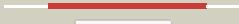

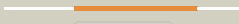

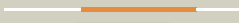







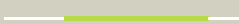











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1356c_(-)_1524035_1524826
Date	Wed Jul 31 22:05:46 BST 2019
Unique Job ID	6c562fc31689e668

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3efaA_	 Alignment		91.9	10	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
2	d2g3aa1	 Alignment		87.9	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
3	c3lodA_	 Alignment		85.9	16	PDB header: transferase Chain: A: PDB Molecule: putative acyl-coa n-acyltransferase; PDBTitle: the crystal structure of the putative acyl-coa n-acyltransferase from2 klebsiella pneumoniae subsp.pneumoniae mgh 78578
4	c3dr8B_	 Alignment		85.8	14	PDB header: transferase Chain: B: PDB Molecule: ynca; PDBTitle: structure of ynca, a putative acetyltransferase from salmonella2 typhimurium with its cofactor acetyl-coa
5	c6ao7A_	 Alignment		76.3	18	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of a gnat family acetyltransferase from2 elizabethkingia anophelis with acetyl-coa bound
6	d1yvka1	 Alignment		74.2	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
7	c5w8cA_	 Alignment		69.7	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: autoinducer synthase; PDBTitle: the structure of a coa-dependent acyl-homoserine lactone synthase,2 bjai, with mta and isovaleryl-coa
8	d1ro5a_	 Alignment		63.0	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Autoinducer synthetase
9	c5t7eD_	 Alignment		60.1	14	PDB header: transferase Chain: D: PDB Molecule: phosphinothricin n-acetyltransferase; PDBTitle: crystal structure of streptomyces hygrosopicus bialaphos resistance2 (bar) protein in complex with coenzyme a and l-phosphinothricin
10	c2huzB_	 Alignment		58.4	16	PDB header: structural genomics, transferase Chain: B: PDB Molecule: glucosamine 6-phosphate n-acetyltransferase; PDBTitle: crystal structure of gnpnat1
11	c3ec4B_	 Alignment		58.2	18	PDB header: transferase Chain: B: PDB Molecule: putative acetyltransferase from the gnat family; PDBTitle: crystal structure of putative acetyltransferase from the gnat family2 (yp_497011.1) from novosphingobium aromaticivorans dsm 12444 at 1.803 a resolution

12	d1ygha_	Alignment		58.1	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
13	d2ae6a1	Alignment		56.7	20	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
14	c2q7ba_	Alignment		55.2	17	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase (np_689019.1) from streptococcus agalactiae 2603 at 2.00 a resolution
15	d1sgva1	Alignment		46.4	37	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
16	d1yx0a1	Alignment		44.9	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
17	c4rs2B_	Alignment		39.3	14	PDB header: transferase Chain: B: PDB Molecule: predicted acyltransferase with acyl-coa n-acyltransferase PDBTitle: 1.55 angstrom crystal structure of gnat family n-acetyltransferase2 (yhbs) from escherichia coli in complex with coa
18	d2cy2a1	Alignment		34.8	20	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
19	d1y9ka1	Alignment		33.3	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
20	c5jtfB_	Alignment		32.7	16	PDB header: transferase Chain: B: PDB Molecule: putative phosphinothricin n-acetyltransferase; PDBTitle: crystal structure of arsn n-acetyltransferase from pseudomonas putida2 kt2440
21	c3vgpA_	Alignment	not modelled	32.4	36	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase, putative; PDBTitle: crystal structure of the c-terminal globular domain of 2 oligosaccharyltransferase (af_0329) from archaeoglobus fulgidus
22	d1rm6b1	Alignment	not modelled	31.2	21	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
23	c2pswA_	Alignment	not modelled	28.9	12	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase 13; PDBTitle: human mak3 homolog in complex with coa
24	c4iusA_	Alignment	not modelled	27.1	24	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: gcn5-related n-acetyltransferase from kribbella flavida.
25	d1xeba_	Alignment	not modelled	25.5	20	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
26	c3vu0B_	Alignment	not modelled	24.2	43	PDB header: transferase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the c-terminal globular domain of 2 oligosaccharyltransferase (afaglb-s2, af_0040, o30195_arclu) from archaeoglobus fulgidus
27	d1y7ra1	Alignment	not modelled	24.1	22	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
28	c2jlmE_	Alignment	not modelled	23.7	17	PDB header: transferase Chain: E: PDB Molecule: putative phosphinothricin n-acetyltransferase; PDBTitle: structure of a putative acetyltransferase (aciad1637)

						from2 acinetobacter baylii adp1
29	c4z9cB_	Alignment	not modelled	23.5	21	PDB header: transferase Chain: B: PDB Molecule: subtilase cytotoxin subunit b-like protein; PDBTitle: ecpltab oxidized
30	c2r7hA_	Alignment	not modelled	23.4	14	PDB header: transferase Chain: A: PDB Molecule: putative d-alanine n-acetyltransferase of gnat family; PDBTitle: crystal structure of a putative acetyltransferase of the gnat family2 (dde_3044) from desulfovibrio desulfuricans subsp. at 1.85 a3 resolution
31	c3p2fA_	Alignment	not modelled	22.3	15	PDB header: signaling protein Chain: A: PDB Molecule: ahl synthase; PDBTitle: crystal structure of tofi in an apo form
32	d1s7ka1	Alignment	not modelled	22.2	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
33	c3fynA_	Alignment	not modelled	21.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron gene cassette protein hfx_cass3; PDBTitle: crystal structure from the mobile metagenome of cole harbour salt2 marsh: integron cassette protein hfx_cass3
34	d1zc6a1	Alignment	not modelled	21.4	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
35	d1c8ua1	Alignment	not modelled	20.7	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
36	c4jxqA_	Alignment	not modelled	20.7	15	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of a gnat superfamily phosphinothricin2 acetyltransferase (pat) from sinorhizobium meliloti 1021
37	d1yvoa1	Alignment	not modelled	19.9	15	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
38	c3wajA_	Alignment	not modelled	19.5	50	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
39	d1q2ya_	Alignment	not modelled	18.5	15	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
40	c1ib1E_	Alignment	not modelled	17.7	8	PDB header: signaling protein/transferase Chain: E: PDB Molecule: serotonin n-acetyltransferase; PDBTitle: crystal structure of the 14-3-3 zeta:serotonin n-acetyltransferase2 complex
41	d2okqa1	Alignment	not modelled	17.5	19	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YbaA-like
42	d2jdca1	Alignment	not modelled	17.0	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
43	c3d8pB_	Alignment	not modelled	16.7	12	PDB header: transferase Chain: B: PDB Molecule: acetyltransferase of gnat family; PDBTitle: crystal structure of acetyltransferase of gnat family (np_373092.1)2 from staphylococcus aureus mu50 at 2.20 a resolution
44	c2r1lB_	Alignment	not modelled	16.1	10	PDB header: transferase Chain: B: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_831484.1) from2 arthrobacter sp. fb24 at 1.65 a resolution
45	d1q1ua_	Alignment	not modelled	15.4	23	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
46	d1vhsa_	Alignment	not modelled	15.1	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
47	c2g0bG_	Alignment	not modelled	15.1	14	PDB header: transferase Chain: G: PDB Molecule: feem; PDBTitle: the structure of feem, an n-acyl amino acid synthase from uncultured2 soil microbes
48	d1ghea_	Alignment	not modelled	14.3	15	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
49	c2zc1A_	Alignment	not modelled	13.9	13	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
50	c4r9zB_	Alignment	not modelled	13.5	6	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: mycobacterium avium subs paratuberculosis tesb protein map1729c
51	c5cupB_	Alignment	not modelled	12.6	29	PDB header: transferase Chain: B: PDB Molecule: phosphate propanoyltransferase; PDBTitle: structure of rhodopseudomonas palustris pdul - phosphate bound form
52	d1z4ra1	Alignment	not modelled	12.6	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
53	d3bzka5	Alignment	not modelled	12.5	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
						Fold: Thioesterase/thiol ester dehydrase-isomerase

54	d1tbua1	Alignment	not modelled	12.4	4	Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
55	c2okqB	Alignment	not modelled	11.9	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ybaa; PDBTitle: crystal structure of unknown conserved ybaa protein from shigella2 flexneri
56	c3hbwA	Alignment	not modelled	11.7	17	PDB header: hormone Chain: A: PDB Molecule: fibroblast growth factor 13; PDBTitle: crystal structure of human fibroblast growth factor2 homologous factor 2a (fhf2a), also referred to as3 fibroblast growth factor 13a (fgf13a)
57	d2ch5a2	Alignment	not modelled	11.7	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
58	c3te4A	Alignment	not modelled	11.4	14	PDB header: transferase Chain: A: PDB Molecule: dopamine n acetyltransferase, isoform a; PDBTitle: crystal structure of dopamine n acetyltransferase in complex with2 acetyl-coa from drosophila melanogaster
59	c3waiA	Alignment	not modelled	11.4	54	PDB header: transferase, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-1, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
60	c3dwqD	Alignment	not modelled	11.2	13	PDB header: toxin Chain: D: PDB Molecule: subtilase cytotoxin, subunit b; PDBTitle: crystal structure of the a-subunit of the ab5 toxin from e.2 coli with neu5gc-2,3gal-1,3glcnac
61	c3eurA	Alignment	not modelled	11.2	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343
62	c5whvF	Alignment	not modelled	10.8	20	PDB header: toxin Chain: F: PDB Molecule: artb protein; PDBTitle: crystal structure of artb
63	d2euia1	Alignment	not modelled	9.8	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
64	d2phcb2	Alignment	not modelled	9.6	19	Fold: DCoH-like Superfamily: PH0987 N-terminal domain-like Family: PH0987 N-terminal domain-like
65	d2fl4a1	Alignment	not modelled	9.6	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
66	d1r57a	Alignment	not modelled	9.3	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
67	d1e6vb1	Alignment	not modelled	9.3	43	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
68	d1hbnb1	Alignment	not modelled	9.1	29	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
69	c2lzeA	Alignment	not modelled	9.1	38	PDB header: de novo protein Chain: A: PDB Molecule: a primordial catalytic fold generated by in vitro PDBTitle: ligase 10c
70	c4nvsB	Alignment	not modelled	9.0	13	PDB header: unknown function Chain: B: PDB Molecule: putative enzyme, glyoxalase family; PDBTitle: crystal structure of the q18cp6_clo46 protein from glyoxalase family.2 northeast structural genomics consortium target cfr3
71	c3nrdB	Alignment	not modelled	9.0	25	PDB header: nucleotide binding protein Chain: B: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
72	c5er3A	Alignment	not modelled	8.9	28	PDB header: solute-binding protein Chain: A: PDB Molecule: sugar abc transporter, periplasmic sugar-binding protein; PDBTitle: crystal structure of abc transporter system solute-binding protein2 from rhodopirellula baltica sh 1
73	d1qsra	Alignment	not modelled	8.8	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
74	c2gupA	Alignment	not modelled	8.8	22	PDB header: transferase Chain: A: PDB Molecule: rok family protein; PDBTitle: structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
75	c5vrvA	Alignment	not modelled	8.7	14	PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: protein regulated by acid ph; PDBTitle: 2.05 angstrom resolution crystal structure of c-terminal domain2 (duf2156) of putative lysylphosphatidylglycerol synthetase from3 agrobacterium fabrum.
76	c5forA	Alignment	not modelled	8.3	30	PDB header: cell cycle Chain: A: PDB Molecule: phosphoinositide 3-kinase adapter protein 1; PDBTitle: cryptic tir
77	c5b02C	Alignment	not modelled	8.2	36	PDB header: transferase, dna binding protein Chain: C: PDB Molecule: moen5,dna-binding protein 7d; PDBTitle: structure of the prenyltransferase moen5 with a fusion protein tag of2 sso7d

78	c2ab9A_	Alignment	not modelled	8.2	38	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: pro-sfti-1; PDBTitle: discovery, structural determination and processing of the2 precursor protein that produces the cyclic trypsin3 inhibitor sfti-1
79	c4lqbA_	Alignment	not modelled	8.0	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein kfla3161
80	c5lnkY_	Alignment	not modelled	7.7	13	PDB header: oxidoreductase Chain: Y: PDB Molecule: mitochondrial complex i, pgiv subunit; PDBTitle: entire ovine respiratory complex i
81	c4zbgA_	Alignment	not modelled	7.7	18	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of a gnat family acetyltransferase from brucella2 melitensis in complex with acetyl-coa
82	c3huhA_	Alignment	not modelled	7.7	7	PDB header: viral protein Chain: A: PDB Molecule: virulence protein stm3117; PDBTitle: the structure of biphenyl-2,3-diol 1,2-dioxygenase iii-related protein2 from salmonella typhimurium
83	d1nofa2	Alignment	not modelled	7.7	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
84	c3o4xE_	Alignment	not modelled	7.5	5	PDB header: protein binding Chain: E: PDB Molecule: protein diaphanous homolog 1; PDBTitle: crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
85	c3o4xF_	Alignment	not modelled	7.5	5	PDB header: protein binding Chain: F: PDB Molecule: protein diaphanous homolog 1; PDBTitle: crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
86	c5vlaZ_	Alignment	not modelled	7.5	50	PDB header: hydrolase Chain: Z: PDB Molecule: thr-val-phe-thr-ser-trp-glu-tyr-leu-asp-trp-val-met- PDBTitle: short pcsk9 delta-p' complex with fusion2 peptide
87	c6niiA_	Alignment	not modelled	7.4	43	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ravd; PDBTitle: crystal structure of ravd (residues 1-200) from legionella pneumophila2 (strain corby)
88	c3qb8A_	Alignment	not modelled	7.4	12	PDB header: transferase Chain: A: PDB Molecule: a654l protein; PDBTitle: paramecium chlorella bursaria virus1 putative orf a654l is a polyamine2 acetyltransferase
89	c2vxkA_	Alignment	not modelled	7.3	15	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate acetyltransferase; PDBTitle: structural comparison between aspergillus fumigatus and2 human gna1
90	c2q0yA_	Alignment	not modelled	7.3	10	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of gcn5-related n-acetyltransferase (yp_295895.1)2 from ralstonia eutropha jmp134 at 1.80 a resolution
91	c1c8uA_	Alignment	not modelled	7.3	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coa thioesterase ii; PDBTitle: crystal structure of the e.coli thioesterase ii, a2 homologue of the human nef-binding enzyme
92	c5b0mB_	Alignment	not modelled	7.2	36	PDB header: transferase, dna binding protein Chain: B: PDB Molecule: moen5.dna-binding protein 7d; PDBTitle: structure of moen5-ss07d fusion protein in complex with beta-dodecyl2 maltoside
93	d2veaa2	Alignment	not modelled	7.2	57	Fold: Profilin-like Superfamily: GAF domain-like Family: Phytochrome-specific domain
94	d1mdwa_	Alignment	not modelled	7.2	18	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Calpain large subunit, catalytic domain (domain II)
95	d3c2wa2	Alignment	not modelled	7.1	43	Fold: Profilin-like Superfamily: GAF domain-like Family: Phytochrome-specific domain
96	d1c5ea_	Alignment	not modelled	7.1	37	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
97	c2ru8A_	Alignment	not modelled	7.1	22	PDB header: replication Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: dnat c-terminal domain
98	c6dk2B_	Alignment	not modelled	6.7	53	PDB header: sugar binding protein Chain: B: PDB Molecule: susd; PDBTitle: bacteroidetes ac2a susd-like
99	d1k91a_	Alignment	not modelled	6.6	25	Fold: P-domain of calnexin/calreticulin Superfamily: P-domain of calnexin/calreticulin Family: P-domain of calnexin/calreticulin