Phyre2

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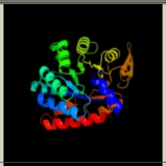
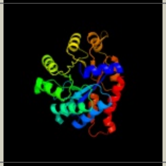
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A877 |
| Date | Thu Jan 5 11:07:06 GMT 2012 |
| Unique Job ID | 8b9e8764ba2ba33c |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3navB_ | Alignment |  | 100.0 | 63 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain;<br>**PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961 |
| 2 | d1qopa_ | Alignment |  | 100.0 | 85 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 3 | c2ekcA_ | Alignment |  | 100.0 | 32 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain;<br>**PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5 |
| 4 | d1ujpa_ | Alignment |  | 100.0 | 28 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 5 | c3thaB_ | Alignment |  | 100.0 | 29 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain;<br>**PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni. |
| 6 | d1rd5a_ | Alignment |  | 100.0 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 7 | d1geqa_ | Alignment |  | 100.0 | 34 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 8 | d1xcfa_ | Alignment |  | 100.0 | 95 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 9 | d1viza_ | Alignment |  | 100.0 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 10 | d2f6ua1 | Alignment |  | 100.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 11 | c3igsB_ | Alignment |  | 100.0 | 16 | **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 |

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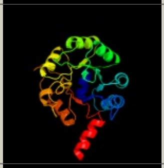
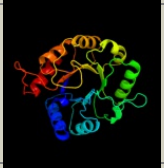
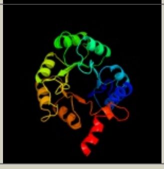
| 12 | d1j5ta_ | Alignment |  | 100.0 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 13 | c3q58A_ | Alignment |  | 100.0 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase;<br>**PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica |
| 14 | c3qc3B_ | Alignment |  | 100.0 | 16 | **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 |
| 15 | d1rpxa_ | Alignment |  | 99.9 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 16 | c2c3zA_ | Alignment |  | 99.9 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase;<br>**PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus |
| 17 | c3ct7E_ | Alignment |  | 99.9 | 18 | **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 |
| 18 | d1tqxa_ | Alignment |  | 99.9 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 19 | c3inpA_ | Alignment |  | 99.9 | 15 | **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. |
| 20 | d1y0ea_ | Alignment |  | 99.9 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 21 | d1q6oa_ | Alignment | not modelled | 99.9 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Decarboxylase |
| 22 | d1yxya1 | Alignment | not modelled | 99.9 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 23 | d1tqja_ | Alignment | not modelled | 99.9 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 24 | d1h1ya_ | Alignment | not modelled | 99.9 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 25 | c3f4wA_ | Alignment | not modelled | 99.9 | 19 | **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 |
| 26 | c3ajxA_ | Alignment | not modelled | 99.9 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**3-hexulose-6-phosphate synthase;<br>**PDBTitle:** crystal structure of 3-hexulose-6-phosphate synthase |
| 27 | d2flia1 | Alignment | not modelled | 99.9 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 28 | c3jr2D_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**biosynthetic protein<br>**Chain:** D: **PDB Molecule:**hexulose-6-phosphate synthase sgbh;<br>**PDBTitle:** x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961 |
| | | | | | | **Fold:**TIM beta/alpha-barrel |

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| 29 | d1dvja_ | Alignment | not modelled | 99.9 | 14 | **Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Decarboxylase |
| 30 | c3exsB_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**rmpd (hexulose-6-phosphate synthase);<br>**PDBTitle:** crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p |
| 31 | d2tpsa_ | Alignment | not modelled | 99.8 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Thiamin phosphate synthase<br>**Family:**Thiamin phosphate synthase |
| 32 | d1piia2 | Alignment | not modelled | 99.8 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 33 | d2czda1 | Alignment | not modelled | 99.8 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Decarboxylase |
| 34 | d1wbha1 | Alignment | not modelled | 99.8 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 35 | d1vhca_ | Alignment | not modelled | 99.8 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 36 | d1wa3a1 | Alignment | not modelled | 99.8 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 37 | c3cu2A_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ribulose-5-phosphate 3-epimerase;<br>**PDBTitle:** crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution |
| 38 | d1vzwa1 | Alignment | not modelled | 99.7 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 39 | c3qjaA_ | Alignment | not modelled | 99.7 | 15 | **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 |
| 40 | d1i4na_ | Alignment | not modelled | 99.7 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 41 | d1mxsa_ | Alignment | not modelled | 99.7 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 42 | d1km4a_ | Alignment | not modelled | 99.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Decarboxylase |
| 43 | c2v82A_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase;<br>**PDBTitle:** kdpgal complexed to kdpgal |
| 44 | d1thfd_ | Alignment | not modelled | 99.7 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 45 | d1h5ya_ | Alignment | not modelled | 99.7 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 46 | d1vc4a_ | Alignment | not modelled | 99.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 47 | d1a53a_ | Alignment | not modelled | 99.7 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 48 | c3nm3D_ | Alignment | not modelled | 99.6 | 12 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme;<br>**PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes |
| 49 | d1xi3a_ | Alignment | not modelled | 99.6 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Thiamin phosphate synthase<br>**Family:**Thiamin phosphate synthase |
| 50 | c1yadD_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**regulatory protein teni;<br>**PDBTitle:** structure of teni from bacillus subtilis |
| 51 | c3o63B_ | Alignment | not modelled | 99.6 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase;<br>**PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis |
| 52 | c3labA_ | Alignment | not modelled | 99.6 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate)<br>**PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica |
| 53 | d1ka9f_ | Alignment | not modelled | 99.6 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 54 | c2y85D_ | Alignment | not modelled | 99.6 | 23 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp |
| | | | | | | **PDB header:**oxidoreductase |

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| 55 | c1gthD_ | Alignment | not modelled | 99.6 | 19 | **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase;<br>**PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil |
| 56 | c2yw3E_ | Alignment | not modelled | 99.5 | 20 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-<br>**PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1 |
| 57 | c2z6jB_ | Alignment | not modelled | 99.5 | 17 | **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 |
| 58 | d1d3ga_ | Alignment | not modelled | 99.5 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 59 | c3ru6C_ | Alignment | not modelled | 99.5 | 14 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**orotidine 5'-phosphate decarboxylase;<br>**PDBTitle:** 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168 |
| 60 | c1tv5A_ | Alignment | not modelled | 99.5 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase homolog, mitochondrial;<br>**PDBTitle:** plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor |
| 61 | d1tv5a1 | Alignment | not modelled | 99.5 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 62 | d1f76a_ | Alignment | not modelled | 99.5 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 63 | c2gjlA_ | Alignment | not modelled | 99.5 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hypothetical protein pa1024;<br>**PDBTitle:** crystal structure of 2-nitropropane dioxygenase |
| 64 | d1w0ma_ | Alignment | not modelled | 99.5 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Triosephosphate isomerase (TIM)<br>**Family:**Triosephosphate isomerase (TIM) |
| 65 | d1gtea2 | Alignment | not modelled | 99.4 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 66 | c2fptA_ | Alignment | not modelled | 99.4 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, mitochondrial;<br>**PDBTitle:** dual binding mode of a novel series of dhodh inhibitors |
| 67 | c3bo9B_ | Alignment | not modelled | 99.4 | 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 |
| 68 | c2htmB_ | Alignment | not modelled | 99.4 | 18 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig;<br>**PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8 |
| 69 | d1hg3a_ | Alignment | not modelled | 99.4 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Triosephosphate isomerase (TIM)<br>**Family:**Triosephosphate isomerase (TIM) |
| 70 | d1juba_ | Alignment | not modelled | 99.3 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 71 | d1tb3a1 | Alignment | not modelled | 99.3 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 72 | d1goxa_ | Alignment | not modelled | 99.3 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 73 | d1vhna_ | Alignment | not modelled | 99.3 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 74 | d1ep3a_ | Alignment | not modelled | 99.3 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 75 | c2e77B_ | Alignment | not modelled | 99.3 | 19 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**lactate oxidase;<br>**PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex |
| 76 | d1jcna1 | Alignment | not modelled | 99.3 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 77 | c3bw2A_ | Alignment | not modelled | 99.3 | 19 | **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 |
| 78 | c2cdh1_ | Alignment | not modelled | 99.3 | 11 | **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. |
| 79 | d1uuma_ | Alignment | not modelled | 99.3 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 80 | d1vrda1 | Alignment | not modelled | 99.3 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| | | | | | | **PDB header:**oxidoreductase |

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| 81 | c1vrdA_ | Alignment | not modelled | 99.3 | 20 | **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 | d1jr1a1 | Alignment | not modelled | 99.3 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 83 | d1eepa_ | Alignment | not modelled | 99.3 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 84 | d1wv2a_ | Alignment | not modelled | 99.3 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**ThiG-like<br>**Family:**ThiG-like |
| 85 | c1jcnA_ | Alignment | not modelled | 99.3 | 19 | **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 |
| 86 | c3ceuA_ | Alignment | not modelled | 99.3 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase;<br>**PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268 |
| 87 | c1ypfB_ | Alignment | not modelled | 99.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**gmp reductase;<br>**PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution |
| 88 | c3oixA_ | Alignment | not modelled | 99.3 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate<br>**PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans |
| 89 | d1xm3a_ | Alignment | not modelled | 99.3 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**ThiG-like<br>**Family:**ThiG-like |
| 90 | c2rduA_ | Alignment | not modelled | 99.3 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1;<br>**PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate |
| 91 | d1zfja1 | Alignment | not modelled | 99.3 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 92 | c3b0vD_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**oxidoreductase/rna<br>**Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase;<br>**PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna |
| 93 | d1p4ca_ | Alignment | not modelled | 99.2 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 94 | c2a7nA_ | Alignment | not modelled | 99.2 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase;<br>**PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase |
| 95 | c2w6rA_ | Alignment | not modelled | 99.2 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit<br>**PDBTitle:** crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels |
| 96 | c3khjE_ | Alignment | not modelled | 99.2 | 12 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase;<br>**PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64 |
| 97 | c1zfjA_ | Alignment | not modelled | 99.2 | 22 | **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 |
| 98 | d2b4ga1 | Alignment | not modelled | 99.2 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 99 | c3r2gA_ | Alignment | not modelled | 99.2 | 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 |
| 100 | c1kbiB_ | Alignment | not modelled | 99.2 | 15 | **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 |
| 101 | c3ffsC_ | Alignment | not modelled | 99.2 | 18 | **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 |
| 102 | c1piiA_ | Alignment | not modelled | 99.2 | 16 | **PDB header:**bifunctional(isomerase and synthase)<br>**Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase;<br>**PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution |
| 103 | c3gr7A_ | Alignment | not modelled | 99.2 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadph dehydrogenase;<br>**PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form |
| | | | | | | **Fold:**TIM beta/alpha-barrel |

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| 104 | d1kbia1 | Alignment | not modelled | 99.2 | 18 | **Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 105 | d1jvna1 | Alignment | not modelled | 99.2 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 106 | c2bdqA_ | Alignment | not modelled | 99.1 | 16 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**copper homeostasis protein cutc;<br>**PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15. |
| 107 | d1p0ka_ | Alignment | not modelled | 99.1 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 108 | d1pvna1 | Alignment | not modelled | 99.1 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 109 | c3hf3A_ | Alignment | not modelled | 99.1 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**chromate reductase;<br>**PDBTitle:** old yellow enzyme from thermus scotoductus sa-01 |
| 110 | c2zrvC_ | Alignment | not modelled | 99.1 | 20 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase;<br>**PDBTitle:** crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fmn. |
| 111 | c3gndC_ | Alignment | not modelled | 99.1 | 18 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**aldolase lsrf;<br>**PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate |
| 112 | c1znnF_ | Alignment | not modelled | 99.1 | 20 | **PDB header:**biosynthetic protein<br>**Chain:** F: **PDB Molecule:**plp synthase;<br>**PDBTitle:** structure of the synthase subunit of plp synthase |
| 113 | c3tfxB_ | Alignment | not modelled | 99.1 | 18 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**orotidine 5'-phosphate decarboxylase;<br>**PDBTitle:** crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus |
| 114 | d1ps9a1 | Alignment | not modelled | 99.0 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 115 | d1znna1 | Alignment | not modelled | 99.0 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**PdxS-like |
| 116 | c2h90A_ | Alignment | not modelled | 99.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**xenobiotic reductase a;<br>**PDBTitle:** xenobiotic reductase a in complex with coumarin |
| 117 | d1vcfa1 | Alignment | not modelled | 99.0 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 118 | d1djqa1 | Alignment | not modelled | 99.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 119 | c1jvnB_ | Alignment | not modelled | 99.0 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf;<br>**PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites |
| 120 | d1z41a1 | Alignment | not modelled | 99.0 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |