



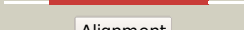

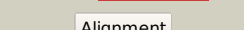

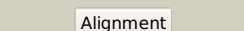




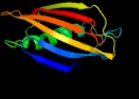
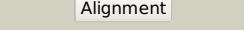

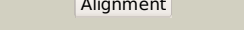
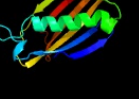
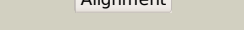

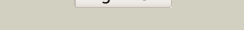
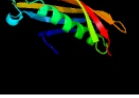











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0356c (-) _434831_435475
Date	Tue Jul 23 14:50:42 BST 2019
Unique Job ID	58f968f2c5b3001f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ov9a1	 Alignment		100.0	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
2	c4ae7A_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
3	c4ae8D_	 Alignment		100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4
4	d2hboa1	 Alignment		99.9	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
5	c3f1tB_	 Alignment		99.9	21	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.
6	c2qwzB_	 Alignment		99.9	17	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
7	d2f0xa1	 Alignment		99.9	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
8	c4i82A_	 Alignment		99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
9	d1wlua1	 Alignment		99.9	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
10	c2pimA_	 Alignment		99.9	18	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
11	c3lbeA_	 Alignment		99.9	15	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

12	d2h4ua1	Alignment		99.9	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
13	c3e8pA	Alignment		99.9	26	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.
14	d2fs2a1	Alignment		99.9	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
15	d1zkia1	Alignment		99.9	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
16	c3nwzD	Alignment		99.9	17	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
17	c3hduB	Alignment		99.9	20	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
18	d2cy9a1	Alignment		99.9	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
19	c5hmcA	Alignment		99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid
20	c3e29C	Alignment		99.9	25	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.
21	c3s4kA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase rv1847/mt1895; PDBTitle: structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
22	d1vh5a	Alignment	not modelled	99.9	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
23	c3e1eE	Alignment	not modelled	99.9	15	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
24	c3dkzA	Alignment	not modelled	99.9	17	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.
25	d1sc0a	Alignment	not modelled	99.9	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
26	d1q4ua	Alignment	not modelled	99.9	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
27	c4m20D	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50
28	c4k02A	Alignment	not modelled	99.9	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
29	d1vh9a_	Alignment	not modelled	99.9	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
30	c4qdbF_	Alignment	not modelled	99.9	10	PDB header: hydrolase Chain: F: PDB Molecule: thioesterase pa1618; PDBTitle: crystal structure of mutant thioesterase pa1618 (q49a) from2 pseudomonas aeruginosa
31	c3gekA_	Alignment	not modelled	99.9	16	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
32	d1ixla_	Alignment	not modelled	99.9	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
33	c3lwgB_	Alignment	not modelled	99.9	14	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis
34	c2prxB_	Alignment	not modelled	99.9	23	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
35	c4rmmA_	Alignment	not modelled	99.9	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the q7nvp2_chrv0 protein from chromobacterium2 violaceum. northeast structural genomics consortium target cvr191
36	c5dm5E_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
37	c3bnvD_	Alignment	not modelled	99.8	7	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
38	d1sh8a_	Alignment	not modelled	99.8	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
39	c4a0zA_	Alignment	not modelled	99.8	14	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
40	d2f41a1	Alignment	not modelled	99.8	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
41	d1ylia1	Alignment	not modelled	99.8	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
42	c2f3xA_	Alignment	not modelled	99.8	18	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
43	c2eisA_	Alignment	not modelled	99.8	15	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
44	c3d6IA_	Alignment	not modelled	99.7	11	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
45	d1t82a_	Alignment	not modelled	99.7	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
46	c2gvhC_	Alignment	not modelled	99.7	11	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
47	d2gvha2	Alignment	not modelled	99.7	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
48	d1yoca1	Alignment	not modelled	99.7	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
49	d1vpma_	Alignment	not modelled	99.7	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
50	c4ienB_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: B: PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
51	c3b7kA_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
52	c4ncpF_	Alignment	not modelled	99.7	14	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
53	c2qq2C_	Alignment	not modelled	99.6	16	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
54	c3lmbA_	Alignment	not modelled	99.6	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;

54	c3mva_	Alignment	not modelled	99.0	9	PDBTitle: the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum t1s
55	d2gvha1	Alignment	not modelled	99.6	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
56	d1y7ua1	Alignment	not modelled	99.6	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
57	c2v1oF_	Alignment	not modelled	99.6	16	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
58	c4zv3B_	Alignment	not modelled	99.5	17	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
59	d2cwza1	Alignment	not modelled	99.0	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
60	c5eo4A_	Alignment	not modelled	98.8	13	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
61	d1s5ua_	Alignment	not modelled	98.8	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
62	d2essa1	Alignment	not modelled	98.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
63	d2cyea1	Alignment	not modelled	98.8	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
64	c2egfE_	Alignment	not modelled	98.8	12	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
65	c5lqID_	Alignment	not modelled	98.8	14	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
66	c3ir3B_	Alignment	not modelled	98.8	13	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
67	c4k00A_	Alignment	not modelled	98.8	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 synechocystis
68	c3bbjA_	Alignment	not modelled	98.8	18	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
69	d2hja1	Alignment	not modelled	98.7	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
70	c3rqbB_	Alignment	not modelled	98.7	9	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
71	d1njka_	Alignment	not modelled	98.7	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
72	c4i4jE_	Alignment	not modelled	98.7	13	PDB header: hydrolase Chain: E: PDB Molecule: acp-polyene thioesterase; PDBTitle: the structure of sgc10, the acp-polyene thioesterase involved in c-2 1027 biosynthesis
73	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
74	c2essaA_	Alignment	not modelled	98.7	16	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
75	c2w3xE_	Alignment	not modelled	98.7	12	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
76	d1z54a1	Alignment	not modelled	98.7	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
77	d2o5ua1	Alignment	not modelled	98.7	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
78	c1c8uA_	Alignment	not modelled	98.7	9	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
79	c3hm0C_	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella henselae
						PDB header: hydrolase

80	c4gakA	Alignment	not modelled	98.6	10	Chain: A: PDB Molecule: acyl- <i>acp</i> thioesterase; PDBTitle: crystal structure of acyl- <i>acp</i> thioesterase from <i>spirosona linguale</i>
81	c5v10B	Alignment	not modelled	98.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the putative <i>tol-pal</i> system-associated acyl- <i>coa2</i> thioesterase from <i>pseudomonas aeruginosa pao1</i>
82	c3cjqA	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of putative thioesterase (yp_496845.1) from <i>novosphingobium aromaticivorans dsm 12444</i> at 1.70 a resolution
83	d2qf6a1	Alignment	not modelled	98.6	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
84	d1c8ua1	Alignment	not modelled	98.6	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
85	d2fuja1	Alignment	not modelled	98.6	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
86	c3ck1B	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: B: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of a putative thioesterase (reut_a2179) from <i>2 ralstonia eutropha jmp134</i> at 1.74 a resolution
87	c5wh9C	Alignment	not modelled	98.6	7	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl- <i>coa</i> thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
88	d2owna1	Alignment	not modelled	98.6	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
89	c4r9zB	Alignment	not modelled	98.6	10	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: mycobacterium avium subs paratuberculosis tesb protein map1729c
90	c3rd7A	Alignment	not modelled	98.5	10	PDB header: hydrolase Chain: A: PDB Molecule: acyl- <i>coa</i> thioesterase; PDBTitle: crystal structure of acyl- <i>coa</i> thioesterase from <i>mycobacterium avium</i>
91	c5byuA	Alignment	not modelled	98.5	10	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from <i>legionella2 pneumophila</i>
92	d2oiwa1	Alignment	not modelled	98.5	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
93	d2owna2	Alignment	not modelled	98.5	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
94	d2oafa1	Alignment	not modelled	98.5	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
95	c2ownA	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: A: PDB Molecule: putative oleoyl-[acyl-carrier protein] thioesterase; PDBTitle: crystal structure of oleoyl thioesterase (putative) (np_784467.1) from <i>2 lactobacillus plantarum</i> at 2.00 a resolution
96	c5x04B	Alignment	not modelled	98.5	14	PDB header: hydrolase Chain: B: PDB Molecule: dodecanoyl-[acyl-carrier-protein] hydrolase, chloroplastic; PDBTitle: 12:0- <i>acp</i> thioesterase from <i>umbellularia californica</i>
97	d2nuja1	Alignment	not modelled	98.5	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
98	c5vpjB	Alignment	not modelled	98.4	12	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesteras from <i>actinomadura2 verrucosospora</i> .
99	c5cpgA	Alignment	not modelled	98.4	13	PDB header: lyase Chain: A: PDB Molecule: (<i>r</i>)-specific enoyl- <i>coa</i> hydratase; PDBTitle: <i>r</i> -hydratase phaj1 from <i>pseudomonas aeruginosa</i> in the unliganded form
100	c2pzhC	Alignment	not modelled	98.4	7	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from <i>helicobacter pylori</i>
101	d1lo7a	Alignment	not modelled	98.4	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
102	c2aliaA	Alignment	not modelled	98.4	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa2801; PDBTitle: structure of protein of unknown function pa2801 from <i>pseudomonas2 aeruginosa</i> , putative thioesterase
103	d2alia1	Alignment	not modelled	98.4	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
104	c3r87A	Alignment	not modelled	98.3	10	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from <i>photobacterium profundum</i>
105	d1iq6a	Alignment	not modelled	98.3	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
106	c3paaA	Alignment	not modelled	98.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;

106	c3q0vA	Alignment	not modelled	98.3	13	PDBTitle: crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
107	d1q6wa	Alignment	not modelled	98.3	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
108	d2hx5a1	Alignment	not modelled	98.3	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
109	c2xf1B	Alignment	not modelled	98.2	17	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
110	c3kuvB	Alignment	not modelled	98.2	14	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.
111	d2q78a1	Alignment	not modelled	98.1	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
112	c3exzA	Alignment	not modelled	98.0	11	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.
113	c5zy8A	Alignment	not modelled	98.0	9	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
114	d2b3na1	Alignment	not modelled	98.0	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
115	d1tbua1	Alignment	not modelled	98.0	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
116	c4ritA	Alignment	not modelled	98.0	8	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
117	c4rv2A	Alignment	not modelled	98.0	5	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein msme1_1340/msme1_1302; PDBTitle: crystal structure of (3r)-hydroxyacyl-ACP dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
118	d2bi0a1	Alignment	not modelled	97.9	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
119	c4ffuA	Alignment	not modelled	97.9	9	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 meliloti 1021
120	d1c8ua2	Alignment	not modelled	97.9	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase