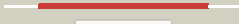



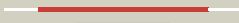




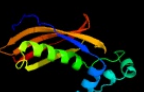





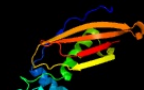

















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3541c (-)_3980838_3981227
Date	Fri Aug 9 18:20:22 BST 2019
Unique Job ID	9f4f371094047a1f

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4w7bD_	 Alignment		100.0	100	PDB header: lyase Chain: D: PDB Molecule: hydratase chsh2; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
2	d1iq6a_	 Alignment		100.0	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
3	c5cpgA_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaJ1 from pseudomonas aeruginosa in the unliganded form
4	c4v12A_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: maoc like domain protein; PDBTitle: crystal structure of the msmeg_6754 dehydratase from mycobacterium2 smegmatis
5	d2b3na1	 Alignment		100.0	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
6	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
7	d1q6wa_	 Alignment		100.0	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
8	c4rv2B_	 Alignment		100.0	24	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
9	c3exzA_	 Alignment		100.0	18	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	c4e3eA_	 Alignment		99.9	17	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
11	d2c2ia1	 Alignment		99.9	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like

12	d2bi0a1	Alignment		99.9	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
13	c4rv2A	Alignment		99.9	20	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein msmeg_1340/msmei_1302; PDBTitle: crystal structure of (3r)-hydroxyacyl- <i>acp</i> dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
14	c5zy8A	Alignment		99.9	16	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein rv0637; PDBTitle: crystal structure of c terminal truncated hadbc (3r)-hydroxyacyl- <i>acp</i> 2 dehydratase) complex from mycobacterium tuberculosis
15	c2bi0A	Alignment		99.9	13	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
16	d1s9ca1	Alignment		99.9	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
17	c4rltA	Alignment		99.9	18	PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: (3r)-hydroxyacyl- <i>acp</i> dehydratase subunit hada; PDBTitle: crystal structure of (3r)-hydroxyacyl- <i>acp</i> dehydratase hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin
18	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)
19	c2vkzH	Alignment		99.9	17	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
20	c2uval	Alignment		99.9	19	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
21	c4w7bG	Alignment	not modelled	99.9	16	PDB header: lyase Chain: G: PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
22	c1s9cK	Alignment	not modelled	99.9	20	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
23	d1pn2a2	Alignment	not modelled	99.9	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
24	c3kh8B	Alignment	not modelled	99.9	18	PDB header: lyase Chain: B: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
25	c4b3yB	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
26	c3khpB	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
27	c2cdhT	Alignment	not modelled	99.9	19	PDB header: transferase Chain: T: PDB Molecule: dehydratase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
28	c3omlA	Alignment	not modelled	99.9	19	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
29	c1pn2D	Alignment	not modelled	99.9	14	PDB header: lyase Chain: D; PDB Molecule: peroxisomal hydratase-dehydrogenase-epimerase; PDBTitle: crystal structure analysis of the selenomethionine labelled 2-enoil-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2
30	d2bi0a2	Alignment	not modelled	99.9	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
31	d1s9ca2	Alignment	not modelled	99.0	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
32	c2f3xA	Alignment	not modelled	98.4	14	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
33	c4a0zA	Alignment	not modelled	98.2	10	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
34	d1ixA	Alignment	not modelled	98.1	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
35	c4ae7A	Alignment	not modelled	97.9	14	PDB header: hydrolase Chain: A; PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
36	d2cwza1	Alignment	not modelled	97.9	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
37	c3lwgB	Alignment	not modelled	97.9	16	PDB header: unknown function Chain: B; PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis
38	c3esiD	Alignment	not modelled	97.9	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
39	c4ae8D	Alignment	not modelled	97.9	10	PDB header: hydrolase Chain: D; PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4
40	c3d6xA	Alignment	not modelled	97.8	9	PDB header: lyase Chain: A; PDB Molecule: (3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of campylobacter jejuni fabz
41	d1pn2a1	Alignment	not modelled	97.8	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
42	c3qooA	Alignment	not modelled	97.8	13	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
43	c5buyA	Alignment	not modelled	97.7	10	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
44	d2ov9a1	Alignment	not modelled	97.7	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
45	c4zw0A	Alignment	not modelled	97.7	10	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
46	c4i82A	Alignment	not modelled	97.7	15	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
47	d2cy9a1	Alignment	not modelled	97.7	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
48	c4h4gG	Alignment	not modelled	97.7	11	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
49	c3gekA	Alignment	not modelled	97.6	17	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
50	c2qlvA	Alignment	not modelled	97.6	11	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
51	c3lbeA	Alignment	not modelled	97.6	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
52	c2qwzB	Alignment	not modelled	97.6	13	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

53	d2f41a1	Alignment	not modelled	97.6	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
54	c3bnvD	Alignment	not modelled	97.6	13	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
55	d2h4ua1	Alignment	not modelled	97.5	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
56	d2fs2a1	Alignment	not modelled	97.5	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
57	d1u1za	Alignment	not modelled	97.4	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
58	d2f0xa1	Alignment	not modelled	97.4	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
59	d1wluu1	Alignment	not modelled	97.3	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
60	c2pimA	Alignment	not modelled	97.3	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
61	c5dm5E	Alignment	not modelled	97.3	9	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
62	d1z6ba1	Alignment	not modelled	97.3	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
63	c5buxB	Alignment	not modelled	97.2	12	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
64	c6qsrB	Alignment	not modelled	97.2	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: beta-hydroxyacyl-(acyl-carrier-protein) dehydratase PDBTitle: the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
65	c4i83A	Alignment	not modelled	97.1	12	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
66	c6qsrA	Alignment	not modelled	97.1	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
67	c5hmcA	Alignment	not modelled	97.1	14	PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid
68	c3nwwD	Alignment	not modelled	97.1	14	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
69	c2eisA	Alignment	not modelled	97.0	11	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
70	d2hboa1	Alignment	not modelled	97.0	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
71	c3f1tB	Alignment	not modelled	97.0	12	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.
72	c2prxB	Alignment	not modelled	97.0	16	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
73	d1s5ua	Alignment	not modelled	97.0	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
74	c5eo4A	Alignment	not modelled	96.9	8	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
75	c3e8pA	Alignment	not modelled	96.9	12	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.
76	d2gvha2	Alignment	not modelled	96.9	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
						PDB header: hydrolase Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa

77	c4k02A_	Alignment	not modelled	96.9	9	thioesterase; PDBTitle: crystal structure of atdhnat1, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from arabidopsis thaliana
78	c3hduB_	Alignment	not modelled	96.9	10	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
79	c4mzqG_	Alignment	not modelled	96.9	18	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
80	c3kuvB_	Alignment	not modelled	96.9	15	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.
81	c3e29C_	Alignment	not modelled	96.8	12	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.
82	d1ylia1	Alignment	not modelled	96.8	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
83	c5byuD_	Alignment	not modelled	96.8	8	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
84	c4ienB_	Alignment	not modelled	96.8	17	PDB header: hydrolase Chain: B: PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
85	d2gvha1	Alignment	not modelled	96.8	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
86	c2gvhC_	Alignment	not modelled	96.7	14	PDB header: hydrolase Chain: C: PDB Molecule: agr_1_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
87	d1c8ua1	Alignment	not modelled	96.7	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
88	c3hm0C_	Alignment	not modelled	96.7	13	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella henselae
89	c3ck1B_	Alignment	not modelled	96.6	17	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
90	d2q78a1	Alignment	not modelled	96.6	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
91	d2hjja1	Alignment	not modelled	96.5	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
92	c4k00A_	Alignment	not modelled	96.5	7	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
93	c5lqID_	Alignment	not modelled	96.5	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
94	d2hx5a1	Alignment	not modelled	96.5	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
95	d1vpma_	Alignment	not modelled	96.5	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
96	c5wh9C_	Alignment	not modelled	96.4	10	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
97	d2essa1	Alignment	not modelled	96.4	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
98	d1zkiA1	Alignment	not modelled	96.4	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
99	d2owna1	Alignment	not modelled	96.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
100	c4ncpF_	Alignment	not modelled	96.3	17	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
101	d1vh5a_	Alignment	not modelled	96.3	5	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
102	d1vh9a_	Alignment	not modelled	96.3	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
						PDB header: hydrolase

103	c3b7kA_	Alignment	not modelled	96.3	15	Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
104	c4i4jE_	Alignment	not modelled	96.3	5	PDB header: hydrolase Chain: E: PDB Molecule: hypothetical protein aq_1494; PDBTitle: the structure of sgce10, the acp-polyene thioesterase involved in c-2 1027 biosynthesis
105	d2owna2	Alignment	not modelled	96.3	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
106	c2egiE_	Alignment	not modelled	96.3	10	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	d1sc0a_	Alignment	not modelled	96.3	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
108	c5byuA_	Alignment	not modelled	96.3	8	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
109	d2oafa1	Alignment	not modelled	96.3	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
110	d1y7ua1	Alignment	not modelled	96.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
111	d1njka_	Alignment	not modelled	96.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
112	c4b8uD_	Alignment	not modelled	96.3	10	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 with 3 n-isobutyl-2-(5-(2-thienyl)-1,2-oxazol-3-yl-methoxy)acetamide
113	d2gf6a1	Alignment	not modelled	96.2	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
114	d2oiwa1	Alignment	not modelled	96.1	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
115	c1c8uA_	Alignment	not modelled	96.1	10	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
116	c4qdbF_	Alignment	not modelled	96.1	8	PDB header: hydrolase Chain: F: PDB Molecule: thioesterase pa1618; PDBTitle: crystal structure of mutant thioesterase pa1618 (q49a) from2 pseudomonas aeruginosa
117	c3d6IA_	Alignment	not modelled	96.1	10	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
118	d2fuja1	Alignment	not modelled	96.0	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
119	d2nuja1	Alignment	not modelled	96.0	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
120	c4gakA_	Alignment	not modelled	96.0	19	PDB header: hydrolase Chain: A: PDB Molecule: acyl-ACP thioesterase; PDBTitle: crystal structure of acyl-ACP thioesterase from spirosona linguale