Phyre^2

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Description	RVBD3389c_(-)_3804099_3804971
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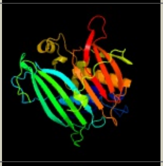
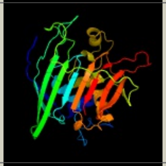
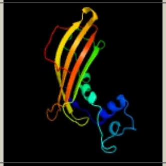
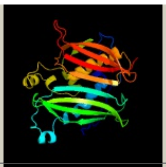
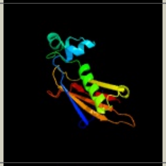
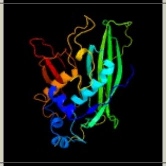
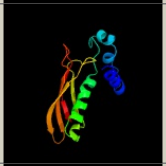
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3khpB_	Alignment		100.0	99	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maoc family protein; **PDBTitle:** crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
2	c3omlA_	Alignment		100.0	39	**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
3	c3kh8B_	Alignment		100.0	36	**PDB header:**lyase **Chain:** B: **PDB Molecule:**maoc-like dehydratase; **PDBTitle:** crystal structure of maoc-like dehydratase from phytophthora capsici
4	c1pn2D_	Alignment		100.0	39	**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
5	c1s9cK_	Alignment		100.0	40	**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
6	c2cdhT_	Alignment		100.0	41	**PDB header:**transferase **Chain:** T: **PDB Molecule:**dehydratase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
7	c4v12A_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**maoc like domain protein; **PDBTitle:** crystal structure of the msmeg_6754 dehydratase from mycobacterium2 smegmatis
8	c4e3eA_	Alignment		100.0	16	**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
9	c2vkzH_	Alignment		100.0	21	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
10	d1pn2a1	Alignment		100.0	31	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
11	c2uval_	Alignment		100.0	18	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400

12	c4b3yB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** cryo-em structure of the mycobacterial fatty acid synthase
13	d1s9ca1	Alignment		100.0	42	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
14	d1pn2a2	Alignment		100.0	49	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
15	d1s9ca2	Alignment		100.0	36	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
16	c2bi0A_	Alignment		100.0	18	**PDB header:**hypothetical protein **Chain:** A: **PDB Molecule:**hypothetical protein rv0216; **PDBTitle:** rv0216, a conserved hypothetical protein from mycobacterium2 tuberculosis that is essential for bacterial survival3 during infection, has a double hotdogfold
17	c4rltA_	Alignment		99.9	20	**PDB header:**lyase/lyase inhibitor **Chain:** A: **PDB Molecule:**(3r)-hydroxyacyl-acp dehydratase subunit hada; **PDBTitle:** crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin
18	c4w7bD_	Alignment		99.8	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**hydratase chsh2; **PDBTitle:** crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
19	d2b3na1	Alignment		99.8	26	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
20	c5cpgA_	Alignment		99.8	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(r)-specific enoyl-coa hydratase; **PDBTitle:** r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
21	c4rv2A_	Alignment	not modelled	99.8	17	**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
22	c5zy8A_	Alignment	not modelled	99.8	21	**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
23	d1iq6a_	Alignment	not modelled	99.8	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
24	c4rv2B_	Alignment	not modelled	99.7	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**maoc family protein; **PDBTitle:** crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
25	d2c2ia1	Alignment	not modelled	99.7	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
26	c4w7bG_	Alignment	not modelled	99.7	8	**PDB header:**lyase **Chain:** G: **PDB Molecule:**hydratase chsh1; **PDBTitle:** crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
27	d2bi0a1	Alignment	not modelled	99.7	24	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
28	d1q6wa_	Alignment	not modelled	99.6	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like

29	d2bi0a2	Alignment	not modelled	99.6	23	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
30	c3exzA_	Alignment	not modelled	99.6	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**maoc-like dehydratase; **PDBTitle:** crystal structure of the maoc-like dehydratase from rhodospirillum2 rubrum. northeast structural genomics consortium target rrr103a.
31	c3ir3B_	Alignment	not modelled	99.6	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-thioester dehydratase 2; **PDBTitle:** crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
32	c4ffuA_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidase; **PDBTitle:** crystal structure of putative maoc-like (monoamine oxidase-like)2 protein, similar to nodn from sinorhizo bium meliloti 1021
33	c2gvhC_	Alignment	not modelled	98.6	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**agr_l_2016p; **PDBTitle:** crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
34	c3b7kA_	Alignment	not modelled	98.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 12; **PDBTitle:** human acyl-coenzyme a thioesterase 12
35	c4gakA_	Alignment	not modelled	98.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-acp thioesterase; **PDBTitle:** crystal structure of acyl-acp thioesterase from spirosoma linguale
36	c3esiD_	Alignment	not modelled	98.1	19	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
37	c2essA_	Alignment	not modelled	98.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-acp thioesterase; **PDBTitle:** crystal structure of an acyl-acp thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution
38	c4zv3B_	Alignment	not modelled	97.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cytosolic acyl coenzyme a thioester hydrolase; **PDBTitle:** crystal structure of the n- and c-terminal domains of mouse acyl-coa2 thioesterase 7
39	c2f3xA_	Alignment	not modelled	97.8	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**transcription factor fapr; **PDBTitle:** crystal structure of fapr (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
40	c2cf2L_	Alignment	not modelled	97.8	14	**PDB header:**transferase **Chain:** L: **PDB Molecule:**fatty acid synthase, dh domain; **PDBTitle:** architecture of mammalian fatty acid synthase
41	c6qsrA_	Alignment	not modelled	97.6	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
42	c2ownA_	Alignment	not modelled	97.6	11	**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
43	c5x04B_	Alignment	not modelled	97.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dodecanoyl-[acyl-carrier-protein] hydrolase, chloroplastic; **PDBTitle:** 12:0-acp thioesterase from umbellularia californica
44	d2gvha1	Alignment	not modelled	96.7	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
45	c4a0zA_	Alignment	not modelled	96.7	12	**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
46	c4zw0A_	Alignment	not modelled	96.7	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; **PDBTitle:** crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from candidatus asiaticum
47	d1ylia1	Alignment	not modelled	96.7	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
48	d1ixla_	Alignment	not modelled	96.7	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
49	c3d6lA_	Alignment	not modelled	96.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
50	c4ae8D_	Alignment	not modelled	96.7	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**thioesterase superfamily member 4; **PDBTitle:** crystal structure of human them4
51	d1z6ba1	Alignment	not modelled	96.6	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
52	c2xflB_	Alignment	not modelled	96.6	20	**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
53	[illegible]	Alignment	not modelled	96.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative acyl-coa hydrolase;

		Alignment	not modelled			**PDBTitle:** crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
54	c3d6xA_	Alignment	not modelled	96.5	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of campylobacter jejuni fabz
55	d2f0xa1	Alignment	not modelled	96.5	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
56	d1mkaa_	Alignment	not modelled	96.5	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**beta-Hydroxydecanol thiol ester dehydrase
57	c3lbeA_	Alignment	not modelled	96.4	14	**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
58	c2qwzB_	Alignment	not modelled	96.4	16	**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
59	d2gvha2	Alignment	not modelled	96.4	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
60	c4ae7A_	Alignment	not modelled	96.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thioesterase superfamily member 5; **PDBTitle:** crystal structure of human them5
61	c4ncpF_	Alignment	not modelled	96.2	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
62	c2eisA_	Alignment	not modelled	96.2	17	**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
63	d2f41a1	Alignment	not modelled	96.2	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
64	c2qq2C_	Alignment	not modelled	96.2	14	**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
65	d2cy9a1	Alignment	not modelled	96.1	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
66	c2prxB_	Alignment	not modelled	96.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**thioesterase superfamily protein; **PDBTitle:** crystal structure of thioesterase superfamily protein (zp_00837258.1)2 from shewanella loihica pv-4 at 1.65 a resolution
67	d2hlja1	Alignment	not modelled	96.1	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
68	c4k00A_	Alignment	not modelled	96.1	20	**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
69	d2h4ua1	Alignment	not modelled	96.1	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
70	c3lwgB_	Alignment	not modelled	96.1	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hp0420 homologue; **PDBTitle:** crystal structure of hp0420-homologue c46a from helicobacter felis
71	d1y7ua1	Alignment	not modelled	96.0	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
72	d1vpma_	Alignment	not modelled	96.0	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
73	c4h4gG_	Alignment	not modelled	96.0	15	**PDB header:**lyase **Chain:** G: **PDB Molecule:**(3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of (3r)-hydroxymyristoyl-[acyl-carrier-protein]2 dehydratase from burkholderia thailandensis e264
74	c2glvA_	Alignment	not modelled	96.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-acyl carrier protein dehydratase; **PDBTitle:** crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
75	c5buyA_	Alignment	not modelled	96.0	14	**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
76	c3gekA_	Alignment	not modelled	95.9	24	**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
77	c5dm5E_	Alignment	not modelled	95.9	16	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative acyl-coa thioester hydrolase; **PDBTitle:** crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
						PDB header:unknown function **Chain:** D: **PDB Molecule:**cj0977;

78	c3bnvD_	Alignment	not modelled	95.8	15	**PDBTitle:** crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
79	d1njka_	Alignment	not modelled	95.8	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
80	d1u1za_	Alignment	not modelled	95.6	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
81	d2o5ua1	Alignment	not modelled	95.4	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
82	d2ov9a1	Alignment	not modelled	95.3	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
83	d1wlua1	Alignment	not modelled	95.3	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
84	c5buxB_	Alignment	not modelled	95.2	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; **PDBTitle:** crystal structure of 3-hydroxyacyl-acp dehydratase (fabz) from2 yersinia pestis with glycerol bound
85	c3r87A_	Alignment	not modelled	95.1	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of orf6 protein from photobacterium profundum
86	c4i83A_	Alignment	not modelled	95.1	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; **PDBTitle:** crystal structure of (3r)-hydroxymyristoyl-acp dehydratase from2 neisseria meningitidis fam18
87	c3f1tB_	Alignment	not modelled	95.0	8	**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.
88	d2cwza1	Alignment	not modelled	95.0	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**TTHA0967-like
89	c5v10B_	Alignment	not modelled	95.0	17	**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
90	c3bbjA_	Alignment	not modelled	94.9	18	**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
91	c5eo4A_	Alignment	not modelled	94.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thioesterase; **PDBTitle:** structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
92	c2w3xE_	Alignment	not modelled	94.8	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cale7; **PDBTitle:** crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
93	c2v1oF_	Alignment	not modelled	94.7	9	**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
94	c4i82A_	Alignment	not modelled	94.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
95	c3rqbB_	Alignment	not modelled	94.7	12	**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
96	c4b8uD_	Alignment	not modelled	94.6	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of 3-hydroxydecanoyl-acyl carrier protein2 dehydratase (faba) from pseudomonas aeruginosa in complex with3 n-isobutyl-2-(5-(2-thienyl)-1,2-oxazol-3-yl-)methoxy)acetamide
97	c4i4jE_	Alignment	not modelled	94.5	8	**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
98	d2essa2	Alignment	not modelled	94.4	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
99	c4mzqG_	Alignment	not modelled	94.3	15	**PDB header:**lyase **Chain:** G: **PDB Molecule:**beta-alanyl-coa:ammonia lyase; **PDBTitle:** beta-alanyl-coa:ammonia lyase from clostridium propionicum in complex2 with propionyl-coa
100	c5byuD_	Alignment	not modelled	94.2	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**thioesterase; **PDBTitle:** crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
101	d2fuja1	Alignment	not modelled	94.2	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
102	c2pimA_	Alignment	not modelled	94.2	15	**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
103	c5vpjB_	Alignment	not modelled	94.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**thioesterase; **PDBTitle:** the crystal structure of a thioesteras from actinomadura2 verrucososporа.
104	c5wh9C_	Alignment	not modelled	94.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**4-hydroxybenzoyl-coa thioesterase; **PDBTitle:** structure of bh1999 gentisyl-coenzyme a thioesterase
105	c5lqlD_	Alignment	not modelled	93.9	16	**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
106	d1lo7a_	Alignment	not modelled	93.9	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
107	c1c8uA_	Alignment	not modelled	93.8	14	**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
108	d2oafa1	Alignment	not modelled	93.8	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
109	d2owna1	Alignment	not modelled	93.7	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
110	d2owna2	Alignment	not modelled	93.7	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
111	d2nuja1	Alignment	not modelled	93.6	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
112	d2gf6a1	Alignment	not modelled	93.5	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
113	d2alia1	Alignment	not modelled	93.3	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
114	c2aliA_	Alignment	not modelled	93.3	12	**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
115	c3ck1B_	Alignment	not modelled	93.2	16	**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
116	d1tbua1	Alignment	not modelled	92.6	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
117	d1s5ua_	Alignment	not modelled	92.6	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
118	d2hx5a1	Alignment	not modelled	92.0	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
119	d1c8ua1	Alignment	not modelled	91.9	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
120	d2essa1	Alignment	not modelled	91.8	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like