

Phyre2

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Description	RVBD1847 (-) _2096884_2097306
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3s4kA_	Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase rv1847/mt1895; PDBTitle: structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
2	d1q4ua_	Alignment		100.0	32	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
3	d1vh5a_	Alignment		100.0	31	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
4	c4qdbF_	Alignment		100.0	22	PDB header: hydrolase Chain: F: PDB Molecule: thioesterase pa1618; PDBTitle: crystal structure of mutant thioesterase pa1618 (q49a) from2 pseudomonas aeruginosa
5	c3hduB_	Alignment		100.0	19	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
6	d1sc0a_	Alignment		100.0	31	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
7	c3e8pA_	Alignment		100.0	20	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.
8	d1vh9a_	Alignment		100.0	33	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
9	c5hmcA_	Alignment		100.0	52	PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid
10	c2qwzB_	Alignment		100.0	21	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
11	c4m20D_	Alignment		100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50

12	c4i82A_	Alignment		99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
13	d1sh8a_	Alignment		99.9	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
14	d1zka1	Alignment		99.9	25	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
15	d2fs2a1	Alignment		99.9	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
16	d2f0xa1	Alignment		99.9	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
17	c3e29C_	Alignment		99.9	21	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.
18	c3f1tB_	Alignment		99.9	16	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.
19	c3dkzA_	Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily protein; PDBTitle: crystal structure of the q7w9w5_borpa protein from2 bordetella parapertussis. northeast structural genomics3 consortium target bpr208c.
20	c2pimA_	Alignment		99.9	21	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
21	c3lbeA_	Alignment	not modelled	99.9	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein smu.793; PDBTitle: the crystal structure of smu.793 from streptococcus mutans ua159 bound2 to acetyl coa
22	c3e1eE_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: E: PDB Molecule: thioesterase family protein; PDBTitle: crystal structure of a thioesterase family protein from2 silicibacter pomeroyi. northeast structural genomics3 target sir180a
23	c4k02A_	Alignment	not modelled	99.9	32	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
24	c4rmmA_	Alignment	not modelled	99.9	20	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the q7nvp2_chrvo protein from chromobacterium2 violaceum. northeast structural genomics consortium target cvr191
25	d1t82a_	Alignment	not modelled	99.9	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
26	d1yoca1	Alignment	not modelled	99.9	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
27	d2hboa1	Alignment	not modelled	99.9	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
28	d1wlua1	Alignment	not modelled	99.9	28	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like

29	d2cy9a1	Alignment	not modelled	99.9	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
30	d2h4ua1	Alignment	not modelled	99.9	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
31	c3lwgB_	Alignment	not modelled	99.9	21	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis
32	c3nzwD_	Alignment	not modelled	99.9	18	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
33	d1ixla_	Alignment	not modelled	99.9	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
34	c3gekA_	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thioesterase yhda; PDBTitle: crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113
35	c3lmbA_	Alignment	not modelled	99.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum t1s
36	c3bnvD_	Alignment	not modelled	99.9	12	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
37	d2ov9a1	Alignment	not modelled	99.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
38	c4ae7A_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
39	d2f41a1	Alignment	not modelled	99.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
40	c4ae8D_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4
41	c2prxB_	Alignment	not modelled	99.8	17	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
42	c4a0zA_	Alignment	not modelled	99.8	16	PDB header: transcription Chain: A: PDB Molecule: transcription factor fapr; PDBTitle: structure of the global transcription regulator fapr from2 staphylococcus aureus in complex with malonyl-coa
43	c2f3xA_	Alignment	not modelled	99.8	16	PDB header: gene regulation Chain: A: PDB Molecule: transcription factor fapr; PDBTitle: crystal structure of fapr (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
44	c5dm5E_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
45	c2eisA_	Alignment	not modelled	99.6	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tthb207; PDBTitle: x-ray structure of acyl-coa hydrolase-like protein, t1379, from2 thermus thermophilus hb8
46	c3d6IA_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
47	d1ylia1	Alignment	not modelled	99.6	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
48	d2gvha2	Alignment	not modelled	99.6	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
49	c2gvhC_	Alignment	not modelled	99.5	27	PDB header: hydrolase Chain: C: PDB Molecule: agr_I_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
50	c3b7kA_	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
51	c4ncpF_	Alignment	not modelled	99.5	20	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 4-hbt like thioesterase sav1878 from2 staphylococcus aureus subsp. aureus mu50
52	c4ienB_	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: B: PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
53	d1vpma_	Alignment	not modelled	99.5	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
54	d2gvha1	Alignment	not modelled	99.4	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like

55	c2qq2C	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: C: PDB Molecule: cytosolic acyl coenzyme a thioester hydrolase; PDBTitle: crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
56	c4zv3B	Alignment	not modelled	99.4	21	PDB header: hydrolase Chain: B: PDB Molecule: cytosolic acyl coenzyme a thioester hydrolase; PDBTitle: crystal structure of the n- and c-terminal domains of mouse acyl-coa2 thioesterase 7
57	d1y7ua1	Alignment	not modelled	99.3	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
58	c2v1oF	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: F: PDB Molecule: cytosolic acyl coenzyme a thioester hydrolase; PDBTitle: crystal structure of n-terminal domain of acyl-coa2 thioesterase 7
59	d2cwza1	Alignment	not modelled	99.1	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
60	d2hlja1	Alignment	not modelled	98.7	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
61	c5byuD	Alignment	not modelled	98.7	11	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
62	c3bbjA	Alignment	not modelled	98.6	25	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase ii; PDBTitle: crystal structure of a putative thioesterase ii (tfu_2367) from2 thermobifida fusca yx at 2.45 a resolution
63	c4k00A	Alignment	not modelled	98.6	12	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 synechocystis
64	d1s5ua	Alignment	not modelled	98.6	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
65	d2cyea1	Alignment	not modelled	98.6	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
66	c5eo4A	Alignment	not modelled	98.6	8	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
67	c5lqID	Alignment	not modelled	98.6	15	PDB header: hydrolase Chain: D: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: high resolution crystal structure of the 4-hydroxybenzoyl coenzyme-a2 thioesterase from staphylococcus aureus
68	c5byuA	Alignment	not modelled	98.5	11	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
69	c4i4jE	Alignment	not modelled	98.5	16	PDB header: hydrolase Chain: E: PDB Molecule: acp-polyene thioesterase; PDBTitle: the structure of sgce10, the acp-polyene thioesterase involved in c-2 1027 biosynthesis
70	c5wh9C	Alignment	not modelled	98.5	10	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
71	c3hm0C	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella henselae
72	d1njka	Alignment	not modelled	98.5	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
73	c3ck1B	Alignment	not modelled	98.5	14	PDB header: hydrolase Chain: B: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of a putative thioesterase (reut_a2179) from2 ralstonia eutropha jmp134 at 1.74 a resolution
74	c2w3xE	Alignment	not modelled	98.5	14	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in edenyne biosynthesis, cale7
75	c2essA	Alignment	not modelled	98.5	9	PDB header: hydrolase Chain: A: PDB Molecule: acyl-acp thioesterase; PDBTitle: crystal structure of an acyl-acp thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution
76	c3rqbB	Alignment	not modelled	98.5	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 alicyclobacillus acidocaldarius
77	d2gf6a1	Alignment	not modelled	98.4	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
78	c5vpjB	Alignment	not modelled	98.4	14	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesteras from actinomadura2 verrucosospora.
79	d2o5ua1	Alignment	not modelled	98.4	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
						Fold: Thioesterase/thiol ester dehydrase-isomerase

80	d2essa1	Alignment	not modelled	98.4	9	Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
81	c2egiE	Alignment	not modelled	98.4	13	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: hypothetical protein aq_1494; PDBTitle: crystal structure of a hypothetical protein(aq1494) from aquifex2 aeolicus
82	d2fuja1	Alignment	not modelled	98.4	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
83	d2oafa1	Alignment	not modelled	98.4	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
84	c5v10B	Alignment	not modelled	98.4	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the putative tol-pal system-associated acyl-coa2 thioesterase from pseudomonas aeruginosa pao1
85	c4gakA	Alignment	not modelled	98.4	7	PDB header: hydrolase Chain: A: PDB Molecule: acyl-acp thioesterase; PDBTitle: crystal structure of acyl-acp thioesterase from spirosona linguale
86	c2pzhC	Alignment	not modelled	98.4	15	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from helicobacter pylori
87	d2owna1	Alignment	not modelled	98.4	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
88	c3qooA	Alignment	not modelled	98.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
89	d1z54a1	Alignment	not modelled	98.3	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
90	c2ownA	Alignment	not modelled	98.3	11	PDB header: hydrolase Chain: A: PDB Molecule: putative oleoyl-[acyl-carrier protein] thioesterase; PDBTitle: crystal structure of oleoyl thioesterase (putative) (np_784467.1) from2 lactobacillus plantarum at 2.00 a resolution
91	d2hx5a1	Alignment	not modelled	98.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
92	c1c8uA	Alignment	not modelled	98.3	17	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
93	c5x04B	Alignment	not modelled	98.3	10	PDB header: hydrolase Chain: B: PDB Molecule: dodecanoyl-[acyl-carrier-protein] hydrolase, chloroplastic; PDBTitle: 12:0-acp thioesterase from umbellularia californica
94	d2oiwa1	Alignment	not modelled	98.2	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
95	c3kuvB	Alignment	not modelled	98.2	21	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.
96	d2nuja1	Alignment	not modelled	98.2	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
97	d1lo7a	Alignment	not modelled	98.2	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
98	d1c8ua1	Alignment	not modelled	98.2	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
99	c3rd7A	Alignment	not modelled	98.2	18	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coa thioesterase; PDBTitle: crystal structure of acyl-coa thioesterase from mycobacterium avium
100	d2alia1	Alignment	not modelled	98.1	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
101	c2aliaA	Alignment	not modelled	98.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa2801; PDBTitle: structure of protein of unknown function pa2801 from pseudomonas2 aeruginosa, putative thioesterase
102	c3r87A	Alignment	not modelled	98.1	12	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from photobacterium profundum
103	c4r9zB	Alignment	not modelled	98.1	13	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: mycobacterium avium subs paratuberculosis tesb protein map1729c
104	d2q78a1	Alignment	not modelled	98.1	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
105	c2xfiB	Alignment	not modelled	98.1	15	PDB header: hydrolase Chain: B: PDB Molecule: dyne7; PDBTitle: induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynemicin3 thioesterase
106	d1q6wa	Alignment	not modelled	98.0	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase

						Family: MaoC-like
107	c3cyaA	Alignment	not modelled	97.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of putative thioesterase (yp_496845.1) from <i>Novosphingobium aromaticivorans</i> DSM 12444 at 1.70 Å resolution
108	d2owna2	Alignment	not modelled	97.8	12	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Acyl-ACP thioesterase-like
109	d1tbua1	Alignment	not modelled	97.8	14	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Acyl-CoA thioesterase
110	c3exzA	Alignment	not modelled	97.8	14	PDB header: lyase Chain: A: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of the maoc-like dehydratase from <i>Rhodospirillum rubrum</i> . Northeast Structural Genomics Consortium target rrr103a.
111	c3ir3B	Alignment	not modelled	97.7	22	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
112	c5cpgA	Alignment	not modelled	97.6	19	PDB header: lyase Chain: A: PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from <i>Pseudomonas aeruginosa</i> in the unliganded form
113	c4rltA	Alignment	not modelled	97.6	17	PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: (3r)-hydroxyacyl-acyl dehydratase subunit hada; PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl dehydratase hadab hetero-2 dimer from <i>Mycobacterium tuberculosis</i> complexed with fisetin
114	d1c8ua2	Alignment	not modelled	97.6	9	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Acyl-CoA thioesterase
115	c4ffuA	Alignment	not modelled	97.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidase; PDBTitle: crystal structure of putative maoc-like (monoamine oxidase-like)2 protein, similar to nodN from <i>Sinorhizobium meliloti</i> 1021
116	c4rv2A	Alignment	not modelled	97.4	17	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein msmeg_1340/msmej_1302; PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl dehydratase hadab hetero-2 dimer from <i>Mycobacterium smegmatis</i>
117	d1iq6a	Alignment	not modelled	97.1	14	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: MaoC-like
118	c5zy8A	Alignment	not modelled	97.1	13	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein rv0637; PDBTitle: crystal structure of C-terminal truncated hadbc (3r-hydroxyacyl-acyl2 dehydratase) complex from <i>Mycobacterium tuberculosis</i>
119	c6qsrB	Alignment	not modelled	96.9	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: beta-hydroxyacyl-(acyl-carrier-protein) dehydratase PDBTitle: the dehydratase heterocomplex apei:p from <i>Xenorhabdus doucetiae</i>
120	c4zw0A	Alignment	not modelled	96.8	9	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 <i>Candidatus asiaticum</i>