


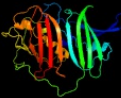




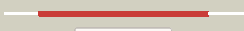
















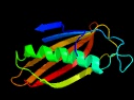







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0499 (- )_589186_590061
Date	Fri Jul 26 01:50:04 BST 2019
Unique Job ID	9cf0f6fa315aa2c6

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3bbjA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase ii; <b>PDBTitle:</b> crystal structure of a putative thioesterase ii (tfu_2367) from2 thermobifida fusca yx at 2.45 a resolution
2	<a href="#">c3rqbB_</a>	 Alignment		100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function with hot2 dog fold from alicyclobacillus acidocaldarius
3	<a href="#">c1c8uA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa thioesterase ii; <b>PDBTitle:</b> crystal structure of the e.coli thioesterase ii, a2 homologue of the human nef-binding enzyme
4	<a href="#">c3cjjA_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of putative thioesterase (yp_496845.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.70 a resolution
5	<a href="#">c3rd7A_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa thioesterase; <b>PDBTitle:</b> crystal structure of acyl-coa thioesterase from mycobacterium avium
6	<a href="#">c4r9zB_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> mycobacterium avium subs paratuberculosis tesb protein map1729c
7	<a href="#">d1c8ua2</a>	 Alignment		99.9	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-CoA thioesterase
8	<a href="#">d1c8ua1</a>	 Alignment		99.9	21	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-CoA thioesterase
9	<a href="#">d1tbua1</a>	 Alignment		99.8	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-CoA thioesterase
10	<a href="#">c2pimA_</a>	 Alignment		99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetic acid degradation-related protein; <b>PDBTitle:</b> crystal structure of a putative thioesterase, phenylacetic acid2 degradation-related protein (reut_b4779) from ralstonia eutropha3 jmp134 at 2.20 a resolution
11	<a href="#">c2qwzB_</a>	 Alignment		99.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylacetic acid degradation-related protein; <b>PDBTitle:</b> crystal structure of a putative thioesterase (tm1040_1390) from2 silicibacter sp. tm1040 at 2.15 a resolution

12	<a href="#">d1zkia1</a>	Alignment		99.4	22	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
13	<a href="#">c4rmmA</a>	Alignment		99.4	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q7nvp2_chrvo protein from chromobacterium2 violaceum. northeast structural genomics consortium target cvr191
14	<a href="#">d2f0xa1</a>	Alignment		99.4	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
15	<a href="#">d1wluu1</a>	Alignment		99.4	21	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
16	<a href="#">c3f1tB</a>	Alignment		99.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein q9i3c8_pseae; <b>PDBTitle:</b> crystal structure of the q9i3c8_pseae protein from pseudomonas2 aeruginosa. northeast structural genomics consortium target par319a.
17	<a href="#">c3nwzD</a>	Alignment		99.3	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> bh2602 protein; <b>PDBTitle:</b> crystal structure of bh2602 protein from bacillus halodurans with coa,2 northeast structural genomics consortium target bhr199
18	<a href="#">d2hb0a1</a>	Alignment		99.3	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
19	<a href="#">c3e8pA</a>	Alignment		99.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the protein q8e9m7 from shewanella oneidensis2 related to thioesterase superfamily. northeast structural genomics3 consortium target sor246.
20	<a href="#">d2h4ua1</a>	Alignment		99.3	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
21	<a href="#">d1vh9a</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
22	<a href="#">c3hduB</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
23	<a href="#">c3e29C</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein q7we92_borbr; <b>PDBTitle:</b> x-ray structure of the protein q7we92_borbr from thioesterase2 superfamily. northeast structural genomics consortium target bor214a.
24	<a href="#">d1vh5a</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
25	<a href="#">d2fs2a1</a>	Alignment	not modelled	99.2	22	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
26	<a href="#">c4k02A</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa thioesterase; <b>PDBTitle:</b> crystal structure of atdhnat1, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from arabidopsis thaliana
27	<a href="#">c4qdbF</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> thioesterase pa1618; <b>PDBTitle:</b> crystal structure of mutant thioesterase pa1618 (q49a) from2 pseudomonas aeruginosa
28	<a href="#">c3s4kA</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase rv1847/mt1895; <b>PDBTitle:</b> structure of a putative esterase rv1847/mt1895 from

					mycobacterium2 tuberculosis
29	<a href="#">d1q4ua_</a>	Alignment	not modelled	99.2	22 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
30	<a href="#">c3b7kA_</a>	Alignment	not modelled	99.2	8 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 12; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 12
31	<a href="#">c2gvhC_</a>	Alignment	not modelled	99.2	14 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> agr_1_2016p; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
32	<a href="#">c3dkzA_</a>	Alignment	not modelled	99.2	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase superfamily protein; <b>PDBTitle:</b> crystal structure of the q7w9w5_borpa protein from2 bordetella parapertussis. northeast structural genomics3 consortium target bpr208c.
33	<a href="#">c3gekA_</a>	Alignment	not modelled	99.2	19 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase yhda; <b>PDBTitle:</b> crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113
34	<a href="#">c3lwgB_</a>	Alignment	not modelled	99.2	14 <b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hp0420 homologue; <b>PDBTitle:</b> crystal structure of hp0420-homologue c46a from helicobacter felis
35	<a href="#">d1ixla_</a>	Alignment	not modelled	99.2	16 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
36	<a href="#">d1sc0a_</a>	Alignment	not modelled	99.2	13 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
37	<a href="#">c4i82A_</a>	Alignment	not modelled	99.1	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
38	<a href="#">c3lbeA_</a>	Alignment	not modelled	99.1	19 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.793; <b>PDBTitle:</b> the crystal structure of smu.793 from streptococcus mutans ua159 bound2 to acetyl coa
39	<a href="#">d2cy9a1</a>	Alignment	not modelled	99.1	20 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
40	<a href="#">c3e1eE_</a>	Alignment	not modelled	99.1	17 <b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> thioesterase family protein; <b>PDBTitle:</b> crystal structure of a thioesterase family protein from2 silicibacter pomeroyi. northeast structural genomics3 target sir180a
41	<a href="#">c4ae7A_</a>	Alignment	not modelled	99.1	7 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase superfamily member 5; <b>PDBTitle:</b> crystal structure of human them5
42	<a href="#">d1t82a_</a>	Alignment	not modelled	99.1	8 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
43	<a href="#">c5hmcA_</a>	Alignment	not modelled	99.1	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> azi13; <b>PDBTitle:</b> crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid
44	<a href="#">c4zv3B_</a>	Alignment	not modelled	99.0	10 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of the n- and c-terminal domains of mouse acyl-coa2 thioesterase 7
45	<a href="#">c4m20D_</a>	Alignment	not modelled	99.0	17 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50
46	<a href="#">d2ov9a1</a>	Alignment	not modelled	99.0	17 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
47	<a href="#">c4a0zA_</a>	Alignment	not modelled	99.0	10 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor fapr; <b>PDBTitle:</b> structure of the global transcription regulator fapr from2 staphylococcus aureus in complex with malonyl-coa
48	<a href="#">c5dm5E_</a>	Alignment	not modelled	98.9	13 <b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative acyl-coa thioester hydrolase; <b>PDBTitle:</b> crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
49	<a href="#">c4ae8D_</a>	Alignment	not modelled	98.9	8 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> thioesterase superfamily member 4; <b>PDBTitle:</b> crystal structure of human them4
50	<a href="#">c2prxB_</a>	Alignment	not modelled	98.9	19 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> thioesterase superfamily protein; <b>PDBTitle:</b> crystal structure of thioesterase superfamily protein (zp_00837258.1)2 from shewanella loihica pv-4 at 1.65 a resolution
51	<a href="#">d2f41a1</a>	Alignment	not modelled	98.9	11 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
52	<a href="#">c3bnvD_</a>	Alignment	not modelled	98.9	9 <b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> cj0977; <b>PDBTitle:</b> crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
53	<a href="#">c2eisA_</a>	Alignment	not modelled	98.9	16 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tthb207; <b>PDBTitle:</b> x-ray structure of acyl-coa hydrolase-like protein, tt1379, from2 thermus thermophilus hb8
54	<a href="#">c2f3vA_</a>	Alignment	not modelled	98.8	9 <b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor fapr;

54	<a href="#">c212AA</a>	Alignment	not modelled	98.8	9	<b>PDBTitle:</b> crystal structure of fapR (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
55	<a href="#">d1sh8a</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
56	<a href="#">c3d61A</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
57	<a href="#">d2gvha2</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
58	<a href="#">d1ylia1</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
59	<a href="#">d2gvha1</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
60	<a href="#">d1yoca1</a>	Alignment	not modelled	98.6	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
61	<a href="#">c4ncpF</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of 4-hbt like thioesterase sav1878 from2 staphylococcus aureus subsp. aureus mu50
62	<a href="#">c2v1oF</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of n-terminal domain of acyl-coa2 thioesterase 7
63	<a href="#">c4ienB</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative acyl-coa hydrolase; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
64	<a href="#">c2qq2C</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
65	<a href="#">d1y7ua1</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
66	<a href="#">c3lmbA</a>	Alignment	not modelled	98.6	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum t1s
67	<a href="#">d1vpma</a>	Alignment	not modelled	98.5	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
68	<a href="#">c3ir3B</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-thioester dehydratase 2; <b>PDBTitle:</b> crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
69	<a href="#">c5cpgA</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (r)-specific enoyl-coa hydratase; <b>PDBTitle:</b> r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
70	<a href="#">c5wh9C</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa thioesterase; <b>PDBTitle:</b> structure of bh1999 gentisyl-coenzyme a thioesterase
71	<a href="#">d1iq6a</a>	Alignment	not modelled	97.1	21	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
72	<a href="#">d2cyea1</a>	Alignment	not modelled	96.9	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
73	<a href="#">d2b3na1</a>	Alignment	not modelled	96.8	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
74	<a href="#">d2hx5a1</a>	Alignment	not modelled	96.8	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
75	<a href="#">c5byuD</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
76	<a href="#">c5buyA</a>	Alignment	not modelled	96.7	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; <b>PDBTitle:</b> crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from francisella tularensis
77	<a href="#">d1u1za</a>	Alignment	not modelled	96.7	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> FabZ-like
78	<a href="#">d2cwza1</a>	Alignment	not modelled	96.6	20	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> TTHA0967-like
79	<a href="#">c4k00A</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa hydrolase; <b>PDBTitle:</b> crystal structure of slr0204, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from synechocystis
80	<a href="#">c3kh8B</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> maoc-like dehydratase;

80	<a href="#">c3k10B</a>	Alignment	not modelled	96.5	10	<b>PDBTitle:</b> crystal structure of maoc-like dehydratase from phytophthora capsici
81	<a href="#">d2gf6a1</a>	Alignment	not modelled	96.5	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
82	<a href="#">d1z54a1</a>	Alignment	not modelled	96.5	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
83	<a href="#">c3d6xA</a>	Alignment	not modelled	96.4	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; <b>PDBTitle:</b> crystal structure of campylobacter jejuni fabz
84	<a href="#">c4i83A</a>	Alignment	not modelled	96.3	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; <b>PDBTitle:</b> crystal structure of (3r)-hydroxymyristoyl-acp dehydratase from2 neisseria meningitidis fam18
85	<a href="#">c4h4gG</a>	Alignment	not modelled	96.3	19	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; <b>PDBTitle:</b> crystal structure of (3r)-hydroxymyristoyl-[acyl-carrier-protein]2 dehydratase from burkholderia thailandensis e264
86	<a href="#">c3hm0C</a>	Alignment	not modelled	96.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable thioesterase; <b>PDBTitle:</b> crystal structure of probable thioesterase from bartonella henselae
87	<a href="#">c5zy8A</a>	Alignment	not modelled	96.2	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0336 protein rv0637; <b>PDBTitle:</b> crystal structure of c terminal truncated hadbc (3r-hydroxyacyl-acp2 dehydratase) complex from mycobacterium tuberculosis
88	<a href="#">c4zw0A</a>	Alignment	not modelled	96.2	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; <b>PDBTitle:</b> crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from candidatus asiaticum
89	<a href="#">d2hlja1</a>	Alignment	not modelled	96.2	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
90	<a href="#">d2oafa1</a>	Alignment	not modelled	96.2	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
91	<a href="#">d1pn2a2</a>	Alignment	not modelled	96.2	22	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
92	<a href="#">d2oiwa1</a>	Alignment	not modelled	96.0	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
93	<a href="#">c5buxB</a>	Alignment	not modelled	96.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-acp dehydratase (fabz) from2 yersinia pestis with glycerol bound
94	<a href="#">c3ck1B</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of a putative thioesterase (reut_a2179) from2 ralstonia eutropha jmp134 at 1.74 a resolution
95	<a href="#">c2uval</a>	Alignment	not modelled	95.8	14	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> fatty acid synthase beta subunits; <b>PDBTitle:</b> 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
96	<a href="#">c3r87A</a>	Alignment	not modelled	95.7	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of orf6 protein from photobacterium profundum
97	<a href="#">c2egiE</a>	Alignment	not modelled	95.7	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> hypothetical protein aq_1494; <b>PDBTitle:</b> crystal structure of a hypothetical protein(aq1494) from aquifex2 aeolicus
98	<a href="#">c5byuA</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
99	<a href="#">c4i4jE</a>	Alignment	not modelled	95.5	5	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> acp-polyene thioesterase; <b>PDBTitle:</b> the structure of sgce10, the acp-polyene thioesterase involved in c-2 1027 biosynthesis
100	<a href="#">d2bi0a1</a>	Alignment	not modelled	95.5	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
101	<a href="#">c2cdhT</a>	Alignment	not modelled	95.4	24	<b>PDB header:</b> transferase <b>Chain:</b> T: <b>PDB Molecule:</b> dehydratase; <b>PDBTitle:</b> architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
102	<a href="#">d1lo7a</a>	Alignment	not modelled	95.2	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
103	<a href="#">c2glvA</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxymyristoyl-acyl carrier protein dehydratase; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
						<b>PDB header:</b> lyase <b>Chain:</b> K: <b>PDB Molecule:</b> peroxisomal multifunctional enzyme type

104	<a href="#">c1s9cK_</a>	Alignment	not modelled	95.1	24	2; <b>PDBTitle:</b> crystal structure analysis of the 2-enoyl-coa hydratase 22 domain of human peroxisomal multifunctional enzyme type 2
105	<a href="#">c5lqID_</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa thioesterase; <b>PDBTitle:</b> high resolution crystal structure of the 4-hydroxybenzoyl coenzyme-a2 thioesterase from staphylococcus aureus
106	<a href="#">c4rltA_</a>	Alignment	not modelled	95.0	18	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxyacyl-accp dehydratase subunit hada; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-accp dehydratase hada hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin
107	<a href="#">c6qsrB_</a>	Alignment	not modelled	95.0	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> beta-hydroxyacyl-(acyl-carrier-protein) dehydratase <b>PDBTitle:</b> the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
108	<a href="#">c5eo4A_</a>	Alignment	not modelled	94.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
109	<a href="#">d1s9ca1</a>	Alignment	not modelled	94.7	25	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
110	<a href="#">d1q6wa_</a>	Alignment	not modelled	94.6	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
111	<a href="#">c3exzA_</a>	Alignment	not modelled	94.5	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> maoc-like dehydratase; <b>PDBTitle:</b> crystal structure of the maoc-like dehydratase from rhodospirillum2 rubrum. northeast structural genomics consortium target rrr103a.
112	<a href="#">d2fuja1</a>	Alignment	not modelled	94.4	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
113	<a href="#">d2bi0a2</a>	Alignment	not modelled	94.3	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
114	<a href="#">c2w3xE_</a>	Alignment	not modelled	94.3	4	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> cale7; <b>PDBTitle:</b> crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
115	<a href="#">c4w7bD_</a>	Alignment	not modelled	94.1	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> hydratase chsh2; <b>PDBTitle:</b> crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
116	<a href="#">c3khpB_</a>	Alignment	not modelled	94.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> maoc family protein; <b>PDBTitle:</b> crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
117	<a href="#">c2vkzH_</a>	Alignment	not modelled	94.0	12	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> fatty acid synthase subunit beta; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
118	<a href="#">d2nuja1</a>	Alignment	not modelled	93.9	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
119	<a href="#">d2owna2</a>	Alignment	not modelled	93.8	7	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
120	<a href="#">d1njka_</a>	Alignment	not modelled	93.5	7	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like