

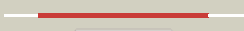
























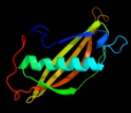







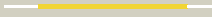

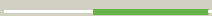
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ylia1	 Alignment		100.0	68	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
2	c3d6lA_	 Alignment		100.0	41	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
3	d1y7ua1	 Alignment		100.0	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
4	c2qq2C_	 Alignment		100.0	27	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
5	d1vpma_	 Alignment		100.0	31	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
6	c2eisA_	 Alignment		100.0	33	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
7	d2gvha1	 Alignment		100.0	25	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
8	c2gvhC_	 Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: agr_I_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
9	c3b7kA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
10	d2gvha2	 Alignment		100.0	25	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
11	c2v1oF_	 Alignment		100.0	25	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

12	d2f0xa1	Alignment		99.9	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
13	c3lwgB_	Alignment		99.9	10	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter2 felis
14	c2qwzB_	Alignment		99.9	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
15	c3e1eE_	Alignment		99.8	18	PDB header: hydrolase Chain: E: PDB Molecule: thioesterase family protein; PDBTitle: crystal structure of a thioesterase family protein from2 silicibacter pomeroyi. northeast structural genomics3 target sir180a
16	d1ixa_	Alignment		99.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
17	d2hboa1	Alignment		99.8	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
18	d2h4ua1	Alignment		99.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
19	c3bnvD_	Alignment		99.8	16	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
20	d2cy9a1	Alignment		99.8	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
21	c2pimA_	Alignment	not modelled	99.8	22	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
22	c3lbeA_	Alignment	not modelled	99.8	17	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
23	d1vh5a_	Alignment	not modelled	99.8	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
24	d1wlua1	Alignment	not modelled	99.8	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
25	d1sc0a_	Alignment	not modelled	99.8	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
26	c3gekA_	Alignment	not modelled	99.8	13	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
27	d1zkia1	Alignment	not modelled	99.8	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
						PDB header: structural genomics, unknown function Chain: D: PDB Molecule: bh2602 protein:

28	c3nzwD_	Alignment	not modelled	99.8	14	PDBTitle: crystal structure of bh2602 protein from bacillus halodurans with coa,2 northeast structural genomics consortium target bhr199
29	d1vh9a_	Alignment	not modelled	99.8	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
30	c3f1tB_	Alignment	not modelled	99.8	14	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.
31	d2fs2a1	Alignment	not modelled	99.8	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
32	d2f41a1	Alignment	not modelled	99.8	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
33	c3s4kA_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase rv1847/mt1895; PDBTitle: structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
34	d1q4ua_	Alignment	not modelled	99.8	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
35	c3e8pA_	Alignment	not modelled	99.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein q8e9m7 from shewanella2 oneidensis related to thioesterase superfamily. northeast3 structural genomics consortium target sor246.
36	c3hduB_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
37	c3dkzA_	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily protein; PDBTitle: crystal structure of the q7w9w5_borpa protein from2 bordetella parapertussis. northeast structural genomics3 consortium target bpr208c.
38	c2f3xA_	Alignment	not modelled	99.7	15	PDB header: gene regulation Chain: A: PDB Molecule: transcription factor fapri; PDBTitle: crystal structure of fapri (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
39	c3e29C_	Alignment	not modelled	99.7	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein q7we92_borbr; PDBTitle: x-ray structure of the protein q7we92_borbr from thioesterase2 superfamily. northeast structural genomics consortium target bor214a.
40	c2prxB_	Alignment	not modelled	99.7	17	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
41	d2ov9a1	Alignment	not modelled	99.6	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
42	d1t82a_	Alignment	not modelled	99.6	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
43	d1sh8a_	Alignment	not modelled	99.6	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
44	d1yoca1	Alignment	not modelled	99.6	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
45	c3lmbA_	Alignment	not modelled	99.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum t1s
46	c3hm0C_	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella2 henselae
47	d1njka_	Alignment	not modelled	99.5	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
48	d2nuja1	Alignment	not modelled	99.5	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
49	c2pzhC_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from helicobacter pylori
50	c2w3xE_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
51	d2gf6a1	Alignment	not modelled	99.4	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
52	c2xf1B_	Alignment	not modelled	99.4	17	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	d2o5ua1	Alignment	not modelled	99.4	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like

54	d2cyea1	Alignment	not modelled	99.4	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
55	c2egiE_	Alignment	not modelled	99.3	15	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: hypothetical protein aq_1494; PDBTitle: crystal structure of a hypothetical protein(aq1494) from aquifex2 aeolicus
56	d2hx5a1	Alignment	not modelled	99.3	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
57	d2hlja1	Alignment	not modelled	99.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
58	d1s5ua_	Alignment	not modelled	99.3	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
59	d1z54a1	Alignment	not modelled	99.3	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
60	d1lo7a_	Alignment	not modelled	99.3	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
61	d2oafa1	Alignment	not modelled	99.2	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
62	d2alia1	Alignment	not modelled	99.2	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
63	c2aliA_	Alignment	not modelled	99.2	16	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
64	d2oiwa1	Alignment	not modelled	99.2	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
65	c3ck1B_	Alignment	not modelled	99.2	19	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
66	d2essa1	Alignment	not modelled	99.1	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
67	d2owna1	Alignment	not modelled	99.1	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
68	d2fuja1	Alignment	not modelled	99.1	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
69	c2essaA_	Alignment	not modelled	98.9	14	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
70	d2cwza1	Alignment	not modelled	98.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
71	c2ownA_	Alignment	not modelled	98.8	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
72	c3bbjA_	Alignment	not modelled	98.3	15	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
73	c3rqbB_	Alignment	not modelled	98.3	14	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
74	c3qoaA_	Alignment	not modelled	98.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
75	d1c8ua1	Alignment	not modelled	98.2	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
76	c1c8uA_	Alignment	not modelled	98.2	16	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
77	c3kuvB_	Alignment	not modelled	98.2	9	PDB header: hydrolase Chain: B: PDB Molecule: fluoroacetyl coenzyme a thioesterase; PDBTitle: structural basis of the activity and substrate specificity of the2 fluoroacetyl-coa thioesterase flk - t42s mutant in complex with3 acetate.
78	c3rd7A_	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coa thioesterase; PDBTitle: crystal structure of acyl-coa thioesterase from mycobacterium avium
79	c3cyaA_	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of putative thioesterase (yp_496845.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.70 a

					resolution
80	d2bi0a1	Alignment	not modelled	98.0	16 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
81	d2owna2	Alignment	not modelled	97.8	9 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
82	d2q78a1	Alignment	not modelled	97.8	21 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
83	d1tbua1	Alignment	not modelled	97.8	13 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
84	c3ir3B	Alignment	not modelled	97.7	14 PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
85	c3d6xA	Alignment	not modelled	97.4	18 PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of campylobacter jejuni fabz
86	c2glvA	Alignment	not modelled	97.4	17 PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-acyl carrier protein PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
87	d1iq6a	Alignment	not modelled	97.3	20 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
88	d2c2ia1	Alignment	not modelled	97.3	17 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
89	c2bi0A	Alignment	not modelled	97.3	16 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
90	d2essa2	Alignment	not modelled	97.1	15 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
91	d2b3na1	Alignment	not modelled	97.0	16 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
92	c3exzA	Alignment	not modelled	97.0	10 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.
93	d2bi0a2	Alignment	not modelled	96.9	13 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
94	d1q6wa	Alignment	not modelled	96.9	21 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
95	d1z6ba1	Alignment	not modelled	96.6	13 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
96	d1u1za	Alignment	not modelled	95.8	12 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
97	c3esiD	Alignment	not modelled	95.6	12 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
98	c3khpB	Alignment	not modelled	95.2	20 PDB header: oxidoreductase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from2 mycobacterium tuberculosis at 2.3a resolution
99	d1c8ua2	Alignment	not modelled	95.1	10 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
100	c3kh8B	Alignment	not modelled	93.9	19 PDB header: lyase Chain: B: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
101	d1pn2a2	Alignment	not modelled	92.1	12 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
102	c2cdhT	Alignment	not modelled	88.6	16 PDB header: transferase Chain: T: PDB Molecule: dehydratase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
103	d1mkaa	Alignment	not modelled	87.3	17 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: beta-Hydroxydecanol thiol ester dehydrase
104	d1s9ca1	Alignment	not modelled	86.1	16 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
105	d1pn2a1	Alignment	not modelled	84.6	5 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like

106	c1s9cK_	 Alignment	not modelled	82.1	14	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
107	c1pn2D_	 Alignment	not modelled	74.6	18	PDB header: lyase Chain: D: PDB Molecule: peroxisomal hydratase-dehydrogenase-epimerase; PDBTitle: crystal structure analysis of the selenomethionine labelled 2-enoyl-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2
108	c2cf2L_	 Alignment	not modelled	72.6	15	PDB header: transferase Chain: L: PDB Molecule: fatty acid synthase, dh domain; PDBTitle: architecture of mammalian fatty acid synthase
109	d1s9ca2	 Alignment	not modelled	62.6	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
110	c3omlA_	 Alignment	not modelled	55.3	12	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