










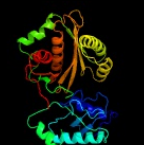





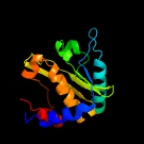



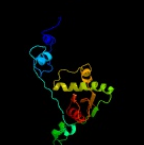











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1619_(-)_1818582_1820036
Date	Fri Aug 2 13:30:21 BST 2019
Unique Job ID	0ec485d87d9d6a3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4v36B_	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: lysyl-trna-dependent l-ysyl-phosphatidylglycerol synthase; PDBTitle: the structure of l-pgs from bacillus licheniformis
2	c5vrvA_	 Alignment		100.0	23	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.
3	c4v34A_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: alanyl-trna-dependent l-alanyl-phosphatidylglycerol PDBTitle: the structure of a-pgs from pseudomonas aeruginosa (semet derivative)
4	c2hqyB_	 Alignment		100.0	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482
5	d1ne9a2	 Alignment		99.3	15	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
6	c1p4nA_	 Alignment		99.3	14	PDB header: transferase/transferase substrate Chain: A: PDB Molecule: femx; PDBTitle: crystal structure of weissella viridescens femx:udp-murnac-2 pentapeptide complex
7	c1lrzA_	 Alignment		99.1	13	PDB header: antibiotic inhibitor Chain: A: PDB Molecule: factor essential for expression of methicillin PDBTitle: x-ray crystal structure of staphylococcus aureus fema
8	d1lrza3	 Alignment		98.9	11	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
9	d2hqya1	 Alignment		97.9	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
10	c4u9wA_	 Alignment		97.1	12	PDB header: transferase Chain: A: PDB Molecule: n-alpha-acetyltransferase 40; PDBTitle: crystal structure of natd bound to h4/h2a peptide and coa
11	c6rftB_	 Alignment		96.9	12	PDB header: antibiotic Chain: B: PDB Molecule: uncharacterized n-acetyltransferase d2e36_21790; PDBTitle: crystal structure of eis2 from mycobacterium abscessus bound to2 acetyl-coa

12	d2aj6a1	Alignment		96.2	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
13	c3n7zD_	Alignment		95.8	11	PDB header: transferase Chain: D: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase from bacillus anthracis
14	c4zm6A_	Alignment		95.4	14	PDB header: hydrolase, transferase Chain: A: PDB Molecule: n-acetyl-beta-d glucosaminidase; PDBTitle: a unique gcn5-related glucosamine n-acetyltransferase region exist in2 the fungal multi-domain gh3 beta-n-acetylglucosaminidase
15	c3lodA_	Alignment		95.3	17	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
16	c2aj6A_	Alignment		95.2	13	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein mw0638; PDBTitle: crystal structure of a putative gnat family acetyltransferase (mw0638)2 from staphylococcus aureus subsp. aureus at 1.63 a resolution
17	d1yx0a1	Alignment		94.5	17	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
18	c2hv2D_	Alignment		94.4	11	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of conserved protein of unknown function from2 enterococcus faecalis v583 at 2.4 a resolution, probable n-3 acyltransferase
19	d2hv2a2	Alignment		94.3	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: EF1021-like
20	c5kf2A_	Alignment		93.9	13	PDB header: transferase Chain: A: PDB Molecule: predicted acetyltransferase; PDBTitle: x-ray structure of a glucosamine n-acetyltransferase from clostridium2 acetobutylicum, apo form, ph 8
21	c3d8pB_	Alignment	not modelled	93.8	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
22	d1y9ka1	Alignment	not modelled	93.5	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
23	c2ozgA_	Alignment	not modelled	93.2	11	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of gcn5-related n-acetyltransferase (yp_325469.1)2 from anabaena variabilis atcc 29413 at 2.00 a resolution
24	d2ozga2	Alignment	not modelled	92.9	11	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: EF1021-like
25	c5i0cA_	Alignment	not modelled	92.5	12	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein yjdj; PDBTitle: crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
26	c4ua3A_	Alignment	not modelled	92.0	8	PDB header: transferase Chain: A: PDB Molecule: uncharacterized n-acetyltransferase c825.04c; PDBTitle: crystal structure of selenomethionine labeled spnatd
27	c3fynA_	Alignment	not modelled	91.7	13	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
28	c5jtfB_	Alignment	not modelled	91.2	12	PDB header: transferase Chain: B: PDB Molecule: putative phosphinothricin n-acetyltransferase;

						PDBTitle: crystal structure of arsn n-acetyltransferase from pseudomonas putida2 kt2440
29	d1r57a_	Alignment	not modelled	90.9	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
30	c3d3sA_	Alignment	not modelled	90.6	13	PDB header: transferase Chain: A: PDB Molecule: l-2,4-diaminobutyric acid acetyltransferase; PDBTitle: crystal structure of l-2,4-diaminobutyric acid acetyltransferase from2 bordetella parapertussis
31	d1n71a_	Alignment	not modelled	90.6	17	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
32	c5f46A_	Alignment	not modelled	90.0	9	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside acetyltransferase meta-aac0020; PDBTitle: crystal structure of an aminoglycoside acetyltransferase meta-aac00202 from an uncultured soil metagenomic sample, apoenzyme form
33	c2pdoG_	Alignment	not modelled	90.0	13	PDB header: transferase Chain: G: PDB Molecule: acetyltransferase ypea; PDBTitle: crystal structure of the putative acetyltransferase of gnat family2 from shigella flexneri
34	d1qsmA_	Alignment	not modelled	89.8	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
35	c2huzB_	Alignment	not modelled	89.7	9	PDB header: structural genomics, transferase Chain: B: PDB Molecule: glucosamine 6-phosphate n-acetyltransferase; PDBTitle: crystal structure of gnpnat1
36	d1y7ra1	Alignment	not modelled	88.9	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
37	c5ygeA_	Alignment	not modelled	88.8	14	PDB header: transferase Chain: A: PDB Molecule: amino-acid acetyltransferase; PDBTitle: arga complexed with acecoa and glutamate
38	c4orfA_	Alignment	not modelled	88.8	20	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase pat; PDBTitle: camp-binding acyltransferase from mycobacterium smegmatis, mutant r95k
39	d2i00a2	Alignment	not modelled	88.7	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: EF1021-like
40	d2atra1	Alignment	not modelled	88.3	21	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
41	c2i00D_	Alignment	not modelled	88.2	11	PDB header: transferase Chain: D: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
42	c2r98A_	Alignment	not modelled	88.1	23	PDB header: transferase Chain: A: PDB Molecule: putative acetylglutamate synthase; PDBTitle: crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
43	c2q0yA_	Alignment	not modelled	88.1	12	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
44	c6ao7A_	Alignment	not modelled	87.8	14	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of a gnat family acetyltransferase from2 elizabethkingia anophelis with acetyl-coa bound
45	c3dr8B_	Alignment	not modelled	87.8	10	PDB header: transferase Chain: B: PDB Molecule: ynca; PDBTitle: structure of ynca, a putative acetyltransferase from salmonella2 typhimurium with its cofactor acetyl-coa
46	c3fxtB_	Alignment	not modelled	86.7	11	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
47	d1yvka1	Alignment	not modelled	86.3	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
48	d1yvoa1	Alignment	not modelled	85.9	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
49	c3r1kA_	Alignment	not modelled	85.7	10	PDB header: transferase Chain: A: PDB Molecule: enhanced intracellular survival protein; PDBTitle: crystal structure of acetyltransferase eis from mycobacterium2 tuberculosis h37rv in complex with coa and an acetamide moiety
50	d2g3aa1	Alignment	not modelled	85.4	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
51	c5hmnE_	Alignment	not modelled	85.3	10	PDB header: transferase Chain: E: PDB Molecule: aac3-i; PDBTitle: crystal structure of an aminoglycoside acetyltransferase hmb0005 from2 an uncultured soil metagenomic sample, unknown active site density3 modeled as polyethylene glycol
52	c4ag9B_	Alignment	not modelled	85.1	16	PDB header: transferase Chain: B: PDB Molecule: glucosamine-6-phosphate n-acetyltransferase; PDBTitle: c. elegans glucosamine-6-phosphate n-acetyltransferase (gna1):2 ternary complex with coenzyme a and glcnc Fold: Acyl-CoA N-acyltransferases (Nat)

53	dlz4ra1	Alignment	not modelled	84.1	7	Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
54	dlghea	Alignment	not modelled	83.6	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
55	c1bo4A	Alignment	not modelled	83.3	9	PDB header: transferase Chain: A: PDB Molecule: protein (serratia marcescens aminoglycoside-3-n- PDBTitle: crystal structure of a gcn5-related n-acetyltransferase: serratia2 marescens aminoglycoside 3-n-acetyltransferase
56	d1bo4a	Alignment	not modelled	83.3	9	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
57	c2q7bA	Alignment	not modelled	83.0	10	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase (np_689019.1) from2 streptococcus agalactiae 2603 at 2.00 a resolution
58	c3i9sA	Alignment	not modelled	82.2	17	PDB header: transferase Chain: A: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of v.cholerae. integron2 cassette protein vch_cass6
59	d1qsra	Alignment	not modelled	81.9	9	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
60	c4e0aB	Alignment	not modelled	81.9	10	PDB header: transferase Chain: B: PDB Molecule: bh1408 protein; PDBTitle: crystal structure of the mutant f44r bh1408 protein from bacillus2 halodurans, northeast structural genomics consortium (nesh) target3 bhr182
61	c4avcA	Alignment	not modelled	81.5	15	PDB header: transferase Chain: A: PDB Molecule: lysine acetyltransferase; PDBTitle: crystal structure of protein lysine acetyltransferase rv09982 in complex with acetyl coa and camp
62	d1cm0a	Alignment	not modelled	80.8	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
63	c3s6fA	Alignment	not modelled	80.7	19	PDB header: transferase Chain: A: PDB Molecule: hypothetical acetyltransferase; PDBTitle: crystal structure of a putative acetyltransferase (dr_1678) from2 deinococcus radiodurans r1 at 1.19 a resolution
64	c3g8wB	Alignment	not modelled	80.0	11	PDB header: transferase Chain: B: PDB Molecule: lactococcal prophage ps3 protein 05; PDBTitle: crystal structure of a probable acetyltransferase from staphylococcus2 epidermidis atcc 12228
65	c4u5yA	Alignment	not modelled	79.8	15	PDB header: ligase Chain: A: PDB Molecule: acyl-coa synthetase; PDBTitle: crystal structure of the complex between the gnat domain of s.2 lividans pat and the acetyl-coa synthetase c-terminal domain of s.3 enterica
66	c3pp9B	Alignment	not modelled	79.6	18	PDB header: transferase Chain: B: PDB Molecule: putative streptothricin acetyltransferase; PDBTitle: 1.6 angstrom resolution crystal structure of putative streptothricin2 acetyltransferase from bacillus anthracis str. ames in complex with3 acetyl coenzyme a
67	c4luaA	Alignment	not modelled	79.2	7	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase; PDBTitle: crystal structure of n-acetyltransferase from staphylococcus aureus2 mu50
68	c3c26A	Alignment	not modelled	78.9	14	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase ta0821; PDBTitle: crystal structure of a putative acetyltransferase (np_394282.1) from2 thermoplasma acidophilum at 2.00 a resolution
69	c2wpaA	Alignment	not modelled	78.1	18	PDB header: transferase Chain: A: PDB Molecule: orf14; PDBTitle: tandem gnat protein from the clavulanic acid biosynthesis pathway2 (without accoa)
70	d2hqya2	Alignment	not modelled	77.9	8	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
71	c3efaA	Alignment	not modelled	77.9	12	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
72	d2fiaa1	Alignment	not modelled	76.8	12	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
73	c4bmaA	Alignment	not modelled	76.7	14	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of sshot
74	c3te4A	Alignment	not modelled	76.1	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
75	c2ozhA	Alignment	not modelled	76.1	23	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein xcc2953; PDBTitle: crystal structure of a putative acetyltransferase belonging to the2 gnat family (xcc2953) from xanthomonas campestris pv. campestris at3 1.40 a resolution
76	d2jdca1	Alignment	not modelled	74.5	12	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
77	d2i6ca1	Alignment	not modelled	74.3	15	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
78	d1mk4a	Alignment	not modelled	74.2	12	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat)

						Family: N-acetyl transferase, NAT
79	c2jlmE_	Alignment	not modelled	72.5	16	PDB header: transferase Chain: E: PDB Molecule: putative phosphinothricin n-acetyltransferase; PDBTitle: structure of a putative acetyltransferase (aciad1637) from2 acinetobacter baylyi adp1
80	c5wjda_	Alignment	not modelled	72.2	11	PDB header: transferase Chain: A: PDB Molecule: cg8481, isoform b; PDBTitle: crystal structure of naa80 bound to acetyl-coa
81	c3zj0A_	Alignment	not modelled	71.7	12	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: the human o-glcnaase c-terminal domain is a pseudo histone2 acetyltransferase
82	c4ubrA_	Alignment	not modelled	70.6	12	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of pseudomonas aeruginosa n-acetyltransferase pa4534
83	c3e0kA_	Alignment	not modelled	67.7	10	PDB header: transferase Chain: A: PDB Molecule: amino-acid acetyltransferase; PDBTitle: crystal structure of c-termianl domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
84	c4e8oB_	Alignment	not modelled	67.3	11	PDB header: transferase Chain: B: PDB Molecule: aac(6')-ih protein; PDBTitle: crystal structure of aminoglycoside antibiotic 6'-n-acetyltransferase2 aac(6')-ih from acinetobacter baumannii
85	d1vkca_	Alignment	not modelled	66.4	15	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
86	d1ygha_	Alignment	not modelled	65.6	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
87	d1vhsa_	Alignment	not modelled	65.2	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
88	c3t90A_	Alignment	not modelled	64.5	10	PDB header: transferase Chain: A: PDB Molecule: glucose-6-phosphate acetyltransferase 1; PDBTitle: crystal structure of glucosamine-6-phosphate n-acetyltransferase from2 arabidopsis thaliana
89	d2beia1	Alignment	not modelled	64.2	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
90	c2r7hA_	Alignment	not modelled	64.0	12	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
91	d1izca_	Alignment	not modelled	62.8	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
92	c1izcA_	Alignment	not modelled	62.8	18	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
93	c2cntD_	Alignment	not modelled	62.4	17	PDB header: transferase Chain: D: PDB Molecule: modification of 30s ribosomal subunit protein s18; PDBTitle: rimi - ribosomal s18 n-alpha-protein acetyltransferase in complex with2 coenzymeA.
94	c2ft0B_	Alignment	not modelled	61.9	23	PDB header: transferase Chain: B: PDB Molecule: tdp-fucosamine acetyltransferase; PDBTitle: crystal structure of tdp-fucosamine acetyltransferase (wecd)- complex2 with acetyl-coa
95	c4tv6A_	Alignment	not modelled	61.8	15	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyglucarate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
96	c2vwtA_	Alignment	not modelled	61.5	6	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
97	c2pswA_	Alignment	not modelled	61.5	10	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase 13; PDBTitle: human mak3 homolog in complex with coa
98	c3t9yA_	Alignment	not modelled	61.3	10	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of gnat family acetyltransferase staphylococcus2 aureus subsp. aureus usa300_tch1516
99	c3blnA_	Alignment	not modelled	59.2	10	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase gnat family; PDBTitle: crystal structure of acetyltransferase gnat family (np_981174.1) from2 bacillus cereus atcc 10987 at 1.31 a resolution
100	d1y9wa1	Alignment	not modelled	59.1	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
101	c3fb3A_	Alignment	not modelled	56.8	15	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase; PDBTitle: crystal structure of trypanosoma brucei acetyltransferase,2 tb11.01.2886
102	d1lrza2	Alignment	not modelled	54.6	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
103	d1q2ya_	Alignment	not modelled	54.2	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
						PDB header: transferase

104	c3fixA_	Alignment	not modelled	53.2	13	Chain: A: PDB Molecule: n-acetyltransferase; PDBTitle: crystal structure of a putative n-acetyltransferase (ta0374) from2 thermoplasma acidophilum
105	c2v5jB_	Alignment	not modelled	52.9	8	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
106	c4b5sB_	Alignment	not modelled	52.3	8	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; PDBTitle: crystal structures of divalent metal dependent pyruvate aldolase,2 hpa1, in complex with pyruvate
107	d1ro5a_	Alignment	not modelled	52.1	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Autoinducer synthetase
108	d1xeba_	Alignment	not modelled	52.0	11	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
109	c2oh1A_	Alignment	not modelled	51.4	10	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase gnat family (yp_013287.1) from2 listeria monocytogenes 4b f2365 at 1.46 a resolution
110	c2hmnA_	Alignment	not modelled	50.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: naphthalene 1,2-dioxygenase alpha subunit; PDBTitle: crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene.
111	c2k5tA_	Alignment	not modelled	50.1	17	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein yhhk; PDBTitle: solution nmr structure of putative n-acetyl transferase2 yhhk from e. coli bound to coenzyme a: northeast3 structural genomics consortium target et106
112	c2gbxE_	Alignment	not modelled	49.6	11	PDB header: oxidoreductase Chain: E: PDB Molecule: biphenyl 2,3-dioxygenase alpha subunit; PDBTitle: crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
113	c4pv6E_	Alignment	not modelled	48.2	15	PDB header: transferase Chain: E: PDB Molecule: n-terminal acetyltransferase complex subunit [ard1]; PDBTitle: crystal structure analysis of ard1 from thermoplasma volcanium
114	c3k9uA_	Alignment	not modelled	46.7	15	PDB header: transferase Chain: A: PDB Molecule: paia acetyltransferase; PDBTitle: crystal structure of paia acetyltransferase (ta0374) from thermoplasma2 acidophilum
115	d1s3za_	Alignment	not modelled	46.2	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
116	d2ae6a1	Alignment	not modelled	45.5	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
117	d2fe7a1	Alignment	not modelled	43.7	11	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
118	d1z4ea1	Alignment	not modelled	43.0	17	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
119	c2r1iB_	Alignment	not modelled	42.6	15	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
120	c4zbpC_	Alignment	not modelled	42.1	14	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase 7; PDBTitle: crystal structure of the ampccr-bound atnudt7