli
2	c5cmoB_	 Alignment		100.0	27	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of holo-[acyl-carrier-protein] synthase (acps) from2 neisseria meningitidis
3	c3hqjA_	 Alignment		100.0	95	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
4	c2jzbA_	 Alignment		100.0	37	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of the streptomyces coelicolor holo-2 [acyl-carrier-protein] synthase (acps) in complex with3 coenzyme a at 1.6 a
5	c3h88A_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of 4'-phosphopantetheinyl transferase acps from2 vibrio cholerae o1 biovar eltor
6	c2qg8A_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: acyl carrier protein synthase py06285; PDBTitle: plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
7	c3ne9B_	 Alignment		100.0	46	PDB header: transferase Chain: B: PDB Molecule: phosphopantetheine protein transferase, ppt1p; PDBTitle: chronobacterium ammoiniagenes apo-acps strucutre
8	d1ftha_	 Alignment		100.0	27	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: Holo-(acyl carrier protein) synthase ACPS
9	d1f7la_	 Alignment		100.0	30	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: Holo-(acyl carrier protein) synthase ACPS
10	c5xukA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of helicobacter pylori holo-[acyl-carrier-protein]2 synthase (acps) in complex with coenzyme a
11	c5xumA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of thermotoga maritima holo-[acyl-carrier-protein]2 synthase (acps)

12	c2wasA	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: structure of the fungal type i fas ppt domain
13	c3f09B	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: 1.82 angstrom resolution crystal structure of holo-(acyl-carrier-2 protein) synthase (acps) from staphylococcus aureus
14	c3hykB	 Alignment		100.0	32	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: 2.31 angstrom resolution crystal structure of a holo-(acyl-carrier-2 protein) synthase from bacillus anthracis str. ames in complex with3 coa (3',5'-adp)
15	c3hmjB	 Alignment		99.4	29	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i
16	d1qr0a2	 Alignment		99.1	14	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: 4'-Phosphopantetheinyl transferase SFP
17	c1qr0A	 Alignment		98.9	17	PDB header: transferase Chain: A: PDB Molecule: 4'-phosphopantetheinyl transferase sfp; PDBTitle: crystal structure of the 4'-phosphopantetheinyl transferase sfp-2 coenzyme a complex
18	d1qr0a1	 Alignment		98.6	20	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: 4'-Phosphopantetheinyl transferase SFP
19	c2cg5A	 Alignment		98.6	21	PDB header: transferase/hydrolase Chain: A: PDB Molecule: l-aminoadipate-semialdehyde dehydrogenase- PDBTitle: structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic acyl3 carrier protein and coenzyme a
20	c4qvhA	 Alignment		98.2	25	PDB header: transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, 4'-phosphopantetheinyl PDBTitle: crystal structure of the essential mycobacterium tuberculosis2 phosphopantetheinyl transferase pptt, solved as a fusion protein with3 maltose binding protein
21	c2pijB	 Alignment	not modelled	9.6	29	PDB header: transcription Chain: B: PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas fluorescens pf-5
22	d1d11a	 Alignment	not modelled	8.8	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
23	c1gk9A	 Alignment	not modelled	8.7	33	PDB header: antibiotic resistance Chain: A: PDB Molecule: penicillin g acylase alpha subunit; PDBTitle: crystal structures of penicillin acylase enzyme-substrate2 complexes: structural insights into the catalytic mechanism
24	d2f1da2	 Alignment	not modelled	8.5	50	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
25	c1ajnA	 Alignment	not modelled	8.3	33	PDB header: antibiotic resistance Chain: A: PDB Molecule: penicillin amidohydrolase; PDBTitle: penicillin acylase complexed with p-nitrophenylacetic acid
26	d2fr2a1	 Alignment	not modelled	8.1	17	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717C-like
27	d2ae8a2	 Alignment	not modelled	8.0	63	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
28	c3qmfA	 Alignment	not modelled	7.6	7	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of an inositol monophosphatase family protein2 (sas2203) from staphylococcus aureus mssa476
		 Alignment				Fold: lambda repressor-like DNA-binding domains

29	d4croa_	Alignment	not modelled	7.5	29	Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
30	d1rhya2	Alignment	not modelled	7.3	38	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
31	c3k8aA	Alignment	not modelled	6.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: putative primosomal replication protein; PDBTitle: neisseria gonorrhoeae prib
32	d1u5tb1	Alignment	not modelled	6.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
33	c4yfbD	Alignment	not modelled	6.2	20	PDB header: hydrolase Chain: D: PDB Molecule: protein related to penicillin acylase; PDBTitle: structure of n-acylhomoserine lactone acylase macq in complex with 2 phenylacetic acid
34	c2ae3A	Alignment	not modelled	6.1	22	PDB header: hydrolase Chain: A: PDB Molecule: glutaryl 7-aminocephalosporanic acid acylase; PDBTitle: glutaryl 7-aminocephalosporanic acid acylase: mutational study of 2 activation mechanism
35	c5uqyB	Alignment	not modelled	5.8	23	PDB header: viral protein/immune system Chain: B: PDB Molecule: envelope glycoprotein gp2; PDBTitle: crystal structure of marburg virus gp in complex with the human 2 survivor antibody mr78
36	c6nvyc	Alignment	not modelled	5.6	33	PDB header: hydrolase Chain: C: PDB Molecule: penicillin g acylase; PDBTitle: crystal structure of penicillin g acylase from bacillus thermotolerans
37	c1yhnB	Alignment	not modelled	5.3	15	PDB header: protein transport Chain: B: PDB Molecule: rab interacting lysosomal protein; PDBTitle: structure basis of rilp recruitment by rab7