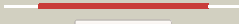



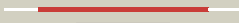

























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2217_(lipB)_2484592_2485284
Date	Mon Aug 5 13:25:34 BST 2019
Unique Job ID	ca31ebe45523bba2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w66a1	 Alignment		100.0	99	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
2	c2qhvA_	 Alignment		100.0	43	PDB header: transferase Chain: A: PDB Molecule: lipoyltransferase; PDBTitle: structural basis of octanoic acid recognition by lipoyl-protein2 ligase b
3	c2qhsA_	 Alignment		100.0	43	PDB header: transferase Chain: A: PDB Molecule: lipoyltransferase; PDBTitle: structural basis of octanoic acid recognition by lipoyl-protein2 ligase b
4	c1vqzA_	 Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: lipoyltransferase; PDBTitle: crystal structure of a putative lipoyl-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
5	c3r07A_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: lipoyltransferase; PDBTitle: structural analysis of an archaeal lipoylation system. a bipartite2 lipoyl protein ligase and its e2 lipoyl domain from thermoplasma3 acidophilum
6	c1x2gB_	 Alignment		100.0	19	PDB header: ligase Chain: B: PDB Molecule: lipoyltransferase; PDBTitle: crystal structure of lipoyl-protein ligase a from2 escherichia coli
7	d2c8ma1	 Alignment		100.0	16	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
8	c2e5aA_	 Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: lipoyltransferase 1; PDBTitle: crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
9	d1vqza2	 Alignment		100.0	21	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
10	d1x2ga2	 Alignment		100.0	17	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
11	d2p5ia1	 Alignment		100.0	15	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like

12	c5ij6A	Alignment		100.0	15	PDB header: ligase,transferase Chain: A: PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-1) in complex with lipoic acid
13	c5ibyA	Alignment		100.0	18	PDB header: ligase,transferase Chain: A: PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-2) in complex with lipoic acid
14	d2p0la1	Alignment		100.0	14	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LpIA-like
15	c5t8uA	Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: lipoate-protein ligase 1; PDBTitle: crystal structure of p. falciparum lip1 in complex lipoate
16	d2zgwa2	Alignment		99.0	14	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Biotin holoenzyme synthetase
17	c2ej9A	Alignment		98.7	13	PDB header: ligase Chain: A: PDB Molecule: putative biotin ligase; PDBTitle: crystal structure of biotin protein ligase from2 methanococcus jannaschii
18	c2eayB	Alignment		98.6	18	PDB header: ligase Chain: B: PDB Molecule: biotin [acetyl-coa-carboxylase] ligase; PDBTitle: crystal structure of biotin protein ligase from aquifex2 aeolicus
19	c2ewnA	Alignment		98.6	21	PDB header: ligase, transcription Chain: A: PDB Molecule: bira bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog
20	c3bfmA	Alignment		98.3	11	PDB header: unknown function Chain: A: PDB Molecule: biotin protein ligase-like protein of unknown function; PDBTitle: crystal structure of a biotin protein ligase-like protein of unknown2 function (tm1040_0394) from silicibacter sp. tm1040 at 1.70 a3 resolution
21	c2dzcA	Alignment	not modelled	98.3	18	PDB header: ligase Chain: A: PDB Molecule: biotin-[acetyl-coa-carboxylase] ligase; PDBTitle: crystal structure of biotin protein ligase from pyrococcus2 horikoshii, mutation r48a
22	c6ck0A	Alignment	not modelled	98.3	13	PDB header: ligase Chain: A: PDB Molecule: biotin acetyl coenzyme a carboxylase synthetase; PDBTitle: crystal structure of biotin acetyl coenzyme a carboxylase synthetase2 from helicobacter pylori with bound biotinylated atp
23	c3rkxA	Alignment	not modelled	98.2	11	PDB header: ligase Chain: A: PDB Molecule: biotin-[acetyl-coa-carboxylase] ligase; PDBTitle: structural characterisation of staphylococcus aureus biotin protein2 ligase
24	d1biaa3	Alignment	not modelled	98.1	21	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Biotin holoenzyme synthetase
25	c2cghB	Alignment	not modelled	98.0	17	PDB header: ligase Chain: B: PDB Molecule: biotin ligase; PDBTitle: crystal structure of biotin ligase from mycobacterium tuberculosis
26	d2ddza1	Alignment	not modelled	95.5	24	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: PH0223-like
27	d1b24a2	Alignment	not modelled	31.7	29	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
28	c3lr4A	Alignment	not modelled	29.6	22	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph

29	c1ponB	Alignment	not modelled	24.5	15	PDB header: calcium-binding protein Chain: B: PDB Molecule: troponin c; PDBTitle: site iii-site iv troponin c heterodimer, nmr
30	c3fxtB	Alignment	not modelled	20.2	27	PDB header: gene regulation Chain: B: PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the n-terminal domain of human nudt6
31	c2xueB	Alignment	not modelled	15.6	22	PDB header: oxidoreductase Chain: B: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of jmjd3
32	c5x1eF	Alignment	not modelled	15.5	19	PDB header: protein transport Chain: F: PDB Molecule: icmo (dotl); PDBTitle: structure of dotl(656-783)-icms-icmw derived from legionella2 pneumophila
33	c3avsA	Alignment	not modelled	14.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6a; PDBTitle: catalytic fragment of utx/kdm6a bound with n-oxyalylglycine, and2 ni(ii)
34	c5yeeA	Alignment	not modelled	13.3	24	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of lokiprofilin1/rabbit actin complex
35	c4ezhA	Alignment	not modelled	12.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: the crystal structure of kdm6b bound with h3k27me3 peptide
36	d3er7a1	Alignment	not modelled	11.0	24	Fold: Cystatin-like Superfamily: NTF2-like Family: Exig0174-like
37	d2bf5a1	Alignment	not modelled	10.7	26	Fold: Monooxygenase (hydroxylase) regulatory protein Superfamily: Monooxygenase (hydroxylase) regulatory protein Family: Monooxygenase (hydroxylase) regulatory protein
38	c5xlA	Alignment	not modelled	10.4	21	PDB header: viral protein Chain: A: PDB Molecule: decoration protein; PDBTitle: nmr structure of the n-terminal domain of the bacteriophage t52 decoration protein pb10
39	c2v9kA	Alignment	not modelled	10.2	19	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein flj32312; PDBTitle: crystal structure of human pus10, a novel pseudouridine2 synthase.
40	d1hqja	Alignment	not modelled	8.6	21	Fold: Monooxygenase (hydroxylase) regulatory protein Superfamily: Monooxygenase (hydroxylase) regulatory protein Family: Monooxygenase (hydroxylase) regulatory protein
41	d2bf2a1	Alignment	not modelled	8.5	26	Fold: Monooxygenase (hydroxylase) regulatory protein Superfamily: Monooxygenase (hydroxylase) regulatory protein Family: Monooxygenase (hydroxylase) regulatory protein
42	d1vyva2	Alignment	not modelled	8.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
43	c4zbpC	Alignment	not modelled	7.6	24	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase 7; PDBTitle: crystal structure of the ampccr-bound atnudt7
44	d1vyua2	Alignment	not modelled	7.5	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
45	c3uotB	Alignment	not modelled	7.2	16	PDB header: cell cycle Chain: B: PDB Molecule: mediator of dna damage checkpoint protein 1; PDBTitle: crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
46	c5dm3A	Alignment	not modelled	7.1	24	PDB header: ligase Chain: A: PDB Molecule: l-glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from chromohalobacter2 salexigens dsm 3043(csa1_0679, target efi-550015) with bound adp
47	d1uc8a1	Alignment	not modelled	7.1	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
48	c6bi6A	Alignment	not modelled	7.0	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yejg; PDBTitle: solution nmr structure of uncharacterized protein yejg
49	d1esfa1	Alignment	not modelled	6.4	36	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
50	c2jpeA	Alignment	not modelled	6.4	16	PDB header: transcription Chain: A: PDB Molecule: nuclear inhibitor of protein phosphatase 1; PDBTitle: fha domain of nipp1
51	d1t3la2	Alignment	not modelled	6.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
52	c2n84A	Alignment	not modelled	5.9	14	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the fha domain of tbpar42
53	c2dchX	Alignment	not modelled	5.9	31	PDB header: hydrolase Chain: X: PDB Molecule: putative homing endonuclease; PDBTitle: crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
54	c2mobA	Alignment	not modelled	5.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (methane monooxygenase regulatory PDBTitle: methane monooxygenase component b Fold: Monooxygenase (hydroxylase) regulatory protein

55	d2moba_	Alignment	not modelled	5.8	24	Superfamily: Monooxygenase (hydroxylase) regulatory protein Family: Monooxygenase (hydroxylase) regulatory protein
56	d1t0hb_	Alignment	not modelled	5.6	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases