



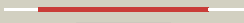


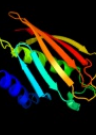






















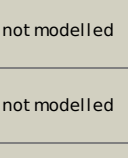


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e8pA_	 Alignment		100.0	48	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein q8e9m7 from shewanella2 oneidensis related to thioesterase superfamily. northeast3 structural genomics consortium target sor246.
2	c3hduB_	 Alignment		100.0	35	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
3	c3f1tB_	 Alignment		100.0	22	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.
4	d2f0xa1	 Alignment		100.0	27	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
5	c2qwzB_	 Alignment		100.0	19	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
6	c3e29C_	 Alignment		100.0	27	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.
7	d1vh9a_	 Alignment		100.0	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
8	d1vh5a_	 Alignment		100.0	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
9	d1sc0a_	 Alignment		100.0	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
10	d2fs2a1	 Alignment		100.0	23	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
11	c2pimA_	 Alignment		100.0	20	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

12	dlq4ua_	Alignment		100.0	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
13	c3e1eE_	Alignment		100.0	27	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
14	d2cy9a1	Alignment		100.0	24	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
15	c3nwzD_	Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: bh2602 protein; PDBTitle: crystal structure of bh2602 protein from bacillus halodurans with coa,2 northeast structural genomics consortium target bhr199
16	c3s4kA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase rv1847/mt1895; PDBTitle: structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
17	d1t82a_	Alignment		100.0	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
18	d1zkia1	Alignment		100.0	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
19	d1sh8a_	Alignment		100.0	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
20	c3dkzA_	Alignment		100.0	27	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.
21	d2h4ua1	Alignment	not modelled	100.0	29	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
22	d1yoca1	Alignment	not modelled	100.0	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
23	d1wlua1	Alignment	not modelled	100.0	27	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
24	c3lbeA_	Alignment	not modelled	100.0	24	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
25	c3lmbA_	Alignment	not modelled	99.9	24	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
26	c3lwqB_	Alignment	not modelled	99.9	18	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter2 felis
27	d2hboa1	Alignment	not modelled	99.9	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
28	c3bnvD_	Alignment	not modelled	99.9	17	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.

29	d1lxl_a	Alignment	not modelled	99.9	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
30	c3gekA	Alignment	not modelled	99.9	15	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
31	d2ov9a1	Alignment	not modelled	99.9	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
32	d2f41a1	Alignment	not modelled	99.9	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
33	c2f3xA	Alignment	not modelled	99.9	19	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
34	c2prxB	Alignment	not modelled	99.8	19	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
35	d1ylia1	Alignment	not modelled	99.7	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
36	c2eisA	Alignment	not modelled	99.7	21	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
37	c3d6lA	Alignment	not modelled	99.7	23	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
38	d2gvha2	Alignment	not modelled	99.7	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
39	c3b7kA	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
40	c2gvhC	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: C: PDB Molecule: agr_1_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
41	d1vpma	Alignment	not modelled	99.6	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
42	d2gvha1	Alignment	not modelled	99.6	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
43	c2qq2C	Alignment	not modelled	99.6	22	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
44	c2v1oF	Alignment	not modelled	99.5	18	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
45	d1y7ua1	Alignment	not modelled	99.4	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
46	d2cwza1	Alignment	not modelled	99.1	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
47	c3bbjA	Alignment	not modelled	98.8	19	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
48	d2hlja1	Alignment	not modelled	98.6	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
49	d1s5ua	Alignment	not modelled	98.6	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
50	c3rqbB	Alignment	not modelled	98.6	16	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
51	d2essa1	Alignment	not modelled	98.5	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
52	c3hm0C	Alignment	not modelled	98.5	6	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella2 henselae
53	d1c8ua1	Alignment	not modelled	98.5	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
54	c2w3xE	Alignment	not modelled	98.5	6	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7 PDB header: hydrolase

55	c2essA	Alignment	not modelled	98.4	14	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
56	d2gf6a1	Alignment	not modelled	98.4	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
57	d1njka	Alignment	not modelled	98.4	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
58	d2cyea1	Alignment	not modelled	98.4	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
59	c1c8uA	Alignment	not modelled	98.4	22	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
60	c3ck1B	Alignment	not modelled	98.4	13	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
61	c3cjqA	Alignment	not modelled	98.4	16	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
62	c2egiE	Alignment	not modelled	98.3	14	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
63	d2o5ua1	Alignment	not modelled	98.3	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
64	d2fuja1	Alignment	not modelled	98.3	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
65	d2owna1	Alignment	not modelled	98.3	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
66	d1z54a1	Alignment	not modelled	98.3	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
67	c3rd7A	Alignment	not modelled	98.2	20	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coa thioesterase; PDBTitle: crystal structure of acyl-coa thioesterase from mycobacterium avium
68	d1lo7a	Alignment	not modelled	98.2	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
69	c3qooA	Alignment	not modelled	98.2	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
70	c2pzhC	Alignment	not modelled	98.2	7	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from helicobacter pylori
71	d2oafa1	Alignment	not modelled	98.2	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
72	d2nuja1	Alignment	not modelled	98.2	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
73	c3ir3B	Alignment	not modelled	98.1	15	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
74	c2ownA	Alignment	not modelled	98.1	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
75	d2oiwa1	Alignment	not modelled	98.0	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
76	d2hx5a1	Alignment	not modelled	98.0	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
77	d1tbua1	Alignment	not modelled	98.0	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
78	d2alia1	Alignment	not modelled	98.0	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
79	c2aliA	Alignment	not modelled	98.0	13	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
80	c3kuvB	Alignment	not modelled	98.0	18	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.

81	c2xf1B_	Alignment	not modelled	97.9	9	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
82	d2q78a1	Alignment	not modelled	97.9	6	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
83	d1q6wa_	Alignment	not modelled	97.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
84	d1c8ua2	Alignment	not modelled	97.7	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
85	d1iq6a_	Alignment	not modelled	97.7	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
86	c3exzA_	Alignment	not modelled	97.6	15	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.
87	d2owna2	Alignment	not modelled	97.6	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
88	c2glvA_	Alignment	not modelled	97.3	13	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
89	d2b3na1	Alignment	not modelled	97.2	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
90	d2bi0a1	Alignment	not modelled	97.0	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
91	d1u1za_	Alignment	not modelled	96.8	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
92	c2bi0A_	Alignment	not modelled	96.0	10	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
93	c3d6xA_	Alignment	not modelled	95.8	15	PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of campylobacter jejuni fabz
94	d2essa2	Alignment	not modelled	95.1	5	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
95	d1pn2a1	Alignment	not modelled	95.1	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
96	d2bi0a2	Alignment	not modelled	93.7	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
97	d1pn2a2	Alignment	not modelled	93.0	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
98	d1mkaa_	Alignment	not modelled	92.1	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: beta-Hydroxydecanol thiol ester dehydrase
99	c3kg8A_	Alignment	not modelled	91.6	11	PDB header: lyase Chain: A: PDB Molecule: curj; PDBTitle: dehydratase domain from curj module of curacin polyketide synthase
100	c3khpB_	Alignment	not modelled	90.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from2 mycobacterium tuberculosis at 2.3a resolution
101	d1s9ca2	Alignment	not modelled	88.8	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
102	d1z6ba1	Alignment	not modelled	87.8	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
103	c2cdhT_	Alignment	not modelled	82.3	15	PDB header: transferase Chain: T: PDB Molecule: dehydratase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
104	c3kg6C_	Alignment	not modelled	79.8	15	PDB header: lyase Chain: C: PDB Molecule: curf; PDBTitle: dehydratase domain from curf module of curacin polyketide synthase
105	d2c2ia1	Alignment	not modelled	79.2	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
106	c3kg7C_	Alignment	not modelled	74.8	12	PDB header: lyase Chain: C: PDB Molecule: curh; PDBTitle: dehydratase domain from curh module of curacin polyketide synthase
107	c3kg9A_	Alignment	not modelled	72.7	13	PDB header: lyase Chain: A: PDB Molecule: curk;

107	c3kg3A	Alignment	not modelled	72.7	13	PDBTitle: dehydratase domain from curk module of curacin polyketide synthase PDB header: lyase
108	c3kh8B	Alignment	not modelled	72.4	12	Chain: B: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
109	c1pn2D	Alignment	not modelled	72.2	20	PDB header: lyase Chain: D: PDB Molecule: peroxisomal hydratase-dehydrogenase-epimerase; PDBTitle: crystal structure analysis of the selenomethionine labelled 2-enoil-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2
110	c1s9cK	Alignment	not modelled	61.7	15	PDB header: lyase Chain: K: PDB Molecule: peroxisomal multifunctional enzyme type 2; PDBTitle: crystal structure analysis of the 2-enoil-coa hydratase 22 domain of human peroxisomal multifunctional enzyme type 2
111	c3omlA	Alignment	not modelled	50.8	8	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
112	c3el6A	Alignment	not modelled	47.1	13	PDB header: lyase Chain: A: PDB Molecule: erythromycin dehydratase; PDBTitle: crystal structure of the erythromycin dehydratase
113	c3esiD	Alignment	not modelled	43.4	13	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
114	d1s9ca1	Alignment	not modelled	36.4	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
115	d2j0pa1	Alignment	not modelled	34.3	24	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
116	d1veha	Alignment	not modelled	30.0	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
117	d1xhja	Alignment	not modelled	25.2	21	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like