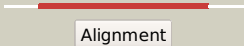
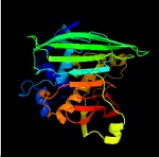
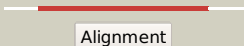

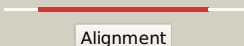










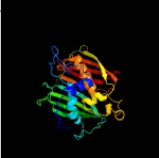

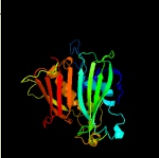

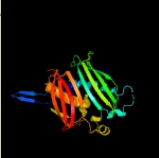


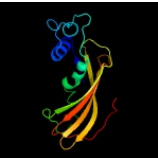







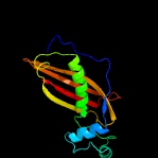


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3538 (-) _3977241_3978101
Date	Fri Aug 9 18:20:21 BST 2019
Unique Job ID	382f8be91bbfe51c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3omlA_	 Alignment		100.0	32	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
2	c3kh8B_	 Alignment		100.0	27	PDB header: lyase Chain: B: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
3	c3khpB_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
4	c1s9cK_	 Alignment		100.0	33	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
5	c1pn2D_	 Alignment		100.0	32	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
6	c2cdhT_	 Alignment		100.0	32	PDB header: transferase Chain: T: PDB Molecule: dehydratase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
7	c4v12A_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: maoc like domain protein; PDBTitle: crystal structure of the msmeg_6754 dehydratase from mycobacterium2 smegmatis
8	c2vkzH_	 Alignment		100.0	21	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
9	c2uval_	 Alignment		100.0	20	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
10	c4b3yB_	 Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
11	c4e3eA_	 Alignment		100.0	15	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

12	d1pn2a1	Alignment		100.0	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
13	d1s9ca1	Alignment		100.0	40	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
14	d1pn2a2	Alignment		100.0	42	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
15	d1s9ca2	Alignment		100.0	26	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
16	c4ritA_	Alignment		99.9	11	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
17	c2bi0A_	Alignment		99.9	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
18	c4rv2A_	Alignment		99.9	11	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
19	c4w7bD_	Alignment		99.8	19	PDB header: lyase Chain: D: PDB Molecule: hydratase chsh2; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
20	c5zy8A_	Alignment		99.8	14	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
21	d2b3na1	Alignment	not modelled	99.8	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
22	c5cpgA_	Alignment	not modelled	99.8	24	PDB header: lyase Chain: A: PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
23	d1iq6a_	Alignment	not modelled	99.8	27	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
24	c4w7bG_	Alignment	not modelled	99.8	13	PDB header: lyase Chain: G: PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
25	d1q6wa_	Alignment	not modelled	99.7	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
26	c4rv2B_	Alignment	not modelled	99.7	24	PDB header: lyase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of (3r)-hydroxyacyl- <i>acp</i> dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
27	d2c2ia1	Alignment	not modelled	99.7	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
28	c3exzA_	Alignment	not modelled	99.7	10	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.

29	d2bi0a1	Alignment	not modelled	99.7	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
30	c4ffuA	Alignment	not modelled	99.6	11	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
31	c3ir3B	Alignment	not modelled	99.6	23	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
32	d2bi0a2	Alignment	not modelled	99.5	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
33	c2cf2L	Alignment	not modelled	98.4	13	PDB header: transferase Chain: L: PDB Molecule: fatty acid synthase, dh domain; PDBTitle: architecture of mammalian fatty acid synthase
34	c2f3xA	Alignment	not modelled	98.1	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
35	c4gakA	Alignment	not modelled	98.1	11	PDB header: hydrolase Chain: A: PDB Molecule: acyl-acyl thioesterase; PDBTitle: crystal structure of acyl-acyl thioesterase from spiroplasma linguale
36	c2essA	Alignment	not modelled	98.0	8	PDB header: hydrolase Chain: A: PDB Molecule: acyl-acyl thioesterase; PDBTitle: crystal structure of an acyl-acyl thioesterase (np_810988.1) from bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution
37	c2gvhC	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: C: PDB Molecule: agr_1_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium tumefaciens at 2.65 a resolution
38	c3esiD	Alignment	not modelled	97.9	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
39	c6qsrA	Alignment	not modelled	97.5	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: the dehydratase heterocomplex ape1:p from xenorhabdus doucetiae
40	c4a0zA	Alignment	not modelled	97.5	11	PDB header: transcription Chain: A: PDB Molecule: transcription factor fapr; PDBTitle: structure of the global transcription regulator fapr from staphylococcus aureus in complex with malonyl-coa
41	c5x04B	Alignment	not modelled	97.2	12	PDB header: hydrolase Chain: B: PDB Molecule: dodecanoyl-[acyl-carrier-protein] hydrolase, chloroplast; PDBTitle: 12:0-acyl thioesterase from umbellularia californica
42	c4i82A	Alignment	not modelled	97.2	5	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from streptococcus pneumoniae tigr4
43	c2ownA	Alignment	not modelled	97.1	9	PDB header: hydrolase Chain: A: PDB Molecule: putative oleoyl-[acyl-carrier protein] thioesterase; PDBTitle: crystal structure of oleoyl thioesterase (putative) (np_784467.1) from lactobacillus plantarum at 2.00 a resolution
44	c3b7kA	Alignment	not modelled	97.0	10	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
45	d1ixla	Alignment	not modelled	97.0	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
46	c3lbeA	Alignment	not modelled	96.9	7	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein smu.793; PDBTitle: the crystal structure of smu.793 from streptococcus mutans ua159 bound to acetyl coa
47	c4ae7A	Alignment	not modelled	96.8	19	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
48	c4ae8D	Alignment	not modelled	96.8	15	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4
49	d2ov9a1	Alignment	not modelled	96.7	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
50	c3bnvD	Alignment	not modelled	96.4	11	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
51	d2h4ua1	Alignment	not modelled	96.2	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
52	c3gekA	Alignment	not modelled	96.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thioesterase yhda; PDBTitle: crystal structure of putative thioesterase yhda from lactococcus lactis. northeast structural genomics consortium target kr113
53	d1z6ba1	Alignment	not modelled	96.1	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
						PDB header: unknown function

54	c3lwgB_	Alignment	not modelled	96.0	9	Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis
55	c5eo4A_	Alignment	not modelled	96.0	14	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
56	d2f41a1	Alignment	not modelled	95.9	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
57	c3d6xA_	Alignment	not modelled	95.7	17	PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of campylobacter jejuni fabz
58	c5lqID_	Alignment	not modelled	95.7	12	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
59	c4h4gG_	Alignment	not modelled	95.7	20	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
60	d2cwza1	Alignment	not modelled	95.6	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
61	d2cy9a1	Alignment	not modelled	95.6	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
62	c4i83A_	Alignment	not modelled	95.6	20	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
63	c4zv3B_	Alignment	not modelled	95.5	13	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
64	c4zw0A_	Alignment	not modelled	95.4	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
65	d1mkaa_	Alignment	not modelled	95.4	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: beta-Hydroxydecanol thiol ester dehydrase
66	c2prxB_	Alignment	not modelled	95.3	11	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
67	c2qwzB_	Alignment	not modelled	95.3	15	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
68	c4i4jE_	Alignment	not modelled	95.3	9	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
69	c3bbjA_	Alignment	not modelled	95.3	15	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
70	d1u1za_	Alignment	not modelled	95.3	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
71	c5byuD_	Alignment	not modelled	95.2	5	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
72	c5buyA_	Alignment	not modelled	95.2	16	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
73	c3e29C_	Alignment	not modelled	95.2	18	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.
74	d2essa1	Alignment	not modelled	95.1	6	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
75	c3rqB_	Alignment	not modelled	95.1	15	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
76	d1wlua1	Alignment	not modelled	95.0	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
77	c3ck1B_	Alignment	not modelled	95.0	13	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
78	d2owna1	Alignment	not modelled	94.9	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like

79	c3f1tB	Alignment	not modelled	94.9	15	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.
80	c3e8pA	Alignment	not modelled	94.9	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.
81	d2f0xa1	Alignment	not modelled	94.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
82	d1s5ua	Alignment	not modelled	94.7	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
83	c5wh9C	Alignment	not modelled	94.5	13	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
84	c2pimA	Alignment	not modelled	94.5	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
85	c3hduB	Alignment	not modelled	94.4	13	PDB header: hydrolase Chain: B: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
86	d1lo7a	Alignment	not modelled	94.3	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
87	c2glvA	Alignment	not modelled	94.3	15	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
88	d2essa2	Alignment	not modelled	93.9	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
89	c4k00A	Alignment	not modelled	93.9	11	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa hydrolase; PDBTitle: crystal structure of slr0204, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from synechocystis
90	c5hmcA	Alignment	not modelled	93.6	13	PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid
91	c4r9zB	Alignment	not modelled	93.6	14	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: mycobacterium avium subs paratuberculosis tesb protein map1729c
92	d2gf6a1	Alignment	not modelled	93.5	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
93	d2hlja1	Alignment	not modelled	93.4	6	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
94	d1sh8a	Alignment	not modelled	93.4	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
95	d1tbua1	Alignment	not modelled	93.4	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
96	d2fs2a1	Alignment	not modelled	93.2	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
97	d2gvha1	Alignment	not modelled	93.1	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
98	d2o5ua1	Alignment	not modelled	93.0	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
99	c3qooA	Alignment	not modelled	92.9	18	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
100	d1njka	Alignment	not modelled	92.8	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
101	c1c8uA	Alignment	not modelled	92.6	15	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
102	d2oafa1	Alignment	not modelled	92.6	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
103	c2xfiB	Alignment	not modelled	92.6	7	PDB header: hydrolase Chain: B: PDB Molecule: dyne7; PDBTitle: induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynamicin3 thioesterase PDB header: lyase Chain: D: PDB Molecule: 3-hydroxydecanoyl-[acyl-carrier-protein]

104	c4b8uD_	Alignment	not modelled	92.4	8	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
105	c3nwzD_	Alignment	not modelled	92.3	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
106	d1vh9a_	Alignment	not modelled	92.1	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
107	c2w3xE_	Alignment	not modelled	92.0	14	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
108	c5dm5E_	Alignment	not modelled	91.7	10	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
109	c5vpjB_	Alignment	not modelled	91.6	10	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesteras from actinomadura2 verrucosospora.
110	c3kuvB_	Alignment	not modelled	91.6	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.
111	c4m20D_	Alignment	not modelled	91.6	6	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50
112	c5buxB_	Alignment	not modelled	91.4	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
113	d2q78a1	Alignment	not modelled	91.3	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
114	d1c8ua1	Alignment	not modelled	91.2	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
115	d1c8ua2	Alignment	not modelled	91.0	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
116	d2oiwa1	Alignment	not modelled	90.8	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
117	d2nuja1	Alignment	not modelled	90.7	6	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
118	d1q4ua_	Alignment	not modelled	90.6	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
119	d1z54a1	Alignment	not modelled	90.2	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
120	d2owna2	Alignment	not modelled	90.1	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like