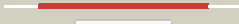



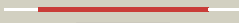








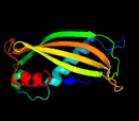

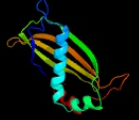








Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0163 (-) _193115_193570 |
| Date | Tue Jul 23 14:50:21 BST 2019 |
| Unique Job ID | 39b48f27cb53faf4 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|--------------------------|---|---|------------|--------|--|
| 1 | d2o5ua1 |  Alignment |  | 100.0 | 43 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 2 | d2nuja1 |  Alignment |  | 100.0 | 21 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 3 | d2oafa1 |  Alignment |  | 100.0 | 24 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 4 | c2xfiB_ |  Alignment |  | 100.0 | 14 | PDB header: hydrolase Chain: B; PDB Molecule: dyne7; PDBTitle: induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynemycin3 thioesterase |
| 5 | c4k00A_ |  Alignment |  | 100.0 | 14 | 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 |
| 6 | c2pzhC_ |  Alignment |  | 100.0 | 14 | PDB header: hydrolase Chain: C; PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from helicobacter pylori |
| 7 | c5vpjB_ |  Alignment |  | 100.0 | 16 | PDB header: hydrolase Chain: B; PDB Molecule: thioesterase; PDBTitle: the crystal structure of a thioesteras from actinomadura2 verrucosospora. |
| 8 | c4i4jE_ |  Alignment |  | 100.0 | 13 | 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 |
| 9 | c5v10B_ |  Alignment |  | 100.0 | 20 | 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 |
| 10 | d2alia1 |  Alignment |  | 100.0 | 28 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 11 | c2aliaA_ |  Alignment |  | 100.0 | 28 | 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 |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c5eo4A_ | Alignment | | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus. |
| 13 | d1njka_ | Alignment | | 100.0 | 17 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 14 | d2oiwa1 | Alignment | | 100.0 | 23 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 15 | c3ck1B_ | Alignment | | 100.0 | 24 | 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 |
| 16 | d2gf6a1 | Alignment | | 100.0 | 23 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 17 | d2hx5a1 | Alignment | | 100.0 | 16 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 18 | c2w3xE_ | Alignment | | 100.0 | 13 | PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7 |
| 19 | d2cyea1 | Alignment | | 100.0 | 30 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 20 | c3r87A_ | Alignment | | 100.0 | 19 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from photobacterium profundum |
| 21 | c5byuA_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila |
| 22 | d1s5ua_ | Alignment | not modelled | 100.0 | 18 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 23 | d1z54a1 | Alignment | not modelled | 100.0 | 24 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 24 | d1lo7a_ | Alignment | not modelled | 100.0 | 14 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 25 | c2egiE_ | Alignment | not modelled | 100.0 | 21 | 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 |
| 26 | d2hja1 | Alignment | not modelled | 100.0 | 15 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 27 | c5lqD_ | Alignment | not modelled | 100.0 | 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 |
| 28 | d2owna1 | Alignment | not modelled | 99.9 | 14 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like |
| | | | | | | PDB header: hydrolase |

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|----|--------------------------|-----------|--------------|------|----|--|
| 29 | c5wh9C_ | Alignment | not modelled | 99.9 | 19 | Chain: C; PDB Molecule: 4-hydroxybenzoyl-coa thioesterase; PDBTitle: structure of bh1999 gentisyl-coenzyme a thioesterase |
| 30 | c3hm0C_ | Alignment | not modelled | 99.9 | 12 | PDB header: hydrolase Chain: C; PDB Molecule: probable thioesterase; PDBTitle: crystal structure of probable thioesterase from bartonella henselae |
| 31 | c5x04B_ | Alignment | not modelled | 99.9 | 11 | PDB header: hydrolase Chain: B; PDB Molecule: dodecanoyl-[acyl-carrier-protein] hydrolase, chloroplast; PDBTitle: 12:0-acyl thioesterase from umbellularia californica |
| 32 | d2essa1 | Alignment | not modelled | 99.9 | 12 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like |
| 33 | d2fuja1 | Alignment | not modelled | 99.9 | 32 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 34 | c4gakA_ | Alignment | not modelled | 99.9 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: acyl-acyl thioesterase; PDBTitle: crystal structure of acyl-acyl thioesterase from spirosona linguale |
| 35 | c2ownA_ | Alignment | not modelled | 99.9 | 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 |
| 36 | c2essaA_ | Alignment | not modelled | 99.9 | 12 | PDB header: hydrolase Chain: A; PDB Molecule: acyl-acyl thioesterase; PDBTitle: crystal structure of an acyl-acyl thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution |
| 37 | c5byuD_ | Alignment | not modelled | 99.9 | 23 | PDB header: hydrolase Chain: D; PDB Molecule: thioesterase; PDBTitle: crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila |
| 38 | d2owna2 | Alignment | not modelled | 99.8 | 17 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like |
| 39 | d2essa2 | Alignment | not modelled | 99.6 | 15 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like |
| 40 | c3d6lA_ | Alignment | not modelled | 99.3 | 12 | PDB header: hydrolase Chain: A; PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni |
| 41 | d1ylia1 | Alignment | not modelled | 99.3 | 15 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 42 | d1vpma_ | Alignment | not modelled | 99.3 | 17 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 43 | c4zv3B_ | Alignment | not modelled | 99.3 | 15 | 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 |
| 44 | c5dm5E_ | Alignment | not modelled | 99.3 | 15 | PDB header: hydrolase Chain: E; PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis |
| 45 | c4ncpF_ | Alignment | not modelled | 99.3 | 13 | 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 |
| 46 | c2eisA_ | Alignment | not modelled | 99.2 | 18 | 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 |
| 47 | c2qq2C_ | Alignment | not modelled | 99.2 | 14 | 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 |
| 48 | c4ienB_ | Alignment | not modelled | 99.2 | 14 | PDB header: hydrolase Chain: B; PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18 |
| 49 | d1y7ua1 | Alignment | not modelled | 99.2 | 16 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 50 | c2v1oF_ | Alignment | not modelled | 99.2 | 14 | 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 |
| 51 | c3b7kA_ | Alignment | not modelled | 99.0 | 16 | PDB header: hydrolase Chain: A; PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12 |
| 52 | d2gvha1 | Alignment | not modelled | 99.0 | 13 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 53 | d2gvha2 | Alignment | not modelled | 98.9 | 23 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like |
| 54 | c2gvhC_ | Alignment | not modelled | 98.9 | 15 | PDB header: hydrolase Chain: C; PDB Molecule: agr_1_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | agrobacterium2 tumefaciens at 2.65 a resolution |
| 55 | c4ae7A | Alignment | not modelled | 98.6 | 8 | PDB header: hydrolase Chain: A: PDB Molecule: thioesterase superfamily member 5; PDBTitle: crystal structure of human them5 |
| 56 | d2f0xa1 | Alignment | not modelled | 98.5 | 14 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 57 | c4i82A | Alignment | not modelled | 98.5 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4 |
| 58 | c3lbeA | Alignment | not modelled | 98.5 | 10 | 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 |
| 59 | c4k02A | Alignment | not modelled | 98.5 | 6 | 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 |
| 60 | c3e1eE | Alignment | not modelled | 98.4 | 13 | 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 |
| 61 | d2h4ua1 | Alignment | not modelled | 98.4 | 14 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 62 | c4ae8D | Alignment | not modelled | 98.4 | 7 | PDB header: hydrolase Chain: D: PDB Molecule: thioesterase superfamily member 4; PDBTitle: crystal structure of human them4 |
| 63 | d2cy9a1 | Alignment | not modelled | 98.4 | 15 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 64 | c5hmcA | Alignment | not modelled | 98.3 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: azi13; PDBTitle: crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid |
| 65 | d1wlua1 | Alignment | not modelled | 98.3 | 23 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 66 | c2qwzB | Alignment | not modelled | 98.3 | 13 | 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 |
| 67 | d1lxa | Alignment | not modelled | 98.3 | 11 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 68 | c3lwgB | Alignment | not modelled | 98.2 | 6 | PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter felis |
| 69 | c3gekA | Alignment | not modelled | 98.2 | 9 | 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 |
| 70 | d1vh5a | Alignment | not modelled | 98.2 | 12 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 71 | c2pimA | Alignment | not modelled | 98.2 | 11 | 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 |
| 72 | d1zka1 | Alignment | not modelled | 98.2 | 14 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 73 | c3nwzD | Alignment | not modelled | 98.1 | 15 | 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 |
| 74 | d2hboa1 | Alignment | not modelled | 98.1 | 12 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 75 | c3s4kA | Alignment | not modelled | 98.1 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: putative esterase rv1847/mt1895; PDBTitle: structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis |
| 76 | d1q4ua | Alignment | not modelled | 98.1 | 10 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 77 | d1sc0a | Alignment | not modelled | 98.0 | 11 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 78 | d2fs2a1 | Alignment | not modelled | 98.0 | 10 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 79 | d2ov9a1 | Alignment | not modelled | 98.0 | 21 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 80 | c2f3xA | Alignment | not modelled | 97.9 | 12 | 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 |
| 81 | d1vh9a | Alignment | not modelled | 97.9 | 14 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 82 | c4qdbF | Alignment | not modelled | 97.9 | 14 | PDB header: hydrolase Chain: F: PDB Molecule: thioesterase pa1618; PDBTitle: crystal structure of mutant thioesterase pa1618 (q49a) from2 pseudomonas aeruginosa |
| 83 | c3f1tB | Alignment | not modelled | 97.8 | 13 | 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. |
| 84 | c4a0zA | Alignment | not modelled | 97.8 | 11 | 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 |
| 85 | c3hduB | Alignment | not modelled | 97.8 | 12 | 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 |
| 86 | d2f41a1 | Alignment | not modelled | 97.8 | 12 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 87 | d2cwza1 | Alignment | not modelled | 97.7 | 13 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like |
| 88 | c4m20D | Alignment | not modelled | 97.7 | 9 | PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50 |
| 89 | c3bnvD | Alignment | not modelled | 97.6 | 13 | PDB header: unknown function Chain: D: PDB Molecule: cj0977; PDBTitle: crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni. |
| 90 | c3dkzA | Alignment | not modelled | 97.6 | 16 | 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. |
| 91 | c3e8pA | Alignment | not modelled | 97.5 | 16 | 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. |
| 92 | c3e29C | Alignment | not modelled | 97.4 | 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. |
| 93 | c2prxB | Alignment | not modelled | 97.3 | 16 | 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 |
| 94 | c4rmmA | Alignment | not modelled | 97.3 | 12 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the q7nvp2_chrvo protein from chromobacterium2 violaceum. northeast structural genomics consortium target cvr191 |
| 95 | c3kuvB | Alignment | not modelled | 97.2 | 9 | 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. |
| 96 | c4rv2A | Alignment | not modelled | 97.1 | 13 | 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 |
| 97 | c3qooA | Alignment | not modelled | 97.0 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hot-dog-like taci_0573 protein from2 thermaerovibrio acidaminovorans |
| 98 | d1yoca1 | Alignment | not modelled | 97.0 | 10 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 99 | d2q78a1 | Alignment | not modelled | 96.8 | 15 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like |
| 100 | c4ritA | Alignment | not modelled | 96.8 | 10 | PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: (3r)-hydroxyacyl- <i>acp</i> dehydratase subunit hada; PDBTitle: crystal structure of (3r)-hydroxyacyl- <i>acp</i> dehydratase hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin |
| 101 | c3ir3B | Alignment | not modelled | 96.8 | 10 | PDB header: lyase Chain: B: PDB Molecule: 3-hydroxyacyl-thioester dehydratase 2; PDBTitle: crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2) |
| 102 | d1t82a | Alignment | not modelled | 96.7 | 16 | Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 103 | c5zy8A | Alignment | not modelled | 96.7 | 10 | PDB header: lyase Chain: A: PDB Molecule: upf0336 protein rv0637; PDBTitle: crystal structure of c terminal truncated hadbc (3r-hydroxyacyl- <i>acp</i> 2 dehydratase) complex from mycobacterium |

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|-----|-------------------------|-----------|--------------|------|---|
| | | | | | tuberculosis |
| 104 | c4mzqG_ | Alignment | not modelled | 96.6 | 11 PDB header: lyase Chain: G: PDB Molecule: beta-alanyl-coa:ammonia lyase; PDBTitle: beta-alanyl-coa:ammonia lyase from clostridium propionicum in complex2 with propionyl-coa |
| 105 | c5buyA_ | Alignment | not modelled | 96.5 | 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 francisella tularensis |
| 106 | c4w7bG_ | Alignment | not modelled | 96.3 | 8 PDB header: lyase Chain: G: PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis |
| 107 | d1sh8a_ | Alignment | not modelled | 96.3 | 17 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like |
| 108 | c3lmbA_ | Alignment | not modelled | 96.2 | 7 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 |
| 109 | d2b3na1 | Alignment | not modelled | 96.1 | 17 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like |
| 110 | d1q6wa_ | Alignment | not modelled | 96.1 | 7 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like |
| 111 | c3khpB_ | Alignment | not modelled | 96.0 | 18 PDB header: oxidoreductase Chain: B: PDB Molecule: maoc family protein; PDBTitle: crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution |
| 112 | d1iq6a_ | Alignment | not modelled | 96.0 | 13 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like |
| 113 | c2glvA_ | Alignment | not modelled | 95.9 | 8 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 |
| 114 | c4ffuA_ | Alignment | not modelled | 95.8 | 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 sinorhizobium meliloti 1021 |
| 115 | c4e3eA_ | Alignment | not modelled | 95.7 | 12 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 |
| 116 | c5cpgA_ | Alignment | not modelled | 95.6 | 20 PDB header: lyase Chain: A: PDB Molecule: (r)-specific enoyl-coa hydratase; PDBTitle: r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form |
| 117 | c3exzA_ | Alignment | not modelled | 95.6 | 19 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. |
| 118 | d1pn2a1 | Alignment | not modelled | 95.1 | 9 Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like |
| 119 | c4hznA_ | Alignment | not modelled | 94.9 | 17 PDB header: transferase Chain: A: PDB Molecule: bifunctional methylmalonyl-coa:acp acetyltransferase/decarboxylase lnmk2 from the leinamycin biosynthetic pathway revealing novel activity for3 a double hot dog fold |
| 120 | c4i83A_ | Alignment | not modelled | 94.8 | 10 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 |