

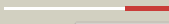


























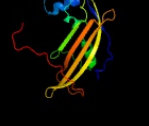



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3542c (-)_3981224_3982159
Date	Fri Aug 9 18:20:22 BST 2019
Unique Job ID	f7f4862c0e0a060e

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4w7bG_	 Alignment		100.0	100	PDB header: lyase Chain: G: PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
2	c6ok1B_	 Alignment		100.0	41	PDB header: transport protein Chain: B: PDB Molecule: chsh2(duf35); PDBTitle: ltp2-chsh2(duf35) aldolase
3	c6et9H_	 Alignment		100.0	26	PDB header: transferase Chain: H: PDB Molecule: pfam duf35; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
4	c5mg5W_	 Alignment		100.0	17	PDB header: transferase Chain: W: PDB Molecule: 2,4-diacetylphloroglucinol biosynthesis protein; PDBTitle: a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (magg)
5	d2gnra1	 Alignment		100.0	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: SSO2064-like
6	c4v12A_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: maoc like domain protein; PDBTitle: crystal structure of the msmeg_6754 dehydratase from mycobacterium2 smegmatis
7	c4rltA_	 Alignment		100.0	16	PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: (3r)-hydroxyacyl-ACP dehydratase subunit hada; PDBTitle: crystal structure of (3r)-hydroxyacyl-ACP dehydratase hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin
8	c4rv2A_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein msmeg_1340/msmei_1302; PDBTitle: crystal structure of (3r)-hydroxyacyl-ACP dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
9	c5zy8A_	 Alignment		99.9	15	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein rv0637; PDBTitle: crystal structure of c terminal truncated hadbc (3r-hydroxyacyl-ACP2 dehydratase) complex from mycobacterium tuberculosis
10	c4e3eA_	 Alignment		99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: maoc domain protein dehydratase; PDBTitle: crystal structure of putative maoc domain protein dehydratase from2 chloroflexus aurantiacus j-10-fl
11	c3exzA_	 Alignment		99.9	18	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.

12	c4ffuA	Alignment		99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidase; PDBTitle: crystal structure of putative maoc-like (monoamine oxidase-like)2 protein, similar to nodn from sinorhizobium meliloti 1021
13	d1q6wa	Alignment		99.9	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
14	d2c2ia1	Alignment		99.9	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
15	c5cpaA	Alignment		99.9	12	PDB header: lyase Chain: A: PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
16	c2bi0A	Alignment		99.8	16	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
17	d1iq6a	Alignment		99.8	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
18	d2bi0a1	Alignment		99.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
19	c3khpB	Alignment		99.8	9	PDB header: oxidoreductase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
20	c4w7bD	Alignment		99.8	14	PDB header: lyase Chain: D: PDB Molecule: hydratase chsh2; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
21	d2b3na1	Alignment	not modelled	99.8	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
22	c3kh8B	Alignment	not modelled	99.7	13	PDB header: lyase Chain: B: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
23	d1pn2a1	Alignment	not modelled	99.7	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
24	d1s9ca2	Alignment	not modelled	99.6	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
25	c1s9cK	Alignment	not modelled	99.6	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
26	c4rv2B	Alignment	not modelled	99.6	18	PDB header: lyase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of (3r)-hydroxyacyl-accp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
27	c1pn2D	Alignment	not modelled	99.5	9	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
28	d2bi0a2	Alignment	not modelled	99.5	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like

29	d1s9ca1	Alignment	not modelled	99.4	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
30	d1pn2a2	Alignment	not modelled	99.4	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
31	c3ir3B_	Alignment	not modelled	99.3	23	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
32	c3om1A_	Alignment	not modelled	99.3	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
33	c2cdhT_	Alignment	not modelled	99.3	14	PDB header: transferase Chain: T: PDB Molecule: dehydratase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
34	c4b3yB_	Alignment	not modelled	98.4	22	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
35	c2uva1_	Alignment	not modelled	98.3	18	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
36	c2vkhZ_	Alignment	not modelled	98.3	15	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
37	c2f3xA_	Alignment	not modelled	97.7	15	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
38	c5wh9C_	Alignment	not modelled	97.4	10	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
39	c4a0zA_	Alignment	not modelled	97.3	10	PDB header: transcription Chain: A: PDB Molecule: transcription factor fapr; PDBTitle: structure of the global transcription regulator fapr from2 staphylococcus aureus in complex with malonyl-coa
40	c3hm0C_	Alignment	not modelled	97.3	15	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella henselae
41	d2gf6a1	Alignment	not modelled	97.3	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
42	d2oafa1	Alignment	not modelled	97.2	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
43	d1mkaa_	Alignment	not modelled	97.1	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: beta-Hydroxydecanol thiol ester dehydrase
44	c5eo4A_	Alignment	not modelled	97.0	8	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
45	d2cyea1	Alignment	not modelled	97.0	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
46	c5byuA_	Alignment	not modelled	97.0	13	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
47	d2hx5a1	Alignment	not modelled	97.0	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
48	c2egiE_	Alignment	not modelled	96.9	22	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
49	d1z54a1	Alignment	not modelled	96.9	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
50	d1s5ua_	Alignment	not modelled	96.9	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
51	d1njka_	Alignment	not modelled	96.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
52	d2oiwa1	Alignment	not modelled	96.8	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
53	c3ck1B_	Alignment	not modelled	96.7	15	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
54	c2cf2L_	Alignment	not modelled	96.7	12	PDB header: transferase Chain: L: PDB Molecule: fatty acid synthase, dh domain; PDBTitle: architecture of mammalian fatty acid synthase

55	c4i4jE	Alignment	not modelled	96.7	16	PDB header: hydrolase Chain: E: PDB Molecule: acp-polyene thioesterase; PDBTitle: the structure of sgce10, the acp-polyene thioesterase involved in c-2 1027 biosynthesis
56	c4k00A	Alignment	not modelled	96.6	6	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa hydrolase; PDBTitle: crystal structure of slr0204, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from synechocystis
57	d1z6ba1	Alignment	not modelled	96.6	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
58	c3r87A	Alignment	not modelled	96.6	13	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from photobacterium profundum
59	d2hlja1	Alignment	not modelled	96.6	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
60	c5vpjB	Alignment	not modelled	96.5	23	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesterase from actinomadura2 verrucosospora.
61	d2o5ua1	Alignment	not modelled	96.5	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
62	c5byuD	Alignment	not modelled	96.5	13	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
63	c5buxB	Alignment	not modelled	96.4	17	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of 3-hydroxyacyl-acp dehydratase (fabz) from2 yersinia pestis with glycerol bound
64	d1lixA	Alignment	not modelled	96.4	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
65	c5v10B	Alignment	not modelled	96.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the putative tol-pal system-associated acyl-coa2 thioesterase from pseudomonas aeruginosa pao1
66	c4b8uD	Alignment	not modelled	96.3	11	PDB header: lyase Chain: D: PDB Molecule: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of 3-hydroxydecanoyl-acyl carrier protein2 dehydratase (fabA) from pseudomonas aeruginosa in complex with3 n-isobutyl-2-(5-(2-thienyl)-1,2-oxazol-3-yl-methoxy)acetamide
67	c6qsrB	Alignment	not modelled	96.3	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: beta-hydroxyacyl-(acyl-carrier-protein) dehydratase PDBTitle: the dehydratase heterocomplex ape:p from xenorhabdus doucetiae
68	c3d6xA	Alignment	not modelled	96.3	12	PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of campylobacter jejuni fabz
69	c5buyA	Alignment	not modelled	96.3	14	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from francisella tularensis
70	c2pzhC	Alignment	not modelled	96.2	11	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from helicobacter pylori
71	c2xfiB	Alignment	not modelled	96.2	18	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
72	c4i83A	Alignment	not modelled	96.2	18	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of (3r)-hydroxymyristoyl-acp dehydratase from2 neisseria meningitidis fam18
73	d2fuja1	Alignment	not modelled	96.2	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
74	d2nuja1	Alignment	not modelled	96.1	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
75	d1u1za	Alignment	not modelled	96.1	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
76	c2w3xE	Alignment	not modelled	96.1	19	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
77	c5lqD	Alignment	not modelled	96.0	10	PDB header: hydrolase Chain: D: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: high resolution crystal structure of the 4-hydroxybenzoyl coenzyme-a2 thioesterase from staphylococcus aureus
78	d2owna1	Alignment	not modelled	95.9	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
						PDB header: lyase Chain: A: PDB Molecule: (3r)-hydroxymyristoyl-acyl carrier protein

79	c2qlvA_	Alignment	not modelled	95.9	18	dehydratase; PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
80	d2owna2	Alignment	not modelled	95.7	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
81	c3lwgB_	Alignment	not modelled	95.7	12	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis
82	c3qooA_	Alignment	not modelled	95.7	16	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
83	c4zw0A_	Alignment	not modelled	95.6	11	PDB header: lyase Chain: A: PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from candidatus asiaticum
84	d1wluw1	Alignment	not modelled	95.4	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
85	c4h4gG_	Alignment	not modelled	95.4	19	PDB header: lyase Chain: G: PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of (3r)-hydroxymyristoyl-[acyl-carrier-protein]2 dehydratase from burkholderia thailandensis e264
86	d2alia1	Alignment	not modelled	95.4	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
87	c2aliaA_	Alignment	not modelled	95.4	15	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
88	d2essa1	Alignment	not modelled	95.2	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
89	c5dm5E_	Alignment	not modelled	95.2	16	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
90	d2f41a1	Alignment	not modelled	95.1	21	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
91	c4gakA_	Alignment	not modelled	95.0	14	PDB header: hydrolase Chain: A: PDB Molecule: acyl-ACP thioesterase; PDBTitle: crystal structure of acyl-ACP thioesterase from spirosona linguale
92	d2hboa1	Alignment	not modelled	95.0	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
93	d2cwza1	Alignment	not modelled	94.8	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
94	c5hmcA_	Alignment	not modelled	94.8	9	PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid
95	c3bnvD_	Alignment	not modelled	94.6	12	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
96	c4ae7A_	Alignment	not modelled	94.4	9	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
97	d2gvha1	Alignment	not modelled	94.1	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
98	c3lbeA_	Alignment	not modelled	93.9	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
99	d2fs2a1	Alignment	not modelled	93.9	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
100	d2cy9a1	Alignment	not modelled	93.6	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
101	c3gekA_	Alignment	not modelled	93.5	5	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
102	d1ylia1	Alignment	not modelled	93.5	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
103	c4ncpF_	Alignment	not modelled	93.4	15	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 4-hbt like thioesterase sav1878 from2 staphylococcus aureus subsp. aureus mu50
104	c6g5iy_	Alignment	not modelled	93.3	8	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r PDB header: hydrolase

105	c4i82A_	Alignment	not modelled	93.2	12	Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
106	d1lo7a_	Alignment	not modelled	93.2	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
107	c2eisA_	Alignment	not modelled	93.0	22	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
108	c2qq2C_	Alignment	not modelled	92.9	17	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
109	c3kuvB_	Alignment	not modelled	92.8	20	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.
110	d2ov9a1	Alignment	not modelled	92.8	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
111	c3d6IA_	Alignment	not modelled	92.7	13	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
112	c2pimA_	Alignment	not modelled	92.6	13	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
113	d1y7ua1	Alignment	not modelled	92.5	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
114	c4ienB_	Alignment	not modelled	92.5	18	PDB header: hydrolase Chain: B: PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
115	d2fiya1	Alignment	not modelled	92.3	10	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
116	c2prxB_	Alignment	not modelled	92.1	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
117	c2gvhC_	Alignment	not modelled	91.9	9	PDB header: hydrolase Chain: C: PDB Molecule: agr_1_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
118	d2q78a1	Alignment	not modelled	91.6	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
119	d1vpma_	Alignment	not modelled	91.3	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
120	c1c8uA_	Alignment	not modelled	90.8	13	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