







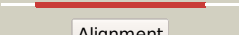

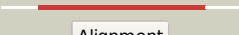













# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2499c_(- )_2813183_2813740
Date	Wed Aug 7 12:50:13 BST 2019
Unique Job ID	37d875f7c47eba48

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2bi0A_</a>	 Alignment		100.0	21	<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="#">d2bi0a1</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
3	<a href="#">c4e3eA_</a>	 Alignment		100.0	26	<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
4	<a href="#">c3exzA_</a>	 Alignment		100.0	28	<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.
5	<a href="#">c4ffuA_</a>	 Alignment		100.0	28	<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 sinorhizo bium melliloti 1021
6	<a href="#">d2bi0a2</a>	 Alignment		100.0	24	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
7	<a href="#">d1q6wa_</a>	 Alignment		100.0	32	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
8	<a href="#">c5cpgA_</a>	 Alignment		100.0	21	<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
9	<a href="#">d2b3na1</a>	 Alignment		100.0	21	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
10	<a href="#">d1iq6a_</a>	 Alignment		100.0	26	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
11	<a href="#">d2c2ia1</a>	 Alignment		100.0	20	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like

12	<a href="#">c4rv2B_</a>	Alignment		99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> maoc family protein; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-accp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
13	<a href="#">c4w7bD_</a>	Alignment		99.9	18	<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
14	<a href="#">c4rltA_</a>	Alignment		99.9	17	<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 hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin
15	<a href="#">c3ir3B_</a>	Alignment		99.9	20	<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)
16	<a href="#">c5zy8A_</a>	Alignment		99.9	17	<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-accp2 dehydratase) complex from mycobacterium tuberculosis
17	<a href="#">c4rv2A_</a>	Alignment		99.9	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0336 protein msmeg_1340/msmej_1302; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-accp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
18	<a href="#">c4v12A_</a>	Alignment		99.9	13	<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
19	<a href="#">c4w7bG_</a>	Alignment		99.9	12	<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="#">d1pn2a2</a>	Alignment		99.9	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
21	<a href="#">d1s9ca1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
22	<a href="#">c3kh8B_</a>	Alignment	not modelled	99.8	20	<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
23	<a href="#">c2vkzH_</a>	Alignment	not modelled	99.8	16	<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
24	<a href="#">c1pn2D_</a>	Alignment	not modelled	99.8	16	<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
25	<a href="#">c2uval_</a>	Alignment	not modelled	99.8	15	<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
26	<a href="#">c3khpB_</a>	Alignment	not modelled	99.8	24	<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
27	<a href="#">c1s9cK_</a>	Alignment	not modelled	99.8	21	<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 <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.
28	<a href="#">c2cdhT_</a>	Alignment	not modelled	99.7	21
29	<a href="#">c3omlA_</a>	Alignment	not modelled	99.7	23
30	<a href="#">c4b3yB_</a>	Alignment	not modelled	99.6	19
31	<a href="#">c2f3xA_</a>	Alignment	not modelled	98.6	14
32	<a href="#">d1s9ca2</a>	Alignment	not modelled	98.6	12
33	<a href="#">c4a0zA_</a>	Alignment	not modelled	98.5	16
34	<a href="#">d1pn2a1</a>	Alignment	not modelled	98.3	10
35	<a href="#">c3qooA_</a>	Alignment	not modelled	98.2	27
36	<a href="#">c4i82A_</a>	Alignment	not modelled	98.1	18
37	<a href="#">c3gekA_</a>	Alignment	not modelled	98.1	11
38	<a href="#">c4zw0A_</a>	Alignment	not modelled	98.1	19
39	<a href="#">c3lbeA_</a>	Alignment	not modelled	98.1	20
40	<a href="#">d1ixla_</a>	Alignment	not modelled	98.0	28
41	<a href="#">c4h4gG_</a>	Alignment	not modelled	98.0	17
42	<a href="#">d1z6ba1</a>	Alignment	not modelled	98.0	20
43	<a href="#">c3lwgB_</a>	Alignment	not modelled	97.9	13
44	<a href="#">d1mkaa_</a>	Alignment	not modelled	97.8	16
45	<a href="#">c3d6xA_</a>	Alignment	not modelled	97.8	19
46	<a href="#">d2fs2a1</a>	Alignment	not modelled	97.8	19
47	<a href="#">c2qwzB_</a>	Alignment	not modelled	97.8	15
48	<a href="#">c4ae7A_</a>	Alignment	not modelled	97.8	9
49	<a href="#">d2cy9a1</a>	Alignment	not modelled	97.8	14
50	<a href="#">c2glvA_</a>	Alignment	not modelled	97.8	20
51	<a href="#">c4b8uD_</a>	Alignment	not modelled	97.7	14

						)methoxy)acetamide
52	<a href="#">c2cf2L</a>	Alignment	not modelled	97.7	15	<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
53	<a href="#">c3bnvD</a>	Alignment	not modelled	97.7	16	<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.
54	<a href="#">c4ae8D</a>	Alignment	not modelled	97.7	4	<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
55	<a href="#">d2ov9a1</a>	Alignment	not modelled	97.7	11	<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="#">d2f41a1</a>	Alignment	not modelled	97.7	15	<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="#">d2h4ua1</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
58	<a href="#">d1q4ua</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
59	<a href="#">d2cwza1</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> TTHA0967-like
60	<a href="#">c5hmcA</a>	Alignment	not modelled	97.6	13	<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
61	<a href="#">c5buyA</a>	Alignment	not modelled	97.6	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 beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from francisella tularensis
62	<a href="#">d1vh9a</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> Paal/Ydil-like
63	<a href="#">d1u1za</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> FabZ-like
64	<a href="#">c3esiD</a>	Alignment	not modelled	97.6	19	<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
65	<a href="#">c3nzwD</a>	Alignment	not modelled	97.6	22	<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
66	<a href="#">d2f0xa1</a>	Alignment	not modelled	97.6	11	<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="#">d1vh5a</a>	Alignment	not modelled	97.6	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
68	<a href="#">c5buxB</a>	Alignment	not modelled	97.6	23	<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-acyl carrier protein (fabz) from2 yersinia pestis with glycerol bound
69	<a href="#">c2pimA</a>	Alignment	not modelled	97.6	23	<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
70	<a href="#">c3fltB</a>	Alignment	not modelled	97.5	14	<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.
71	<a href="#">d2hboa1</a>	Alignment	not modelled	97.5	8	<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="#">c3kuvB</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fluoroacetyl coenzyme a thioesterase; <b>PDBTitle:</b> structural basis of the activity and substrate specificity of the2 fluoroacetyl-coa thioesterase flk - t42s mutant in complex with3 acetate.
73	<a href="#">d1sc0a</a>	Alignment	not modelled	97.5	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
74	<a href="#">d1wlua1</a>	Alignment	not modelled	97.5	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
75	<a href="#">c4i83A</a>	Alignment	not modelled	97.4	22	<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)-hydroxymristoyl-acyl carrier protein dehydratase from2 neisseria meningitidis fam18
						<b>PDB header:</b> hydrolase

76	<a href="#">c3s4kA</a>	Alignment	not modelled	97.4	15	<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
77	<a href="#">c6qsrB</a>	Alignment	not modelled	97.4	16	<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
78	<a href="#">c6qsrA</a>	Alignment	not modelled	97.3	15	<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
79	<a href="#">c3hduB</a>	Alignment	not modelled	97.2	12	<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
80	<a href="#">c4k02A</a>	Alignment	not modelled	97.2	14	<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
81	<a href="#">c2eisA</a>	Alignment	not modelled	97.1	15	<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
82	<a href="#">c3e29C</a>	Alignment	not modelled	97.1	13	<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.
83	<a href="#">c2prxB</a>	Alignment	not modelled	97.0	16	<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
84	<a href="#">c4qdbF</a>	Alignment	not modelled	97.0	13	<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
85	<a href="#">d1s5ua</a>	Alignment	not modelled	96.9	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
86	<a href="#">c5eo4A</a>	Alignment	not modelled	96.8	10	<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.
87	<a href="#">d1zkiA1</a>	Alignment	not modelled	96.8	15	<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="#">c3e8pA</a>	Alignment	not modelled	96.7	14	<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.
89	<a href="#">c4rmmA</a>	Alignment	not modelled	96.7	13	<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_chrv0 protein from chromobacterium2 violaceum. northeast structural genomics consortium target cvr191
90	<a href="#">d1ylia1</a>	Alignment	not modelled	96.7	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
91	<a href="#">d2gvha1</a>	Alignment	not modelled	96.7	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
92	<a href="#">c2gvhC</a>	Alignment	not modelled	96.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> agr_I_2016p; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
93	<a href="#">d2gvha2</a>	Alignment	not modelled	96.6	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
94	<a href="#">c5lqID</a>	Alignment	not modelled	96.6	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
95	<a href="#">d1sh8a</a>	Alignment	not modelled	96.6	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
96	<a href="#">c3rqbB</a>	Alignment	not modelled	96.6	18	<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
97	<a href="#">c4m20D</a>	Alignment	not modelled	96.5	10	<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
98	<a href="#">d2essa1</a>	Alignment	not modelled	96.5	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
99	<a href="#">c3dkzA</a>	Alignment	not modelled	96.5	23	<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.
100	<a href="#">d2owna1</a>	Alignment	not modelled	96.4	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like

101	<a href="#">c4ienB_</a>	Alignment	not modelled	96.4	20	<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
102	<a href="#">d1c8ua1</a>	Alignment	not modelled	96.4	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-CoA thioesterase
103	<a href="#">d1t82a_</a>	Alignment	not modelled	96.4	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
104	<a href="#">c4mzqG_</a>	Alignment	not modelled	96.3	17	<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
105	<a href="#">c3ck1B_</a>	Alignment	not modelled	96.3	17	<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
106	<a href="#">d2hjja1</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
107	<a href="#">c3hm0C_</a>	Alignment	not modelled	96.3	13	<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
108	<a href="#">d1vpma_</a>	Alignment	not modelled	96.3	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
109	<a href="#">c3bbjA_</a>	Alignment	not modelled	96.2	17	<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
110	<a href="#">c3e1eE_</a>	Alignment	not modelled	96.2	13	<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
111	<a href="#">d1tbua1</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> Acyl-CoA thioesterase
112	<a href="#">d2gf6a1</a>	Alignment	not modelled	96.2	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
113	<a href="#">c5dm5E_</a>	Alignment	not modelled	96.2	18	<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
114	<a href="#">c2w3xE_</a>	Alignment	not modelled	96.1	11	<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="#">d1y7ua1</a>	Alignment	not modelled	96.1	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
116	<a href="#">c2qq2C_</a>	Alignment	not modelled	96.1	18	<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
117	<a href="#">c4gakA_</a>	Alignment	not modelled	96.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-ACP thioesterase; <b>PDBTitle:</b> crystal structure of acyl-ACP thioesterase from spiroplasma linguale
118	<a href="#">c4k00A_</a>	Alignment	not modelled	96.1	17	<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
119	<a href="#">c5vpjB_</a>	Alignment	not modelled	96.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> the crystal structure of a thioesterase from actinomadura2 verrucosospora.
120	<a href="#">c1c8uA_</a>	Alignment	not modelled	96.1	12	<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