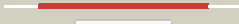



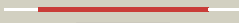




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0130_(-)_157845_158300
Date	Tue Jul 23 14:50:17 BST 2019
Unique Job ID	143788700505e93a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2c2ia1	 Alignment		100.0	99	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
2	c4e3eA	 Alignment		100.0	16	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-fl
3	d2bi0a1	 Alignment		100.0	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
4	c2bi0A	 Alignment		100.0	14	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
5	c4ffuA	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidase; PDBTitle: crystal structure of putative maoc-like (monoamine oxidase-like)2 protein, similar to nodn from sinorhizo bium melliloti 1021
6	d1q6wa	 Alignment		100.0	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
7	c3exzA	 Alignment		100.0	21	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.
8	d2b3na1	 Alignment		99.9	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
9	c5cpgA	 Alignment		99.9	24	PDB header: lyase Chain: A: PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
10	d1iq6a	 Alignment		99.9	28	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
11	c4w7bG	 Alignment		99.9	17	PDB header: lyase Chain: G: PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis

12	d2bi0a2	Alignment		99.9	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
13	c5zy8A_	Alignment		99.9	18	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
14	c4rltA_	Alignment		99.9	11	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
15	c4rv2A_	Alignment		99.9	14	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
16	c4w7bD_	Alignment		99.9	16	PDB header: lyase Chain: D: PDB Molecule: hydratase chsh2; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
17	c4v12A_	Alignment		99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: maoc like domain protein; PDBTitle: crystal structure of the msmeg_6754 dehydratase from mycobacterium2 smegmatis
18	c4rv2B_	Alignment		99.9	20	PDB header: lyase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
19	c3ir3B_	Alignment		99.9	25	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
20	d1s9ca1	Alignment		99.8	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
21	d1pn2a2	Alignment	not modelled	99.8	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
22	c3kh8B_	Alignment	not modelled	99.8	23	PDB header: lyase Chain: B: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
23	c1pn2D_	Alignment	not modelled	99.8	23	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
24	c1s9cK_	Alignment	not modelled	99.7	21	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
25	c3khpB_	Alignment	not modelled	99.7	27	PDB header: oxidoreductase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
26	c2cdhT_	Alignment	not modelled	99.7	22	PDB header: transferase Chain: T: PDB Molecule: dehydratase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
27	c3omIA_	Alignment	not modelled	99.7	27	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
						PDB header: transferase

28	c2vkzH_	Alignment	not modelled	99.6	18	Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
29	c2uval_	Alignment	not modelled	99.6	18	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
30	c4b3yB_	Alignment	not modelled	99.5	19	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
31	d1s9ca2	Alignment	not modelled	99.1	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
32	d1pn2a1	Alignment	not modelled	99.0	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
33	c2f3xA_	Alignment	not modelled	98.2	21	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
34	d1z6ba1	Alignment	not modelled	98.2	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
35	c3d6xA_	Alignment	not modelled	97.9	18	PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of campylobacter jejuni fabz
36	c4a0zA_	Alignment	not modelled	97.9	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
37	c4zw0A_	Alignment	not modelled	97.7	13	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 candidatus asiaticum
38	c5buyA_	Alignment	not modelled	97.7	19	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
39	c4h4gG_	Alignment	not modelled	97.6	18	PDB header: lyase Chain: G: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of (3r)-hydroxymyristoyl-[acyl-carrier-protein]2 dehydratase from burkholderia thailandensis e264
40	c2qlvA_	Alignment	not modelled	97.5	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
41	c4b8uD_	Alignment	not modelled	97.4	16	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
42	d2gvha1	Alignment	not modelled	97.4	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
43	d1ixla_	Alignment	not modelled	97.4	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
44	c6qsrB_	Alignment	not modelled	97.4	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: beta-hydroxyacyl-(acyl-carrier-protein) dehydratase PDBTitle: the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
45	c3d6lA_	Alignment	not modelled	97.4	22	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
46	c5buxB_	Alignment	not modelled	97.4	19	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of 3-hydroxyacyl-ACP dehydratase (fabz) from2 yersinia pestis with glycerol bound
47	d1mkaa_	Alignment	not modelled	97.3	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: beta-Hydroxydecanol thiol ester dehydrase
48	d1ulza_	Alignment	not modelled	97.3	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
49	c3esiD_	Alignment	not modelled	97.3	11	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
50	c2eisA_	Alignment	not modelled	97.2	24	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
						Fold: Thioesterase/thiol ester dehydrase-isomerase

51	d2f41a1	Alignment	not modelled	97.2	22	Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
52	d1ylia1	Alignment	not modelled	97.2	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
53	c5dm5E_	Alignment	not modelled	97.1	15	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
54	c4i83A_	Alignment	not modelled	97.1	13	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
55	c3bnvD_	Alignment	not modelled	97.1	12	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
56	c4mzqG_	Alignment	not modelled	97.0	14	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
57	c2qq2C_	Alignment	not modelled	97.0	14	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
58	d2h4ua1	Alignment	not modelled	97.0	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
59	c3lwgB_	Alignment	not modelled	97.0	11	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis
60	c4ncpF_	Alignment	not modelled	96.9	16	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
61	c2gvhC_	Alignment	not modelled	96.9	16	PDB header: hydrolase Chain: C: PDB Molecule: agr_l_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
62	c2cf2L_	Alignment	not modelled	96.9	17	PDB header: transferase Chain: L: PDB Molecule: fatty acid synthase, dh domain; PDBTitle: architecture of mammalian fatty acid synthase
63	c4ae7A_	Alignment	not modelled	96.9	20	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
64	d2f0xa1	Alignment	not modelled	96.8	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
65	c4ienB_	Alignment	not modelled	96.8	18	PDB header: hydrolase Chain: B: PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
66	d2gvha2	Alignment	not modelled	96.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
67	c3b7kA_	Alignment	not modelled	96.7	15	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
68	d1vpma_	Alignment	not modelled	96.7	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
69	d1y7ua1	Alignment	not modelled	96.6	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
70	c6qsrA_	Alignment	not modelled	96.5	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
71	c4ae8D_	Alignment	not modelled	96.5	18	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4
72	c3gekA_	Alignment	not modelled	96.4	14	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
73	d1wlua1	Alignment	not modelled	96.4	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
74	c2v1oF_	Alignment	not modelled	96.4	14	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
75	c4zv3B_	Alignment	not modelled	96.3	14	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
76	c4k00A_	Alignment	not modelled	96.1	13	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
77	d2cy9a1	Alignment	not modelled	96.0	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
78	d2hja1	Alignment	not modelled	96.0	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
79	d2gf6a1	Alignment	not modelled	96.0	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
80	d2hb0a1	Alignment	not modelled	95.9	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
81	c5byuD	Alignment	not modelled	95.8	7	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
82	c2qwzB	Alignment	not modelled	95.8	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
83	c3f1tB	Alignment	not modelled	95.7	11	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.
84	d1njka	Alignment	not modelled	95.6	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
85	d2ov9a1	Alignment	not modelled	95.6	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
86	d2hx5a1	Alignment	not modelled	95.6	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
87	d2o5ua1	Alignment	not modelled	95.5	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
88	c3r87A	Alignment	not modelled	95.5	11	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from photobacterium profundum
89	c2prxB	Alignment	not modelled	95.5	10	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
90	d2cyea1	Alignment	not modelled	95.5	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
91	c2xfiB	Alignment	not modelled	95.4	13	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
92	c4rmmA	Alignment	not modelled	95.3	14	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
93	d2oafa1	Alignment	not modelled	95.3	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
94	c5v10B	Alignment	not modelled	95.3	13	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
95	d2cwza1	Alignment	not modelled	95.1	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
96	c3hm0C	Alignment	not modelled	95.0	12	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella henselae
97	c3qooA	Alignment	not modelled	94.9	15	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
98	c2pimA	Alignment	not modelled	94.9	15	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
99	c2w3xE	Alignment	not modelled	94.7	13	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
100	c5vpjB	Alignment	not modelled	94.7	21	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesteras from actinomadura2 verrucospora.
101	d2nuja1	Alignment	not modelled	94.5	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
						PDB header: hydrolase

102	c4i4jE_	Alignment	not modelled	94.1	10	Chain: E: PDB Molecule: acp-polyene thioesterase; PDBTitle: the structure of sgce10, the acp-polyene thioesterase involved in c-2 1027 biosynthesis
103	c4i82A_	Alignment	not modelled	94.1	11	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
104	c5wh9C_	Alignment	not modelled	94.0	11	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
105	d2fuja1	Alignment	not modelled	93.7	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
106	c2egjE_	Alignment	not modelled	93.7	11	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
107	c4k02A_	Alignment	not modelled	93.7	13	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
108	d1s5ua_	Alignment	not modelled	93.3	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
109	d2q78a1	Alignment	not modelled	93.3	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
110	c3nwdD_	Alignment	not modelled	93.2	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
111	d1z54a1	Alignment	not modelled	93.2	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
112	c3kuvB_	Alignment	not modelled	93.0	19	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.
113	d1zkiA1	Alignment	not modelled	92.9	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
114	c5lqID_	Alignment	not modelled	92.8	6	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
115	c5byuA_	Alignment	not modelled	92.8	6	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
116	c3ck1B_	Alignment	not modelled	92.8	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
117	c3lbeA_	Alignment	not modelled	92.7	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
118	c3e1eE_	Alignment	not modelled	92.5	16	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
119	c2pzhC_	Alignment	not modelled	92.4	14	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from helicobacter pylori
120	d2fs2a1	Alignment	not modelled	92.2	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like