

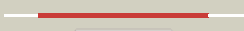














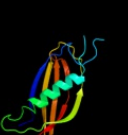
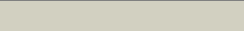





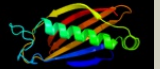
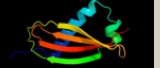
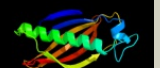






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2glvA_</a>	 Alignment		100.0	42	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxymyristoyl-acyl carrier protein <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
2	<a href="#">dlz6ba1</a>	 Alignment		100.0	47	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> FabZ-like
3	<a href="#">c3d6xA_</a>	 Alignment		100.0	45	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; <b>PDBTitle:</b> crystal structure of campylobacter jejuni fabz
4	<a href="#">dlulza_</a>	 Alignment		100.0	55	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> FabZ-like
5	<a href="#">dlmkaa_</a>	 Alignment		100.0	26	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> beta-Hydroxydecanol thiol ester dehydrase
6	<a href="#">c2cf2L_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> L: <b>PDB Molecule:</b> fatty acid synthase, dh domain; <b>PDBTitle:</b> architecture of mammalian fatty acid synthase
7	<a href="#">c3esiD_</a>	 Alignment		99.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from2 erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
8	<a href="#">c2qwzB_</a>	 Alignment		98.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylacetic acid degradation-related protein; <b>PDBTitle:</b> crystal structure of a putative thioesterase (tm1040_1390) from2 silicibacter sp. tm1040 at 2.15 a resolution
9	<a href="#">c3ir3B_</a>	 Alignment		98.4	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-thioester dehydratase 2; <b>PDBTitle:</b> crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
10	<a href="#">dlwlua1</a>	 Alignment		98.3	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
11	<a href="#">dlixa_</a>	 Alignment		98.2	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like

12	<a href="#">c2f3xA</a>	Alignment		98.2	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor fapr; <b>PDBTitle:</b> crystal structure of fapr (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
13	<a href="#">d2b3na1</a>	Alignment		98.1	22	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
14	<a href="#">d1zkia1</a>	Alignment		98.1	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
15	<a href="#">d1q6wa</a>	Alignment		98.0	23	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
16	<a href="#">c3lwqB</a>	Alignment		98.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hp0420 homologue; <b>PDBTitle:</b> crystal structure of hp0420-homologue c46a from helicobacter2 felis
17	<a href="#">d1sc0a</a>	Alignment		97.9	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
18	<a href="#">c2pimA</a>	Alignment		97.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetic acid degradation-related protein; <b>PDBTitle:</b> crystal structure of a putative thioesterase, phenylacetic acid2 degradation-related protein (reut_b4779) from ralstonia eutropha3 jmp134 at 2.20 a resolution
19	<a href="#">c3qooA</a>	Alignment		97.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
20	<a href="#">d2f41a1</a>	Alignment		97.8	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
21	<a href="#">d2f0xa1</a>	Alignment	not modelled	97.8	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
22	<a href="#">c3f1tB</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein q9i3c8_pseae; <b>PDBTitle:</b> crystal structure of the q9i3c8_pseae protein from pseudomonas2 aeruginosa. northeast structural genomics consortium target par319a.
23	<a href="#">d1iq6a</a>	Alignment	not modelled	97.7	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
24	<a href="#">d2h4ua1</a>	Alignment	not modelled	97.7	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
25	<a href="#">c3kg9A</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> curk; <b>PDBTitle:</b> dehydratase domain from curk module of curacin polyketide synthase
26	<a href="#">c3bnvD</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> cj0977; <b>PDBTitle:</b> crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
27	<a href="#">c2gvhC</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> agr_1_2016p; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
28	<a href="#">c3exzA</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> maoc-like dehydratase; <b>PDBTitle:</b> crystal structure of the maoc-like dehydratase from rhodospirillum2 rubrum. northeast structural genomics consortium

					target rrr103a.
29	<a href="#">c3kg6C_</a>	Alignment	not modelled	97.6	15 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> curf; <b>PDBTitle:</b> dehydratase domain from curf module of curacin polyketide synthase
30	<a href="#">c3el6A_</a>	Alignment	not modelled	97.6	17 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> erythromycin dehydratase; <b>PDBTitle:</b> crystal structure of the erythromycin dehydratase
31	<a href="#">d1vh9a_</a>	Alignment	not modelled	97.6	14 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
32	<a href="#">c3hduB_</a>	Alignment	not modelled	97.5	14 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
33	<a href="#">d2gvha2</a>	Alignment	not modelled	97.5	18 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
34	<a href="#">d1y7ua1</a>	Alignment	not modelled	97.5	18 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
35	<a href="#">c2v1oF_</a>	Alignment	not modelled	97.4	16 <b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of n-terminal domain of acyl-coa2 thioesterase 7
36	<a href="#">d1ylia1</a>	Alignment	not modelled	97.4	18 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
37	<a href="#">c2bi0A_</a>	Alignment	not modelled	97.4	14 <b>PDB header:</b> hypothetical protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv0216; <b>PDBTitle:</b> rv0216, a conserved hypothetical protein from mycobacterium2 tuberculosis that is essential for bacterial survival3 during infection, has a double hotdogfold
38	<a href="#">c3kh8B_</a>	Alignment	not modelled	97.3	16 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> maoc-like dehydratase; <b>PDBTitle:</b> crystal structure of maoc-like dehydratase from phytophthora capsici
39	<a href="#">d2oiwa1</a>	Alignment	not modelled	97.3	7 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
40	<a href="#">c3e29C_</a>	Alignment	not modelled	97.3	14 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein q7we92_borbr; <b>PDBTitle:</b> x-ray structure of the protein q7we92_borbr from thioesterase2 superfamily. northeast structural genomics consortium target bor214a.
41	<a href="#">d1vpma_</a>	Alignment	not modelled	97.3	17 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
42	<a href="#">c2eisA_</a>	Alignment	not modelled	97.3	21 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tthb207; <b>PDBTitle:</b> x-ray structure of acyl-coa hydrolase-like protein, tt1379, from2 thermus thermophilus hbb
43	<a href="#">d2c2ia1</a>	Alignment	not modelled	97.2	17 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
44	<a href="#">d2bi0a1</a>	Alignment	not modelled	97.2	15 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
45	<a href="#">c3e8pA_</a>	Alignment	not modelled	97.1	11 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the protein q8e9m7 from shewanella2 oneidensis related to thioesterase superfamily. northeast3 structural genomics consortium target sor246.
46	<a href="#">c3hm0C_</a>	Alignment	not modelled	97.1	12 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable thioesterase; <b>PDBTitle:</b> crystal structure of probable thioesterase from bartonella2 henselae
47	<a href="#">c3lbeA_</a>	Alignment	not modelled	97.1	13 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.793; <b>PDBTitle:</b> the crystal structure of smu.793 from streptococcus mutans ua159 bound2 to acetyl coa
48	<a href="#">c3kuvB_</a>	Alignment	not modelled	97.1	11 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fluoroacetyl coenzyme a thioesterase; <b>PDBTitle:</b> structural basis of the activity and substrate specificity of the2 fluoroacetyl-coa thioesterase flk - t42s mutant in complex with3 acetate.
49	<a href="#">d2cy9a1</a>	Alignment	not modelled	97.1	13 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
50	<a href="#">c3kg8A_</a>	Alignment	not modelled	97.1	14 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> curj; <b>PDBTitle:</b> dehydratase domain from curj module of curacin polyketide synthase
51	<a href="#">d1vh5a_</a>	Alignment	not modelled	97.1	10 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
52	<a href="#">d2fs2a1</a>	Alignment	not modelled	97.0	16 <b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
53	<a href="#">c3d6lA_</a>	Alignment	not modelled	97.0	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni

54	<a href="#">c3rd7A_</a>	Alignment	not modelled	97.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa thioesterase; <b>PDBTitle:</b> crystal structure of acyl-coa thioesterase from mycobacterium avium
55	<a href="#">d2gvha1</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
56	<a href="#">c3nwzD_</a>	Alignment	not modelled	96.9	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> bh2602 protein; <b>PDBTitle:</b> crystal structure of bh2602 protein from bacillus halodurans with coa,2 northeast structural genomics consortium target bhr199
57	<a href="#">c3b7kA_</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 12; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 12
58	<a href="#">c3gekA_</a>	Alignment	not modelled	96.9	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase yhda; <b>PDBTitle:</b> crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113
59	<a href="#">d1pn2a2</a>	Alignment	not modelled	96.9	22	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
60	<a href="#">d2fuja1</a>	Alignment	not modelled	96.9	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
61	<a href="#">d1s9ca1</a>	Alignment	not modelled	96.8	21	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
62	<a href="#">d1q4ua_</a>	Alignment	not modelled	96.8	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
63	<a href="#">d2gf6a1</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
64	<a href="#">d1c8ua1</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-CoA thioesterase
65	<a href="#">c3hrqB_</a>	Alignment	not modelled	96.7	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> afatoxin biosynthesis polyketide synthase; <b>PDBTitle:</b> the product template domain from pksa with palmitate bound
66	<a href="#">c3s4kA_</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase rv1847/mt1895; <b>PDBTitle:</b> structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
67	<a href="#">d2cyea1</a>	Alignment	not modelled	96.7	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
68	<a href="#">d2cwza1</a>	Alignment	not modelled	96.7	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> TTHA0967-like
69	<a href="#">d2hboa1</a>	Alignment	not modelled	96.7	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
70	<a href="#">c2qq2C_</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
71	<a href="#">c1pn2D_</a>	Alignment	not modelled	96.6	22	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> peroxisomal hydratase-dehydrogenase-epimerase; <b>PDBTitle:</b> crystal structure analysis of the selenomethionine labelled2 2-enoyl-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2
72	<a href="#">c1c8uA_</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa thioesterase ii; <b>PDBTitle:</b> crystal structure of the e.coli thioesterase ii, a2 homologue of the human nef-binding enzyme
73	<a href="#">c3khpB_</a>	Alignment	not modelled	96.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> maoc family protein; <b>PDBTitle:</b> crystal structure of a possible dehydrogenase from2 mycobacterium tuberculosis at 2.3a resolution
74	<a href="#">c3bbjA_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase ii; <b>PDBTitle:</b> crystal structure of a putative thioesterase ii (tfu_2367) from2 thermobifida fusca yx at 2.45 a resolution
75	<a href="#">c1s9cK_</a>	Alignment	not modelled	96.5	20	<b>PDB header:</b> lyase <b>Chain:</b> K: <b>PDB Molecule:</b> peroxisomal multifunctional enzyme type 2; <b>PDBTitle:</b> crystal structure analysis of the 2-enoyl-coa hydratase 22 domain of human peroxisomal multifunctional enzyme type 2
76	<a href="#">d2hx5a1</a>	Alignment	not modelled	96.5	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
77	<a href="#">d2q78a1</a>	Alignment	not modelled	96.4	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> TTHA0967-like
78	<a href="#">c2egiE_</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> hypothetical protein aq_1494; <b>PDBTitle:</b> crystal structure of a hypothetical protein(aq1494) from aquifex2 aeolicus

79	<a href="#">c3rqbB</a>	Alignment	not modelled	96.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function with hot2 dog fold from alicyclobacillus acidocaldarius
80	<a href="#">c2cdhT</a>	Alignment	not modelled	96.3	21	<b>PDB header:</b> transferase <b>Chain:</b> T: <b>PDB Molecule:</b> dehydratase; <b>PDBTitle:</b> architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
81	<a href="#">d2hlja1</a>	Alignment	not modelled	96.1	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
82	<a href="#">c3kg7C</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> curh; <b>PDBTitle:</b> dehydratase domain from curh module of curacin polyketide synthase
83	<a href="#">d2oafa1</a>	Alignment	not modelled	96.1	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
84	<a href="#">c2aliaA</a>	Alignment	not modelled	96.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa2801; <b>PDBTitle:</b> structure of protein of unknown function pa2801 from pseudomonas2 aeruginosa, putative thioesterase
85	<a href="#">d2alia1</a>	Alignment	not modelled	96.0	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
86	<a href="#">c3cjqA</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of putative thioesterase (yp_496845.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.70 a resolution
87	<a href="#">d2ov9a1</a>	Alignment	not modelled	95.8	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
88	<a href="#">c2uval</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> fatty acid synthase beta subunits; <b>PDBTitle:</b> 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
89	<a href="#">d1tbua1</a>	Alignment	not modelled	95.7	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-CoA thioesterase
90	<a href="#">d1njka</a>	Alignment	not modelled	95.5	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
91	<a href="#">d1z54a1</a>	Alignment	not modelled	95.4	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
92	<a href="#">d2bi0a2</a>	Alignment	not modelled	95.3	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
93	<a href="#">d2o5ua1</a>	Alignment	not modelled	95.2	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
94	<a href="#">c3e1eE</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> thioesterase family protein; <b>PDBTitle:</b> crystal structure of a thioesterase family protein from2 silicibacter pomeroyi. northeast structural genomics3 target sir180a
95	<a href="#">c3omlA</a>	Alignment	not modelled	95.0	20	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal multifunctional enzyme type 2, cg3415; <b>PDBTitle:</b> structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster
96	<a href="#">c2pzhC</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein hp_0496; <b>PDBTitle:</b> ybgc thioesterase (hp0496) from helicobacter pylori
97	<a href="#">c2xflB</a>	Alignment	not modelled	94.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dyne7; <b>PDBTitle:</b> induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynemicin3 thioesterase
98	<a href="#">d1t82a</a>	Alignment	not modelled	94.6	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
99	<a href="#">d1sh8a</a>	Alignment	not modelled	94.2	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
100	<a href="#">d2nuja1</a>	Alignment	not modelled	94.1	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
101	<a href="#">c2vkzH</a>	Alignment	not modelled	94.1	13	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> fatty acid synthase subunit beta; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
102	<a href="#">d2owna2</a>	Alignment	not modelled	94.0	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
103	<a href="#">c2w3xE</a>	Alignment	not modelled	93.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> cale7; <b>PDBTitle:</b> crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
						<b>PDB header:</b> hydrolase



104	<a href="#">c3dkzA_</a>	Alignment	not modelled	93.8	12	<b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase superfamily protein; <b>PDBTitle:</b> crystal structure of the q7w9w5_borpa protein from2 bordetella parapertussis. northeast structural genomics3 consortium target bpr208c.
105	<a href="#">d1s5ua_</a>	Alignment	not modelled	93.7	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
106	<a href="#">d2owna1</a>	Alignment	not modelled	93.4	6	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
107	<a href="#">c3ck1B_</a>	Alignment	not modelled	93.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of a putative thioesterase (reut_a2179) from2 ralstonia eutropha jmp134 at 1.74 a resolution
108	<a href="#">c2essaA_</a>	Alignment	not modelled	92.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-acp thioesterase; <b>PDBTitle:</b> crystal structure of an acyl-acp thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution
109	<a href="#">d2essa1</a>	Alignment	not modelled	91.9	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
110	<a href="#">c2prxB_</a>	Alignment	not modelled	91.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> thioesterase superfamily protein; <b>PDBTitle:</b> crystal structure of thioesterase superfamily protein (zp_00837258.1)2 from shewanella loihica pv-4 at 1.65 a resolution
111	<a href="#">c2ownA_</a>	Alignment	not modelled	88.9	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oleoyl-[acyl-carrier protein] thioesterase; <b>PDBTitle:</b> crystal structure of oleoyl thioesterase (putative) (np_784467.1) from2 lactobacillus plantarum at 2.00 a resolution
112	<a href="#">d1lo7a_</a>	Alignment	not modelled	88.1	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
113	<a href="#">c3lmbA_</a>	Alignment	not modelled	85.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum t1s
114	<a href="#">d2essa2</a>	Alignment	not modelled	80.5	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
115	<a href="#">d1yoca1</a>	Alignment	not modelled	79.4	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
116	<a href="#">d1s9ca2</a>	Alignment	not modelled	78.3	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
117	<a href="#">d1c8ua2</a>	Alignment	not modelled	65.9	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-CoA thioesterase