Phyre2

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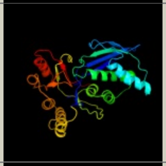
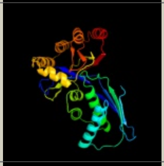
| Email | l.a.kelley@imperial.ac.uk |
| Description | P62615 |
| Date | Thu Jan 5 12:07:40 GMT 2012 |
| Unique Job ID | f9e057f533ef95cf |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1oj4B_ | Alignment |  | 100.0 | 98 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**4-diphosphocytidyl-2-c-methyl-d-erythritol<br>**PDBTitle:** ternary complex of2 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase |
| 2 | c1uekA_ | Alignment |  | 100.0 | 36 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**4-(cytidine 5'-diphospho)-2c-methyl-d-erythritol<br>**PDBTitle:** crystal structure of 4-(cytidine 5'-diphospho)-2c-methyl-d-2 erythritol kinase |
| 3 | c2v34B_ | Alignment |  | 100.0 | 30 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**4-diphosphocytidyl-2c-methyl-d-erythritol kinase;<br>**PDBTitle:** ispe in complex with cytidine and ligand |
| 4 | d1oj4a1 | Alignment |  | 100.0 | 97 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 5 | c1fwlD_ | Alignment |  | 100.0 | 20 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**homoserine kinase;<br>**PDBTitle:** crystal structure of homoserine kinase |
| 6 | d1ueka1 | Alignment |  | 100.0 | 44 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 7 | c3hulA_ | Alignment |  | 100.0 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**homoserine kinase;<br>**PDBTitle:** structure of putative homoserine kinase thrb from listeria2 monocytogenes |
| 8 | c2gs8A_ | Alignment |  | 100.0 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**mevalonate pyrophosphate decarboxylase;<br>**PDBTitle:** structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes |
| 9 | c2hfuB_ | Alignment |  | 100.0 | 15 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**mevalonate kinase, putative;<br>**PDBTitle:** crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate |
| 10 | c1kkhA_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mevalonate kinase;<br>**PDBTitle:** crystal structure of the methanococcus jannaschii2 mevalonate kinase |
| 11 | c2x7iA_ | Alignment |  | 100.0 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mevalonate kinase;<br>**PDBTitle:** crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252 |

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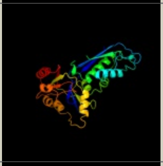
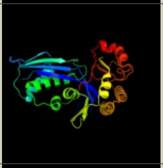
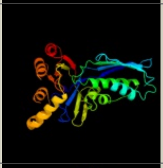
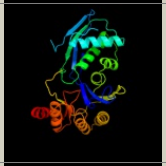
| 12 | c2hk3A_ | Alignment |  | 100.0 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**diphosphomevalonate decarboxylase;<br>**PDBTitle:** crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form) |
| 13 | c2oi2A_ | Alignment |  | 100.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mevalonate kinase;<br>**PDBTitle:** streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate |
| 14 | c2cz9A_ | Alignment |  | 100.0 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable galactokinase;<br>**PDBTitle:** crystal structure of galactokinase from pyrococcus horikoshi |
| 15 | c3k17A_ | Alignment |  | 100.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**lin0012 protein;<br>**PDBTitle:** crystal structure of a lin0012 protein from listeria innocua |
| 16 | c3ltoB_ | Alignment |  | 100.0 | 16 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**mevalonate diphosphate decarboxylase;<br>**PDBTitle:** crystal structure of a mevalonate diphosphate decarboxylase2 from legionella pneumophila |
| 17 | c3k85B_ | Alignment |  | 100.0 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**d-glycero-d-manno-heptose 1-phosphate kinase;<br>**PDBTitle:** crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron |
| 18 | c2r42A_ | Alignment |  | 100.0 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mevalonate kinase;<br>**PDBTitle:** the biochemical and structural basis for feedback2 inhibition of mevalonate kinase and isoprenoid metabolism |
| 19 | c1pieA_ | Alignment |  | 100.0 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**galactokinase;<br>**PDBTitle:** crystal structure of lactococcus lactis galactokinase2 complexed with galactose |
| 20 | c1k47F_ | Alignment |  | 100.0 | 16 | **PDB header:**transferase<br>**Chain:** F: **PDB Molecule:**phosphomevalonate kinase;<br>**PDBTitle:** crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk) |
| 21 | c1wuuA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**galactokinase;<br>**PDBTitle:** crystal structure of human galactokinase complexed with2 mgamppnp and galactose |
| 22 | c2a2cA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**n-acetylgalactosamine kinase;<br>**PDBTitle:** x-ray structure of human n-acetyl galactosamine kinase2 complexed with mg-adp and n-acetyl galactosamine 1-3 phosphate |
| 23 | c2aj4B_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**galactokinase;<br>**PDBTitle:** crystal structure of saccharomyces cerevisiae galactokinase2 in complex with galactose and mg:amppnp |
| 24 | d1oj4a2 | Alignment | not modelled | 100.0 | 98 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE |
| 25 | d1h72c1 | Alignment | not modelled | 100.0 | 20 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 26 | d1kkha1 | Alignment | not modelled | 99.9 | 20 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 27 | c2hkeB_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**diphosphomevalonate decarboxylase, putative;<br>**PDBTitle:** mevalonate diphosphate decarboxylase from trypanosoma brucei |
| 28 | d1fi4a1 | Alignment | not modelled | 99.9 | 17 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |

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| 29 | d1piea1 | Alignment | not modelled | 99.9 | 24 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 30 | d1k47a1 | Alignment | not modelled | 99.9 | 18 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 31 | d1wuua1 | Alignment | not modelled | 99.9 | 23 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 32 | d1ueka2 | Alignment | not modelled | 99.9 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE |
| 33 | d1s4ea1 | Alignment | not modelled | 99.8 | 22 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 34 | d1kvka1 | Alignment | not modelled | 99.8 | 25 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 35 | d1h72c2 | Alignment | not modelled | 99.7 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Homoserine kinase |
| 36 | c1fi4A_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**mevalonate 5-diphosphate decarboxylase;<br>**PDBTitle:** the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution. |
| 37 | c3f0nB_ | Alignment | not modelled | 99.1 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**mevalonate pyrophosphate decarboxylase;<br>**PDBTitle:** mus musculus mevalonate pyrophosphate decarboxylase |
| 38 | d1kvka2 | Alignment | not modelled | 98.6 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Mevalonate kinase |
| 39 | d1k47a2 | Alignment | not modelled | 98.6 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Phosphomevalonate kinase (PMK) |
| 40 | d1kkha2 | Alignment | not modelled | 98.4 | 17 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Mevalonate kinase |
| 41 | d1s4ea2 | Alignment | not modelled | 97.8 | 21 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Galactokinase |
| 42 | d1wuua2 | Alignment | not modelled | 97.5 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Galactokinase |
| 43 | d1piea2 | Alignment | not modelled | 97.4 | 15 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Galactokinase |
| 44 | c3mnfA_ | Alignment | not modelled | 20.3 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**pac2 family protein;<br>**PDBTitle:** crystal structure of pac2 family protein from streptomyces avermitilis2 ma |
| 45 | d1xxaa_ | Alignment | not modelled | 18.5 | 13 | **Fold:**DCoH-like<br>**Superfamily:**C-terminal domain of arginine repressor<br>**Family:**C-terminal domain of arginine repressor |
| 46 | d1b4ba_ | Alignment | not modelled | 15.8 | 17 | **Fold:**DCoH-like<br>**Superfamily:**C-terminal domain of arginine repressor<br>**Family:**C-terminal domain of arginine repressor |
| 47 | c3gaaB_ | Alignment | not modelled | 15.1 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein ta1441;<br>**PDBTitle:** the crystal structure of the protein with unknown function from2 thermoplasma acidophilum |
| 48 | d2p90a1 | Alignment | not modelled | 14.4 | 10 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Cgl1923-like<br>**Family:**Cgl1923-like |
| 49 | c2p90B_ | Alignment | not modelled | 13.4 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical protein cgl1923;<br>**PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032 |
| 50 | c3cagF_ | Alignment | not modelled | 12.6 | 11 | **PDB header:**dna binding protein<br>**Chain:** F: **PDB Molecule:**arginine repressor;<br>**PDBTitle:** crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines. |
| 51 | c3fuxB_ | Alignment | not modelled | 11.2 | 21 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dimethyladenosine transferase;<br>**PDBTitle:** t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121 |
| 52 | c2wamB_ | Alignment | not modelled | 10.9 | 21 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**conserved hypothetical alanine and leucine rich<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714 |
| 53 | d2p5ma1 | Alignment | not modelled | 10.9 | 13 | **Fold:**DCoH-like<br>**Superfamily:**C-terminal domain of arginine repressor<br>**Family:**C-terminal domain of arginine repressor |
| 54 | c3e0dA_ | Alignment | not modelled | 10.7 | 17 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha;<br>**PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha- |

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|  |  |  |  |  |  | subunit |
| 55 | d1yrxa1 | Alignment | not modelled | 10.2 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**BLUF domain |
| 56 | d1a6qa1 | Alignment | not modelled | 8.5 | 35 | **Fold:**Another 3-helical bundle<br>**Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain<br>**Family:**Protein serine/threonine phosphatase 2C, C-terminal domain |
| 57 | d2byca1 | Alignment | not modelled | 8.5 | 10 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**BLUF domain |
| 58 | c2hnhA_ | Alignment | not modelled | 8.3 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit;<br>**PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii |
| 59 | c2diuA_ | Alignment | not modelled | 8.1 | 13 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**kiaa0430 protein;<br>**PDBTitle:** solution structure of the rrm domain of kiaa0430 protein |
| 60 | c3m05A_ | Alignment | not modelled | 8.1 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480;<br>**PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745 |
| 61 | d1o51a_ | Alignment | not modelled | 8.1 | 17 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**DUF190/COG1993 |
| 62 | c2hfnJ_ | Alignment | not modelled | 7.8 | 13 | **PDB header:**electron transport<br>**Chain:** J: **PDB Molecule:**synechocystis photoreceptor (slr1694);<br>**PDBTitle:** crystal structures of the synechocystis photoreceptor slr1694 reveal2 distinct structural states related to signaling |
| 63 | d1mwqa_ | Alignment | not modelled | 6.2 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**YciI-like |
| 64 | c3v4gA_ | Alignment | not modelled | 5.8 | 13 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**arginine repressor;<br>**PDBTitle:** 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6 |
| 65 | d1vkra_ | Alignment | not modelled | 5.6 | 14 | **Fold:**Phosphotyrosine protein phosphatases I-like<br>**Superfamily:**PTS system IIB component-like<br>**Family:**PTS system, Lactose/Cellobiose specific IIB subunit |
| 66 | c1vkrA_ | Alignment | not modelled | 5.6 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components;<br>**PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii |
| 67 | d8ohma2 | Alignment | not modelled | 5.5 | 14 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**RNA helicase |
| 68 | d2gdwa1 | Alignment | not modelled | 5.4 | 26 | **Fold:**Acyl carrier protein-like<br>**Superfamily:**ACP-like<br>**Family:**Peptidyl carrier domain |