
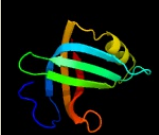
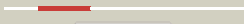
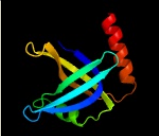

























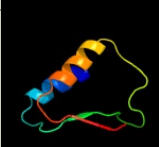



Phyre2

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|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1108c_(xseA)_1234218_1235465 |
| Date | Wed Jul 31 22:05:19 BST 2019 |
| Unique Job ID | b46ff0e5fe02e042 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3f2cA_ |  Alignment |  | 97.1 | 13 | PDB header: transferase/dna Chain: A: PDB Molecule: geobacillus kaustophilus dna polc; PDBTitle: dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn |
| 2 | c3kf6A_ |  Alignment |  | 97.1 | 13 | PDB header: structural protein Chain: A: PDB Molecule: protein stn1; PDBTitle: crystal structure of s. pombe stn1-ten1 complex |
| 3 | c4gopB_ |  Alignment |  | 96.8 | 19 | PDB header: dna binding protein/dna Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna |
| 4 | c6i52B_ |  Alignment |  | 96.7 | 17 | PDB header: dna binding protein Chain: B: PDB Molecule: replication factor a protein 2; PDBTitle: yeast rpa bound to ssdna |
| 5 | c4joiA_ |  Alignment |  | 96.5 | 16 | PDB header: dna binding protein Chain: A: PDB Molecule: cst complex subunit stn1; PDBTitle: crystal structure of the human telomeric stn1-ten1 complex |
| 6 | d1l0wa1 |  Alignment |  | 96.1 | 20 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 7 | d1c0aa1 |  Alignment |  | 96.0 | 17 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 8 | c3zdrA_ |  Alignment |  | 96.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase domain of the bifunctional PDBTitle: structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3 thermoglucosidasius ncimb 11955 |
| 9 | c3bfjK_ |  Alignment |  | 95.9 | 24 | PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase |
| 10 | d1vlja_ |  Alignment |  | 95.8 | 27 | Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase |
| 11 | c3ox4D_ |  Alignment |  | 95.5 | 26 | PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | c5groA_ | Alignment |  | 95.4 | 22 | PDB header: ligase Chain: A: PDB Molecule: aspartate--trna(asp/asn) ligase; PDBTitle: crystal structure of the n-terminal anticodon-binding domain of non-2 discriminating aspartyl-trna synthetase from helicobacter pylori |
| 13 | d1e1oa1 | Alignment |  | 95.4 | 24 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 14 | c3okfA_ | Alignment |  | 95.3 | 16 | PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae |
| 15 | d1n9wa1 | Alignment |  | 95.3 | 17 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 16 | d1oj7a_ | Alignment |  | 95.2 | 24 | Fold: Dehydroquinate synthase-like Superfamily: Dehydroquinate synthase-like Family: Iron-containing alcohol dehydrogenase |
| 17 | c5fkvA_ | Alignment |  | 95.2 | 14 | PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex) |
| 18 | d1gm5a2 | Alignment |  | 95.0 | 18 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain |
| 19 | c3fduF_ | Alignment |  | 94.8 | 30 | PDB header: isomerase Chain: F: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii |
| 20 | d1rrma_ | Alignment |  | 94.7 | 26 | Fold: Dehydroquinate synthase-like Superfamily: Dehydroquinate synthase-like Family: Iron-containing alcohol dehydrogenase |
| 21 | c3e0eA_ | Alignment | not modelled | 94.7 | 13 | PDB header: replication Chain: A: PDB Molecule: replication protein a; PDBTitle: crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targ mrr110b |
| 22 | c5eksB_ | Alignment | not modelled | 94.6 | 17 | PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: structure of 3-dehydroquinate synthase from acinetobacter baumannii in2 complex with nad |
| 23 | d1bbua1 | Alignment | not modelled | 94.5 | 25 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 24 | d1o2da_ | Alignment | not modelled | 94.5 | 24 | Fold: Dehydroquinate synthase-like Superfamily: Dehydroquinate synthase-like Family: Iron-containing alcohol dehydrogenase |
| 25 | d1jq5a_ | Alignment | not modelled | 94.4 | 15 | Fold: Dehydroquinate synthase-like Superfamily: Dehydroquinate synthase-like Family: Iron-containing alcohol dehydrogenase |
| 26 | c6c76A_ | Alignment | not modelled | 94.4 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioreducens in an orthorhombic crystal form |
| 27 | c1z9fA_ | Alignment | not modelled | 94.3 | 14 | PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution |
| 28 | c5zxID_ | Alignment | not modelled | 94.2 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli |
| 29 | c2xtB_ | Alignment | not modelled | 94.1 | 12 | PDB header: ligase Chain: B: PDB Molecule: asparaginyl-trna synthetase, cytoplasmic; |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c2ygtb_ | Alignment | not modelled | 94.1 | 12 | PDBTitle: asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate |
| 30 | c2pi2A_ | Alignment | not modelled | 94.0 | 17 | PDB header: replication, dna binding protein Chain: A: PDB Molecule: replication protein a 32 kda subunit; PDBTitle: full-length replication protein a subunits rpa14 and rpa32 |
| 31 | d1ujna_ | Alignment | not modelled | 94.0 | 15 | Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS |
| 32 | c3jzdA_ | Alignment | not modelled | 94.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution |
| 33 | c5yvma_ | Alignment | not modelled | 94.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq |
| 34 | c3qviB_ | Alignment | not modelled | 94.0 | 23 | PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae |
| 35 | d1b8aa1 | Alignment | not modelled | 94.0 | 19 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 36 | d2pi2a1 | Alignment | not modelled | 93.9 | 16 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB |
| 37 | c3moyA_ | Alignment | not modelled | 93.8 | 25 | PDB header: lyase Chain: A: PDB Molecule: probable enoyl-coa hydratase; PDBTitle: crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis |
| 38 | c3gizB_ | Alignment | not modelled | 93.8 | 17 | PDB header: immune system Chain: B: PDB Molecule: microcin immunity protein mccf; PDBTitle: crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames |
| 39 | c4fr2A_ | Alignment | not modelled | 93.7 | 20 | PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni |
| 40 | c1eqrC_ | Alignment | not modelled | 93.6 | 17 | PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli |
| 41 | c3bjuB_ | Alignment | not modelled | 93.5 | 17 | PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna synthetase |
| 42 | d2nu7b1 | Alignment | not modelled | 93.5 | 25 | Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains |
| 43 | c3gkbA_ | Alignment | not modelled | 93.5 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative enoyl-coa hydratase; PDBTitle: crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis |
| 44 | c2qq3F_ | Alignment | not modelled | 93.4 | 30 | PDB header: lyase Chain: F: PDB Molecule: enoyl-coa hydratase subunit i; PDBTitle: crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426 |
| 45 | c4nnqB_ | Alignment | not modelled | 93.3 | 26 | PDB header: lyase Chain: B: PDB Molecule: putative enoyl-coa hydratase; PDBTitle: crystal structure of lnmf protein from streptomyces amphibiosporus |
| 46 | c4gn5A_ | Alignment | not modelled | 93.2 | 19 | PDB header: de novo protein/hydrolase Chain: A: PDB Molecule: obody am3115; PDBTitle: obody am3115 bound to hen egg-white lysozyme |
| 47 | c4mcaB_ | Alignment | not modelled | 93.1 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a |
| 48 | c6csjD_ | Alignment | not modelled | 93.1 | 15 | PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of a bacillus coagulans polyol dehydrogenase double mutant2 with an acquired d-lactate dehydrogenase activity |
| 49 | c4fzwa_ | Alignment | not modelled | 93.1 | 26 | PDB header: isomerase/lyase Chain: A: PDB Molecule: 2,3-dehydroadipyl-coa hydratase; PDBTitle: crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli |
| 50 | c3hl0B_ | Alignment | not modelled | 93.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens |
| 51 | c4jcsA_ | Alignment | not modelled | 93.0 | 25 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase from cupriavidus2 metallidurans ch34 |
| 52 | d1eova1 | Alignment | not modelled | 92.7 | 17 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain |
| 53 | c2vlbC_ | Alignment | not modelled | 92.6 | 19 | PDB header: lyase Chain: C: PDB Molecule: arylmalonate decarboxylase; PDBTitle: structure of unliganded arylmalonate decarboxylase |
| 54 | c4fzwd_ | Alignment | not modelled | 92.5 | 30 | PDB header: isomerase/lyase Chain: D: PDB Molecule: 1,2-epoxyphenylacetyl-coa isomerase; PDBTitle: crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli |
| 55 | c2ej5B_ | Alignment | not modelled | 92.5 | 30 | 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 |

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|----|-------------------------|-----------|--------------|------|----|--|
| 56 | c4e5sC | Alignment | not modelled | 92.4 | 20 | PDB header: hydrolase Chain: C: PDB Molecule: mcdflike protein (ba_5613); PDBTitle: crystal structure of mcdflike protein (ba_5613) from bacillus2 anthracis str. ames |
| 57 | c3mybA | Alignment | not modelled | 92.2 | 26 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase mycobacterium smegmatis |
| 58 | c3tlgB | Alignment | not modelled | 92.2 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: mcdf; PDBTitle: microcin c7 self immunity protein mddf in the inactive mutant apo2 state |
| 59 | d1q52a | Alignment | not modelled | 92.1 | 26 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 60 | c4owxB | Alignment | not modelled | 92.1 | 13 | PDB header: dna binding protein/dna Chain: B: PDB Molecule: soas complex subunit b1; PDBTitle: structural basis of soas1 in complex with a 12nt ssdna |
| 61 | c2x58B | Alignment | not modelled | 92.1 | 26 | PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: the crystal structure of mfe1 liganded with coa |
| 62 | d1uiva | Alignment | not modelled | 92.0 | 34 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 63 | c6jkdD | Alignment | not modelled | 91.9 | 20 | PDB header: oxidoreductase Chain: D: PDB Molecule: methanol dehydrogenase; PDBTitle: crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+ |
| 64 | c5o34C | Alignment | not modelled | 91.8 | 33 | PDB header: lyase Chain: C: PDB Molecule: enoyl-coa hydratase carb homologue; PDBTitle: thne from s.clavuligerus |
| 65 | c2lexA | Alignment | not modelled | 91.8 | 28 | PDB header: lyase Chain: A: PDB Molecule: dihydroxynaphthoic acid synthetase; PDBTitle: crystal structure of dihydroxynaphthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426 |
| 66 | c4k2nA | Alignment | not modelled | 91.7 | 30 | 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 |
| 67 | c2q35A | Alignment | not modelled | 91.5 | 17 | PDB header: lyase Chain: A: PDB Molecule: curf; PDBTitle: crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lynqbya majuscula |
| 68 | d1wdka4 | Alignment | not modelled | 91.5 | 19 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 69 | c2eq5D | Alignment | not modelled | 91.5 | 21 | PDB header: isomerase Chain: D: PDB Molecule: 228aa long hypothetical hydantoin racemase; PDBTitle: crystal structure of hydantoin racemase from pyrococcus horikoshii ot3 |
| 70 | c3lkeA | Alignment | not modelled | 91.4 | 19 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from bacillus halodurans |
| 71 | c1rjnC | Alignment | not modelled | 91.4 | 25 | PDB header: lyase Chain: C: PDB Molecule: menb; PDBTitle: the crystal structure of menb (rv0548c) from mycobacterium2 tuberculosis in complex with the coa portion of naphthoyl coa |
| 72 | c2ppyE | Alignment | not modelled | 91.3 | 15 | PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426 |
| 73 | c3h0uB | Alignment | not modelled | 91.3 | 17 | PDB header: lyase Chain: B: PDB Molecule: putative enoyl-coa hydratase; PDBTitle: crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis |
| 74 | c3h81A | Alignment | not modelled | 91.3 | 35 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase echa8; PDBTitle: crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis |
| 75 | c3hrxD | Alignment | not modelled | 91.2 | 24 | PDB header: lyase Chain: D: PDB Molecule: probable enoyl-coa hydratase; PDBTitle: crystal structure of phenylacetic acid degradation protein paag |
| 76 | c4wj4A | Alignment | not modelled | 91.2 | 16 | PDB header: ligase/rna Chain: A: PDB Molecule: aspartate--trna(asp/asn) ligase; PDBTitle: crystal structure of non-discriminating aspartyl-trna synthetase from2 pseudomonas aeruginosa complexed with trna(asn) and aspartic acid |
| 77 | d1szoa | Alignment | not modelled | 91.2 | 28 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 78 | c5jxbB | Alignment | not modelled | 91.1 | 24 | PDB header: lyase Chain: B: PDB Molecule: 3-hydroxybutyryl-coa dehydratase; PDBTitle: crystal structure of liuc in complex with coenzyme a and malonic acid |
| 79 | c3m4qA | Alignment | not modelled | 91.1 | 15 | PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase, putative; PDBTitle: entamoeba histolytica asparaginyl-trna synthetase (asnr5) |
| 80 | c1efwA | Alignment | not modelled | 91.1 | 20 | PDB header: ligase/rna Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli |
| 81 | c5vzrE | Alignment | not modelled | 91.0 | 23 | PDB header: lyase Chain: F: PDB Molecule: enoyl-coa hydratase; |

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|-----|--------------------------|-----------|--------------|------|----|--|
| 81 | c9azul_ | Alignment | not modelled | 91.0 | 25 | PDBTitle: structure of acryloyl-coa hydratase acuh from roseovarius nubinhibens2 ism |
| 82 | d1hzda_ | Alignment | not modelled | 91.0 | 26 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 83 | c2vx2D_ | Alignment | not modelled | 90.9 | 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) |
| 84 | c3rsiA_ | Alignment | not modelled | 90.9 | 22 | PDB header: isomerase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196 |
| 85 | c2fbmB_ | Alignment | not modelled | 90.8 | 25 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: y chromosome chromodomain protein 1, telomeric isoform b; PDBTitle: acetyltransferase domain of cdy1 |
| 86 | d2a7ka1_ | Alignment | not modelled | 90.8 | 26 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 87 | c3g64A_ | Alignment | not modelled | 90.7 | 35 | PDB header: lyase Chain: A: PDB Molecule: putative enoyl-coa hydratase; PDBTitle: crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2) |
| 88 | d1mj3a_ | Alignment | not modelled | 90.6 | 25 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 89 | c3e9hB_ | Alignment | not modelled | 90.6 | 24 | PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine |
| 90 | d1ef8a_ | Alignment | not modelled | 90.5 | 33 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 91 | c5elnC_ | Alignment | not modelled | 90.5 | 16 | PDB header: ligase Chain: C: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine |
| 92 | c4upaA_ | Alignment | not modelled | 90.3 | 17 | PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with ampnpn |
| 93 | c4p53A_ | Alignment | not modelled | 90.3 | 18 | PDB header: lyase Chain: A: PDB Molecule: cyclase; PDBTitle: vala (2-epi-5-epi-valiolone synthase) from streptomyces hygrosopicus2 subsp. jinggangensis 5008 with nad+ and zn2+ bound |
| 94 | c4zu2A_ | Alignment | not modelled | 90.2 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: putative isohexenylglutaconyl-coa hydratase; PDBTitle: pseudomonas aeruginosa atue |
| 95 | c3i7fA_ | Alignment | not modelled | 90.1 | 14 | PDB header: ligase Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: aspartyl trna synthetase from entamoeba histolytica |
| 96 | c4wczB_ | Alignment | not modelled | 90.1 | 33 | PDB header: isomerase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans |
| 97 | c3rstH_ | Alignment | not modelled | 90.0 | 20 | PDB header: hydrolase Chain: H: PDB Molecule: signal peptide peptidase sppa; PDBTitle: crystal structure of bacillus subtilis signal peptide peptidase a |
| 98 | c4jfcA_ | Alignment | not modelled | 89.9 | 28 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a enoyl-coa hydratase from polaromonas sp. js666 |
| 99 | c3iv7B_ | Alignment | not modelled | 89.9 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase iv; PDBTitle: crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution |
| 100 | c3omeE_ | Alignment | not modelled | 89.9 | 22 | PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis |
| 101 | d1nzya_ | Alignment | not modelled | 89.9 | 20 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 102 | c4i4zE_ | Alignment | not modelled | 89.9 | 30 | PDB header: lyase Chain: E: PDB Molecule: naphthoate synthase; PDBTitle: synechocystis sp. pcc 6803 1,4-dihydroxy-2-naphthoyl-coenzyme a2 synthase (menb) in complex with salicylyl-coa |
| 103 | c5ve2J_ | Alignment | not modelled | 89.7 | 28 | PDB header: isomerase,lyase Chain: J: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase from2 pseudoalteromonas atlantica t6c at 2.3 a resolution. |
| 104 | c2j5gL_ | Alignment | not modelled | 89.7 | 30 | PDB header: hydrolase Chain: L: PDB Molecule: alr4455 protein; PDBTitle: the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120 |
| 105 | c3ce9A_ | Alignment | not modelled | 89.5 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution |
| 106 | c3bptA_ | Alignment | not modelled | 89.5 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: 3-hydroxyisobutyryl-coa hydrolase; PDBTitle: crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 107 | d1jvna2 | Alignment | not modelled | 89.4 | 21 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT) |
| 108 | c1gm5A_ | Alignment | not modelled | 89.3 | 18 | PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction |
| 109 | c3peaD_ | Alignment | not modelled | 89.2 | 20 | 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' |
| 110 | c5z7rA_ | Alignment | not modelled | 89.1 | 20 | PDB header: lyase Chain: A: PDB Molecule: short-chain-enoyl-coa hydratase; PDBTitle: crystal strcture of crotonase from clostridium acetobutylicum |
| 111 | c5wybB_ | Alignment | not modelled | 89.1 | 20 | PDB header: isomerase Chain: B: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: structure of pseudomonas aeruginosa dspi |
| 112 | c4olqD_ | Alignment | not modelled | 89.1 | 26 | 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 |
| 113 | c4h02B_ | Alignment | not modelled | 89.1 | 14 | PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of p. falciparum lysyl-trna synthetase |
| 114 | c3zokB_ | Alignment | not modelled | 89.0 | 13 | PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinat synthase; PDBTitle: structure of 3-dehydroquinat synthase from actinidia chinensis in2 complex with nad |
| 115 | c4mi2C_ | Alignment | not modelled | 89.0 | 28 | PDB header: isomerase Chain: C: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus |
| 116 | d1rjma_ | Alignment | not modelled | 89.0 | 23 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 117 | c3njbA_ | Alignment | not modelled | 88.9 | 22 | PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak |
| 118 | d2fw2a1 | Alignment | not modelled | 88.9 | 23 | Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like |
| 119 | c4og1A_ | Alignment | not modelled | 88.9 | 30 | 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 |
| 120 | c1n9wA_ | Alignment | not modelled | 88.9 | 17 | PDB header: biosynthetic protein Chain: A: PDB Molecule: aspartyl-trna synthetase 2; PDBTitle: crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus |