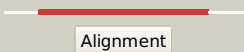

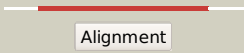



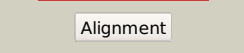



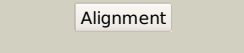

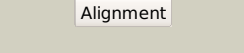



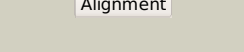

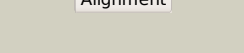

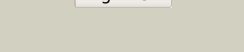









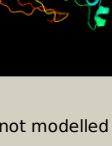


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0241c (-)_289812_290654
Date	Tue Jul 23 14:50:30 BST 2019
Unique Job ID	bade8733e821e924

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pn2D_			100.0	16	PDB header: lyase Chain: D; PDB Molecule: peroxisomal hydratase-dehydrogenase-epimerase; PDBTitle: crystal structure analysis of the selenomethionine labelled 2-enoil-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2
2	c3kh8B_			100.0	19	PDB header: lyase Chain: B; PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
3	c3om1A_			100.0	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
4	c3khpB_			100.0	19	PDB header: oxidoreductase Chain: B; PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
5	c1s9cK_			100.0	16	PDB header: lyase Chain: K; PDB Molecule: peroxisomal multifunctional enzyme type 2; PDBTitle: crystal structure analysis of the 2-enoil-coa hydratase 22 domain of human peroxisomal multifunctional enzyme type 2
6	c2cdhT_			100.0	15	PDB header: transferase Chain: T; PDB Molecule: dehydratase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
7	c2uval_			100.0	21	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
8	c2vkhH_			100.0	22	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
9	c4b3yB_			100.0	20	PDB header: transferase Chain: B; PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
10	c4v12A_			100.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: maoc like domain protein; PDBTitle: crystal structure of the msmeg_6754 dehydratase from mycobacterium2 smegmatis
11	c4e3eA_			100.0	16	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

12	d1s9ca1	Alignment		99.9	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
13	d1pn2a2	Alignment		99.9	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
14	c4w7bD	Alignment		99.9	19	PDB header: lyase Chain: D: PDB Molecule: hydratase chsh2; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
15	d2b3na1	Alignment		99.9	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
16	d1pn2a1	Alignment		99.9	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
17	c5cpgA	Alignment		99.8	25	PDB header: lyase Chain: A: PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
18	d1iq6a	Alignment		99.8	27	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
19	d2c2ia1	Alignment		99.8	27	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
20	c4rv2B	Alignment		99.7	33	PDB header: lyase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
21	c4ffuA	Alignment	not modelled	99.7	23	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
22	c2bi0A	Alignment	not modelled	99.7	15	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
23	c4ritA	Alignment	not modelled	99.7	12	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
24	c5zy8A	Alignment	not modelled	99.7	16	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
25	d1q6wa	Alignment	not modelled	99.6	27	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
26	c3ir3B	Alignment	not modelled	99.6	15	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
27	c3exzA	Alignment	not modelled	99.6	20	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.
28	c4rv2A	Alignment	not modelled	99.6	19	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein msmeg_1340/msmei_1302; PDBTitle: crystal structure of (3r)-hydroxyacyl- <i>acp</i> dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
29	c4w7bG	Alignment	not modelled	99.6	21	PDB header: lyase Chain: G: PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
30	d2bi0a1	Alignment	not modelled	99.6	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
31	d1s9ca2	Alignment	not modelled	99.5	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
32	d2bi0a2	Alignment	not modelled	99.4	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
33	c2gvhC	Alignment	not modelled	97.6	17	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
34	c5x04B	Alignment	not modelled	97.6	11	PDB header: hydrolase Chain: B: PDB Molecule: dodecanoyl-[acyl-carrier-protein] hydrolase, chloroplastic; PDBTitle: 12:0- <i>acp</i> thioesterase from umbellularia californica
35	c2f3xA	Alignment	not modelled	97.4	14	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	c4gakA	Alignment	not modelled	97.3	12	PDB header: hydrolase Chain: A: PDB Molecule: acyl- <i>acp</i> thioesterase; PDBTitle: crystal structure of acyl- <i>acp</i> thioesterase from spirosona linguale
37	c2essA	Alignment	not modelled	97.3	15	PDB header: hydrolase Chain: A: PDB Molecule: acyl- <i>acp</i> thioesterase; PDBTitle: crystal structure of an acyl- <i>acp</i> thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution
38	c5byuD	Alignment	not modelled	96.3	12	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
39	c5wh9C	Alignment	not modelled	95.9	16	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
40	d2oafa1	Alignment	not modelled	95.9	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
41	c6qsrA	Alignment	not modelled	95.9	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
42	c2xfiB	Alignment	not modelled	95.8	21	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
43	d2gf6a1	Alignment	not modelled	95.8	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
44	d1wlua1	Alignment	not modelled	95.7	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
45	c3esiD	Alignment	not modelled	95.7	11	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
46	c4i82A	Alignment	not modelled	95.6	5	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
47	c3lbeA	Alignment	not modelled	95.5	11	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
48	d2oiwa1	Alignment	not modelled	95.4	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
49	c4a0zA	Alignment	not modelled	95.1	13	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
50	c2ownA	Alignment	not modelled	95.0	14	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
51	d1ixa	Alignment	not modelled	94.9	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
52	c2pimA	Alignment	not modelled	94.8	15	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
53	d2h4ua1	Alignment	not modelled	94.4	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
54	c3hm0C_	Alignment	not modelled	94.4	12	PDB header: hydrolase Chain: C: PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella henselae
55	c4h4gG_	Alignment	not modelled	94.3	13	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
56	d2o5ua1	Alignment	not modelled	94.2	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
57	d2h1ja1	Alignment	not modelled	94.1	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
58	c2w3xE_	Alignment	not modelled	94.1	14	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
59	d2hboa1	Alignment	not modelled	94.0	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
60	c3b7kA_	Alignment	not modelled	94.0	12	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
61	c2egiE_	Alignment	not modelled	93.9	12	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
62	d2owna1	Alignment	not modelled	93.7	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
63	d1njka_	Alignment	not modelled	93.6	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
64	d1z54a1	Alignment	not modelled	93.6	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
65	c5eo4A_	Alignment	not modelled	93.6	12	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
66	d2f41a1	Alignment	not modelled	93.5	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
67	d2hx5a1	Alignment	not modelled	93.5	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
68	d2cyea1	Alignment	not modelled	93.5	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
69	c3kuvB_	Alignment	not modelled	93.2	12	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.
70	c4k00A_	Alignment	not modelled	93.2	11	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
71	c3f1tB_	Alignment	not modelled	92.5	12	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.
72	d2gvha1	Alignment	not modelled	92.5	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
73	c5byuA_	Alignment	not modelled	92.2	14	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
74	c3ck1B_	Alignment	not modelled	92.0	10	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
75	c3qooA_	Alignment	not modelled	92.0	12	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
76	d1lo7a_	Alignment	not modelled	92.0	5	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
77	d2q78a1	Alignment	not modelled	91.7	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
78	d2cy9a1	Alignment	not modelled	91.5	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like

79	c5il5A_	Alignment	not modelled	91.3	9	PDB header: lyase Chain: A: PDB Molecule: mlnd; PDBTitle: crystal structure of the dehydratase domain of mlnd from bacillus2 amyloliquefaciens
80	c4zw0A_	Alignment	not modelled	91.0	13	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
81	c5vpiB_	Alignment	not modelled	90.8	11	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesterase from actinomadura2 verrucosospora.
82	c5lqID_	Alignment	not modelled	90.3	13	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
83	d2f0xa1	Alignment	not modelled	89.9	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
84	c3bnvD_	Alignment	not modelled	89.9	8	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
85	c5v10B_	Alignment	not modelled	89.7	13	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
86	c5buyA_	Alignment	not modelled	89.5	12	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
87	c4ae8D_	Alignment	not modelled	89.4	19	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4
88	c3r87A_	Alignment	not modelled	89.3	7	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from photobacterium profundum
89	c3e29C_	Alignment	not modelled	89.3	9	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.
90	c2prxB_	Alignment	not modelled	89.0	8	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
91	c3bbjA_	Alignment	not modelled	88.9	18	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
92	d1zkiA1	Alignment	not modelled	88.7	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
93	d2ov9a1	Alignment	not modelled	87.7	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
94	d2nuja1	Alignment	not modelled	87.5	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
95	d2fs2a1	Alignment	not modelled	87.5	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
96	c4ae7A_	Alignment	not modelled	87.2	18	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
97	c5dm5E_	Alignment	not modelled	87.2	18	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
98	d1z6ba1	Alignment	not modelled	86.9	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
99	c2pzhC_	Alignment	not modelled	86.6	13	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from helicobacter pylori
100	d2owna2	Alignment	not modelled	86.4	6	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
101	c2v1oF_	Alignment	not modelled	86.1	8	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
102	d1s5ua_	Alignment	not modelled	86.1	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
103	d2fuja1	Alignment	not modelled	85.8	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
104	c1c8rA_	Alignment	not modelled	85.8	10	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coa thioesterase ii;

104	c1c6uA	Alignment	not modelled	85.8	19	PDBTitle: crystal structure of the e.coli thioesterase ii, a2 homologue of the human nef-binding enzyme PDB header: hydrolase
105	c2qwzB	Alignment	not modelled	85.7	12	Chain: B; PDB Molecule: phenylacetic acid degradation-related protein; PDBTitle: crystal structure of a putative thioesterase (tm1040_1390) from <i>Silicibacter</i> sp. tm1040 at 2.15 Å resolution
106	d2essa2	Alignment	not modelled	85.7	6	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Acyl-ACP thioesterase-like
107	d1u1za	Alignment	not modelled	85.2	5	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: FabZ-like
108	c2glvA	Alignment	not modelled	84.8	14	PDB header: lyase Chain: A; PDB Molecule: (3r)-hydroxymyristoyl-acyl carrier protein dehydratase; PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from <i>Helicobacter pylori</i>
109	c3rqbB	Alignment	not modelled	84.7	24	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 <i>Alicyclobacillus acidocaldarius</i>
110	c4i4jE	Alignment	not modelled	84.6	11	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
111	c4ienB	Alignment	not modelled	84.5	8	PDB header: hydrolase Chain: B; PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from <i>Neisseria meningitidis</i> 2 fam18
112	d2essa1	Alignment	not modelled	84.4	10	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Acyl-ACP thioesterase-like
113	c5buxB	Alignment	not modelled	82.4	15	PDB header: lyase Chain: B; PDB Molecule: 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; PDBTitle: crystal structure of 3-hydroxyacyl-acyl carrier protein (fabz) from <i>Yersinia pestis</i> with glycerol bound
114	c3e8pA	Alignment	not modelled	81.6	7	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein q8e9m7 from <i>Shewanella oneidensis</i> 2 related to thioesterase superfamily. northeast structural genomics3 consortium target sor246.
115	c3lwgB	Alignment	not modelled	81.2	6	PDB header: unknown function Chain: B; PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from <i>Helicobacter felis</i>
116	d1sh8a	Alignment	not modelled	80.6	14	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Paal/Ydil-like
117	c2cf2L	Alignment	not modelled	80.6	12	PDB header: transferase Chain: L; PDB Molecule: fatty acid synthase, dh domain; PDBTitle: architecture of mammalian fatty acid synthase
118	d1t82a	Alignment	not modelled	80.4	15	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: Paal/Ydil-like
119	d1ylia1	Alignment	not modelled	79.3	15	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: 4HBT-like
120	d2cwza1	Alignment	not modelled	79.2	12	Fold: Thioesterase/thiol ester dehydratase-isomerase Superfamily: Thioesterase/thiol ester dehydratase-isomerase Family: TTHA0967-like