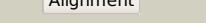
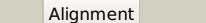
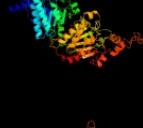
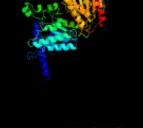
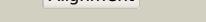
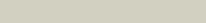
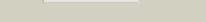
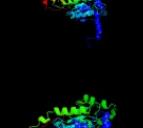
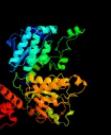
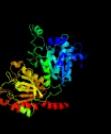


Phyre²

| | |
|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3799c_(accD4)_4254558_4256126 |
| Date | Fri Aug 9 18:20:50 BST 2019 |
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Detailed template information

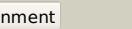
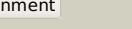
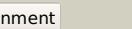
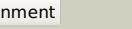
| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c1xnwD_ |  |  | 100.0 | 50 | PDB header: ligase Chain: D: PDB Molecule: propionyl-coa carboxylase complex b subunit; PDBTitle: acyl-coa carboxylase beta subunit from s. coelicolor (pccb),2 apo form #2, mutant d422i |
| 2 | c1on3E_ |  |  | 100.0 | 46 | PDB header: transferase Chain: E: PDB Molecule: methylmalonyl-coa carboxyltransferase 12s PDBTitle: transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound) |
| 3 | c2a7sD_ |  |  | 100.0 | 49 | PDB header: ligase Chain: D: PDB Molecule: probable propionyl-coa carboxylase beta chain 5; PDBTitle: crystal structure of the acyl-coa carboxylase, accd5, from2 mycobacterium tuberculosis |
| 4 | c1x0uB_ |  |  | 100.0 | 44 | PDB header: lyase Chain: B: PDB Molecule: hypothetical methylmalonyl-coa decarboxylase alpha subunit; PDBTitle: crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfobolus tokodaii |
| 5 | c5ingC_ |  |  | 100.0 | 48 | PDB header: transferase Chain: C: PDB Molecule: putative carboxyl transferase; PDBTitle: a crotonyl-coa reductase-carboxylase independent pathway for assembly2 of unusual alkylmalonyl-coa polyketide synthase extender unit |
| 6 | c1vrgE_ |  |  | 100.0 | 45 | PDB header: ligase Chain: E: PDB Molecule: propionyl-coa carboxylase, beta subunit; PDBTitle: crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution |
| 7 | c3n6rF_ |  |  | 100.0 | 47 | PDB header: ligase Chain: F: PDB Molecule: propionyl-coa carboxylase, beta subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc) |
| 8 | c3u9rB_ |  |  | 100.0 | 30 | PDB header: ligase Chain: B: PDB Molecule: methylcrotonyl-coa carboxylase, beta-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc), beta subunit |
| 9 | c4q0gC_ |  |  | 100.0 | 31 | PDB header: ligase Chain: C: PDB Molecule: probable acetyl-/propionyl-coa carboxylase (beta subunit) PDBTitle: crystal structure of beta subunit of acyl-coa carboxylase accd1 from2 mycobacterium tuberculosis |
| 10 | c5fifD_ |  |  | 100.0 | 28 | PDB header: ligase Chain: D: PDB Molecule: carboxylase; PDBTitle: carboxyltransferase domain of a single-chain bacterial carboxylase |
| 11 | c5iklD_ |  |  | 100.0 | 28 | PDB header: ligase Chain: D: PDB Molecule: geranyl-coa carboxylase, beta-subunit; PDBTitle: crystal structure of p. aeruginosa geranyl-coa carboxylase (gcc), beta2 subunit |

| | | | | | | |
|----|------------------------|-----------|---|-------|----|--|
| 12 | c4rcnA | Alignment |  | 100.0 | 29 | PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase |
| 13 | c1pixB | Alignment |  | 100.0 | 24 | PDB header: lyase Chain: B: PDB Molecule: glutaconyl-coa decarboxylase a subunit; PDBTitle: crystal structure of the carboxyltransferase subunit of the bacterial ion pump glutaconyl-coenzyme a decarboxylase |
| 14 | c3glmD | Alignment |  | 100.0 | 22 | PDB header: lyase Chain: D: PDB Molecule: glutaconyl-coa decarboxylase subunit a; PDBTitle: glutaconyl-coa decarboxylase a subunit from clostridium symbiosum co-2 crystallized with crotonyl-coa |
| 15 | c4l6wB | Alignment |  | 100.0 | 35 | PDB header: ligase Chain: B: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase |
| 16 | c4l6wA | Alignment |  | 100.0 | 38 | PDB header: ligase Chain: A: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase |
| 17 | c4wyob | Alignment |  | 100.0 | 19 | PDB header: ligase/ligase inhibitor Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of human-yeast chimera acetyl coa carboxylase ct2 domain bound to compound 1 |
| 18 | c3h0jA | Alignment |  | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2 |
| 19 | c1uyvB | Alignment |  | 100.0 | 19 | PDB header: transferase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain l1705i/2 v1967i mutant |
| 20 | c2x24B | Alignment |  | 100.0 | 24 | PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor |
| 21 | c1od4C | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain |
| 22 | c3ff6D | Alignment | not modelled | 100.0 | 23 | PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186 |
| 23 | c1uytC | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: C: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain |
| 24 | c5i6fA | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase |
| 25 | c5i6fB | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase |
| 26 | c5i6hA | Alignment | not modelled | 100.0 | 20 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of cd-ct domains of chaetomium thermophilum acetyl-2 coa carboxylase |
| 27 | c5cskB | Alignment | not modelled | 100.0 | 19 | PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated |
| 28 | c6g2dC | Alignment | not modelled | 100.0 | 22 | PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution |
| | | | | | | PDB header: ligase |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | c5csIA | Alignment | not modelled | 100.0 | 20 | Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer |
| 30 | d1xnya1 | Alignment | not modelled | 100.0 | 54 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 31 | d2a7sa1 | Alignment | not modelled | 100.0 | 49 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 32 | d1on3a1 | Alignment | not modelled | 100.0 | 46 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 33 | d1pixa3 | Alignment | not modelled | 100.0 | 24 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 34 | d1on3a2 | Alignment | not modelled | 100.0 | 45 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 35 | d1vrga2 | Alignment | not modelled | 100.0 | 46 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 36 | d2a7sa2 | Alignment | not modelled | 100.0 | 48 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 37 | d1xnya2 | Alignment | not modelled | 100.0 | 48 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 38 | d1vrga1 | Alignment | not modelled | 100.0 | 45 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 39 | d1pixa2 | Alignment | not modelled | 100.0 | 22 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 40 | d2f9yb1 | Alignment | not modelled | 100.0 | 24 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 41 | c2f9yB | Alignment | not modelled | 100.0 | 24 | PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli |
| 42 | c5vipB | Alignment | not modelled | 100.0 | 26 | PDB header: transferase Chain: B: PDB Molecule: mdcd; PDBTitle: crystal structure of pseudomonas malonate decarboxylase mdcd-mdc2 hetero-dimer |
| 43 | d1uyra1 | Alignment | not modelled | 100.0 | 20 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 44 | d1uyra2 | Alignment | not modelled | 100.0 | 20 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 45 | c2f9iD | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus |
| 46 | d2f9ya1 | Alignment | not modelled | 100.0 | 25 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain |
| 47 | c2f9iC | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: C: PDB Molecule: acetyl-coenzyme a carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus |
| 48 | c5vj1M | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: M: PDB Molecule: mdce; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with coenzyme a |
| 49 | c4hnkl | Alignment | not modelled | 99.1 | 12 | PDB header: hydrolase Chain: I: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: crystal structure of an enzyme |
| 50 | c3bezC | Alignment | not modelled | 99.0 | 19 | PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppe),2 sement crystals |
| 51 | c3r6hA | Alignment | not modelled | 98.6 | 14 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase, echa3; PDBTitle: crystal structure of an enoyl-coa hydratase (ech3) from mycobacterium2 marinum |
| 52 | d2fw2a1 | Alignment | not modelled | 98.5 | 14 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 53 | d2f6ia1 | Alignment | not modelled | 98.5 | 19 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, Clp subunit |
| 54 | c4jfca | Alignment | not modelled | 98.5 | 10 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a enoyl-coa hydratase from polaromonas sp. js666 |
| 55 | c4fznd | Alignment | not modelled | 98.5 | 13 | PDB header: isomerase/lyase Chain: D: PDB Molecule: 1,2-epoxyphenylacetyl-coa isomerase; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 55 | c4izwd_ | Alignment | not modelled | 98.5 | 13 | PDBTitle: crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli PDB header: lyase Chain: B: PDB Molecule: 3-hydroxybutyryl-coa dehydratase; PDBTitle: crystal structure of liuc in complex with coenzyme a and malonic acid |
| 56 | c5jbxB_ | Alignment | not modelled | 98.4 | 12 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 57 | d1q52a_ | Alignment | not modelled | 98.4 | 15 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase from cupriavidus2 metallidurans ch34 |
| 58 | c4jcsA_ | Alignment | not modelled | 98.4 | 20 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 59 | d1wz8a1 | Alignment | not modelled | 98.4 | 13 | PDB header: isomerase Chain: A: PDB Molecule: peroxisomal 3,2-trans-enoyl-coa isomerase; PDBTitle: the crystal structure of human peroxisomal delta3, delta2 enoyl coa2 isomerase (peci) |
| 60 | c2f6qA_ | Alignment | not modelled | 98.4 | 12 | PDB header: lyase Chain: A: PDB Molecule: enoyl coa hydratase/isomerase (crotonase); PDBTitle: crystal structure of putative enoyl coa hydratase/isomerase2 (crotonase) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 |
| 61 | c3i47A_ | Alignment | not modelled | 98.4 | 13 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: y chromosome chromodomain protein 1, telomeric isoform b; PDBTitle: acetyltransferase domain of cdy1 |
| 62 | c2fbmB_ | Alignment | not modelled | 98.4 | 13 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 63 | d1uiya_ | Alignment | not modelled | 98.4 | 16 | PDB header: lyase Chain: D: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase family2 protein from hyphomonas neptunium |
| 64 | c4olqD_ | Alignment | not modelled | 98.4 | 17 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 65 | d1xx4a_ | Alignment | not modelled | 98.4 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: 3-hydroxypropionyl-coenzyme a dehydratase; PDBTitle: crystal strcuture of 3-hydroxypropionyl-coa dehydratase from2 metallosphaera sedula |
| 66 | c5zaiB_ | Alignment | not modelled | 98.4 | 12 | PDB header: hydrolase Chain: G: PDB Molecule: atp-dependent clp protease, putative; PDBTitle: crystal structure of the clpp protease catalytic domain from2 plasmodium falciparum |
| 67 | c2f6iG_ | Alignment | not modelled | 98.3 | 17 | PDB header: isomerase Chain: D: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of enoyl-coa hydratase from bacillus anthracis str.2 'ames ancestor' |
| 68 | c3peaD_ | Alignment | not modelled | 98.3 | 14 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 69 | d1nzya_ | Alignment | not modelled | 98.3 | 15 | PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans dsm 12444 |
| 70 | c4jyjA_ | Alignment | not modelled | 98.3 | 16 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 71 | d1rjma_ | Alignment | not modelled | 98.3 | 18 | PDB header: lyase Chain: A: PDB Molecule: short-chain-enoyl-coa hydratase; PDBTitle: crystal strcture of crotonase from clostridium acetobutylicum |
| 72 | c5z7ra_ | Alignment | not modelled | 98.3 | 12 | PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a enoyl-coa hydratase from shewanella pealeana2 atcc 700345 |
| 73 | c4kpkA_ | Alignment | not modelled | 98.3 | 22 | PDB header: isomerase Chain: D: PDB Molecule: enoyl-coa hydratase domain-containing protein 3; PDBTitle: crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3) |
| 74 | c2vx2D_ | Alignment | not modelled | 98.3 | 10 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, Clp subunit |
| 75 | d1yg6a1 | Alignment | not modelled | 98.3 | 14 | PDB header: isomerase Chain: C: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis |
| 76 | c3rrvC_ | Alignment | not modelled | 98.3 | 13 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, Clp subunit |
| 77 | d2cbya1 | Alignment | not modelled | 98.3 | 18 | PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a enoyl-coa hydratase from mycobacterium avium2 subsp. paratuberculosis k-10 |
| 78 | c4lk5B_ | Alignment | not modelled | 98.3 | 18 | PDB header: isomerase Chain: F: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa |
| 79 | c3fdudF | Alignment | not modelled | 98.3 | 17 | |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | hydratase/isomerase from2 acinetobacter baumannii |
| 80 | d2f6qa1 | Alignment | not modelled | 98.3 | 11 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 81 | c1y7oE | Alignment | not modelled | 98.3 | 18 | PDB header: hydrolase Chain: E: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: the structure of streptococcus pneumoniae a153p clpp |
| 82 | c3isaA | Alignment | not modelled | 98.2 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis |
| 83 | c3p2ID | Alignment | not modelled | 98.2 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: crystal structure of atp-dependent clp protease subunit p from2 francisella tularensis |
| 84 | c4jcqU | Alignment | not modelled | 98.2 | 10 | PDB header: hydrolase Chain: U: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: clpp1 from listeria monocytogenes |
| 85 | c4izbB | Alignment | not modelled | 98.2 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of dmdd, a crotonase superfamily enzyme that2 catalyzes the hydration and hydrolysis of methylthioacryloyl-coa |
| 86 | c3p5mB | Alignment | not modelled | 98.2 | 19 | PDB header: isomerase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium |
| 87 | c4di1A | Alignment | not modelled | 98.2 | 13 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase echa17; PDBTitle: crystal structure of enoyl-coa hydratase echa17 from mycobacterium2 marinum |
| 88 | c2ej5B | Alignment | not modelled | 98.2 | 14 | PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase subunit ii; PDBTitle: crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus |
| 89 | c4jvtA | Alignment | not modelled | 98.2 | 15 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of tfu_1878, a putative enoyl-coa hydratase2 fromthermobifida fusca yx in complex with coa |
| 90 | c2d3tB | Alignment | not modelled | 98.2 | 12 | PDB header: lyase, oxidoreductase/transferase Chain: B: PDB Molecule: fatty acid beta-oxidation complex alpha subunit; PDBTitle: fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v |
| 91 | c3q1tB | Alignment | not modelled | 98.2 | 16 | PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from mycobacterium avium |
| 92 | c4jyIE | Alignment | not modelled | 98.2 | 14 | PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from thermoplasma volcanium2 gss1 |
| 93 | c5yloA | Alignment | not modelled | 98.2 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: structural of pseudomonas aeruginosa pa4980 |
| 94 | c4kd6A | Alignment | not modelled | 98.2 | 20 | PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a enoyl-coa hydratase/isomerase from burkholderia2 graminis c4d1m |
| 95 | c3oc7A | Alignment | not modelled | 98.2 | 15 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of an enoyl-coa hydratase from mycobacterium avium |
| 96 | c3q7hM | Alignment | not modelled | 98.2 | 15 | PDB header: hydrolase Chain: M: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: structure of the clpp subunit of the atp-dependent clp protease from2 coxiella burnetii |
| 97 | c4k2nA | Alignment | not modelled | 98.2 | 12 | PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/carnithine racemase; PDBTitle: crystal structure of an enoyl-coa hydratase/ carnithine racemase from2 magnetospirillum magneticum |
| 98 | d1y7oa1 | Alignment | not modelled | 98.2 | 18 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit |
| 99 | c4nekD | Alignment | not modelled | 98.2 | 19 | PDB header: isomerase Chain: D: PDB Molecule: enoyl-coa hydratase/carnithine racemase; PDBTitle: putative enoyl-coa hydratase/carnithine racemase from magnetospirillum2 magneticum amb-1 |
| 100 | c2q35A | Alignment | not modelled | 98.2 | 10 | PDB header: lyase Chain: A: PDB Molecule: curf; PDBTitle: crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula |
| 101 | d1wdka4 | Alignment | not modelled | 98.2 | 13 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 102 | c2cbyG | Alignment | not modelled | 98.1 | 18 | PDB header: hydrolase Chain: G: PDB Molecule: atp-dependent clp protease proteolytic subunit 1; PDBTitle: crystal structure of the atp-dependent clp protease proteolytic2 subunit 1 (clpp1) from mycobacterium tuberculosis |
| 103 | c3g64A | Alignment | not modelled | 98.1 | 18 | PDB header: lyase Chain: A: PDB Molecule: putative enoyl-coa hydratase; PDBTitle: crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2) |
| 104 | d2a7ka1 | Alignment | not modelled | 98.1 | 14 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase |

| | | | | | | Family: Crotonase-like |
|-----|-------------------------|---|-----------|--------------|------|---|
| 105 | c3hrxD_ |  | Alignment | not modelled | 98.1 | 15 PDB header: lyase Chain: D; PDB Molecule: probable enoyl-coa hydratase; PDBTitle: crystal structure of phenylacetic acid degradation protein paag |
| 106 | c3hinA_ |  | Alignment | not modelled | 98.1 | 12 PDB header: lyase Chain: A; PDB Molecule: putative 3-hydroxybutyryl-coa dehydratase; PDBTitle: crystal structure of putative enoyl-coa hydratase from2 rhodopseudomonas palustris cga009 |
| 107 | c4og1A_ |  | Alignment | not modelled | 98.1 | 14 PDB header: lyase Chain: A; PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444 |
| 108 | d1piha_ |  | Alignment | not modelled | 98.1 | 14 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 109 | c3lkeA_ |  | Alignment | not modelled | 98.1 | 14 PDB header: lyase Chain: A; PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from bacillus halodurans |
| 110 | d1dcia_ |  | Alignment | not modelled | 98.1 | 16 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 111 | c2iexA_ |  | Alignment | not modelled | 98.1 | 12 PDB header: lyase Chain: A; PDB Molecule: dihydroxynapthoic acid synthetase; PDBTitle: crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426 |
| 112 | c3kqfC_ |  | Alignment | not modelled | 98.1 | 12 PDB header: isomerase Chain: C; PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: 1.8 angstrom resolution crystal structure of enoyl-coa hydratase from2 bacillus anthracis. |
| 113 | c3omeE_ |  | Alignment | not modelled | 98.1 | 11 PDB header: lyase Chain: E; PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis |
| 114 | c5wybB_ |  | Alignment | not modelled | 98.1 | 17 PDB header: isomerase Chain: B; PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: structure of pseudomonas aeruginosa dspi |
| 115 | c2ppyE_ |  | Alignment | not modelled | 98.1 | 20 PDB header: lyase Chain: E; PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426 |
| 116 | c3ot6A_ |  | Alignment | not modelled | 98.1 | 12 PDB header: isomerase Chain: A; PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase family protein2 from psudomonas syringae |
| 117 | c2j5iF_ |  | Alignment | not modelled | 98.0 | 15 PDB header: lyase Chain: F; PDB Molecule: p-hydroxycinnamoyl coa hydratase/lyase; PDBTitle: crystal structure of hydroxycinnamoyl-coa hydratase-lyase |
| 118 | c3h02F_ |  | Alignment | not modelled | 98.0 | 11 PDB header: lyase Chain: F; PDB Molecule: naphthoate synthase; PDBTitle: 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium. |
| 119 | d1sg4a1 |  | Alignment | not modelled | 98.0 | 13 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 120 | c3t88A_ |  | Alignment | not modelled | 98.0 | 11 PDB header: lyase/lyase inhibitor Chain: A; PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa synthase; PDBTitle: crystal structure of escherichia coli membr in complex with substrate2 analogue, osb-ncoa |