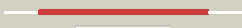












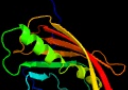





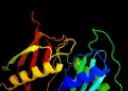

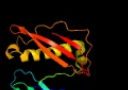











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1618_(tesB1)_1817622_1818524
 Date Fri Aug 2 13:30:21 BST 2019
 Unique Job ID cb6ea548fda49926

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c8uA_	 Alignment		100.0	30	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	30	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coa thioesterase; PDBTitle: crystal structure of acyl-coa thioesterase from mycobacterium avium
3	c4r9zB_	 Alignment		100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: mycobacterium avium subs paratuberculosis tesb protein map1729c
4	c3bbjA_	 Alignment		100.0	14	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	c3rqbB_	 Alignment		100.0	20	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
6	c3cjqA_	 Alignment		100.0	24	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
7	d1c8ua2	 Alignment		100.0	31	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
8	d1c8ua1	 Alignment		100.0	30	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
9	d1tbua1	 Alignment		100.0	33	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
10	c3b7kA_	 Alignment		99.2	11	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
11	c2gvhC_	 Alignment		99.0	14	PDB header: hydrolase Chain: C: PDB Molecule: agr_I_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution

12	c2pimA	Alignment		99.0	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
13	c4zv3B	Alignment		99.0	11	PDB header: hydrolase Chain: B: PDB Molecule: cytosolic acyl coenzyme a thioester hydrolase; PDBTitle: crystal structure of the n- and c-terminal domains of mouse acyl-coa2 thioesterase 7
14	d1wlu1	Alignment		99.0	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
15	d1zka1	Alignment		98.9	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
16	c2qwzB	Alignment		98.9	15	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
17	d2hboa1	Alignment		98.8	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
18	d2f0xa1	Alignment		98.7	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
19	d2h4ua1	Alignment		98.7	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
20	c3lwgB	Alignment		98.7	12	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis
21	d1ixla	Alignment	not modelled	98.7	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
22	c4rmmA	Alignment	not modelled	98.6	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the q7nvp2_chrv0 protein from chromobacterium2 violaceum. northeast structural genomics consortium target cvr191
23	c3lbeA	Alignment	not modelled	98.6	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
24	c4a0zA	Alignment	not modelled	98.6	12	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
25	c4i82A	Alignment	not modelled	98.6	12	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
26	c3f1tB	Alignment	not modelled	98.6	17	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.
27	d2fs2a1	Alignment	not modelled	98.6	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
28	d2cy9a1	Alignment	not modelled	98.6	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like

29	c3e29C_	Alignment	not modelled	98.5	18	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.
30	c3nwd_	Alignment	not modelled	98.5	8	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
31	d1vh5a_	Alignment	not modelled	98.4	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
32	c3s4kA_	Alignment	not modelled	98.4	14	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase rv1847/mt1895; PDBTitle: structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
33	c2f3xA_	Alignment	not modelled	98.4	9	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
34	c4k02A_	Alignment	not modelled	98.4	12	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa thioesterase; PDBTitle: crystal structure of atdhnat1, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from arabidopsis thaliana
35	d1vh9a_	Alignment	not modelled	98.4	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
36	d1q4ua_	Alignment	not modelled	98.4	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
37	c3gekA_	Alignment	not modelled	98.3	11	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
38	c3dkzA_	Alignment	not modelled	98.3	14	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.
39	d2ov9a1	Alignment	not modelled	98.3	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
40	c5dm5E_	Alignment	not modelled	98.3	9	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
41	c3e8pA_	Alignment	not modelled	98.3	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein q8e9m7 from shewanella oneidensis2 related to thioesterase superfamily. northeast structural genomics3 consortium target sor246.
42	c3bnvD_	Alignment	not modelled	98.3	8	PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
43	c5hmcA_	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid
44	c4qdbF_	Alignment	not modelled	98.3	12	PDB header: hydrolase Chain: F: PDB Molecule: thioesterase pa1618; PDBTitle: crystal structure of mutant thioesterase pa1618 (q49a) from2 pseudomonas aeruginosa
45	c4m20D_	Alignment	not modelled	98.2	11	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50
46	c3e1eE_	Alignment	not modelled	98.2	11	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
47	c3hduB_	Alignment	not modelled	98.2	15	PDB header: hydrolase Chain: B: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
48	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
49	c2eisA_	Alignment	not modelled	98.1	21	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
50	c4ae7A_	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5
51	d1t82a_	Alignment	not modelled	98.1	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
52	c2qq2C_	Alignment	not modelled	98.1	15	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

53	d1sc0a_	Alignment	not modelled	98.0	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
54	c4ncpF_	Alignment	not modelled	98.0	17	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
55	d2gvha1	Alignment	not modelled	98.0	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
56	d1ylia1	Alignment	not modelled	98.0	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
57	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
58	d1sh8a_	Alignment	not modelled	98.0	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
59	d2f41a1	Alignment	not modelled	98.0	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
60	c4ienB_	Alignment	not modelled	98.0	13	PDB header: hydrolase Chain: B; PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
61	c3d61A_	Alignment	not modelled	97.9	20	PDB header: hydrolase Chain: A; PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
62	c3ir3B_	Alignment	not modelled	97.9	8	PDB header: lyase Chain: B; PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
63	d1vpma_	Alignment	not modelled	97.9	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
64	d2gvha2	Alignment	not modelled	97.8	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
65	d1y7ua1	Alignment	not modelled	97.8	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
66	c4ae8D_	Alignment	not modelled	97.8	12	PDB header: hydrolase Chain: D; PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4
67	d1yoca1	Alignment	not modelled	97.7	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
68	c5cpgA_	Alignment	not modelled	97.2	11	PDB header: lyase Chain: A; PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
69	c2ownA_	Alignment	not modelled	97.1	12	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
70	d1iq6a_	Alignment	not modelled	97.1	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
71	c3lmbA_	Alignment	not modelled	96.9	14	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 t1s
72	c4h4gG_	Alignment	not modelled	96.8	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
73	c3d6xA_	Alignment	not modelled	96.7	12	PDB header: lyase Chain: A; PDB Molecule: (3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of campylobacter jejuni fabz
74	c4zw0A_	Alignment	not modelled	96.7	17	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
75	c5buxB_	Alignment	not modelled	96.7	13	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
76	d1u1za_	Alignment	not modelled	96.6	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
77	c4i83A_	Alignment	not modelled	96.5	16	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
						Fold: Thioesterase/thiol ester dehydrase-isomerase

78	d2hx5a1	Alignment	not modelled	96.3	13	Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
79	c5buyA	Alignment	not modelled	95.9	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
80	c5lqID	Alignment	not modelled	95.8	17	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
81	d2oafa1	Alignment	not modelled	95.7	16	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
82	c6qsrB	Alignment	not modelled	95.7	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: beta-hydroxyacyl-(acyl-carrier-protein) dehydratase PDBTitle: the dehydratase heterocomplex apei:p from xenorhabdus doucetiae
83	d2b3na1	Alignment	not modelled	95.5	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
84	c2qlvA	Alignment	not modelled	95.4	19	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 helicobacter pylori
85	c4ritA	Alignment	not modelled	95.4	9	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
86	c5eo4A	Alignment	not modelled	95.4	7	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
87	c5v10B	Alignment	not modelled	95.4	10	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
88	d2oiwa1	Alignment	not modelled	95.3	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
89	c4k00A	Alignment	not modelled	95.2	13	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
90	d1q6wa	Alignment	not modelled	95.2	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
91	d2essa1	Alignment	not modelled	94.9	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
92	c5byuA	Alignment	not modelled	94.9	9	PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
93	d2cyea1	Alignment	not modelled	94.8	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
94	c3exzA	Alignment	not modelled	94.8	12	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.
95	d1s5ua	Alignment	not modelled	94.8	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
96	c2alia	Alignment	not modelled	94.6	10	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
97	d2alia1	Alignment	not modelled	94.6	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
98	c5byuD	Alignment	not modelled	94.5	9	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
99	c3kh8B	Alignment	not modelled	94.1	10	PDB header: lyase Chain: B: PDB Molecule: maoc-like dehydratase; PDBTitle: crystal structure of maoc-like dehydratase from phytophthora capsici
100	d1njka	Alignment	not modelled	94.0	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
101	c4ffuA	Alignment	not modelled	94.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidase; PDBTitle: crystal structure of putative maoc-like (monoamine oxidase-like)2 protein, similar to nodn from sinorhizo bium melliloti 1021
102	d1pn2a1	Alignment	not modelled	93.9	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like

103	c5wh9C_	Alignment	not modelled	93.8	9	PDB header: hydrolase Chain: C: PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase
104	c4w7bG_	Alignment	not modelled	93.7	15	PDB header: lyase Chain: G: PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
105	c4rv2A_	Alignment	not modelled	93.6	6	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
106	d2hja1	Alignment	not modelled	93.5	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
107	c3kg9A_	Alignment	not modelled	93.4	11	PDB header: lyase Chain: A: PDB Molecule: curk; PDBTitle: dehydratase domain from curk module of curacin polyketide synthase
108	c2w3xE_	Alignment	not modelled	93.2	9	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
109	d2owna1	Alignment	not modelled	93.1	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
110	d2gfa1	Alignment	not modelled	92.9	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
111	c2egiE_	Alignment	not modelled	92.8	6	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
112	d1z6ba1	Alignment	not modelled	92.6	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: FabZ-like
113	c5vpjB_	Alignment	not modelled	92.6	13	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesterase from actinomadura2 verrucosospora.
114	d2o5ua1	Alignment	not modelled	92.4	8	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
115	d1pn2a2	Alignment	not modelled	92.1	10	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
116	c3omIA_	Alignment	not modelled	92.1	11	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
117	c3ck1B_	Alignment	not modelled	92.0	13	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
118	c3kg8A_	Alignment	not modelled	91.9	14	PDB header: lyase Chain: A: PDB Molecule: curj; PDBTitle: dehydratase domain from curj module of curacin polyketide synthase
119	d2owna2	Alignment	not modelled	91.7	7	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
120	d1s9ca2	Alignment	not modelled	91.6	6	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like