

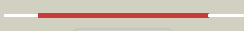























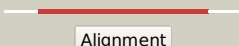













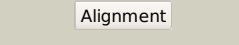



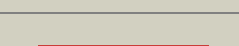
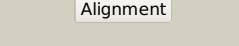
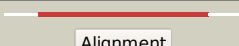


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0216 (-) _258913_259926
Date	Tue Jul 23 14:50:27 BST 2019
Unique Job ID	ebeebcd84872e777

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2bi0A_</a>	 Alignment		100.0	99	<b>PDB header:</b> hypothetical protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv0216; <b>PDBTitle:</b> rv0216, a conserved hypothetical protein from mycobacterium2 tuberculosis that is essential for bacterial survival3 during infection, has a double hotdogfold
2	<a href="#">c4e3eA_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> maoc domain protein dehydratase; <b>PDBTitle:</b> crystal structure of putative maoc domain protein dehydratase from2 chloroflexus aurantiacus j-10-fl
3	<a href="#">d2bi0a1</a>	 Alignment		100.0	98	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
4	<a href="#">d2bi0a2</a>	 Alignment		100.0	95	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
5	<a href="#">c4v12A_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> maoc like domain protein; <b>PDBTitle:</b> crystal structure of the msmeG_6754 dehydratase from mycobacterium2 smegmatis
6	<a href="#">c4ffuA_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidase; <b>PDBTitle:</b> crystal structure of putative maoc-like (monoamine oxidase-like)2 protein, similar to nodN from sinorhizobium meliloti 1021
7	<a href="#">c3exzA_</a>	 Alignment		100.0	17	<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.
8	<a href="#">d1q6wa_</a>	 Alignment		100.0	22	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
9	<a href="#">c5cpgA_</a>	 Alignment		100.0	19	<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
10	<a href="#">d1iq6a_</a>	 Alignment		100.0	23	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
11	<a href="#">d2b3na1</a>	 Alignment		100.0	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like

12	<a href="#">d2c2ia1</a>	 Alignment		100.0	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
13	<a href="#">c3ir3B_</a>	 Alignment		99.9	12	<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)
14	<a href="#">c3khpB_</a>	 Alignment		99.9	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
15	<a href="#">c4rv2B_</a>	 Alignment		99.9	18	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> maoc family protein; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl- <i>acp</i> dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
16	<a href="#">c4ritA_</a>	 Alignment		99.9	16	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> (3r)-hydroxyacyl- <i>acp</i> dehydratase subunit hada; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl- <i>acp</i> dehydratase hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin
17	<a href="#">c4w7bD_</a>	 Alignment		99.9	15	<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
18	<a href="#">c5zy8A_</a>	 Alignment		99.9	15	<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- <i>acp</i> 2 dehydratase) complex from mycobacterium tuberculosis
19	<a href="#">c4w7bG_</a>	 Alignment		99.9	15	<b>PDB header:</b> lyase <b>Chain:</b> G; <b>PDB Molecule:</b> hydratase chsh1; <b>PDBTitle:</b> crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
20	<a href="#">c4rv2A_</a>	 Alignment		99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> upf0336 protein msmeq_1340/msmei_1302; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl- <i>acp</i> dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
21	<a href="#">c3kh8B_</a>	 Alignment	not modelled	99.9	14	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> maoc-like dehydratase; <b>PDBTitle:</b> crystal structure of maoc-like dehydratase from phytophthora capsici
22	<a href="#">c1s9cK_</a>	 Alignment	not modelled	99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> K; <b>PDB Molecule:</b> peroxisomal multifunctional enzyme type 2; <b>PDBTitle:</b> crystal structure analysis of the 2-enoyl-coa hydratase 22 domain of human peroxisomal multifunctional enzyme type 2
23	<a href="#">d1s9ca1</a>	 Alignment	not modelled	99.8	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
24	<a href="#">d1pn2a2</a>	 Alignment	not modelled	99.8	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
25	<a href="#">c1pn2D_</a>	 Alignment	not modelled	99.8	14	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> peroxisomal hydratase-dehydrogenase-epimerase; <b>PDBTitle:</b> crystal structure analysis of the selenomethionine labelled2 2-enoyl-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2
26	<a href="#">c2cdhT_</a>	 Alignment	not modelled	99.8	17	<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.
27	<a href="#">c3om1A_</a>	 Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> peroxisomal multifunctional enzyme type 2, cg3415; <b>PDBTitle:</b> structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster <b>PDB header:</b> transferase

28	<a href="#">c2vkzH_</a>	Alignment	not modelled	99.3	17	<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
29	<a href="#">c2uval_</a>	Alignment	not modelled	99.3	17	<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
30	<a href="#">c4b3yB_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> cryo-em structure of the mycobacterial fatty acid synthase
31	<a href="#">c2gvhC_</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> agr_l_2016p; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
32	<a href="#">c2f3xA_</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor fapr; <b>PDBTitle:</b> crystal structure of fapr (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
33	<a href="#">c3b7kA_</a>	Alignment	not modelled	98.2	13	<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
34	<a href="#">c4a0zA_</a>	Alignment	not modelled	98.2	13	<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
35	<a href="#">d1s9ca2</a>	Alignment	not modelled	98.2	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
36	<a href="#">d1pn2a1</a>	Alignment	not modelled	98.0	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
37	<a href="#">c2cf2L_</a>	Alignment	not modelled	98.0	8	<b>PDB header:</b> transferase <b>Chain:</b> L: <b>PDB Molecule:</b> fatty acid synthase, dh domain; <b>PDBTitle:</b> architecture of mammalian fatty acid synthase
38	<a href="#">c4zv3B_</a>	Alignment	not modelled	97.8	9	<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
39	<a href="#">c4h4gG_</a>	Alignment	not modelled	97.7	13	<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
40	<a href="#">d1z6ba1</a>	Alignment	not modelled	97.6	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> FabZ-like
41	<a href="#">c4zw0A_</a>	Alignment	not modelled	97.5	15	<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
42	<a href="#">d2gvha1</a>	Alignment	not modelled	97.4	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
43	<a href="#">c4ae7A_</a>	Alignment	not modelled	97.4	13	<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
44	<a href="#">c3d6xA_</a>	Alignment	not modelled	97.4	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 campylobacter jejuni fabz
45	<a href="#">c3gekA_</a>	Alignment	not modelled	97.4	9	<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
46	<a href="#">d1ixla_</a>	Alignment	not modelled	97.3	19	<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="#">c3esiD_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from2 erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
48	<a href="#">c5buyA_</a>	Alignment	not modelled	97.3	18	<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
49	<a href="#">c4i82A_</a>	Alignment	not modelled	97.2	15	<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
50	<a href="#">d2cy9a1</a>	Alignment	not modelled	97.2	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
51	<a href="#">d2h4ua1</a>	Alignment	not modelled	97.1	15	<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="#">c3lhaA_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.793;

52	<a href="#">c3lveA</a>	Alignment	not modelled	97.1	10	<b>PDBTitle:</b> the crystal structure of smu.793 from streptococcus mutans ua159 bound2 to acetyl coa <b>PDB header:</b> structural genomics, unknown function
53	<a href="#">c3qooA</a>	Alignment	not modelled	97.1	12	<b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
54	<a href="#">c2eisA</a>	Alignment	not modelled	97.1	12	<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
55	<a href="#">c2glvA</a>	Alignment	not modelled	97.1	19	<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
56	<a href="#">d2fs2a1</a>	Alignment	not modelled	97.1	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
57	<a href="#">d1vpma</a>	Alignment	not modelled	97.0	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
58	<a href="#">d1mkaa</a>	Alignment	not modelled	97.0	10	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> beta-Hydroxydecanol thiol ester dehydrase
59	<a href="#">d1ylia1</a>	Alignment	not modelled	97.0	7	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
60	<a href="#">d1ulza</a>	Alignment	not modelled	97.0	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> FabZ-like
61	<a href="#">c5dm5E</a>	Alignment	not modelled	97.0	14	<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
62	<a href="#">d2hboa1</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
63	<a href="#">c6qsrB</a>	Alignment	not modelled	96.9	10	<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
64	<a href="#">c4ienB</a>	Alignment	not modelled	96.9	11	<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
65	<a href="#">c3lwqB</a>	Alignment	not modelled	96.8	10	<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
66	<a href="#">d2f41a1</a>	Alignment	not modelled	96.8	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
67	<a href="#">c5buxB</a>	Alignment	not modelled	96.8	18	<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
68	<a href="#">c4mzqG</a>	Alignment	not modelled	96.8	14	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> beta-alanyl-coa:ammonia lyase; <b>PDBTitle:</b> beta-alanyl-coa:ammonia lyase from clostridium propionicum in complex2 with propionyl-coa
69	<a href="#">c4i83A</a>	Alignment	not modelled	96.8	17	<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
70	<a href="#">d1y7ua1</a>	Alignment	not modelled	96.7	6	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
71	<a href="#">d2f0xa1</a>	Alignment	not modelled	96.7	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
72	<a href="#">c4ncpF</a>	Alignment	not modelled	96.7	11	<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
73	<a href="#">c4ae8D</a>	Alignment	not modelled	96.7	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
74	<a href="#">c2ownA</a>	Alignment	not modelled	96.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oleoyl-[acyl-carrier protein] thioesterase; <b>PDBTitle:</b> crystal structure of oleoyl thioesterase (putative) (np_784467.1) from2 lactobacillus plantarum at 2.00 a resolution
75	<a href="#">d2essa1</a>	Alignment	not modelled	96.6	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
76	<a href="#">c3e29C</a>	Alignment	not modelled	96.6	18	<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.
77	<a href="#">c4nqA</a>	Alignment	not modelled	96.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-ACP thioesterase;

77	<a href="#">c4gdaA</a>	Alignment	not modelled	96.8	12	<b>PDBTitle:</b> crystal structure of acyl-acyl thioesterase from spiroplasma linguale <b>PDB header:</b> hydrolase
78	<a href="#">c2qwzB</a>	Alignment	not modelled	96.6	17	<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
79	<a href="#">c6qsrA</a>	Alignment	not modelled	96.6	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
80	<a href="#">c5hmcA</a>	Alignment	not modelled	96.5	22	<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
81	<a href="#">c2qq2C</a>	Alignment	not modelled	96.5	7	<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
82	<a href="#">c3bnvD</a>	Alignment	not modelled	96.5	8	<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.
83	<a href="#">d1s5ua</a>	Alignment	not modelled	96.3	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
84	<a href="#">c4b8uD</a>	Alignment	not modelled	96.3	12	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase; <b>PDBTitle:</b> 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)-methoxyacetamide
85	<a href="#">c3s4kA</a>	Alignment	not modelled	96.3	22	<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
86	<a href="#">c2pimA</a>	Alignment	not modelled	96.3	14	<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
87	<a href="#">d2ov9a1</a>	Alignment	not modelled	96.3	10	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
88	<a href="#">c3nwdD</a>	Alignment	not modelled	96.3	13	<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
89	<a href="#">d1wlua1</a>	Alignment	not modelled	96.3	22	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
90	<a href="#">c3f1tB</a>	Alignment	not modelled	96.2	11	<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.
91	<a href="#">c2v1oF</a>	Alignment	not modelled	96.2	14	<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
92	<a href="#">c2prxB</a>	Alignment	not modelled	96.1	15	<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
93	<a href="#">c3d6IA</a>	Alignment	not modelled	96.1	14	<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
94	<a href="#">c5lqlD</a>	Alignment	not modelled	96.0	9	<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
95	<a href="#">d2gvha2</a>	Alignment	not modelled	95.9	10	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
96	<a href="#">c3ck1B</a>	Alignment	not modelled	95.7	20	<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
97	<a href="#">d2owna1</a>	Alignment	not modelled	95.7	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
98	<a href="#">d1q4ua</a>	Alignment	not modelled	95.6	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
99	<a href="#">c5eo4A</a>	Alignment	not modelled	95.6	12	<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.
100	<a href="#">c5vpjB</a>	Alignment	not modelled	95.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> the crystal structure of a thioesteras from actinomadura2 verrucosospora.

101	<a href="#">d1vh9a_</a>	Alignment	not modelled	95.5	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
102	<a href="#">d1vh5a_</a>	Alignment	not modelled	95.4	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
103	<a href="#">c3hduB_</a>	Alignment	not modelled	95.3	18	<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
104	<a href="#">c2essA_</a>	Alignment	not modelled	95.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl- <i>acp</i> thioesterase; <b>PDBTitle:</b> crystal structure of an acyl- <i>acp</i> thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution
105	<a href="#">d2gf6a1</a>	Alignment	not modelled	95.3	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
106	<a href="#">c4k00A_</a>	Alignment	not modelled	95.1	12	<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
107	<a href="#">d1njka_</a>	Alignment	not modelled	95.0	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
108	<a href="#">d2cwza1</a>	Alignment	not modelled	95.0	10	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> TTHA0967-like
109	<a href="#">d1sc0a_</a>	Alignment	not modelled	94.9	10	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
110	<a href="#">d2nuja1</a>	Alignment	not modelled	94.9	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
111	<a href="#">c3r87A_</a>	Alignment	not modelled	94.9	15	<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
112	<a href="#">c4k02A_</a>	Alignment	not modelled	94.8	11	<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 atdhna1, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from arabidopsis thaliana
113	<a href="#">c2xfiB_</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dyne7; <b>PDBTitle:</b> induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynemicin3 thioesterase
114	<a href="#">c3e8pA_</a>	Alignment	not modelled	94.8	10	<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.
115	<a href="#">c4i4jE_</a>	Alignment	not modelled	94.5	20	<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
116	<a href="#">c3dkzA_</a>	Alignment	not modelled	94.5	19	<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.
117	<a href="#">d2hlja1</a>	Alignment	not modelled	94.4	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
118	<a href="#">d1t82a_</a>	Alignment	not modelled	94.4	7	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
119	<a href="#">d2fuja1</a>	Alignment	not modelled	94.3	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
120	<a href="#">c4qdbF_</a>	Alignment	not modelled	94.1	10	<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