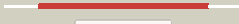



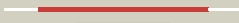








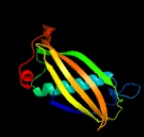

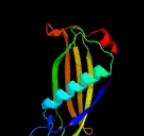














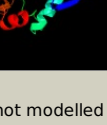


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2001 (-) _2246840_2247592
Date	Mon Aug 5 13:25:10 BST 2019
Unique Job ID	16ef71ae06528b1e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2essa_	 Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: acyl- <i>acp</i> thioesterase; PDBTitle: crystal structure of an acyl- <i>acp</i> thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution
2	c5x04B_	 Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: dodecanoyl-[acyl-carrier-protein] hydrolase, chloroplastic; PDBTitle: 12:0- <i>acp</i> thioesterase from umbellularia californica
3	c4gakA_	 Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: acyl- <i>acp</i> thioesterase; PDBTitle: crystal structure of acyl- <i>acp</i> thioesterase from spirosona linguale
4	c2ownA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative oleoyl-[acyl-carrier protein] thioesterase; PDBTitle: crystal structure of oleoyl thioesterase (putative) (np_784467.1) from2 lactobacillus plantarum at 2.00 a resolution
5	d2essa1	 Alignment		100.0	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
6	d2owna1	 Alignment		100.0	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
7	c5byuA_	 Alignment		99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
8	d1s5ua_	 Alignment		99.9	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
9	d2oiwa1	 Alignment		99.9	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
10	c5v10B_	 Alignment		99.9	18	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
11	d2gf6a1	 Alignment		99.9	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like

12	d2alia1	Alignment		99.9	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
13	c2aliA	Alignment		99.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa2801; PDBTitle: structure of protein of unknown function pa2801 from pseudomonas2 aeruginosa, putative thioesterase
14	c2egiE	Alignment		99.9	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
15	d2o5ua1	Alignment		99.9	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
16	d2oafa1	Alignment		99.9	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
17	c4k00A	Alignment		99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa hydrolase; PDBTitle: crystal structure of slr0204, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from synechocystis
18	d1njka	Alignment		99.9	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
19	c5lqID	Alignment		99.9	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
20	d2cyea1	Alignment		99.9	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
21	c5eo4A	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
22	c3hm0C	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella henselae
23	d2nuja1	Alignment	not modelled	99.9	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
24	c3ck1B	Alignment	not modelled	99.9	15	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
25	d2hx5a1	Alignment	not modelled	99.9	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
26	d1z54a1	Alignment	not modelled	99.9	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
27	c5wh9C	Alignment	not modelled	99.9	9	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
28	c3r87A	Alignment	not modelled	99.9	10	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from photobacterium profundum
						PDB header: hydrolase

29	c5vpjB_	Alignment	not modelled	99.9	9	Chain: B: PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesterase from actinomadura2 verrucosospora.
30	c4i4jE_	Alignment	not modelled	99.9	7	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
31	c2w3xE_	Alignment	not modelled	99.9	9	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
32	c2pzhC_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from helicobacter pylori
33	d1lo7a_	Alignment	not modelled	99.8	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
34	d2essa2	Alignment	not modelled	99.8	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
35	c2xfIB_	Alignment	not modelled	99.8	11	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
36	d2hlja1	Alignment	not modelled	99.8	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
37	d2fuja1	Alignment	not modelled	99.8	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
38	c5byuD_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
39	d2owna2	Alignment	not modelled	99.7	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
40	c4zv3B_	Alignment	not modelled	99.0	11	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
41	c3b7kA_	Alignment	not modelled	98.7	6	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
42	c2gvhC_	Alignment	not modelled	98.5	10	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
43	c5dm5E_	Alignment	not modelled	98.5	11	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
44	d1ylia1	Alignment	not modelled	98.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
45	c3d6IA_	Alignment	not modelled	98.3	11	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
46	c4ienB_	Alignment	not modelled	98.2	9	PDB header: hydrolase Chain: B: PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
47	d1vpma_	Alignment	not modelled	98.2	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
48	c2eisA_	Alignment	not modelled	98.1	10	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
49	c3lbeA_	Alignment	not modelled	98.1	6	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
50	c4i82A_	Alignment	not modelled	97.9	9	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
51	c4ncpF_	Alignment	not modelled	97.8	13	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 4-hbt like thioesterase sav1878 from2 staphylococcus aureus subsp. aureus mu50
52	d1y7ua1	Alignment	not modelled	97.8	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
53	d2gvha2	Alignment	not modelled	97.8	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
54	c2v1oF_	Alignment	not modelled	97.8	10	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
						PDB header: hydrolase

55	c4ae7A_	Alignment	not modelled	97.8	11	Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
56	c4ae8D_	Alignment	not modelled	97.8	15	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4
57	c2qq2C_	Alignment	not modelled	97.7	12	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	d1wlua1	Alignment	not modelled	97.6	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
59	d2hboa1	Alignment	not modelled	97.5	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
60	d2ov9a1	Alignment	not modelled	97.4	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
61	d2gvha1	Alignment	not modelled	97.4	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
62	d1zkia1	Alignment	not modelled	97.4	6	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
63	d1ixla_	Alignment	not modelled	97.2	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
64	c1s9cK_	Alignment	not modelled	97.2	7	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
65	d2h4ua1	Alignment	not modelled	97.2	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
66	c3kuvB_	Alignment	not modelled	96.9	9	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.
67	c3s4kA_	Alignment	not modelled	96.9	8	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase rv1847/mt1895; PDBTitle: structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
68	c3kh8B_	Alignment	not modelled	96.8	14	PDB header: lyase Chain: B: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
69	c2pimA_	Alignment	not modelled	96.6	7	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
70	c3gekA_	Alignment	not modelled	96.4	9	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
71	c2cdhT_	Alignment	not modelled	96.4	8	PDB header: transferase Chain: T: PDB Molecule: dehydratase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
72	c2qwzB_	Alignment	not modelled	96.4	7	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
73	d2f0xa1	Alignment	not modelled	96.3	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
74	d1sc0a_	Alignment	not modelled	96.3	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
75	c3nzwD_	Alignment	not modelled	96.2	9	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
76	d2fs2a1	Alignment	not modelled	96.1	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
77	d2cy9a1	Alignment	not modelled	96.0	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
78	d2cwza1	Alignment	not modelled	96.0	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
79	c5hmcA_	Alignment	not modelled	96.0	10	PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid PDB header: hydrolase

80	c4k02A	Alignment	not modelled	95.8	10	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
81	c3qooA	Alignment	not modelled	95.7	12	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
82	c5zy8A	Alignment	not modelled	95.6	6	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
83	d1vh5a	Alignment	not modelled	95.4	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
84	c4rmmA	Alignment	not modelled	95.4	10	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
85	c4qdbF	Alignment	not modelled	95.3	10	PDB header: hydrolase Chain: F: PDB Molecule: thioesterase pa1618; PDBTitle: crystal structure of mutant thioesterase pa1618 (q49a) from2 pseudomonas aeruginosa
86	c3lwgB	Alignment	not modelled	95.2	14	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis
87	c3hduB	Alignment	not modelled	95.1	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
88	c3dkzA	Alignment	not modelled	95.0	7	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.
89	c3khpB	Alignment	not modelled	95.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
90	d1q4ua	Alignment	not modelled	94.9	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
91	c4rv2A	Alignment	not modelled	94.8	6	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein msmeg_1340/msmei_1302; PDBTitle: crystal structure of (3r)-hydroxyacyl-ACP dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
92	c3e1eE	Alignment	not modelled	94.7	9	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
93	c4m20D	Alignment	not modelled	94.4	6	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50
94	c3f1tB	Alignment	not modelled	94.3	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.
95	c4a0zA	Alignment	not modelled	94.3	8	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
96	c3omlA	Alignment	not modelled	92.8	8	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
97	c2qlvA	Alignment	not modelled	92.5	8	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
98	d2q78a1	Alignment	not modelled	92.4	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
99	c3e8pA	Alignment	not modelled	91.3	16	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.
100	c3rd7A	Alignment	not modelled	90.9	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coa thioesterase; PDBTitle: crystal structure of acyl-coa thioesterase from mycobacterium avium
101	c4ffuA	Alignment	not modelled	90.5	12	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
102	d2f41a1	Alignment	not modelled	90.1	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
103	c4v12A	Alignment	not modelled	89.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: maoc like domain protein; PDBTitle: crystal structure of the msmeg_6754 dehydratase from

						mycobacterium2 smegmatis
104	c4ritA	Alignment	not modelled	89.6	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
105	c4e3eA	Alignment	not modelled	89.3	7	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
106	d1vh9a	Alignment	not modelled	88.6	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
107	d2b3na1	Alignment	not modelled	88.2	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
108	c4w7bD	Alignment	not modelled	88.1	12	PDB header: lyase Chain: D: PDB Molecule: hydratase chsh2; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
109	c5buyA	Alignment	not modelled	87.5	8	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
110	c3e29C	Alignment	not modelled	87.0	10	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.
111	d1tbua1	Alignment	not modelled	86.5	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
112	c1c8uA	Alignment	not modelled	86.3	7	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
113	c3bbjA	Alignment	not modelled	86.2	3	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
114	c1pn2D	Alignment	not modelled	85.7	11	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
115	d1q6wa	Alignment	not modelled	85.7	5	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
116	d1u1za	Alignment	not modelled	83.7	5	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
117	c3ir3B	Alignment	not modelled	83.6	10	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
118	d1c8ua1	Alignment	not modelled	82.6	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
119	c3rqbB	Alignment	not modelled	82.5	4	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
120	c4i83A	Alignment	not modelled	82.3	3	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of (3r)-hydroxymyristoyl- <i>acp</i> dehydratase from2 neisseria meningitidis fam18