







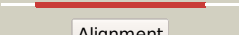

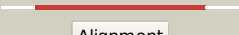






















# Phyre2

|               |                                  |
|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD3039c_echA17_3399430_3400194 |
| Date          | Thu Aug 8 16:20:21 BST 2019      |
| Unique Job ID | 6c124d1ad8353ce1                 |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c5jbxB_</a> |  Alignment   |    | 100.0      | 29     | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydratase;<br><b>PDBTitle:</b> crystal structure of liuc in complex with coenzyme a and malonic acid                               |
| 2  | <a href="#">c4di1A_</a> |  Alignment   |    | 100.0      | 83     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase echa17;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa17 from mycobacterium2 marinum                               |
| 3  | <a href="#">c5zaiB_</a> |  Alignment   |    | 100.0      | 27     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B; <b>PDB Molecule:</b> 3-hydroxypropionyl-coenzyme a dehydratase;<br><b>PDBTitle:</b> crystal structure of 3-hydroxypropionyl-coa dehydratase from2 metallosphaera sedula    |
| 4  | <a href="#">c3hinA_</a> |  Alignment   |   | 100.0      | 24     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative 3-hydroxybutyryl-coa dehydratase;<br><b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase from2 rhodospseudomonas palustris cga009 |
| 5  | <a href="#">c4jcsA_</a> |  Alignment |  | 100.0      | 21     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase from cupriavidus2 metallidurans ch34                |
| 6  | <a href="#">c3moyA_</a> |  Alignment |  | 100.0      | 31     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> probable enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis                         |
| 7  | <a href="#">d1nzya_</a> |  Alignment |  | 100.0      | 26     | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like  |
| 8  | <a href="#">c5z7rA_</a> |  Alignment |  | 100.0      | 27     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> short-chain-enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of crotonase from clostridium acetobutylicum                                       |
| 9  | <a href="#">c3g64A_</a> |  Alignment |  | 100.0      | 30     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)                   |
| 10 | <a href="#">c4jfcA_</a> |  Alignment |  | 100.0      | 28     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from polaromonas sp. js666  |
| 11 | <a href="#">c2hw5F_</a> |  Alignment |  | 100.0      | 27     | <b>PDB header:</b> lyase<br><b>Chain:</b> F; <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1                            |

|    |                         |           |   |       |    |  |
|----|-------------------------|-----------|---|-------|----|--|
| 12 | <a href="#">d1mj3a_</a> | Alignment |    | 100.0 | 28 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 13 | <a href="#">c4mi2C_</a> | Alignment |    | 100.0 | 30 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus            |
| 14 | <a href="#">c2ppyE_</a> | Alignment |    | 100.0 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426                                     |
| 15 | <a href="#">c2ej5B_</a> | Alignment |    | 100.0 | 29 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase subunit ii;<br><b>PDBTitle:</b> crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus              |
| 16 | <a href="#">c2qq3F_</a> | Alignment |    | 100.0 | 30 | <b>PDB header:</b> lyase<br><b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase subunit i;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426      |
| 17 | <a href="#">c2vx2D_</a> | Alignment |    | 100.0 | 22 | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase domain-containing protein 3;<br><b>PDBTitle:</b> crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3) |
| 18 | <a href="#">d1wdka4</a> | Alignment |  | 100.0 | 27 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 19 | <a href="#">c4zu2A_</a> | Alignment |  | 100.0 | 25 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative isohexenylglutaconyl-coa hydratase;<br><b>PDBTitle:</b> pseudomonas aeruginosa atue   |
| 20 | <a href="#">c4fzwA_</a> | Alignment |  | 100.0 | 31 | <b>PDB header:</b> isomerase/lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-dehydroadipyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli                           |
| 21 | <a href="#">c3hrxD_</a> | Alignment | not modelled  | 100.0 | 30 | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> probable enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of phenylacetic acid degradation protein paag  |
| 22 | <a href="#">c3kqfC_</a> | Alignment | not modelled  | 100.0 | 28 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;<br><b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of enoyl-coa hydratase from2 bacillus anthracis.     |
| 23 | <a href="#">c3mybA_</a> | Alignment | not modelled  | 100.0 | 26 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase mycobacterium smegmatis  |
| 24 | <a href="#">d1xx4a_</a> | Alignment | not modelled  | 100.0 | 23 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 25 | <a href="#">c3h81A_</a> | Alignment | not modelled  | 100.0 | 34 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa8;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis   |
| 26 | <a href="#">d1hzda_</a> | Alignment | not modelled  | 100.0 | 33 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 27 | <a href="#">c3peaD_</a> | Alignment | not modelled  | 100.0 | 28 | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from bacillus anthracis str.2 'ames ancestor'         |
| 28 | <a href="#">c3i47A_</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl coa hydratase/isomerase (crotonase);   |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 28 | <a href="#">c347A</a>   | Alignment | not modelled | 100.0 | 29 | <b>PDBTitle:</b> crystal structure of putative enoyl coa hydratase/isomerase2 (crotonase) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1  |
| 29 | <a href="#">d1uiya</a>  | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 30 | <a href="#">c3trrA</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus                    |
| 31 | <a href="#">c4lk5B</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from mycobacterium avium2 subsp. paratuberculosis k-10                                     |
| 32 | <a href="#">d1wz8a1</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 33 | <a href="#">d2fw2a1</a> | Alignment | not modelled | 100.0 | 20 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 34 | <a href="#">c2d3tB</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> lyase, oxidoreductase/transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty oxidation complex alpha subunit;<br><b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v           |
| 35 | <a href="#">c2x58B</a>  | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme;<br><b>PDBTitle:</b> the crystal structure of mfe1 liganded with coa  |
| 36 | <a href="#">c3t88A</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> lyase/lyase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase;<br><b>PDBTitle:</b> crystal structure of escherichia coli menb in complex with substrate2 analogue, osb-ncoa           |
| 37 | <a href="#">c5wybB</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> structure of pseudomonas aeruginosa dspi   |
| 38 | <a href="#">c4nekD</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/carnithine racemase;<br><b>PDBTitle:</b> putative enoyl-coa hydratase/carnithine racemase from magnetospirillum2 magneticum amb-1                      |
| 39 | <a href="#">c2fbmB</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> y chromosome chromodomain protein 1, telomeric isoform b;<br><b>PDBTitle:</b> acetyltransferase domain of cdy1                                 |
| 40 | <a href="#">c5ve2j</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> isomerase,lyase<br><b>Chain:</b> J: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase from2 pseudoalteromonas atlantica t6c at 2.3 a resolution.               |
| 41 | <a href="#">d1dcia</a>  | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 42 | <a href="#">c3p5mB</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium   |
| 43 | <a href="#">c3rsiA</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196 |
| 44 | <a href="#">c3lkeA</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from bacillus halodurans   |
| 45 | <a href="#">c4olqD</a>  | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;<br><b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase family2 protein from hyphomonas neptunium      |
| 46 | <a href="#">c4k2nA</a>  | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/carnithine racemase;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/ carnithine racemase from2 magnetospirillum magneticum            |
| 47 | <a href="#">c2iexA</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxynaphthoic acid synthetase;<br><b>PDBTitle:</b> crystal structure of dihydroxynaphthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426                 |
| 48 | <a href="#">c4fzwD</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> isomerase/lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 1,2-epoxyphenylacetyl-coa isomerase;<br><b>PDBTitle:</b> crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli                                 |
| 49 | <a href="#">c3q1tB</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium avium   |
| 50 | <a href="#">c3swwB</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus                    |
| 51 | <a href="#">c3gkbA</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis           |
| 52 | <a href="#">d2f6qa1</a> | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 53 | <a href="#">c4q1jA</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyketide biosynthesis enoyl-coa isomerase pksi;<br><b>PDBTitle:</b> structure and mechanism of a dehydratase/decarboxylase enzyme couple2 involved in polyketide             |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
|    |                         |           |              |       |    | beta-branching   |
| 54 | <a href="#">c3bptA</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyryl-coa hydrolase;<br><b>PDBTitle:</b> crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin  |
| 55 | <a href="#">c4jylE</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> lyase<br><b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from thermoplasma volcanium2 gss1  |
| 56 | <a href="#">c2f6qA</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal 3,2-trans-enoyl-coa isomerase;<br><b>PDBTitle:</b> the crystal structure of human peroxisomal delta3, delta2 enoyl coa2 isomerase (peci)   |
| 57 | <a href="#">c3rrvC</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis  |
| 58 | <a href="#">c4hdtA</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyryl-coa hydrolase;<br><b>PDBTitle:</b> crystal structure of a carnitiny-coa dehydratase from mycobacterium2 thermoresistibile  |
| 59 | <a href="#">c4og1A</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444   |
| 60 | <a href="#">c4j2uA</a>  | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase from rhodobacter2 sphaeroides 2.4.1   |
| 61 | <a href="#">c3h0uB</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis   |
| 62 | <a href="#">c4izbB</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;<br><b>PDBTitle:</b> crystal structure of dmdd, a crotonase superfamily enzyme that2 catalyzes the hydration and hydrolysis of methylthioacryloyl-coa |
| 63 | <a href="#">c3njbA</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak   |
| 64 | <a href="#">c3ju1A</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> lyase, isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase family protein   |
| 65 | <a href="#">d1q52a</a>  | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 66 | <a href="#">c3qxzA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> lyase, isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus  |
| 67 | <a href="#">c3qxiA</a>  | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa1;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum  |
| 68 | <a href="#">c3r0oA</a>  | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> carnitiny-coa dehydratase;<br><b>PDBTitle:</b> crystal structure of carnitiny-coa hydratase from mycobacterium avium   |
| 69 | <a href="#">c4i4zE</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> E: <b>PDB Molecule:</b> naphthoate synthase;<br><b>PDBTitle:</b> synechocystis sp. pcc 6803 1,4-dihydroxy-2-naphthoyl-coenzyme a2 synthase (menb) in complex with salicylyl-coa  |
| 70 | <a href="#">c3l3sF</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> isomerase<br><b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydrotase/isomerase family2 protein from silicibacter pomeroyi                                 |
| 71 | <a href="#">c2wtbA</a>  | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atmfp2);<br><b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2   |
| 72 | <a href="#">c4mouA</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase family member,2 nysgrc target 028282                                       |
| 73 | <a href="#">c4b3hA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase, transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid beta-oxidation complex alpha-chain fadB;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis fatty acid2 beta-oxidation complex                       |
| 74 | <a href="#">c4f47A</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa19;<br><b>PDBTitle:</b> the structure of enoyl-coa hydratase echa19 from mycobacterium marinum   |
| 75 | <a href="#">c4jwvA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short chain enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of putative short chain enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444                                     |
| 76 | <a href="#">c5yloA</a>  | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> structural of pseudomonas aeruginosa pa4980  |
| 77 | <a href="#">d1sg4a1</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |

|     |                         |           |              |       |    |  |
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| 78  | <a href="#">c4k3wA</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 marinobacter aquaeolei  |
| 79  | <a href="#">c5xzdF</a>  | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> lyase<br><b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> structure of acryloyl-coa hydratase acuh from roseovarius nubinhibens2 ism  |
| 80  | <a href="#">c4jvtA</a>  | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of tfu_1878, a putative enoyl-coa hydratase2 fromthermobifida fusca yx in complex with coa                                  |
| 81  | <a href="#">c3sllC</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus                            |
| 82  | <a href="#">c3tlfF</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> isomerase<br><b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis                                      |
| 83  | <a href="#">c4kpkA</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from shewanella pealeana2 atcc 700345  |
| 84  | <a href="#">c2q35A</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> curf;<br><b>PDBTitle:</b> crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula   |
| 85  | <a href="#">c6ojmB</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase;<br><b>PDBTitle:</b> crystal structure of 1,4-dihydroxy-2-naphthoyl-coa synthase2 elizabethkingia anophelis nuhp1                               |
| 86  | <a href="#">d1ef8a</a>  | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 87  | <a href="#">d1pjha</a>  | Alignment | not modelled | 100.0 | 15 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 88  | <a href="#">c3r6hA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, echa3;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum  |
| 89  | <a href="#">c3qkaB</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase, echa5;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa5 from mycobacterium2 marinum   |
| 90  | <a href="#">c3oc7A</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase from mycobacterium avium  |
| 91  | <a href="#">c3ot6A</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase family protein2 from psudomonas syringae                   |
| 92  | <a href="#">c2j5fF</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> lyase<br><b>Chain:</b> F: <b>PDB Molecule:</b> p-hydroxycinnamoyl coa hydratase/lyase;<br><b>PDBTitle:</b> crystal structure of hydroxycinnamoyl-coa hydratase-lyase  |
| 93  | <a href="#">d2a7ka1</a> | Alignment | not modelled | 100.0 | 27 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 94  | <a href="#">c4jotA</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, putative;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydrotase from deinococcus radiodurans2 r1   |
| 95  | <a href="#">c6iunB</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/delta(3)-cis-delta(2)-trans-enoyl-coa<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase (ech) from ralstonia eutropha2 h16 in complex with nad |
| 96  | <a href="#">c3p85A</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure enoyl-coa hydratase from mycobacterium avium  |
| 97  | <a href="#">d1szoa</a>  | Alignment | not modelled | 100.0 | 16 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 98  | <a href="#">c4nngB</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative enoyl-coa hydratase;<br><b>PDBTitle:</b> crystal structure of lnmf protein from streptomyces amphibiosporus   |
| 99  | <a href="#">c4jyJA</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans dsm 12444                     |
| 100 | <a href="#">c3he2C</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase echa6;<br><b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis   |
| 101 | <a href="#">c3isaA</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis                             |
| 102 | <a href="#">c4k29A</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;<br><b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 xanthobacter autotrophicus py2                                      |
|     |                         |           |              |       |    | <b>PDB header:</b> lyase   |



|     |                         |           |              |       |    |  |
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| 103 | <a href="#">c3h02F_</a> | Alignment | not modelled | 100.0 | 27 | <b>Chain:</b> F; <b>PDB Molecule:</b> naphthoate synthase; <b>PDBTitle:</b> 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.  |
| 104 | <a href="#">c4wczB_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B; <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans    |
| 105 | <a href="#">c3laoA_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> lyase, isomerase<br><b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from pseudomonas2 aeruginosa pa01                      |
| 106 | <a href="#">c3fduF_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> isomerase<br><b>Chain:</b> F; <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii   |
| 107 | <a href="#">c2w3pB_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> benzoyl-coa-dihydrodiol lyase; <b>PDBTitle:</b> boxc crystal structure   |
| 108 | <a href="#">c5fusB_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> putative enoyl coa hydratase; <b>PDBTitle:</b> crystal structure of b. cenocepacia dfsa  |
| 109 | <a href="#">c3hp0B_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> putative polyketide biosynthesis enoyl-coa hydratase (pksh) from bacillus subtilis   |
| 110 | <a href="#">c5zqzC_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> lyase,hydrolase/transferase<br><b>Chain:</b> C; <b>PDB Molecule:</b> trifunctional enzyme subunit alpha, mitochondrial; <b>PDBTitle:</b> structure of human mitochondrial trifunctional protein, tetramer |
| 111 | <a href="#">c3omeE_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> lyase<br><b>Chain:</b> E; <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis                                    |
| 112 | <a href="#">c1rjnC_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> lyase<br><b>Chain:</b> C; <b>PDB Molecule:</b> menb; <b>PDBTitle:</b> the crystal structure of menb (rv0548c) from mycobacterium2 tuberculosis in complex with the coa portion of naphthoyl coa           |
| 113 | <a href="#">c3m6nA_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> rpff protein; <b>PDBTitle:</b> crystal structure of rpff   |
| 114 | <a href="#">d1rjma_</a> | Alignment | not modelled | 100.0 | 20 | <b>Fold:</b> ClpP/crotonase<br><b>Superfamily:</b> ClpP/crotonase<br><b>Family:</b> Crotonase-like   |
| 115 | <a href="#">c4kd6A_</a> | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase/isomerase from burkholderia2 graminis c4d1m                 |
| 116 | <a href="#">c2j5gL_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> L; <b>PDB Molecule:</b> alr4455 protein; <b>PDBTitle:</b> the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120                     |
| 117 | <a href="#">c2pg8C_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> ligand binding protein<br><b>Chain:</b> C; <b>PDB Molecule:</b> dpgc; <b>PDBTitle:</b> crystal structure of r254k mutant of dpgc with bound substrate analog  |
| 118 | <a href="#">c3qreA_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase, echa12_1; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase echa12_1 from2 mycobacterium marinum                           |
| 119 | <a href="#">c3qmjA_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase, echa8_6; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa8_6 from mycobacterium2 marinum                                |
| 120 | <a href="#">c5o34C_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> lyase<br><b>Chain:</b> C; <b>PDB Molecule:</b> enoyl-coa hydratase carb homologue; <b>PDBTitle:</b> thne from s.clavuligerus  |