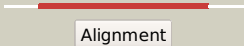

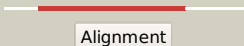

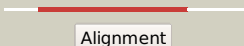


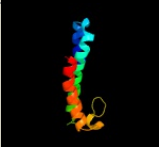


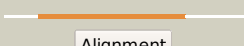

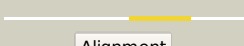
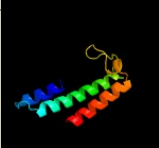
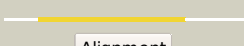

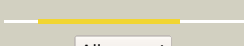

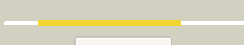
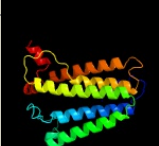

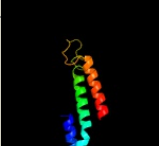
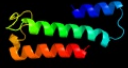










Phyre2

| | |
|---------------|--------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0534c_(menA)_625565_626443 |
| Date | Fri Jul 26 01:50:08 BST 2019 |
| Unique Job ID | bc6e7ffb72513b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4od5C_ |  Alignment |  | 100.0 | 13 | PDB header: transferase Chain: C; PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1 |
| 2 | c3m9uD_ |  Alignment |  | 95.9 | 12 | PDB header: transferase Chain: D; PDB Molecule: farnesyl-diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from2 lactobacillus brevis atcc 367 |
| 3 | c3ts7B_ |  Alignment |  | 95.9 | 10 | PDB header: transferase Chain: B; PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of farnesyl diphosphate synthase (target efi-501951)2 from methylococcus capsulatus |
| 4 | c3npkB_ |  Alignment |  | 84.8 | 16 | PDB header: transferase Chain: B; PDB Molecule: geranyltranstransferase; PDBTitle: the crystal structure of geranyltranstransferase from campylobacter2 jejuni |
| 5 | c3kraB_ |  Alignment |  | 82.1 | 13 | PDB header: transferase Chain: B; PDB Molecule: geranyl diphosphate synthase small subunit; PDBTitle: mint heterotetrameric geranyl pyrophosphate synthase in complex with2 magnesium |
| 6 | c5xn5A_ |  Alignment |  | 81.4 | 12 | PDB header: transferase Chain: A; PDB Molecule: os07g0580900 protein; PDBTitle: homo-dimer crystal structure of geranylgeranyl diphosphate synthases 12 from oryza sativa |
| 7 | c3p8lB_ |  Alignment |  | 79.0 | 24 | PDB header: transferase Chain: B; PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase from enterococcus faecalis2 v583 |
| 8 | c3oacD_ |  Alignment |  | 73.2 | 13 | 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 |
| 9 | c3wjnA_ |  Alignment |  | 72.6 | 12 | 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) |
| 10 | c5h9dB_ |  Alignment |  | 70.8 | 12 | PDB header: transferase Chain: B; PDB Molecule: farnesyl pyrophosphate synthetase; PDBTitle: crystal structure of heptaprenyl diphosphate synthase from2 staphylococcus aureus |
| 11 | c3ipiA_ |  Alignment |  | 69.2 | 16 | PDB header: transferase Chain: A; PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a geranyltranstransferase from the methanosarcina2 mazei |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|---|
| 12 | c2ftzA_ | Alignment |  | 66.1 | 18 | 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 |
| 13 | c2j1oA_ | Alignment |  | 64.7 | 15 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from sinapis alba |
| 14 | d1rqja_ | Alignment |  | 63.3 | 12 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 15 | c3ez3A_ | Alignment |  | 59.7 | 15 | 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 |
| 16 | c3lsnA_ | Alignment |  | 58.7 | 17 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of putative geranyltranstransferase from pseudomonas2 fluorescens pf-5 complexed with magnesium |
| 17 | c3oyrB_ | Alignment |  | 58.4 | 19 | PDB header: transferase Chain: B: PDB Molecule: trans-isoprenyl diphosphate synthase; PDBTitle: crystal structure of polyprenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate |
| 18 | c4lfgB_ | Alignment |  | 57.0 | 12 | 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; |
| 19 | c1wy0A_ | Alignment |  | 56.9 | 12 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthetase from2 pyrococcus horikoshii ot3 |
| 20 | c2o1oB_ | Alignment |  | 56.3 | 10 | 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. |
| 21 | c2e8xB_ | Alignment | not modelled | 55.9 | 17 | PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: s. cerevisiae geranylgeranyl pyrophosphate synthase in2 complex with magnesium and gpp |
| 22 | c2forB_ | Alignment | not modelled | 54.2 | 21 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of the shigella flexneri farnesyl pyrophosphate2 synthase complex with an isopentenyl pyrophosphate |
| 23 | c3llwA_ | Alignment | not modelled | 49.7 | 10 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase (ispa); PDBTitle: crystal structure of geranyltransferase from helicobacter pylori 26695 |
| 24 | c5e8kA_ | Alignment | not modelled | 47.3 | 23 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthase 10, mitochondrial; PDBTitle: crystal structure of polyprenyl pyrophosphate synthase 2 from2 arabidopsis thaliana |
| 25 | c3m0gB_ | Alignment | not modelled | 44.1 | 17 | PDB header: transferase Chain: B: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of putative farnesyl diphosphate synthase from2 rhodobacter capsulatus |
| 26 | c2l4fA_ | Alignment | not modelled | 41.0 | 42 | PDB header: protein binding Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: nmr structure of the uba domain of s. cerevisiae dcn1 bound to2 ubiquitin |
| 27 | c5aypA_ | Alignment | not modelled | 39.1 | 27 | PDB header: transferase Chain: A: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of bacillus stearothermophilus farnesyl2 pyrophosphate synthase |
| 28 | c5ifnB_ | Alignment | not modelled | 34.1 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; |

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|----|-------------------------|-----------|--------------|------|----|--|
| 28 | c3jqb_ | Alignment | not modelled | 34.1 | 13 | PDBTitle: geranylgeranyl pyrophosphate synthetase from archaeon geoglobus2 acetivorans PDB header: transferase |
| 29 | c1wmwA_ | Alignment | not modelled | 33.4 | 15 | Chain: A: PDB Molecule: geranylgeranyl diphosphate synthetase; PDBTitle: crystal structure of geranylgeranyl diphosphate synthase from thermus2 thermophilus |
| 30 | c2h8oA_ | Alignment | not modelled | 31.9 | 22 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: the 1.6a crystal structure of the geranyltransferase from2 agrobacterium tumefaciens |
| 31 | c3mzvB_ | Alignment | not modelled | 29.5 | 16 | PDB header: transferase Chain: B: PDB Molecule: decaprenyl diphosphate synthase; PDBTitle: crystal structure of a decaprenyl diphosphate synthase from2 rhodobacter capsulatus |
| 32 | c3p8rA_ | Alignment | not modelled | 25.1 | 18 | PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase from vibrio cholerae |
| 33 | d1v4ea_ | Alignment | not modelled | 22.9 | 12 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 34 | c3aqbD_ | Alignment | not modelled | 22.2 | 10 | 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 |
| 35 | c4lltB_ | Alignment | not modelled | 19.2 | 18 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; 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 |
| 36 | c6b07B_ | Alignment | not modelled | 18.2 | 13 | 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) |
| 37 | c3nf2A_ | Alignment | not modelled | 17.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: putative polyprenyl synthetase; PDBTitle: crystal structure of polyprenyl synthetase from streptomyces2 coelicolor a3(2) |
| 38 | c4kkmB_ | Alignment | not modelled | 16.0 | 14 | 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 |
| 39 | c3aq0G_ | Alignment | not modelled | 14.5 | 13 | 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) |
| 40 | c4f62B_ | Alignment | not modelled | 13.8 | 18 | PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a putative farnesyl-diphosphate synthase from2 marinomonas sp. med121 (target efi-501980) |
| 41 | d1fpsa_ | Alignment | not modelled | 13.5 | 11 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 42 | d1ezfa_ | Alignment | not modelled | 10.9 | 15 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Squalene synthase |
| 43 | d2q80a1 | Alignment | not modelled | 9.3 | 9 | Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases |
| 44 | c3cp6A_ | Alignment | not modelled | 9.2 | 11 | PDB header: transferase Chain: A: PDB Molecule: farnesyl pyrophosphate synthetase; PDBTitle: crystal structure of human farnesyl diphosphate synthase (t201a2 mutant) complexed with mg and biphosphonate inhibitor |
| 45 | c2jlpB_ | Alignment | not modelled | 8.8 | 12 | PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from sinapis alba in2 complex with ggpp |
| 46 | c5yo8B_ | Alignment | not modelled | 8.4 | 8 | PDB header: lyase Chain: B: PDB Molecule: tetraprenyl-beta-curcumen synthase; PDBTitle: crystal structure of beta-c25/c30/c35-prene synthase |
| 47 | c2zcpA_ | Alignment | not modelled | 8.2 | 31 | 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 |
| 48 | c4dhdA_ | Alignment | not modelled | 7.4 | 13 | PDB header: transferase Chain: A: PDB Molecule: polyprenyl synthetase; PDBTitle: crystal structure of isoprenoid synthase a3msh1 (target efi-501992)2 from pyrobaculum caldifontis |
| 49 | c3h87D_ | Alignment | not modelled | 6.9 | 44 | PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis |
| 50 | c2pnvA_ | Alignment | not modelled | 6.8 | 19 | PDB header: membrane protein Chain: A: PDB Molecule: small conductance calcium-activated potassium PDBTitle: crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus |
| 51 | c5ldwf_ | Alignment | not modelled | 6.0 | 18 | PDB header: oxidoreductase Chain: F: PDB Molecule: nahd dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class1 |
| 52 | c5lc5f_ | Alignment | not modelled | 6.0 | 18 | PDB header: oxidoreductase Chain: F: PDB Molecule: nahd dehydrogenase [ubiquinone] flavoprotein 1, |

| | | | | | |
|----|-------------------------|-----------|--------------|-----|---|
| | | | | | PDBTitle: structure of mammalian respiratory complex i, class2 PDB header: transferase |
| 53 | c3tc1A_ | Alignment | not modelled | 6.0 | 13 Chain: A: PDB Molecule: octaprenyl pyrophosphate synthase; PDBTitle: crystal structure of octaprenyl pyrophosphate synthase from2 helicobacter pylori |
| 54 | c2azjB_ | Alignment | not modelled | 5.6 | 9 PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: crystal structure for the mutant d81c of sulfolobus2 solfataricus hexaprenyl pyrophosphate synthase |
| 55 | c4jyrG_ | Alignment | not modelled | 5.1 | 25 PDB header: hydrolase Chain: G: PDB Molecule: d,d-heptose 1,7-bisphosphate phosphatase; PDBTitle: crystal structure of d,d-heptose 1,7-bisphosphate phosphatase from2 burkholderia thailandensis |