Phyre2

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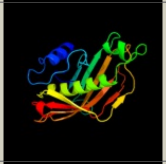
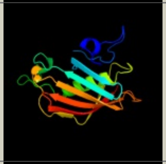
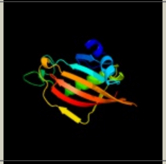
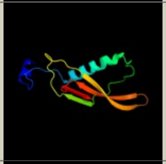
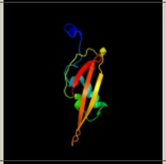
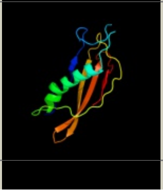
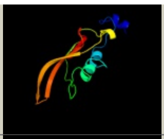
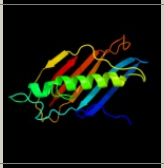
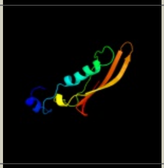
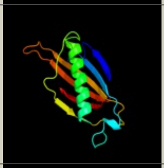
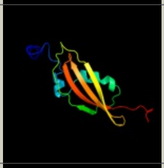
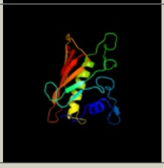
Unique Job ID	e652ff88bb39756e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mkaa_	Alignment		100.0	100	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**beta-Hydroxydecanol thiol ester dehydrase
2	c2cf2L_	Alignment		100.0	99	**PDB header:**transferase **Chain:** L: **PDB Molecule:**fatty acid synthase, dh domain; **PDBTitle:** architecture of mammalian fatty acid synthase
3	d1z6ba1	Alignment		100.0	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
4	c2glvA_	Alignment		100.0	26	**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
5	d1u1za_	Alignment		100.0	22	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
6	c3d6xA_	Alignment		100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of campylobacter jejuni fabz
7	c3esiD_	Alignment		99.8	24	**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
8	d1q6wa_	Alignment		97.5	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
9	d1iq6a_	Alignment		97.5	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
10	c2bi0A_	Alignment		97.4	11	**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
11	c3ir3B_	Alignment		97.4	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-thioester dehydratase 2; **PDBTitle:** crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)

12	c3exzA_	Alignment		97.4	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.
13	c2pimA_	Alignment		97.3	18	**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
14	d1wlua1	Alignment		97.2	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
15	d2c2ia1	Alignment		97.0	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
16	d2b3na1	Alignment		97.0	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
17	d1zkia1	Alignment		97.0	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
18	d2bi0a1	Alignment		96.9	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
19	d1vh9a_	Alignment		96.8	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
20	c2qwzB_	Alignment		96.6	11	**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
21	c3kg9A_	Alignment	not modelled	96.6	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curk; **PDBTitle:** dehydratase domain from curk module of curacin polyketide synthase
22	d1sc0a_	Alignment	not modelled	96.5	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
23	d2h4ua1	Alignment	not modelled	96.4	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
24	c2f3xA_	Alignment	not modelled	96.2	12	**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
25	c3f1tB_	Alignment	not modelled	96.2	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.
26	d2f0xa1	Alignment	not modelled	96.0	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
27	c3kg6C_	Alignment	not modelled	96.0	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**curf; **PDBTitle:** dehydratase domain from curf module of curacin polyketide synthase
28	c3kh8B_	Alignment	not modelled	95.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**maoc-like dehydratase; **PDBTitle:** crystal structure of maoc-like dehydratase from phytophthora capsici
						PDB header:oxidoreductase

29	c3khpB_	Alignment	not modelled	95.8	18	**Chain:** B: **PDB Molecule:**maoc family protein; **PDBTitle:** crystal structure of a possible dehydrogenase from2 mycobacterium tuberculosis at 2.3a resolution
30	d1vh5a_	Alignment	not modelled	95.8	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
31	c3kg7C_	Alignment	not modelled	95.6	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**curh; **PDBTitle:** dehydratase domain from curh module of curacin polyketide synthase
32	c3hrqB_	Alignment	not modelled	95.3	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**aflatoxin biosynthesis polyketide synthase; **PDBTitle:** the product template domain from pksa with palmitate bound
33	c1pn2D_	Alignment	not modelled	95.2	20	**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
34	d2bi0a2	Alignment	not modelled	95.1	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
35	c3kg8A_	Alignment	not modelled	95.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curj; **PDBTitle:** dehydratase domain from curj module of curacin polyketide synthase
36	d1s9ca1	Alignment	not modelled	95.0	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
37	c3el6A_	Alignment	not modelled	94.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**erythromycin dehydratase; **PDBTitle:** crystal structure of the erythromycin dehydratase
38	d1pn2a2	Alignment	not modelled	94.7	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
39	c2cdhT_	Alignment	not modelled	94.5	14	**PDB header:**transferase **Chain:** T: **PDB Molecule:**dehydratase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
40	d1pn2a1	Alignment	not modelled	94.2	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
41	c1s9cK_	Alignment	not modelled	94.1	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
42	d1ixla_	Alignment	not modelled	93.7	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
43	c3omlA_	Alignment	not modelled	92.7	16	**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
44	d2gf6a1	Alignment	not modelled	92.0	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
45	c3e29C_	Alignment	not modelled	91.2	15	**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.
46	d2hx5a1	Alignment	not modelled	90.1	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
47	c3lwgB_	Alignment	not modelled	89.5	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hp0420 homologue; **PDBTitle:** crystal structure of hp0420-homologue c46a from helicobacter2 felis
48	d2cy9a1	Alignment	not modelled	89.1	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
49	d2oiwa1	Alignment	not modelled	88.9	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
50	c3hm0C_	Alignment	not modelled	88.0	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable thioesterase; **PDBTitle:** crystal structure of probable thioesterase from bartonella2 henselae
51	d2oafa1	Alignment	not modelled	86.9	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
52	d1t82a_	Alignment	not modelled	86.8	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
53	c2gvhC_	Alignment	not modelled	86.5	10	**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
						PDB header:transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits;

54	c2uval_	Alignment	not modelled	84.8	14	**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
55	d2ov9a1	Alignment	not modelled	84.7	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
56	d1tbua1	Alignment	not modelled	83.8	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
57	c3lbeA_	Alignment	not modelled	83.4	12	**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	d2hboa1	Alignment	not modelled	83.4	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
59	c3hduB_	Alignment	not modelled	82.8	15	**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
60	d1y7ua1	Alignment	not modelled	82.3	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
61	d2cyea1	Alignment	not modelled	82.3	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
62	c2w3xE_	Alignment	not modelled	81.2	8	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cale7; **PDBTitle:** crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
63	d2gvha2	Alignment	not modelled	81.1	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
64	d2gvha1	Alignment	not modelled	80.4	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
65	d1s9ca2	Alignment	not modelled	80.3	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
66	d1ylia1	Alignment	not modelled	79.5	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
67	d2f41a1	Alignment	not modelled	78.7	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
68	c2prxB_	Alignment	not modelled	76.7	6	**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
69	d2fs2a1	Alignment	not modelled	76.0	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
70	c3gekA_	Alignment	not modelled	75.6	12	**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
71	c3e8pA_	Alignment	not modelled	73.2	15	**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.
72	c1c8uA_	Alignment	not modelled	72.2	9	**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
73	d2owna2	Alignment	not modelled	71.8	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
74	c2eisA_	Alignment	not modelled	71.4	16	**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
75	c3s4kA_	Alignment	not modelled	70.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase rv1847/mt1895; **PDBTitle:** structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
76	c3rqbB_	Alignment	not modelled	70.2	15	**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
77	c2vkzH_	Alignment	not modelled	69.8	14	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
78	c2egiE_	Alignment	not modelled	69.4	8	**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
79	d1c8ua1	Alignment	not modelled	67.6	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase

						Family: Acyl-CoA thioesterase
80	d1vpma_	Alignment	not modelled	67.5	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
81	c3cjyA_	Alignment	not modelled	67.5	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
82	c3rd7A_	Alignment	not modelled	66.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coa thioesterase; **PDBTitle:** crystal structure of acyl-coa thioesterase from mycobacterium avium
83	c3qooA_	Alignment	not modelled	66.0	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
84	c3bbjA_	Alignment	not modelled	64.9	12	**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
85	d1q4ua_	Alignment	not modelled	64.7	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
86	c3dkzA_	Alignment	not modelled	62.9	16	**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.
87	d1yoca1	Alignment	not modelled	62.8	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
88	c3d6lA_	Alignment	not modelled	60.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
89	c3ck1B_	Alignment	not modelled	60.3	11	**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
90	d1njka_	Alignment	not modelled	59.7	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
91	c3nwzD_	Alignment	not modelled	56.4	9	**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
92	c2qq2C_	Alignment	not modelled	56.2	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
93	c3e1eE_	Alignment	not modelled	55.3	17	**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
94	d1z54a1	Alignment	not modelled	55.1	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
95	c3b7kA_	Alignment	not modelled	54.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 12; **PDBTitle:** human acyl-coenzyme a thioesterase 12
96	c2v1oF_	Alignment	not modelled	51.6	10	**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
97	d2owna1	Alignment	not modelled	50.7	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
98	d2hlja1	Alignment	not modelled	50.3	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
99	c2pzhC_	Alignment	not modelled	49.5	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hypothetical protein hp_0496; **PDBTitle:** ybgc thioesterase (hp0496) from helicobacter pylori
100	c2xflB_	Alignment	not modelled	48.5	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
101	d1sh8a_	Alignment	not modelled	46.4	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
102	c3bnvD_	Alignment	not modelled	45.4	7	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cj0977; **PDBTitle:** crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
103	c3lmbA_	Alignment	not modelled	43.4	10	**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 tls
104	d2q78a1	Alignment	not modelled	40.5	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase

						Family:TTHA0967-like
105	c3kuvB_	Alignment	not modelled	38.6	15	**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.
106	d2fuja1	Alignment	not modelled	37.2	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
107	d1s5ua_	Alignment	not modelled	26.8	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like