Phyre^2

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Description	P0A8Y8
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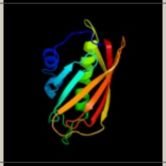
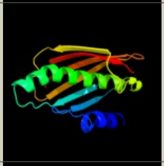
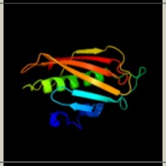
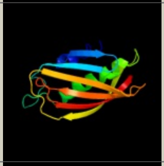
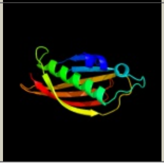
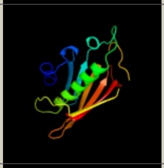
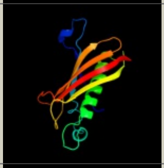
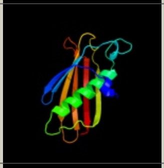
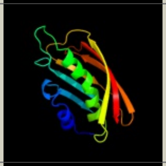
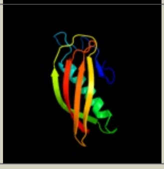
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vh9a_	Alignment		100.0	99	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
2	d1vh5a_	Alignment		100.0	59	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
3	d1sc0a_	Alignment		100.0	48	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
4	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
5	c3hduB_	Alignment		100.0	10	**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
6	d1q4ua_	Alignment		100.0	31	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
7	c3e8pA_	Alignment		100.0	17	**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.
8	c3s4kA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase rv1847/mt1895; **PDBTitle:** structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
9	c3e1eE_	Alignment		99.9	20	**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
10	c2pimA_	Alignment		99.9	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
11	d1zkia1	Alignment		99.9	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like

12	d2f0xa1	Alignment		99.9	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
13	c3f1tB_	Alignment		99.9	15	**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.
14	c3e29C_	Alignment		99.9	20	**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.
15	d2fs2a1	Alignment		99.9	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
16	c3dkzA_	Alignment		99.9	17	**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.
17	c3gekA_	Alignment		99.9	27	**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
18	d2h4ua1	Alignment		99.9	22	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
19	d1sh8a_	Alignment		99.9	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
20	c3nwzD_	Alignment		99.9	27	**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
21	c3lbeA_	Alignment	not modelled	99.9	13	**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
22	d1wlua1	Alignment	not modelled	99.9	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
23	d2cy9a1	Alignment	not modelled	99.9	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
24	d1yoca1	Alignment	not modelled	99.9	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
25	c3lwgB_	Alignment	not modelled	99.9	8	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hp0420 homologue; **PDBTitle:** crystal structure of hp0420-homologue c46a from helicobacter2 felis
26	d2hboa1	Alignment	not modelled	99.9	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
27	d1ixla_	Alignment	not modelled	99.9	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
28	d1t82a_	Alignment	not modelled	99.9	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
						PDB header:structural genomics, unknown function

29	c3lmbA_	Alignment	not modelled	99.9	20	**Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum tls
30	c3bnvD_	Alignment	not modelled	99.9	7	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cj0977; **PDBTitle:** crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
31	d2f41a1	Alignment	not modelled	99.8	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
32	d2ov9a1	Alignment	not modelled	99.8	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
33	c2prxB_	Alignment	not modelled	99.8	15	**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
34	c2f3xA_	Alignment	not modelled	99.8	13	**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
35	c2eisA_	Alignment	not modelled	99.7	20	**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
36	d1ylia1	Alignment	not modelled	99.7	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
37	c3d6lA_	Alignment	not modelled	99.7	12	**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	99.6	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
39	c3b7kA_	Alignment	not modelled	99.6	8	**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	17	**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
41	c2qq2C_	Alignment	not modelled	99.6	11	**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
42	d1vpma_	Alignment	not modelled	99.5	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
43	d2gvha1	Alignment	not modelled	99.5	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
44	d1y7ua1	Alignment	not modelled	99.5	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
45	c2v1oF_	Alignment	not modelled	99.4	12	**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
46	d2cwza1	Alignment	not modelled	99.2	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**TTHA0967-like
47	c3qooA_	Alignment	not modelled	98.5	13	**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
48	c3bbjA_	Alignment	not modelled	98.5	21	**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
49	c3kuvB_	Alignment	not modelled	98.4	19	**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.
50	d1s5ua_	Alignment	not modelled	98.4	6	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
51	c3rqbB_	Alignment	not modelled	98.4	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
52	d2cyea1	Alignment	not modelled	98.4	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
53	d2hlja1	Alignment	not modelled	98.3	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
54	c3hm0C_	Alignment	not modelled	98.3	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable thioesterase; **PDBTitle:** crystal structure of probable thioesterase from bartonella2 henselae
						PDB header:hydrolase

55	c2w3xE_	Alignment	not modelled	98.3	8	**Chain:** E: **PDB Molecule:**cale7; **PDBTitle:** crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
56	d1njka_	Alignment	not modelled	98.3	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
57	d2q78a1	Alignment	not modelled	98.3	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**TTHA0967-like
58	d1c8ua1	Alignment	not modelled	98.3	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
59	c3ck1B_	Alignment	not modelled	98.2	9	**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
60	c2essA_	Alignment	not modelled	98.2	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
61	c3rd7A_	Alignment	not modelled	98.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coa thioesterase; **PDBTitle:** crystal structure of acyl-coa thioesterase from mycobacterium avium
62	c1c8uA_	Alignment	not modelled	98.2	8	**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
63	d2essa1	Alignment	not modelled	98.2	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
64	d2gf6a1	Alignment	not modelled	98.2	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
65	c2egiE_	Alignment	not modelled	98.1	13	**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
66	d2o5ua1	Alignment	not modelled	98.1	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
67	d2fuja1	Alignment	not modelled	98.1	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
68	d1lo7a_	Alignment	not modelled	98.1	7	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
69	c2pzhC_	Alignment	not modelled	98.1	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hypothetical protein hp_0496; **PDBTitle:** ybgc thioesterase (hp0496) from helicobacter pylori
70	d2nuja1	Alignment	not modelled	98.1	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
71	d2owna1	Alignment	not modelled	98.1	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
72	d2hx5a1	Alignment	not modelled	98.0	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
73	c3d6xA_	Alignment	not modelled	98.0	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of campylobacter jejuni fabz
74	d2oafa1	Alignment	not modelled	98.0	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
75	d1z54a1	Alignment	not modelled	97.9	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
76	c2ownA_	Alignment	not modelled	97.9	10	**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
77	c2xflB_	Alignment	not modelled	97.8	12	**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
78	d1tbua1	Alignment	not modelled	97.8	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
79	c3cjyA_	Alignment	not modelled	97.8	13	**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	d2oiwa1	Alignment	not modelled	97.8	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
81	c2glyA_	Alignment	not modelled	97.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-acyl carrier protein

81	c2glvA_	Alignment	not modelled	97.8	11	**PDBTitle:** crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
82	d2alia1	Alignment	not modelled	97.8	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
83	c2aliA_	Alignment	not modelled	97.8	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
84	c3ir3B_	Alignment	not modelled	97.6	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-thioester dehydratase 2; **PDBTitle:** crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
85	c3exzA_	Alignment	not modelled	97.5	14	**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.
86	d1q6wa_	Alignment	not modelled	97.4	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
87	d1iq6a_	Alignment	not modelled	97.3	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
88	d2owna2	Alignment	not modelled	97.3	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
89	d1c8ua2	Alignment	not modelled	97.3	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
90	d1mkaa_	Alignment	not modelled	97.1	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**beta-Hydroxydecanol thiol ester dehydrase
91	d1z6ba1	Alignment	not modelled	96.5	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
92	d1u1za_	Alignment	not modelled	96.0	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
93	d2bi0a1	Alignment	not modelled	95.9	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
94	c2bi0A_	Alignment	not modelled	95.2	13	**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
95	d2b3na1	Alignment	not modelled	95.2	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
96	d1pn2a1	Alignment	not modelled	93.1	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
97	d1s9ca2	Alignment	not modelled	92.6	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
98	c3kg8A_	Alignment	not modelled	91.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curj; **PDBTitle:** dehydratase domain from curj module of curacin polyketide synthase
99	d2essa2	Alignment	not modelled	91.4	7	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
100	c3khpB_	Alignment	not modelled	91.3	17	**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	c2cf2L_	Alignment	not modelled	85.0	15	**PDB header:**transferase **Chain:** L: **PDB Molecule:**fatty acid synthase, dh domain; **PDBTitle:** architecture of mammalian fatty acid synthase
102	d2bi0a2	Alignment	not modelled	76.9	21	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
103	c3kg6C_	Alignment	not modelled	72.6	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**curf; **PDBTitle:** dehydratase domain from curf module of curacin polyketide synthase
104	c3omlA_	Alignment	not modelled	72.4	15	**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
105	c3kh8B_	Alignment	not modelled	69.8	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**maoc-like dehydratase; **PDBTitle:** crystal structure of maoc-like dehydratase from phytophthora capsici
106	c1pn2D_	Alignment	not modelled	67.5	16	**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
						PDB header:structural genomics, unknown function

107	c3esiD_	Alignment	not modelled	67.0	13	**Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
108	c3kg7C_	Alignment	not modelled	65.1	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**curh; **PDBTitle:** dehydratase domain from curh module of curacin polyketide synthase
109	c2cdhT_	Alignment	not modelled	61.7	16	**PDB header:**transferase **Chain:** T: **PDB Molecule:**dehydratase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
110	d1pn2a2	Alignment	not modelled	58.8	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
111	c3kg9A_	Alignment	not modelled	58.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curk; **PDBTitle:** dehydratase domain from curk module of curacin polyketide synthase
112	d2c2ia1	Alignment	not modelled	54.1	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
113	d2hq2a1	Alignment	not modelled	45.9	7	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
114	c3el6A_	Alignment	not modelled	43.5	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**erythromycin dehydratase; **PDBTitle:** crystal structure of the erythromycin dehydratase
115	c1s9cK_	Alignment	not modelled	41.7	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
116	d2j0pa1	Alignment	not modelled	34.4	6	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
117	d1s9ca1	Alignment	not modelled	27.7	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like