Phyre²

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Description	P0AGG2
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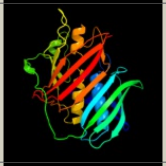
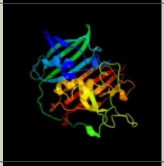
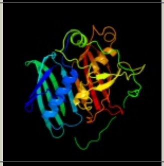
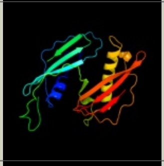
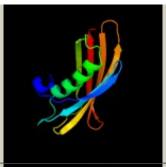
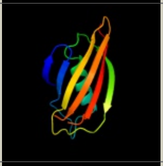
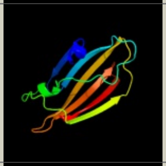
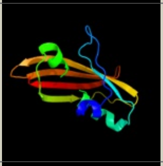
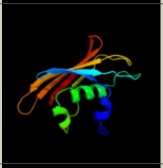
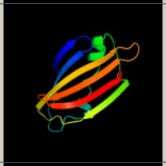
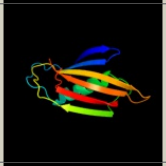
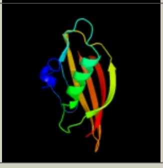
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c8uA_	Alignment		100.0	100	**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
2	c3rd7A_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coa thioesterase; **PDBTitle:** crystal structure of acyl-coa thioesterase from mycobacterium avium
3	c3rqbB_	Alignment		100.0	22	**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
4	c3bbjA_	Alignment		100.0	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
5	c3cjyA_	Alignment		100.0	22	**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
6	d1c8ua2	Alignment		100.0	100	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
7	d1c8ua1	Alignment		100.0	100	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
8	d1tbua1	Alignment		100.0	35	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
9	c3b7kA_	Alignment		99.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 12; **PDBTitle:** human acyl-coenzyme a thioesterase 12
10	c2gvhC_	Alignment		99.1	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**agr_l_2016p; **PDBTitle:** crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
11	c2pimA_	Alignment		99.0	19	**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	d1wlua1	Alignment		99.0	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
13	c2qwzB_	Alignment		99.0	14	**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
14	d1zkia1	Alignment		98.9	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
15	d2h4ua1	Alignment		98.8	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
16	d2hboa1	Alignment		98.8	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
17	d2f0xa1	Alignment		98.8	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
18	c3lbeA_	Alignment		98.7	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
19	c3f1tB_	Alignment		98.7	20	**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.
20	d2fs2a1	Alignment		98.7	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
21	d1ixla_	Alignment	not modelled	98.7	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
22	c3lwgB_	Alignment	not modelled	98.7	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hp0420 homologue; **PDBTitle:** crystal structure of hp0420-homologue c46a from helicobacter2 felis
23	c3e29C_	Alignment	not modelled	98.6	14	**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.
24	c3e8pA_	Alignment	not modelled	98.5	22	**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.
25	d2cy9a1	Alignment	not modelled	98.5	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
26	c3s4kA_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase rv1847/mt1895; **PDBTitle:** structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
27	d1q4ua_	Alignment	not modelled	98.5	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
28	c3nwzD_	Alignment	not modelled	98.5	16	**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
29	d2ov9a1	Alignment	not modelled	98.5	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
30	d1vh9a_	Alignment	not modelled	98.5	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
31	c3gekA_	Alignment	not modelled	98.5	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
32	c3dkzA_	Alignment	not modelled	98.4	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.
33	d1vh5a_	Alignment	not modelled	98.4	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
34	c3hduB_	Alignment	not modelled	98.4	22	**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
35	c2f3xA_	Alignment	not modelled	98.4	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
36	c3e1eE_	Alignment	not modelled	98.3	22	**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
37	c2eisA_	Alignment	not modelled	98.3	14	**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
38	d2f41a1	Alignment	not modelled	98.3	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
39	d1vpma_	Alignment	not modelled	98.2	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
40	c3bnvD_	Alignment	not modelled	98.2	13	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cj0977; **PDBTitle:** crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
41	c2v1oF_	Alignment	not modelled	98.2	11	**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
42	d2gvha1	Alignment	not modelled	98.2	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
43	d1t82a_	Alignment	not modelled	98.2	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
44	c2qq2C_	Alignment	not modelled	98.2	12	**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
45	d1ylia1	Alignment	not modelled	98.2	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
46	d1sc0a_	Alignment	not modelled	98.1	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
47	d1sh8a_	Alignment	not modelled	98.1	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
48	d2gvha2	Alignment	not modelled	98.1	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
49	c3d6lA_	Alignment	not modelled	98.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
50	c2prxB_	Alignment	not modelled	98.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**thioesterase superfamily protein; **PDBTitle:** crystal structure of thioesterase superfamily protein (zp_00837258.1)2 from shewanella loihica pv-4 at 1.65 a resolution
51	d1y7ua1	Alignment	not modelled	98.0	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
52	d1yoca1	Alignment	not modelled	97.9	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
53	c3ir3B_	Alignment	not modelled	97.8	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-thioester dehydratase 2; **PDBTitle:** crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)

54	d1iq6a_	Alignment	not modelled	97.1	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
55	c3lmbA_	Alignment	not modelled	97.0	18	**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
56	d2b3na1	Alignment	not modelled	96.8	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
57	c2ownA_	Alignment	not modelled	96.7	9	**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
58	d1u1za_	Alignment	not modelled	96.7	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
59	d2bi0a1	Alignment	not modelled	96.7	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
60	d2hx5a1	Alignment	not modelled	96.5	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
61	c3d6xA_	Alignment	not modelled	96.4	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of campylobacter jejuni fabz
62	c3kh8B_	Alignment	not modelled	96.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**maoc-like dehydratase; **PDBTitle:** crystal structure of maoc-like dehydratase from phytophthora capsici
63	c2glvA_	Alignment	not modelled	96.1	14	**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
64	d2oafa1	Alignment	not modelled	95.9	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
65	d2gf6a1	Alignment	not modelled	95.8	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
66	d2cyea1	Alignment	not modelled	95.7	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
67	d2owna2	Alignment	not modelled	95.4	6	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
68	d2oiwa1	Alignment	not modelled	95.3	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
69	c3hm0C_	Alignment	not modelled	95.3	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable thioesterase; **PDBTitle:** crystal structure of probable thioesterase from bartonella2 henselae
70	d1q6wa_	Alignment	not modelled	95.1	21	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
71	d2essa1	Alignment	not modelled	95.0	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
72	d1pn2a2	Alignment	not modelled	95.0	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
73	d2hlja1	Alignment	not modelled	94.8	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
74	c2essA_	Alignment	not modelled	94.8	8	**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
75	d1s5ua_	Alignment	not modelled	94.6	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
76	c2w3xE_	Alignment	not modelled	94.4	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cale7; **PDBTitle:** crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
77	c2aliA_	Alignment	not modelled	94.2	6	**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
78	d2alia1	Alignment	not modelled	94.2	6	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
79	d1z6ba1	Alignment	not modelled	94.1	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
80	d2owna1	Alignment	not modelled	93.9	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase

						Family: Acyl-ACP thioesterase-like
81	d1pn2a1	Alignment	not modelled	93.6	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
82	c2egiE_	Alignment	not modelled	93.6	5	**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
83	d1s9ca1	Alignment	not modelled	93.6	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
84	c2cdhT_	Alignment	not modelled	93.3	9	**PDB header:**transferase **Chain:** T: **PDB Molecule:**dehydratase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
85	d1njka_	Alignment	not modelled	93.1	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
86	d1s9ca2	Alignment	not modelled	93.0	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
87	c3kg9A_	Alignment	not modelled	92.7	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curk; **PDBTitle:** dehydratase domain from curk module of curacin polyketide synthase
88	c3exzA_	Alignment	not modelled	92.5	9	**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.
89	d2essa2	Alignment	not modelled	92.4	5	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
90	d2o5ua1	Alignment	not modelled	92.1	5	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
91	c2uvaI_	Alignment	not modelled	92.0	9	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
92	d1z54a1	Alignment	not modelled	91.8	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
93	d1lo7a_	Alignment	not modelled	91.2	5	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
94	c2bi0A_	Alignment	not modelled	90.4	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
95	c3khpB_	Alignment	not modelled	88.7	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
96	c3ck1B_	Alignment	not modelled	88.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative thioesterase; **PDBTitle:** crystal structure of a putative thioesterase (reut_a2179) from2 ralstonia eutropha jmp134 at 1.74 a resolution
97	d2cwza1	Alignment	not modelled	88.0	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**TTHA0967-like
98	c1s9cK_	Alignment	not modelled	88.0	10	**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
99	c2pzhC_	Alignment	not modelled	87.4	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hypothetical protein hp_0496; **PDBTitle:** ybgc thioesterase (hp0496) from helicobacter pylori
100	c1pn2D_	Alignment	not modelled	86.0	10	**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
101	d1mkaa_	Alignment	not modelled	85.8	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**beta-Hydroxydecanol thiol ester dehydrase
102	c2xflB_	Alignment	not modelled	85.8	13	**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
103	c2vkzH_	Alignment	not modelled	84.8	7	**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
104	d2fuja1	Alignment	not modelled	83.6	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
						PDB header:oxidoreductase, hydrolase

105	c3omlA_	Alignment	not modelled	82.5	15	**Chain:** A: **PDB Molecule:**peroxisomal multifunctional enzyme type 2, cg3415; **PDBTitle:** structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster
106	d2bi0a2	Alignment	not modelled	80.7	23	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
107	d2nuja1	Alignment	not modelled	78.7	5	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
108	c3jzhA_	Alignment	not modelled	73.0	3	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb protein eed; **PDBTitle:** eed-h3k79me3
109	d2c2ia1	Alignment	not modelled	71.5	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
110	c3esiD_	Alignment	not modelled	65.5	9	**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
111	d1tbga_	Alignment	not modelled	61.5	19	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
112	c2pbiB_	Alignment	not modelled	61.1	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein subunit beta 5; **PDBTitle:** the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure
113	c1nr0A_	Alignment	not modelled	56.2	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** two seven-bladed beta-propeller domains revealed by the2 structure of a c. elegans homologue of yeast actin3 interacting protein 1 (aip1).
114	c2pm9A_	Alignment	not modelled	54.6	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec31; **PDBTitle:** crystal structure of yeast sec13/31 vertex element of the2 copii vesicular coat
115	c3kg7C_	Alignment	not modelled	53.2	9	**PDB header:**lyase **Chain:** C: **PDB Molecule:**curh; **PDBTitle:** dehydratase domain from curh module of curacin polyketide synthase
116	c3eweC_	Alignment	not modelled	48.7	19	**PDB header:**protein transport,structural protein **Chain:** C: **PDB Molecule:**nucleoporin seh1; **PDBTitle:** crystal structure of the nup85/seh1 complex
117	c3qooA_	Alignment	not modelled	47.0	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
118	c2qxvA_	Alignment	not modelled	46.4	8	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**embryonic ectoderm development; **PDBTitle:** structural basis of ezh2 recognition by eed
119	c3iz6a_	Alignment	not modelled	46.3	19	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
120	c3kg8A_	Alignment	not modelled	46.1	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curj; **PDBTitle:** dehydratase domain from curj module of curacin polyketide synthase