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|---|---|
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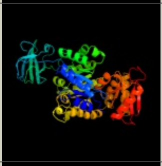
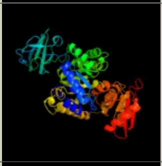
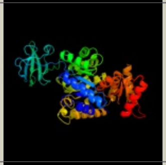
| Description | P0AD61 |
| Date | Thu Jan 5 11:20:06 GMT 2012 |
| Unique Job ID | 342435d3803d8d22 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2e28A_ | Alignment |  | 100.0 | 52 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus |
| 2 | c3t07D_ | Alignment |  | 100.0 | 48 | **PDB header:**transferase/transferase inhibitor<br>**Chain:** D: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid |
| 3 | c1t5aB_ | Alignment |  | 100.0 | 49 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme;<br>**PDBTitle:** human pyruvate kinase m2 |
| 4 | c1aqfB_ | Alignment |  | 100.0 | 49 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate |
| 5 | c3ma8A_ | Alignment |  | 100.0 | 44 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum |
| 6 | c3e0vB_ | Alignment |  | 100.0 | 44 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions |
| 7 | c1a3wB_ | Alignment |  | 100.0 | 43 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+ |
| 8 | c3eoeC_ | Alignment |  | 100.0 | 47 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007 |
| 9 | c1pklB_ | Alignment |  | 100.0 | 44 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**protein (pyruvate kinase);<br>**PDBTitle:** the structure of leishmania pyruvate kinase |
| 10 | c2vgbB_ | Alignment |  | 100.0 | 48 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l;<br>**PDBTitle:** human erythrocyte pyruvate kinase |
| 11 | c1e0tD_ | Alignment |  | 100.0 | 99 | **PDB header:**phosphotransferase<br>**Chain:** D: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** r292d mutant of e. coli pyruvate kinase |

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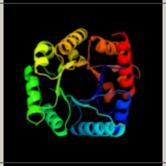
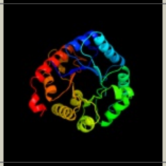
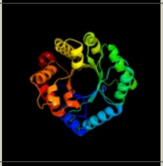
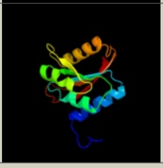
|---|---|---|---|---|---|---|
| 12 | c3khdC_ | Alignment |  | 100.0 | 53 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure of pff1300w. |
| 13 | d1pkla2 | Alignment |  | 100.0 | 56 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Pyruvate kinase |
| 14 | d2g50a2 | Alignment |  | 100.0 | 59 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Pyruvate kinase |
| 15 | d1a3xa2 | Alignment |  | 100.0 | 58 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Pyruvate kinase |
| 16 | d1liua2 | Alignment |  | 100.0 | 55 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Pyruvate kinase |
| 17 | d1e0ta2 | Alignment |  | 100.0 | 100 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Pyruvate kinase |
| 18 | d1e0ta3 | Alignment |  | 100.0 | 100 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**Pyruvate kinase, C-terminal domain |
| 19 | d1liua3 | Alignment |  | 100.0 | 34 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**Pyruvate kinase, C-terminal domain |
| 20 | d2g50a3 | Alignment |  | 100.0 | 34 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**Pyruvate kinase, C-terminal domain |
| 21 | d1pkla3 | Alignment | not modelled | 100.0 | 28 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**Pyruvate kinase, C-terminal domain |
| 22 | d1a3xa3 | Alignment | not modelled | 99.9 | 32 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**Pyruvate kinase, C-terminal domain |
| 23 | d1e0ta1 | Alignment | not modelled | 99.9 | 100 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**Pyruvate kinase beta-barrel domain |
| 24 | d2g50a1 | Alignment | not modelled | 99.8 | 39 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**Pyruvate kinase beta-barrel domain |
| 25 | d1pkma1 | Alignment | not modelled | 99.8 | 39 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**Pyruvate kinase beta-barrel domain |
| 26 | d1liua1 | Alignment | not modelled | 99.8 | 41 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**Pyruvate kinase beta-barrel domain |
| 27 | d1a3xa1 | Alignment | not modelled | 99.8 | 33 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**Pyruvate kinase beta-barrel domain |
| 28 | d1pkla1 | Alignment | not modelled | 99.8 | 32 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**Pyruvate kinase beta-barrel domain |
| 29 | d1dxea_ | Alignment | not modelled | 99.1 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain |

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| | | | | | | **Family:**HpcH/HpaI aldolase |
| 30 | c2v5jB_ | Alignment | not modelled | 99.1 | 16 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase;<br>**PDBTitle:** apo class ii aldolase hpch |
| 31 | c2vwtA_ | Alignment | not modelled | 99.0 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase;<br>**PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex |
| 32 | c3qz6A_ | Alignment | not modelled | 99.0 | 18 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**hpch/hpai aldolase;<br>**PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2 |
| 33 | c1sgjB_ | Alignment | not modelled | 98.9 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**citrate lyase, beta subunit;<br>**PDBTitle:** crystal structure of citrate lyase beta subunit |
| 34 | d1sgja_ | Alignment | not modelled | 98.9 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**HpcH/HpaI aldolase |
| 35 | c3qllB_ | Alignment | not modelled | 98.8 | 18 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**citrate lyase;<br>**PDBTitle:** crystal structure of ripc from yersinia pestis |
| 36 | d1izca_ | Alignment | not modelled | 98.8 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**HpcH/HpaI aldolase |
| 37 | c1izcA_ | Alignment | not modelled | 98.8 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase;<br>**PDBTitle:** crystal structure analysis of macrophomate synthase |
| 38 | c3qqwC_ | Alignment | not modelled | 98.4 | 13 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**putative citrate lyase;<br>**PDBTitle:** crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution |
| 39 | c1u5vA_ | Alignment | not modelled | 98.4 | 18 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**cite;<br>**PDBTitle:** structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis |
| 40 | d1u5ha_ | Alignment | not modelled | 98.3 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**HpcH/HpaI aldolase |
| 41 | c3r4iB_ | Alignment | not modelled | 98.1 | 14 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**citrate lyase;<br>**PDBTitle:** crystal structure of a citrate lyase (bxe_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution |
| 42 | c3cuzA_ | Alignment | not modelled | 97.7 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**malate synthase a;<br>**PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design |
| 43 | c2hroA_ | Alignment | not modelled | 97.6 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase;<br>**PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus |
| 44 | c3pugA_ | Alignment | not modelled | 97.6 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**malate synthase;<br>**PDBTitle:** haloferax volcanii malate synthase native at 3mm glyoxylate |
| 45 | c2bg5C_ | Alignment | not modelled | 97.6 | 13 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase;<br>**PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts) |
| 46 | c2hwgA_ | Alignment | not modelled | 97.5 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase;<br>**PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system |
| 47 | c2olsA_ | Alignment | not modelled | 97.4 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase;<br>**PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis |
| 48 | c1kblA_ | Alignment | not modelled | 97.4 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase;<br>**PDBTitle:** pyruvate phosphate dikinase |
| 49 | c1zfjA_ | Alignment | not modelled | 97.3 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase;<br>**PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes |
| 50 | c1h6zA_ | Alignment | not modelled | 97.3 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase;<br>**PDBTitle:** 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei |
| 51 | c3cuxA_ | Alignment | not modelled | 97.1 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**malate synthase;<br>**PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design |
| 52 | d1vbga1 | Alignment | not modelled | 97.1 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Pyruvate phosphate dikinase, C-terminal domain |
| 53 | d1kbla1 | Alignment | not modelled | 97.1 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Pyruvate phosphate dikinase, C-terminal domain |
| 54 | c1vbhA_ | Alignment | not modelled | 96.9 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase;<br>**PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from |

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| | | | | | | maize |
| 55 | d1h6za1 | Alignment | not modelled | 96.6 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Pyruvate phosphate dikinase, C-terminal domain |
| 56 | d1jr1a1 | Alignment | not modelled | 96.6 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 57 | c3odmE_ | Alignment | not modelled | 96.6 | 22 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**phosphoenolpyruvate carboxylase;<br>**PDBTitle:** archaeal-type phosphoenolpyruvate carboxylase |
| 58 | c1jcnA_ | Alignment | not modelled | 96.1 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase i;<br>**PDBTitle:** binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp |
| 59 | d1zfja1 | Alignment | not modelled | 95.8 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 60 | c3f4wA_ | Alignment | not modelled | 94.0 | 12 | **PDB header:**synthase, lyase<br>**Chain:** A: **PDB Molecule:**putative hexulose 6 phosphate synthase;<br>**PDBTitle:** the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium |
| 61 | d1t57a_ | Alignment | not modelled | 94.0 | 21 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**MTH1675-like |
| 62 | c3gndC_ | Alignment | not modelled | 93.6 | 16 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**aldolase lsrf;<br>**PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate |
| 63 | c3khjE_ | Alignment | not modelled | 93.6 | 18 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase;<br>**PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64 |
| 64 | c3bo9B_ | Alignment | not modelled | 93.6 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative nitroalkan dioxygenase;<br>**PDBTitle:** crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution |
| 65 | d2flia1 | Alignment | not modelled | 93.5 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 66 | d1xcfa_ | Alignment | not modelled | 93.2 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 67 | c2gjlA_ | Alignment | not modelled | 92.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hypothetical protein pa1024;<br>**PDBTitle:** crystal structure of 2-nitropropane dioxygenase |
| 68 | c3r2gA_ | Alignment | not modelled | 92.5 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase;<br>**PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila |
| 69 | c2h90A_ | Alignment | not modelled | 92.4 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**xenobiotic reductase a;<br>**PDBTitle:** xenobiotic reductase a in complex with coumarin |
| 70 | d1h1ya_ | Alignment | not modelled | 92.2 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 71 | d1vp8a_ | Alignment | not modelled | 91.7 | 25 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**MTH1675-like |
| 72 | c2qr6A_ | Alignment | not modelled | 90.4 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**imp dehydrogenase/gmp reductase;<br>**PDBTitle:** crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution |
| 73 | c1vrdA_ | Alignment | not modelled | 90.4 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase;<br>**PDBTitle:** crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution |
| 74 | d1vrda1 | Alignment | not modelled | 88.7 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 75 | d1ps9a1 | Alignment | not modelled | 88.3 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 76 | d1y0ea_ | Alignment | not modelled | 88.2 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 77 | c3ffsC_ | Alignment | not modelled | 87.2 | 21 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase;<br>**PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase |
| 78 | c2z6jB_ | Alignment | not modelled | 86.4 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**trans-2-enoyl-acp reductase ii;<br>**PDBTitle:** crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor |
| 79 | c3nm3D_ | Alignment | not modelled | 86.4 | 16 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme; |

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| 79 | c3hm3D_ | Alignment | not modelled | 86.4 | 16 | **PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes |
| 80 | d1rpxa_ | Alignment | not modelled | 85.9 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 81 | c2vp8A_ | Alignment | not modelled | 85.8 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dihydropteroate synthase 2;<br>**PDBTitle:** structure of mycobacterium tuberculosis rv1207 |
| 82 | d1kbia1 | Alignment | not modelled | 84.1 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 83 | d1ojxa_ | Alignment | not modelled | 83.9 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 84 | c3igsB_ | Alignment | not modelled | 82.3 | 17 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2;<br>**PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase |
| 85 | c2y0fD_ | Alignment | not modelled | 82.2 | 16 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase;<br>**PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27 |
| 86 | c3inpA_ | Alignment | not modelled | 81.8 | 8 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase;<br>**PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis. |
| 87 | c3ct7E_ | Alignment | not modelled | 81.6 | 10 | **PDB header:**isomerase<br>**Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase;<br>**PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12 |
| 88 | c3cwcB_ | Alignment | not modelled | 81.2 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**putative glycerate kinase 2;<br>**PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2 |
| 89 | d1f76a_ | Alignment | not modelled | 80.6 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 90 | d1tqja_ | Alignment | not modelled | 80.2 | 9 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 91 | c3qc3B_ | Alignment | not modelled | 79.7 | 9 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase;<br>**PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution |
| 92 | d2tpsa_ | Alignment | not modelled | 79.0 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Thiamin phosphate synthase<br>**Family:**Thiamin phosphate synthase |
| 93 | c2qjhH_ | Alignment | not modelled | 78.9 | 20 | **PDB header:**lyase<br>**Chain:** H: **PDB Molecule:**putative aldolase mj0400;<br>**PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate |
| 94 | d1jqoa_ | Alignment | not modelled | 78.7 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate carboxylase |
| 95 | c1jqoA_ | Alignment | not modelled | 78.7 | 17 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase;<br>**PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize |
| 96 | c2p10D_ | Alignment | not modelled | 78.4 | 13 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**mll9387 protein;<br>**PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution |
| 97 | d1eepa_ | Alignment | not modelled | 78.0 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 98 | d1vcva1 | Alignment | not modelled | 77.8 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 99 | d1ajza_ | Alignment | not modelled | 77.1 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Dihydropteroate synthetase-like<br>**Family:**Dihydropteroate synthetase |
| 100 | c3qjaA_ | Alignment | not modelled | 76.1 | 12 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase;<br>**PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form |
| 101 | c2htmB_ | Alignment | not modelled | 75.7 | 14 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig;<br>**PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8 |
| 102 | c3q58A_ | Alignment | not modelled | 75.5 | 23 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase;<br>**PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica |
| 103 | d1tqxa_ | Alignment | not modelled | 74.9 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 104 | d2cu0a1 | Alignment | not modelled | 74.9 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| | | | | | | **Fold:**TIM beta/alpha-barrel |

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|---|---|---|---|---|---|---|
| 105 | d1jqna_ | Alignment | not modelled | 74.0 | 20 | **Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate carboxylase |
| 106 | d3bofa1 | Alignment | not modelled | 73.9 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Dihydropteroate synthetase-like<br>**Family:**Methyltetrahydrofolate-utiluzing methyltransferases |
| 107 | d1jcna1 | Alignment | not modelled | 72.7 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 108 | c3thaB_ | Alignment | not modelled | 72.6 | 9 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain;<br>**PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni. |
| 109 | c3ktsA_ | Alignment | not modelled | 71.1 | 20 | **PDB header:**transcriptional regulator<br>**Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein;<br>**PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365 |
| 110 | c2fptA_ | Alignment | not modelled | 70.5 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, mitochondrial;<br>**PDBTitle:** dual binding mode of a novel series of dhodh inhibitors |
| 111 | d1q6oa_ | Alignment | not modelled | 69.5 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Decarboxylase |
| 112 | c3pg8B_ | Alignment | not modelled | 69.4 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase;<br>**PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima |
| 113 | c2v82A_ | Alignment | not modelled | 69.3 | 12 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase;<br>**PDBTitle:** kdpgal complexed to kdpgal |
| 114 | d1pvna1 | Alignment | not modelled | 69.1 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 115 | c3tr9A_ | Alignment | not modelled | 67.8 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dihydropteroate synthase;<br>**PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii |
| 116 | c1ps9A_ | Alignment | not modelled | 67.6 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase;<br>**PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase |
| 117 | c2vefB_ | Alignment | not modelled | 67.0 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dihydropteroate synthase;<br>**PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae |
| 118 | d1xi3a_ | Alignment | not modelled | 67.0 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Thiamin phosphate synthase<br>**Family:**Thiamin phosphate synthase |
| 119 | d1tx2a_ | Alignment | not modelled | 67.0 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Dihydropteroate synthetase-like<br>**Family:**Dihydropteroate synthetase |
| 120 | c1tx2A_ | Alignment | not modelled | 67.0 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase;<br>**PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis |