







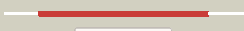
















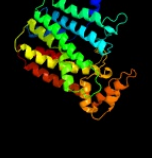
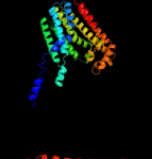
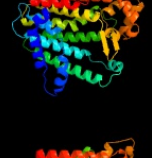
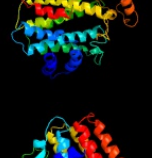

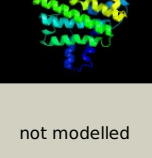


Phyre2

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 Date Fri Jul 26 01:50:11 BST 2019
 Unique Job ID f4679f0e317015d1

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c3mzvB_ |  Alignment |  | 100.0 | 32 | PDB header: transferase Chain: B: PDB Molecule: decaprenyl diphosphate synthase; PDBTitle: crystal structure of a decaprenyl diphosphate synthase from2 rhodobacter capsulatus |
| 2 | c3oyrB_ |  Alignment |  | 100.0 | 33 | PDB header: transferase Chain: B: PDB Molecule: trans-isoprenyl diphosphate synthase; PDBTitle: crystal structure of a polyprenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate |
| 3 | c1wy0A_ |  Alignment |  | 100.0 | 30 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthetase from2 pyrococcus horikoshii ot3 |
| 4 | c5h9dB_ |  Alignment |  | 100.0 | 29 | PDB header: transferase Chain: B: PDB Molecule: farnesyl pyrophosphate synthetase; PDBTitle: crystal structure of heptaprenyl diphosphate synthase from2 staphylococcus aureus |
| 5 | c3aqbD_ |  Alignment |  | 100.0 | 26 | PDB header: transferase Chain: D: PDB Molecule: component b of hexaprenyl diphosphate synthase; PDBTitle: m. luteus b-p 26 heterodimeric hexaprenyl diphosphate synthase in2 complex with magnesium |
| 6 | c3nf2A_ |  Alignment |  | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: putative polyprenyl synthetase; PDBTitle: crystal structure of polyprenyl synthetase from streptomyces2 coelicolor a3(2) |
| 7 | c4lobA_ |  Alignment |  | 100.0 | 28 | PDB header: transferase Chain: A: PDB Molecule: polyprenyl synthetase; PDBTitle: crystal structure of polyprenyl diphosphate synthase a1s_2732 (target2 efi-509223) from acinetobacter baumannii |
| 8 | c3wjnA_ |  Alignment |  | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: octaprenyl diphosphate synthase; PDBTitle: crystal structure of octaprenyl pyrophosphate synthase from2 escherichia coli with farnesyl s-thiol-pyrophosphate (fsp) |
| 9 | c3lmdA_ |  Alignment |  | 100.0 | 50 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from2 corynebacterium glutamicum atcc 13032 |
| 10 | c1wmwA_ |  Alignment |  | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl diphosphate synthetase; PDBTitle: crystal structure of geranylgeranyl diphosphate synthase from thermus2 thermophilus |
| 11 | c5jfqB_ |  Alignment |  | 100.0 | 30 | PDB header: oxidoreductase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl pyrophosphate synthetase from archaeon geoglobus2 acetivorans |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c3n3dB_ | Alignment |  | 100.0 | 24 | PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from <i>Lactobacillus brevis</i> atcc 367 |
| 13 | c4dhdA_ | Alignment |  | 100.0 | 28 | PDB header: transferase Chain: A: PDB Molecule: polyprenyl synthetase; PDBTitle: crystal structure of isoprenoid synthase a3msh1 (target efi-501992)2 from <i>Pyrobaculum calidifontis</i> |
| 14 | d1fpa_ | Alignment |  | 100.0 | 20 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 15 | c6b07B_ | Alignment |  | 100.0 | 18 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of cffpps2, a lepidopteran type-ii farnesyl2 diphosphate synthase, complexed with [1-phosphono-2-(1-propylpyridin-3-2-yl)ethyl]phosphonic acid (inhibitor 1d) |
| 16 | c3aq0G_ | Alignment |  | 100.0 | 31 | PDB header: transferase Chain: G: PDB Molecule: geranyl diphosphate synthase; PDBTitle: ligand-bound form of Arabidopsis medium/long-chain length prenyl2 pyrophosphate synthase (surface polar residue mutant) |
| 17 | c4jyxE_ | Alignment |  | 100.0 | 27 | PDB header: transferase Chain: E: PDB Molecule: trans-hexaprenyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase patl_3739 (target efi-509195)2 from <i>Pseudoalteromonas atlantica</i> , complex with inorganic phosphate3 and an unknown ligand |
| 18 | c3cp6A_ | Alignment |  | 100.0 | 18 | PDB header: transferase Chain: A: PDB Molecule: farnesyl pyrophosphate synthetase; PDBTitle: crystal structure of human farnesyl diphosphate synthase (t201a2 mutant) complexed with mg and bisphosphonate inhibitor |
| 19 | c3oacD_ | Alignment |  | 100.0 | 28 | PDB header: transferase Chain: D: PDB Molecule: geranyl diphosphate synthase large subunit; PDBTitle: mint deletion mutant of heterotetrameric geranyl pyrophosphate2 synthase in complex with ligands |
| 20 | c4kk2B_ | Alignment |  | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: monoterpene synthase fds-5, chloroplast - farnesyl PDBTitle: crystal structure of a chimeric fpp/gfpp synthase (target efi-502313c)2 from <i>Artemisia spiciformis</i> (1-72:gi751454468,73-346:gi75233326), apo3 structure |
| 21 | c4jzbA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: crystal structure of leishmaniasis major farnesyl diphosphate synthase2 in complex with 1-(2-hydroxy-2,2-diphosphonoethyl)-3-3 phenylpyridinium, ipp and ca2+ |
| 22 | c2f94F_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: F: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of human fpps in complex with ibandronate |
| 23 | d2q80a1 | Alignment | not modelled | 100.0 | 23 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 24 | c3rmgB_ | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: B: PDB Molecule: octaprenyl-diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from <i>Bacteroides thetaiotaomicron</i> |
| 25 | c3ez3A_ | Alignment | not modelled | 100.0 | 19 | PDB header: lyase Chain: A: PDB Molecule: farnesyl pyrophosphate synthase, putative; PDBTitle: crystal structure of Plasmodium vivax geranylgeranylpyrophosphate2 synthase pvx_092040 with zoledronate and ipp bound |
| 26 | c3oyrA_ | Alignment | not modelled | 100.0 | 34 | PDB header: transferase Chain: A: PDB Molecule: trans-isoprenyl diphosphate synthase; PDBTitle: crystal structure of polyprenyl synthase from <i>Caulobacter crescentus</i> 2 cb15 complexed with calcium and isoprenyl diphosphate |
| 27 | c2ogdB_ | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: B: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: t. brucei farnesyl diphosphate synthase complexed with bisphosphonate2 bph-527 |
| | | | | | | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 28 | c4lltB_ | Alignment | not modelled | 100.0 | 32 | PDBTitle: crystal structure of a farnesyl diphosphate synthase from roseobacter2 denitrificans och 114, target efi-509393, with two ipp and calcium3 bound in active site PDB header: transferase |
| 29 | c2e8xB_ | Alignment | not modelled | 100.0 | 21 | Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: s. cerevisiae geranylgeranyl pyrophosphate synthase in2 complex with magnesium and gpp PDB header: transferase |
| 30 | c3lk5A_ | Alignment | not modelled | 100.0 | 24 | Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthase; PDBTitle: crystal structure of putative geranylgeranyl pyrophosphate synthase2 from corynebacterium glutamicum |
| 31 | d1v4ea_ | Alignment | not modelled | 100.0 | 25 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 32 | c5eroB_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: fuscococcadiene synthase; PDBTitle: crystal structure of elongation domain of phomopsis amygdali2 fusicoccadiene synthase complexed with cobalt ions and pamidronate |
| 33 | d1rqja_ | Alignment | not modelled | 100.0 | 31 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 34 | c1yhlA_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: structure of the complex of trypanosoma cruzi farnesyl diphosphate2 synthase with risedronate, dmapp and mg+2 |
| 35 | c3m9uD_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: D: PDB Molecule: farnesyl-diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from2 lactobacillus brevis atcc 367 |
| 36 | c3tc1A_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: octaprenyl pyrophosphate synthase; PDBTitle: crystal structure of octaprenyl pyrophosphate synthase from2 helicobacter pylori |
| 37 | c2o1oB_ | Alignment | not modelled | 100.0 | 17 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative farnesyl pyrophosphate synthase; PDBTitle: cryptosporidium parvum putative polyprenyl pyrophosphate synthase2 (cgd4_2550) in complex with risedronate. |
| 38 | c4ifgB_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl diphosphate synthase sub12742 (target efi-509455) from streptococcus uberis 0140j with bound3 magnesium and isopentyl diphosphate, fully liganded complex; |
| 39 | c3ts7B_ | Alignment | not modelled | 100.0 | 34 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of farnesyl diphosphate synthase (target efi-501951)2 from methylococcus capsulatus |
| 40 | c5xn5A_ | Alignment | not modelled | 100.0 | 31 | PDB header: transferase Chain: A: PDB Molecule: os07g0580900 protein; PDBTitle: homo-dimer crystal structure of geranylgeranyl diphosphate synthases 12 from oryza sativa |
| 41 | c3ipiA_ | Alignment | not modelled | 100.0 | 31 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a geranyltranstransferase from the methanosarcina2 mazei |
| 42 | d1rtra_ | Alignment | not modelled | 100.0 | 29 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 43 | c2forB_ | Alignment | not modelled | 100.0 | 31 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of the shigella flexneri farnesyl pyrophosphate2 synthase complex with an isopentenyl pyrophosphate |
| 44 | c2j1pB_ | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from sinapis alba in2 complex with gppp |
| 45 | c4kkmB_ | Alignment | not modelled | 100.0 | 31 | PDB header: transferase Chain: B: PDB Molecule: polyprenyl synthetase; PDBTitle: crystal structure of a fpp/gfpp synthase (target efi-501952) from2 zymomonas mobilis, apo structure |
| 46 | c3lomA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of geranyltransferase from legionella pneumophila |
| 47 | c3p8lB_ | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase from enterococcus faecalis2 v583 |
| 48 | c3ucaB_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of isoprenoid synthase (target efi-501974) from2 clostridium perfringens |
| 49 | c3lsnA_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of putative geranyltranstransferase from pseudomonas2 fluorescens pf-5 complexed with magnesium |
| 50 | c2h8oA_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: the 1.6a crystal structure of the geranyltransferase from2 agrobacterium tumefaciens |
| 51 | c5e8kA_ | Alignment | not modelled | 100.0 | 28 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthase 10, mitochondrial; PDBTitle: crystal structure of polyprenyl pyrophosphate synthase 2 from2 arabidopsis thaliana |
| 52 | c2azjB_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: crystal structure for the mutant d81c of sulfolobus2 solfataricus hexaprenyl pyrophosphate synthase |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 53 | c6c57B_ | Alignment | not modelled | 100.0 | 26 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthase; PDBTitle: crystal structure of mutant human geranylgeranyl pyrophosphate2 synthase (y246d) in complex with bisphosphonate inhibitor fv0109 |
| 54 | c3llwA_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase (ispa); PDBTitle: crystal structure of geranyltransferase from helicobacter pylori 26695 |
| 55 | c3m0gB_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: B: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of putative farnesyl diphosphate synthase from2 rhodobacter capsulatus |
| 56 | c3npkB_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: the crystal structure of geranyltranstransferase from campylobacter2 jejuni |
| 57 | c2ftzA_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of geranyltranstransferase (ec 2.5.1.10) (tm0161)2 from thermotoga maritima at 1.90 a resolution |
| 58 | c2j1oA_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from sinapis alba |
| 59 | c5aypA_ | Alignment | not modelled | 100.0 | 26 | PDB header: transferase Chain: A: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of bacillus stearothermophilus farnesyl2 pyrophosphate synthase |
| 60 | c3qkcB_ | Alignment | not modelled | 100.0 | 16 | PDB header: transferase Chain: B: PDB Molecule: geranyl diphosphate synthase small subunit; PDBTitle: crystal structure of geranyl diphosphate synthase small subunit from2 antirrhinum majus |
| 61 | c5xn6D_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: D: PDB Molecule: os02g0668100 protein; PDBTitle: heterodimer crystal structure of geranylgeranyl diphosphate synthases2 1 with ggpps recruiting protein(osgrp) from oryza sativa |
| 62 | c3kraB_ | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: B: PDB Molecule: geranyl diphosphate synthase small subunit; PDBTitle: mint heterotetrameric geranyl pyrophosphate synthase in complex with2 magnesium |
| 63 | c3p8rA_ | Alignment | not modelled | 100.0 | 28 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase from vibrio cholerae |
| 64 | c4fp4A_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: polyprenyl synthetase; PDBTitle: crystal structure of isoprenoid synthase a3mx09 (target efi-501993)2 from pyrobaculum calidifontis |
| 65 | c4f62B_ | Alignment | not modelled | 100.0 | 33 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a putative farnesyl-diphosphate synthase from2 marinomonas sp. med121 (target efi-501980) |
| 66 | d1ezfa_ | Alignment | not modelled | 98.2 | 18 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Squalene synthase |
| 67 | c2zcpA_ | Alignment | not modelled | 98.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: dehydrosqualene synthase; PDBTitle: crystal structure of the c(30) carotenoid dehydrosqualene synthase2 from staphylococcus aureus complexed with farnesyl thiopyrophosphate |
| 68 | c5nx4A_ | Alignment | not modelled | 97.8 | 13 | PDB header: ligase Chain: A: PDB Molecule: pentalenene synthase; PDBTitle: crystal structure of linalool/nerolidol synthase from streptomyces2 clavuligerus |
| 69 | c5b0mB_ | Alignment | not modelled | 97.7 | 19 | PDB header: transferase, dna binding protein Chain: B: PDB Molecule: moen5,dna-binding protein 7d; PDBTitle: structure of moen5-ss07d fusion protein in complex with beta-dodecyl2 maltoside |
| 70 | c5b02C_ | Alignment | not modelled | 97.7 | 19 | PDB header: transferase, dna binding protein Chain: C: PDB Molecule: moen5,dna-binding protein 7d; PDBTitle: structure of the prenyltransferase moen5 with a fusion protein tag of2 sso7d |
| 71 | c4hd1A_ | Alignment | not modelled | 97.7 | 25 | PDB header: transferase Chain: A: PDB Molecule: squalene synthase hpnc; PDBTitle: crystal structure of squalene synthase hpnc from alicyclobacillus2 acidocaldarius |
| 72 | c3lg5A_ | Alignment | not modelled | 97.6 | 15 | PDB header: lyase Chain: A: PDB Molecule: epi-isozizaene synthase; PDBTitle: f198a epi-isozizaene synthase: complex with mg, inorganic2 pyrophosphate and benzyl triethyl ammonium cation |
| 73 | c3wccC_ | Alignment | not modelled | 97.5 | 18 | PDB header: transferase Chain: C: PDB Molecule: farnesyltransferase, putative; PDBTitle: the complex structure of tcsqs with ligand, e5700 |
| 74 | c5ermA_ | Alignment | not modelled | 97.0 | 19 | PDB header: lyase Chain: A: PDB Molecule: fusicoccadiene synthase; PDBTitle: crystal structure of cyclization domain of phomopsis amygdali2 fusicoccadiene synthase complexed with magnesium ions and pamidronate |
| 75 | c5a0iA_ | Alignment | not modelled | 96.8 | 19 | PDB header: lyase Chain: A: PDB Molecule: labdane-related diterpene synthase; PDBTitle: crystallographic structure of the bacterial labdane-related diterpene2 synthase lrdc in complex with mg and ppi at 2.57 a resolution. |
| 76 | c6q4sA_ | Alignment | not modelled | 96.8 | 12 | PDB header: unknown function Chain: A: PDB Molecule: pentalenene synthase; PDBTitle: crystal structure of a-eudesmol synthase |
| | | | | | | PDB header: transferase |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 77 | c4okmA | Alignment | not modelled | 96.6 | 15 | Chain: A: PDB Molecule: terpene synthase metal-binding domain-containing protein; PDBTitle: selinadiene synthase apo and in complex with diphosphate |
| 78 | c3we9A | Alignment | not modelled | 96.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: putative phytoene/squalene synthase yisp; PDBTitle: the crystal structure of yisp from bacillus subtilis subsp. subtilis2 strain 168 |
| 79 | c5iysA | Alignment | not modelled | 95.8 | 16 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: phytoene synthase; PDBTitle: crystal structure of a dehydrosqualene synthase in complex with ligand |
| 80 | c5i1uB | Alignment | not modelled | 95.8 | 14 | PDB header: lyase Chain: B: PDB Molecule: germacradien-4-ol synthase; PDBTitle: crystal structure of germacradien-4-ol synthase from streptomyces2 citricolor |
| 81 | c5nx6A | Alignment | not modelled | 95.4 | 15 | PDB header: lyase Chain: A: PDB Molecule: pentalenene synthase; PDBTitle: crystal structure of 1,8-cineole synthase from streptomyces2 clavuligerus in complex with 2-fluoronyl diphosphate |
| 82 | d1di1a | Alignment | not modelled | 95.3 | 14 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Aristolochene/pentalenene synthase |
| 83 | c6egkB | Alignment | not modelled | 94.7 | 14 | PDB header: lyase Chain: B: PDB Molecule: cucumene synthase; PDBTitle: t181n cucumene synthase |
| 84 | c2oa6B | Alignment | not modelled | 94.6 | 16 | PDB header: lyase Chain: B: PDB Molecule: aristolochene synthase; PDBTitle: aristolochene synthase from aspergillus terreus complexed with2 pyrophosphate |
| 85 | c3n0fA | Alignment | not modelled | 92.6 | 12 | PDB header: lyase Chain: A: PDB Molecule: isoprene synthase; PDBTitle: crystal structure of isoprene synthase from grey poplar leaves2 (populus x canescens) |
| 86 | c3g4dB | Alignment | not modelled | 92.4 | 17 | PDB header: lyase Chain: B: PDB Molecule: (+)-delta-cadinene synthase isozyme xc1; PDBTitle: crystal structure of (+)-delta-cadinene synthase from gossypium2 arboreum and evolutionary divergence of metal binding motifs for3 catalysis |
| 87 | c4mc8A | Alignment | not modelled | 92.3 | 15 | PDB header: lyase Chain: A: PDB Molecule: putative sesquiterpene cyclase; PDBTitle: hedyacaryl synthase in complex with hepes |
| 88 | c3saeA | Alignment | not modelled | 91.8 | 20 | PDB header: lyase Chain: A: PDB Molecule: alpha-bisabolene synthase; PDBTitle: structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production |
| 89 | c2ongA | Alignment | not modelled | 89.4 | 20 | PDB header: lyase Chain: A: PDB Molecule: 4s-limonene synthase; PDBTitle: crystal structure of limonene synthase with 2-2 fluorogeranyl diphosphate (fgpp). |
| 90 | c2j5cB | Alignment | not modelled | 89.2 | 17 | PDB header: lyase Chain: B: PDB Molecule: 1,8-cineole synthase; PDBTitle: rational conversion of substrate and product specificity in a2 monoterpene synthase. structural insights into the molecular basis of3 rapid evolution. |
| 91 | c1n20A | Alignment | not modelled | 89.1 | 17 | PDB header: isomerase Chain: A: PDB Molecule: (+)-bornyl diphosphate synthase; PDBTitle: (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2,2,3-dihydrogeranyl diphosphate |
| 92 | c3s9vD | Alignment | not modelled | 89.1 | 14 | PDB header: lyase, isomerase Chain: D: PDB Molecule: abietadiene synthase, chloroplastic; PDBTitle: abietadiene synthase from abies grandis |
| 93 | c5dw7A | Alignment | not modelled | 89.0 | 18 | PDB header: lyase Chain: A: PDB Molecule: germacradienol/geosmin synthase; PDBTitle: crystal structure of the unliganded geosmin synthase n-terminal domain2 from streptomyces coelicolor |
| 94 | d1ps1a | Alignment | not modelled | 88.7 | 14 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Aristolochene/pentalenene synthase |
| 95 | c1hm4A | Alignment | not modelled | 88.5 | 13 | PDB header: lyase Chain: A: PDB Molecule: pentalenene synthase; PDBTitle: n219l pentalenene synthase |
| 96 | c3p5rB | Alignment | not modelled | 88.3 | 18 | PDB header: lyase Chain: B: PDB Molecule: taxadiene synthase; PDBTitle: crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate |
| 97 | c4zq8B | Alignment | not modelled | 88.0 | 18 | PDB header: transferase Chain: B: PDB Molecule: isoprenoid synthase; PDBTitle: crystal structure of a terpene synthase from streptomyces lydicus,2 target efi-540129 |
| 98 | c5zzjC | Alignment | not modelled | 86.1 | 18 | PDB header: lyase Chain: C: PDB Molecule: santalene synthase; PDBTitle: crystal structure of a enzyme from santalum album |
| 99 | d1n1ba2 | Alignment | not modelled | 84.9 | 19 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Terpenoid cyclase C-terminal domain |
| 100 | c5uv1A | Alignment | not modelled | 84.5 | 16 | PDB header: lyase Chain: A: PDB Molecule: (+)-limonene synthase; PDBTitle: crystal structure of (+)-limonene synthase complexed with 2-2 fluorogeranyl diphosphate |
| 101 | c1hx9A | Alignment | not modelled | 83.5 | 17 | PDB header: lyase Chain: A: PDB Molecule: 5-epi-aristolochene synthase; PDBTitle: crystal structure of teas w273s form 1 |
| | | | | | | PDB header: lyase Chain: A: PDB Molecule: 2-methylisoborneol synthase; |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 102 | c3v1xA_ | Alignment | not modelled | 82.0 | 15 | PDBTitle: crystal structure of 2-methylisoborneol synthase from streptomyces2 coelicolor a3(2) in complex with mg2+ and 2-fluorogeranyl diphosphate |
| 103 | c3v1vA_ | Alignment | not modelled | 80.1 | 17 | PDB header: lyase Chain: A: PDB Molecule: 2-methylisoborneol synthase; PDBTitle: crystal structure of 2-methylisoborneol synthase from streptomyces2 coelicolor a3(2) in complex with mg2+ and geranyl-s-thiolodiphosphate |
| 104 | c4gaxA_ | Alignment | not modelled | 78.1 | 18 | PDB header: lyase Chain: A: PDB Molecule: amorpha-4,11-diene synthase; PDBTitle: crystal structure of an alpha-bisabolol synthase mutant |
| 105 | d5easa2 | Alignment | not modelled | 73.1 | 17 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Terpenoid cyclase C-terminal domain |
| 106 | c5c05A_ | Alignment | not modelled | 72.6 | 18 | PDB header: biosynthetic protein Chain: A: PDB Molecule: putative gamma-terpinene synthase; PDBTitle: crystal structure of gamma-terpinene synthase from thymus vulgaris |
| 107 | c6o9qA_ | Alignment | not modelled | 57.6 | 16 | PDB header: lyase Chain: A: PDB Molecule: sesquisabinene b synthase 1; PDBTitle: wild-type sasqs1 |
| 108 | c5yo8B_ | Alignment | not modelled | 51.1 | 22 | PDB header: lyase Chain: B: PDB Molecule: tetraprenyl-beta-curcumene synthase; PDBTitle: crystal structure of beta-c25/c30/c35-prene synthase |
| 109 | d2o3la1 | Alignment | not modelled | 31.6 | 17 | Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like |
| 110 | c5h9dD_ | Alignment | not modelled | 28.1 | 21 | PDB header: transferase Chain: D: PDB Molecule: heptaprenyl diphosphate synthase (hepp synthase) subunit 1 PDBTitle: crystal structure of heptaprenyl diphosphate synthase from2 staphylococcus aureus |
| 111 | d2hh6a1 | Alignment | not modelled | 24.8 | 25 | Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like |