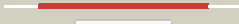



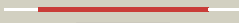


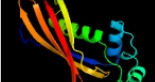
















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0636 (-)_732396_732824
Date	Fri Jul 26 01:50:20 BST 2019
Unique Job ID	978dc93fb8341575

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4rv2B_	 Alignment		100.0	85	PDB header: lyase Chain: B; PDB Molecule: maoc family protein; PDBTitle: crystal structure of (3r)-hydroxyacyl-accp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
2	c4v12A_	 Alignment		100.0	51	PDB header: oxidoreductase Chain: A; PDB Molecule: maoc like domain protein; PDBTitle: crystal structure of the msmeg_6754 dehydratase from mycobacterium2 smegmatis
3	d2b3na1	 Alignment		100.0	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
4	c4w7bD_	 Alignment		100.0	22	PDB header: lyase Chain: D; PDB Molecule: hydratase chsh2; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
5	c4ffuA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: oxidase; PDBTitle: crystal structure of putative maoc-like (monoamine oxidase-like)2 protein, similar to nodn from sinorhizobium melliloti 1021
6	c5cpgA_	 Alignment		100.0	27	PDB header: lyase Chain: A; PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
7	c4e3eA_	 Alignment		100.0	6	PDB header: oxidoreductase Chain: A; PDB Molecule: maoc domain protein dehydratase; PDBTitle: crystal structure of putative maoc domain protein dehydratase from2 chloroflexus aurantiacus j-10-fi
8	d1q6wa_	 Alignment		100.0	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
9	c3exzA_	 Alignment		100.0	15	PDB header: lyase Chain: A; PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of the maoc-like dehydratase from rhodospirillum2 rubrum. northeast structural genomics consortium target rrr103a.
10	d1iq6a_	 Alignment		100.0	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
11	d2bi0a1	 Alignment		100.0	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like

12	c2bi0A_	Alignment		99.9	17	PDB header: hypothetical protein Chain: A; PDB Molecule: hypothetical protein rv0216; PDBTitle: rv0216, a conserved hypothetical protein from mycobacterium2 tuberculosis that is essential for bacterial survival3 during infection, has a double hotdogfold
13	d2c2ia1	Alignment		99.9	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
14	d2bi0a2	Alignment		99.9	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
15	c5zy8A_	Alignment		99.9	13	PDB header: lyase Chain: A; PDB Molecule: upf0336 protein rv0637; PDBTitle: crystal structure of c terminal truncated hadbc (3r-hydroxyacyl-acp2 dehydratase) complex from mycobacterium tuberculosis
16	c3ir3B_	Alignment		99.9	21	PDB header: lyase Chain: B; PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
17	c4rv2A_	Alignment		99.9	15	PDB header: lyase Chain: A; PDB Molecule: upf0336 protein msmeg_1340/msmej_1302; PDBTitle: crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
18	c4ritA_	Alignment		99.9	13	PDB header: lyase/lyase inhibitor Chain: A; PDB Molecule: (3r)-hydroxyacyl-acp dehydratase subunit hada; PDBTitle: crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin
19	d1s9ca1	Alignment		99.9	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
20	d1pn2a2	Alignment		99.8	27	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
21	c2vkzH_	Alignment	not modelled	99.8	25	PDB header: transferase Chain: H; PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
22	c4w7bG_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: G; PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
23	c2uval_	Alignment	not modelled	99.8	27	PDB header: transferase Chain: I; PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
24	c3omlA_	Alignment	not modelled	99.8	26	PDB header: oxidoreductase, hydrolase Chain: A; PDB Molecule: peroxisomal multifunctional enzyme type 2, cg3415; PDBTitle: structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster
25	c3kh8B_	Alignment	not modelled	99.8	28	PDB header: lyase Chain: B; PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
26	c1pn2D_	Alignment	not modelled	99.8	24	PDB header: lyase Chain: D; PDB Molecule: peroxisomal hydratase-dehydrogenase-epimerase; PDBTitle: crystal structure analysis of the selenomethionine labelled2 2-enoyl-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2
27	c1s9cK_	Alignment	not modelled	99.8	25	PDB header: lyase Chain: K; PDB Molecule: peroxisomal multifunctional enzyme type 2; PDBTitle: crystal structure analysis of the 2-enoyl-coa hydratase 22

					domain of human peroxisomal multifunctional enzyme type 2 PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
28	c4b3yB_	Alignment	not modelled	99.8	27
29	c3khpB_	Alignment	not modelled	99.8	28
30	c2cdhT_	Alignment	not modelled	99.8	24
31	c2f3xA_	Alignment	not modelled	98.1	20
32	d1s9ca2	Alignment	not modelled	98.0	12
33	c4a0zA_	Alignment	not modelled	97.5	15
34	d1z6ba1	Alignment	not modelled	97.3	10
35	d1ixla_	Alignment	not modelled	97.3	24
36	d2ov9a1	Alignment	not modelled	97.2	18
37	d2f41a1	Alignment	not modelled	97.0	16
38	c4h4gG_	Alignment	not modelled	96.9	9
39	c4ae8D_	Alignment	not modelled	96.9	12
40	c4ae7A_	Alignment	not modelled	96.9	14
41	c3qooA_	Alignment	not modelled	96.8	12
42	d1pn2a1	Alignment	not modelled	96.8	10
43	c4i82A_	Alignment	not modelled	96.8	14
44	c3lwgB_	Alignment	not modelled	96.7	12
45	c3d6xA_	Alignment	not modelled	96.6	11
46	d2cwza1	Alignment	not modelled	96.5	14
47	c4zw0A_	Alignment	not modelled	96.5	7
48	c3lbeA_	Alignment	not modelled	96.5	16
49	c3gekA_	Alignment	not modelled	96.1	7
50	c3esiD_	Alignment	not modelled	96.0	11
51	d2cy9a1	Alignment	not modelled	95.8	22
52	d2fs2a1	Alignment	not modelled	95.8	13
					Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
					PDB header: unknown function

53	c3bnvD	Alignment	not modelled	95.8	10	Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
54	c6qsrA	Alignment	not modelled	95.6	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
55	c2pimA	Alignment	not modelled	95.5	16	PDB header: hydrolase Chain: A: PDB Molecule: phenylacetic acid degradation-related protein; PDBTitle: crystal structure of a putative thioesterase, phenylacetic acid2 degradation-related protein (reut_b4779) from ralstonia eutropha3 jmp134 at 2.20 a resolution
56	c5buyA	Alignment	not modelled	95.3	12	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from francisella tularensis
57	c3nwdD	Alignment	not modelled	95.0	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: bh2602 protein; PDBTitle: crystal structure of bh2602 protein from bacillus halodurans with coa,2 northeast structural genomics consortium target bhr199
58	c3hduB	Alignment	not modelled	95.0	13	PDB header: hydrolase Chain: B: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
59	c3e29C	Alignment	not modelled	94.6	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein q7we92_borbr; PDBTitle: x-ray structure of the protein q7we92_borbr from thioesterase2 superfamily. northeast structural genomics consortium target bor214a.
60	d1u1za	Alignment	not modelled	94.6	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
61	c4mzqG	Alignment	not modelled	94.3	26	PDB header: lyase Chain: G: PDB Molecule: beta-alanyl-coa:ammonia lyase; PDBTitle: beta-alanyl-coa:ammonia lyase from clostridium propionicum in complex2 with propionyl-coa
62	c2glvA	Alignment	not modelled	94.2	14	PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-acyl carrier protein dehydratase; PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
63	c3e8pA	Alignment	not modelled	94.1	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein q8e9m7 from shewanella oneidensis2 related to thioesterase superfamily. northeast structural genomics3 consortium target sor246.
64	d2h4ua1	Alignment	not modelled	94.1	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
65	c3f1tB	Alignment	not modelled	93.6	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein q9i3c8_pseae; PDBTitle: crystal structure of the q9i3c8_pseae protein from pseudomonas2 aeruginosa. northeast structural genomics consortium target par319a.
66	c2qwzB	Alignment	not modelled	93.4	14	PDB header: hydrolase Chain: B: PDB Molecule: phenylacetic acid degradation-related protein; PDBTitle: crystal structure of a putative thioesterase (tm1040_1390) from2 silicibacter sp. tm1040 at 2.15 a resolution
67	d2gvha2	Alignment	not modelled	93.3	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
68	c2prxB	Alignment	not modelled	93.3	18	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase superfamily protein; PDBTitle: crystal structure of thioesterase superfamily protein (zp_00837258.1)2 from shewanella loihica pv-4 at 1.65 a resolution
69	d2hboa1	Alignment	not modelled	93.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
70	c6qsrB	Alignment	not modelled	93.2	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: beta-hydroxyacyl-(acyl-carrier-protein) dehydratase PDBTitle: the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
71	d1ylia1	Alignment	not modelled	93.2	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
72	c5byuD	Alignment	not modelled	93.1	17	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
73	d1vh5a	Alignment	not modelled	92.6	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
74	d2f0xa1	Alignment	not modelled	92.4	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
75	c4i83A	Alignment	not modelled	92.4	9	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of (3r)-hydroxymyristoyl-acp dehydratase from2 neisseria meningitidis fam18
76	d1wlua1	Alignment	not modelled	92.3	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like

77	c5buxB_	Alignment	not modelled	92.1	8	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of 3-hydroxyacyl-acyl carrier protein dehydratase (fabz) from <i>Yersinia pestis</i> with glycerol bound
78	c5eo4A_	Alignment	not modelled	91.9	11	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from <i>Staphylococcus aureus</i> .
79	c5lqD_	Alignment	not modelled	91.8	13	PDB header: hydrolase Chain: D: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: high resolution crystal structure of the 4-hydroxybenzoyl coenzyme-a2 thioesterase from <i>Staphylococcus aureus</i>
80	c3ck1B_	Alignment	not modelled	91.5	19	PDB header: hydrolase Chain: B: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of a putative thioesterase (reut_a2179) from <i>Ralstonia eutropha</i> jmp134 at 1.74 Å resolution
81	c3rqbB_	Alignment	not modelled	91.1	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved protein of unknown function with hot2 dog fold from <i>Alicyclobacillus acidocaldarius</i>
82	d1vh9a_	Alignment	not modelled	90.4	14	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Paal/Ydil-like
83	c2w3xE_	Alignment	not modelled	90.1	13	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
84	d1q4ua_	Alignment	not modelled	90.1	9	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Paal/Ydil-like
85	c4rmmA_	Alignment	not modelled	89.9	11	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the q7nvp2_chrv0 protein from <i>Chromobacterium violaceum</i> . northeast structural genomics consortium target cvr191
86	d1zkiA1	Alignment	not modelled	89.8	13	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Paal/Ydil-like
87	d2owna1	Alignment	not modelled	89.8	15	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Acyl-ACP thioesterase-like
88	d1s5ua_	Alignment	not modelled	89.8	12	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: 4HBT-like
89	c3kuvB_	Alignment	not modelled	89.8	16	PDB header: hydrolase Chain: B: PDB Molecule: fluoroacetyl coenzyme a thioesterase; PDBTitle: structural basis of the activity and substrate specificity of the2 fluoroacetyl-coa thioesterase flk - t42s mutant in complex with3 acetate.
90	c2gvhC_	Alignment	not modelled	89.5	15	PDB header: hydrolase Chain: C: PDB Molecule: agr_1_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from <i>Agrobacterium tumefaciens</i> at 2.65 Å resolution
91	d2essa1	Alignment	not modelled	89.3	11	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Acyl-ACP thioesterase-like
92	c3dkzA_	Alignment	not modelled	89.1	14	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily protein; PDBTitle: crystal structure of the q7w9w5_borpa protein from <i>Bordetella parapertussis</i> . northeast structural genomics3 consortium target bpr208c.
93	d2gvha1	Alignment	not modelled	89.1	13	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: 4HBT-like
94	c4k00A_	Alignment	not modelled	88.9	11	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa hydrolase; PDBTitle: crystal structure of slr0204, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from <i>Synechocystis</i>
95	c4ienB_	Alignment	not modelled	88.7	18	PDB header: hydrolase Chain: B: PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from <i>Neisseria meningitidis</i> 2 fam18
96	c5hmcA_	Alignment	not modelled	88.6	11	PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of <i>S. sahachiroi</i> azig complexed with 5-methyl2 naphthoic acid
97	c4qdbF_	Alignment	not modelled	88.5	13	PDB header: hydrolase Chain: F: PDB Molecule: thioesterase pa1618; PDBTitle: crystal structure of mutant thioesterase pa1618 (q49a) from <i>Pseudomonas aeruginosa</i>
98	d2nuja1	Alignment	not modelled	88.2	16	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: 4HBT-like
99	d1vpma_	Alignment	not modelled	87.7	12	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: 4HBT-like
100	d2owna2	Alignment	not modelled	87.6	10	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Acyl-ACP thioesterase-like
101	c5dm5E_	Alignment	not modelled	87.5	11	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from <i>Yersinia pestis</i>
						Fold: Thioesterase/thiol ester dehydratase-isomerase

102	d1njka_	Alignment	not modelled	87.3	13	Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
103	c2eisA_	Alignment	not modelled	87.2	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tthb207; PDBTitle: x-ray structure of acyl-coa hydrolase-like protein, tt1379, from2 thermus thermophilus hb8
104	d1sc0a_	Alignment	not modelled	87.0	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
105	c3s4kA_	Alignment	not modelled	87.0	8	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase rv1847/mt1895; PDBTitle: structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
106	c3d6IA_	Alignment	not modelled	86.7	14	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
107	d2gf6a1	Alignment	not modelled	86.7	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
108	c5wh9C_	Alignment	not modelled	86.6	11	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
109	c5byuA_	Alignment	not modelled	86.2	17	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
110	d2fuja1	Alignment	not modelled	86.1	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
111	c4m20D_	Alignment	not modelled	86.0	11	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50
112	d1y7ua1	Alignment	not modelled	85.6	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
113	c1c8uA_	Alignment	not modelled	85.3	12	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
114	c4k02A_	Alignment	not modelled	84.4	14	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa thioesterase; PDBTitle: crystal structure of atdhnat1, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from arabidopsis thaliana
115	d2oafa1	Alignment	not modelled	84.3	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
116	c4b8uD_	Alignment	not modelled	84.2	14	PDB header: lyase Chain: D: PDB Molecule: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of 3-hydroxydecanoyl-acyl carrier protein2 dehydratase (faba) from pseudomonas aeruginosa in complex with3 n-isobutyl-2-(5-(2-thienyl)-1,2-oxazol-3-yl-methoxy)acetamide
117	d2hjja1	Alignment	not modelled	83.2	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
118	d1sh8a_	Alignment	not modelled	82.9	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
119	d1tbua1	Alignment	not modelled	81.7	6	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
120	d2o5ua1	Alignment	not modelled	81.4	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like