# Phyre$^2$

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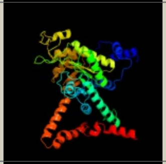
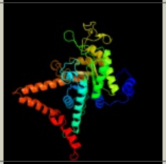
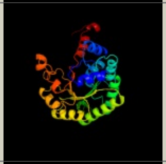
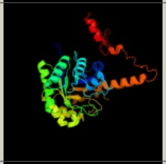
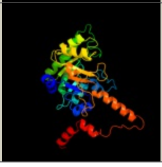
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A9G6 |
| Date | Thu Jan 5 11:10:09 GMT 2012 |
| Unique Job ID | e8fda1584905a9bc |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1dqua_ | Alignment |  | 100.0 | 41 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like |
| 2 | d1igwa_ | Alignment |  | 100.0 | 100 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like |
| 3 | d1f61a_ | Alignment |  | 100.0 | 61 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like |
| 4 | c3e5bB_ | Alignment |  | 100.0 | 62 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**isocitrate lyase;<br>**PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis |
| 5 | c3eooL_ | Alignment |  | 100.0 | 32 | **PDB header:**lyase<br>**Chain:** L: **PDB Molecule:**methylisocitrate lyase;<br>**PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei |
| 6 | c3b8iF_ | Alignment |  | 100.0 | 26 | **PDB header:**lyase<br>**Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase;<br>**PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+. |
| 7 | c3ih1A_ | Alignment |  | 100.0 | 30 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**methylisocitrate lyase;<br>**PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis |
| 8 | d1muma_ | Alignment |  | 100.0 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like |
| 9 | c3fa4D_ | Alignment |  | 100.0 | 26 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase;<br>**PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form |
| 10 | c1zlpA_ | Alignment |  | 100.0 | 29 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**petal death protein;<br>**PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct |
| 11 | c3lyeA_ | Alignment |  | 100.0 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase;<br>**PDBTitle:** crystal structure of oxaloacetate acetylhydrolase |

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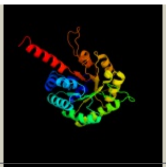
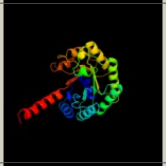
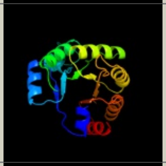
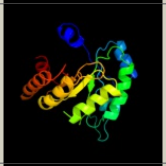
| 12 | c2hjpA_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase;<br>**PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++ |
| 13 | d1s2wa_ | Alignment |  | 100.0 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like |
| 14 | d1ujqa_ | Alignment |  | 100.0 | 33 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like |
| 15 | c2qiwA_ | Alignment |  | 100.0 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pep phosphonomutase;<br>**PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution |
| 16 | c2ze3A_ | Alignment |  | 100.0 | 26 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**dfa0005;<br>**PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus |
| 17 | d1m3ua_ | Alignment |  | 99.9 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Ketopantoate hydroxymethyltransferase PanB |
| 18 | c3ez4B_ | Alignment |  | 99.9 | 20 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase;<br>**PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei |
| 19 | d1oy0a_ | Alignment |  | 99.8 | 25 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Ketopantoate hydroxymethyltransferase PanB |
| 20 | d1o66a_ | Alignment |  | 97.5 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Ketopantoate hydroxymethyltransferase PanB |
| 21 | c2p10D_ | Alignment | not modelled | 96.9 | 24 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**mll9387 protein;<br>**PDBTitle:** crystal structure of a putative phosphopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution |
| 22 | c3si9B_ | Alignment | not modelled | 96.7 | 17 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae |
| 23 | d1o5ka_ | Alignment | not modelled | 96.7 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 24 | c3daqB_ | Alignment | not modelled | 96.4 | 20 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus |
| 25 | c3b4uB_ | Alignment | not modelled | 96.3 | 20 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58 |
| 26 | c3lerA_ | Alignment | not modelled | 96.3 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168 |
| 27 | c2yxgD_ | Alignment | not modelled | 96.3 | 21 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa) |
| 28 | c3noeA_ | Alignment | not modelled | 96.1 | 22 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa |

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| 29 | d2a6na1 | Alignment | not modelled | 96.1 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 30 | c3g0sA_ | Alignment | not modelled | 96.0 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2 |
| 31 | c2rfgB_ | Alignment | not modelled | 96.0 | 17 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution |
| 32 | c3cprB_ | Alignment | not modelled | 96.0 | 20 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase;<br>**PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution |
| 33 | c3h5dD_ | Alignment | not modelled | 95.9 | 17 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae |
| 34 | c3s5oA_ | Alignment | not modelled | 95.9 | 17 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial;<br>**PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate |
| 35 | c2r8wB_ | Alignment | not modelled | 95.8 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**agr_c_1641p;<br>**PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58 |
| 36 | c3fkkA_ | Alignment | not modelled | 95.8 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase;<br>**PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase |
| 37 | c3eb2A_ | Alignment | not modelled | 95.6 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution |
| 38 | c3na8A_ | Alignment | not modelled | 95.6 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase;<br>**PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa |
| 39 | d1f74a_ | Alignment | not modelled | 95.5 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 40 | c3lciA_ | Alignment | not modelled | 95.5 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase;<br>**PDBTitle:** the d-sialic acid aldolase mutant v251w |
| 41 | d1xm3a_ | Alignment | not modelled | 95.5 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**ThiG-like<br>**Family:**ThiG-like |
| 42 | d1xxxa1 | Alignment | not modelled | 95.4 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 43 | c3fluD_ | Alignment | not modelled | 95.4 | 20 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis |
| 44 | c3e96B_ | Alignment | not modelled | 95.4 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii |
| 45 | c3d0cB_ | Alignment | not modelled | 95.3 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution |
| 46 | c3pueA_ | Alignment | not modelled | 95.3 | 24 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution |
| 47 | d1xkya1 | Alignment | not modelled | 94.8 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 48 | c3qfeB_ | Alignment | not modelled | 94.7 | 18 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**putative dihydrodipicolinate synthase family protein;<br>**PDBTitle:** crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis |
| 49 | c3n2xB_ | Alignment | not modelled | 94.5 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**uncharacterized protein yage;<br>**PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate |
| 50 | d1vr6a1 | Alignment | not modelled | 94.4 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I DAHP synthetase |
| 51 | c1kbiB_ | Alignment | not modelled | 94.2 | 24 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**cytochrome b2;<br>**PDBTitle:** crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme |
| 52 | c3bw2A_ | Alignment | not modelled | 94.2 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase;<br>**PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes |
| 53 | c2v9dB_ | Alignment | not modelled | 94.2 | 14 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**yage;<br>**PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12 |

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| 54 | d1goxa_ | Alignment | not modelled | 93.8 | 26 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 55 | c2nuxB_ | Alignment | not modelled | 93.8 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate<br>**PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution |
| 56 | d1tb3a1 | Alignment | not modelled | 93.6 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 57 | d1w3ia_ | Alignment | not modelled | 93.6 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 58 | c1zfjA_ | Alignment | not modelled | 93.6 | 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 |
| 59 | d1tzza1 | Alignment | not modelled | 93.5 | 27 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 60 | d1rvka1 | Alignment | not modelled | 93.2 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 61 | c3ffsC_ | Alignment | not modelled | 93.1 | 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 |
| 62 | c3sqsA_ | Alignment | not modelled | 92.8 | 11 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein;<br>**PDBTitle:** crystal structure of a putative mandelate racemase/muconate2 lactonizing protein from dinoroseobacter shibae dfl 12 |
| 63 | c2vc6A_ | Alignment | not modelled | 92.5 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** structure of mosa from s. meliloti with pyruvate bound |
| 64 | d2p10a1 | Alignment | not modelled | 92.4 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Mll9387-like |
| 65 | d1jcna1 | Alignment | not modelled | 92.3 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 66 | c3bi8A_ | Alignment | not modelled | 92.3 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum |
| 67 | c1jcnA_ | Alignment | not modelled | 92.2 | 21 | **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 |
| 68 | d2mnra1 | Alignment | not modelled | 92.2 | 27 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 69 | c2ehhE_ | Alignment | not modelled | 91.9 | 17 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus |
| 70 | d1kbia1 | Alignment | not modelled | 91.7 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 71 | d1hl2a_ | Alignment | not modelled | 91.6 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 72 | d1zfja1 | Alignment | not modelled | 91.3 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 73 | c2qr6A_ | Alignment | not modelled | 91.1 | 22 | **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 |
| 74 | c3nvtA_ | Alignment | not modelled | 91.1 | 16 | **PDB header:**transferase/isomerase<br>**Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase;<br>**PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e |
| 75 | c3khjE_ | Alignment | not modelled | 90.7 | 20 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase;<br>**PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64 |
| 76 | c1zcoA_ | Alignment | not modelled | 90.5 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase;<br>**PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase |
| 77 | c3rcyC_ | Alignment | not modelled | 90.4 | 25 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme-like<br>**PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme-2 like protein from roseovarius sp. tm1035 |

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| 78 | c1vs1B_ | Alignment | not modelled | 89.8 | 20 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**3-deoxy-7-phosphoheptulonate synthase;<br>**PDBTitle:** crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep |
| 79 | d1jr1a1 | Alignment | not modelled | 89.6 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 80 | c2htmB_ | Alignment | not modelled | 89.2 | 15 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig;<br>**PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8 |
| 81 | c1vrdA_ | Alignment | not modelled | 89.1 | 22 | **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 |
| 82 | c3dz1A_ | Alignment | not modelled | 89.0 | 13 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution |
| 83 | d1jpma1 | Alignment | not modelled | 88.8 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 84 | c1me9A_ | Alignment | not modelled | 88.8 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase;<br>**PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound |
| 85 | c3cxoA_ | Alignment | not modelled | 88.7 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative galactonate dehydratase;<br>**PDBTitle:** crystal structure of l-rhamnonate dehydratase from2 salmonella typhimurium complexed with mg and 3-deoxy-l-3 rhamnonate |
| 86 | c2e77B_ | Alignment | not modelled | 88.4 | 24 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**lactate oxidase;<br>**PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex |
| 87 | c1rvkA_ | Alignment | not modelled | 87.9 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**isomerase/lactonizing enzyme;<br>**PDBTitle:** crystal structure of enolase agr_l_2751 from agrobacterium tumefaciens |
| 88 | d2gdqa1 | Alignment | not modelled | 87.4 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 89 | d1p4ca_ | Alignment | not modelled | 87.1 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 90 | d1vrda1 | Alignment | not modelled | 87.1 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 91 | c2r94B_ | Alignment | not modelled | 86.5 | 22 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase;<br>**PDBTitle:** crystal structure of kd(p)ga from t.tenax |
| 92 | c3fv9D_ | Alignment | not modelled | 86.5 | 13 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme;<br>**PDBTitle:** crystal structure of putative mandelate racemase/muconatelactonizing2 enzyme from roseovarius nubinhibens ism complexed with magnesium |
| 93 | c3cyjA_ | Alignment | not modelled | 86.2 | 23 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme-like<br>**PDBTitle:** crystal structure of a mandelate racemase/muconate lactonizing enzyme-2 like protein from rubrobacter xylanophilus |
| 94 | c2a7rD_ | Alignment | not modelled | 86.1 | 14 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**gmp reductase 2;<br>**PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2) |
| 95 | c2gjlA_ | Alignment | not modelled | 86.0 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hypothetical protein pa1024;<br>**PDBTitle:** crystal structure of 2-nitropropane dioxygenase |
| 96 | c3px5A_ | Alignment | not modelled | 85.9 | 21 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**enzyme of enolase superfamily;<br>**PDBTitle:** structure of efi enolase target en500555, a putative dipeptide2 epimerase: apo structure |
| 97 | c3stgA_ | Alignment | not modelled | 85.9 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase;<br>**PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis |
| 98 | c3bo9B_ | Alignment | not modelled | 85.7 | 18 | **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 |
| 99 | c2rduA_ | Alignment | not modelled | 85.2 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1;<br>**PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate |
| 100 | c3r2gA_ | Alignment | not modelled | 84.9 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase;<br>**PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila |
| 101 | c2a7pA_ | Alignment | not modelled | 84.1 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase; |

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| 101 | c2a7nA_ | Alignment | not modelled | 84.1 | 25 | **PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase |
| 102 | d2gl5a1 | Alignment | not modelled | 84.0 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 103 | c2z6jB_ | Alignment | not modelled | 83.4 | 26 | **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 |
| 104 | c2gdqB_ | Alignment | not modelled | 81.8 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**yitf;<br>**PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from bacillus subtilis at 1.8 a resolution |
| 105 | c2pp1C_ | Alignment | not modelled | 81.4 | 27 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**l-talarate/galactarate dehydratase;<br>**PDBTitle:** crystal structure of l-talarate/galactarate dehydratase from2 salmonella typhimurium lt2 liganded with mg and l-lyxarohydroxamate |
| 106 | c3jw7E_ | Alignment | not modelled | 81.0 | 23 | **PDB header:**isomerase<br>**Chain:** E: **PDB Molecule:**dipeptide epimerase;<br>**PDBTitle:** crystal structure of dipeptide epimerase from enterococcus faecalis2 v583 complexed with mg and dipeptide l-ile-l-tyr |
| 107 | d1y0ea_ | Alignment | not modelled | 79.5 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 108 | d2chra1 | Alignment | not modelled | 79.2 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 109 | c2hmcA_ | Alignment | not modelled | 78.9 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens |
| 110 | c3pg8B_ | Alignment | not modelled | 78.3 | 22 | **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 |
| 111 | d2a21a1 | Alignment | not modelled | 76.8 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I DAHP synthetase |
| 112 | d1yeya1 | Alignment | not modelled | 76.7 | 25 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 113 | c2qjjC_ | Alignment | not modelled | 76.3 | 20 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme;<br>**PDBTitle:** crystal structure of d-mannonate dehydratase from novosphingobium2 aromaticivorans |
| 114 | c2qdeA_ | Alignment | not modelled | 76.3 | 30 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family<br>**PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1 |
| 115 | c3dipA_ | Alignment | not modelled | 76.2 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**enolase;<br>**PDBTitle:** crystal structure of an enolase protein from the2 environmental genome shotgun sequencing of the sargasso sea |
| 116 | d1muca1 | Alignment | not modelled | 75.5 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 117 | c2oz8B_ | Alignment | not modelled | 75.3 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**mll7089 protein;<br>**PDBTitle:** crystal structure of putative mandelate racemase from mesorhizobium2 loti |
| 118 | c2cdh1_ | Alignment | not modelled | 74.9 | 25 | **PDB header:**transferase<br>**Chain:** 1: **PDB Molecule:**enoyl reductase;<br>**PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution. |
| 119 | c3t8qA_ | Alignment | not modelled | 74.9 | 22 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family<br>**PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 family protein from hoeflea phototrophica |
| 120 | c3q45E_ | Alignment | not modelled | 71.6 | 23 | **PDB header:**isomerase<br>**Chain:** E: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family;<br>**PDBTitle:** crystal structure of dipeptide epimerase from cytophaga hutchinsonii2 complexed with mg and dipeptide d-ala-l-val |