# Phyre$^2$

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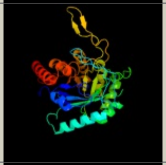
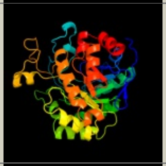
| Description | P25889 |
| Date | Thu Jan 5 11:42:42 GMT 2012 |
| Unique Job ID | 67679a0c70f61f3e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1gthD_ | Alignment |  | 100.0 | 37 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase;<br>**PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil |
| 2 | d1tv5a1 | Alignment |  | 100.0 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 3 | c1tv5A_ | Alignment |  | 100.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase homolog, mitochondrial;<br>**PDBTitle:** plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor |
| 4 | d1d3ga_ | Alignment |  | 100.0 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 5 | c2fptA_ | Alignment |  | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, mitochondrial;<br>**PDBTitle:** dual binding mode of a novel series of dhodh inhibitors |
| 6 | d1uuma_ | Alignment |  | 100.0 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 7 | d1f76a_ | Alignment |  | 100.0 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 8 | c3oixA_ | Alignment |  | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate<br>**PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans |
| 9 | d1juba_ | Alignment |  | 100.0 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 10 | d2b4ga1 | Alignment |  | 100.0 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 11 | c3gyeA_ | Alignment |  | 100.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, putative;<br>**PDBTitle:** didydroorotate dehydrogenase from leishmania major |

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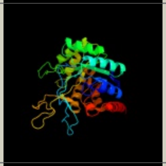
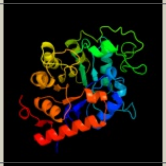
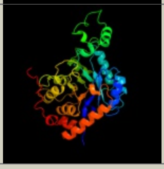
| 12 | d1ep3a_ | Alignment |  | 100.0 | 25 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 13 | d1gtea2 | Alignment |  | 100.0 | 36 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 14 | c2zrvC_ | Alignment |  | 100.0 | 17 | **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. |
| 15 | d1vcfa1 | Alignment |  | 100.0 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 16 | d1goxa_ | Alignment |  | 100.0 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 17 | c2rduA_ | Alignment |  | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1;<br>**PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate |
| 18 | c2e77B_ | Alignment |  | 100.0 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**lactate oxidase;<br>**PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex |
| 19 | d1tb3a1 | Alignment |  | 100.0 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 20 | c1kbiB_ | Alignment |  | 100.0 | 17 | **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 |
| 21 | d1p4ca_ | Alignment | not modelled | 100.0 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 22 | d1p0ka_ | Alignment | not modelled | 100.0 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 23 | c2a7nA_ | Alignment | not modelled | 100.0 | 16 | **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 |
| 24 | d1kbia1 | Alignment | not modelled | 100.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 25 | d1vhna_ | Alignment | not modelled | 99.9 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 26 | c3khjE_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase;<br>**PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64 |
| 27 | c3b0vD_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**oxidoreductase/rna<br>**Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase;<br>**PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna |
| 28 | d1eepa_ | Alignment | not modelled | 99.9 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| | | | | | | **PDB header:**oxidoreductase |

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| 29 | c1vrdA_ | Alignment | not modelled | 99.9 | 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 |
| 30 | d1jr1a1 | Alignment | not modelled | 99.9 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 31 | d1vrda1 | Alignment | not modelled | 99.9 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 32 | c2qr6A_ | Alignment | not modelled | 99.9 | 18 | **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 |
| 33 | d1jcna1 | Alignment | not modelled | 99.9 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 34 | d1zfja1 | Alignment | not modelled | 99.9 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 35 | c3ffsC_ | Alignment | not modelled | 99.9 | 22 | **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 |
| 36 | c1ypfB_ | Alignment | not modelled | 99.9 | 14 | **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 |
| 37 | c1jcnA_ | Alignment | not modelled | 99.9 | 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 |
| 38 | c3gr7A_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadph dehydrogenase;<br>**PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form |
| 39 | c3r2gA_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase;<br>**PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila |
| 40 | c1me9A_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase;<br>**PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound |
| 41 | c2a7rD_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**gmp reductase 2;<br>**PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2) |
| 42 | d1pvna1 | Alignment | not modelled | 99.9 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 43 | d2cu0a1 | Alignment | not modelled | 99.9 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Inosine monophosphate dehydrogenase (IMPDH)<br>**Family:**Inosine monophosphate dehydrogenase (IMPDH) |
| 44 | d1geqa_ | Alignment | not modelled | 99.9 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 45 | c2cu0B_ | Alignment | not modelled | 99.9 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase;<br>**PDBTitle:** crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3 |
| 46 | c3hf3A_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**chromate reductase;<br>**PDBTitle:** old yellow enzyme from thermus scotoductus sa-01 |
| 47 | c2cdh1_ | Alignment | not modelled | 99.9 | 21 | **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. |
| 48 | d1ps9a1 | Alignment | not modelled | 99.9 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 49 | c2h90A_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**xenobiotic reductase a;<br>**PDBTitle:** xenobiotic reductase a in complex with coumarin |
| 50 | c3kruC_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nadh:flavin oxidoreductase/nadh oxidase;<br>**PDBTitle:** crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39 |
| 51 | c2htmB_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig;<br>**PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8 |
| 52 | d1z41a1 | Alignment | not modelled | 99.8 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 53 | c1zfjA_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; |

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|---|---|---|---|---|---|---|
| 53 | c1zfjA_ | Alignment | not modelled | 99.8 | 19 | **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes |
| 54 | d1djqa1 | Alignment | not modelled | 99.8 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 55 | c1ps9A_ | Alignment | not modelled | 99.8 | 16 | **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 |
| 56 | c1djnB_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**trimethylamine dehydrogenase;<br>**PDBTitle:** structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1) |
| 57 | d1rd5a_ | Alignment | not modelled | 99.8 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 58 | c2gjlA_ | Alignment | not modelled | 99.7 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hypothetical protein pa1024;<br>**PDBTitle:** crystal structure of 2-nitropropane dioxygenase |
| 59 | c2z6jB_ | Alignment | not modelled | 99.7 | 22 | **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 |
| 60 | d1gwja_ | Alignment | not modelled | 99.7 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 61 | d1gtea5 | Alignment | not modelled | 99.7 | 32 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 62 | c3bo9B_ | Alignment | not modelled | 99.7 | 21 | **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 |
| 63 | d1vyra_ | Alignment | not modelled | 99.7 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 64 | c3k30B_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**histamine dehydrogenase;<br>**PDBTitle:** histamine dehydrogenase from nocardiodes simplex |
| 65 | c2gq8A_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**oxidoreductase, fmn-binding;<br>**PDBTitle:** structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone |
| 66 | c3bw2A_ | Alignment | not modelled | 99.6 | 20 | **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 |
| 67 | d1xm3a_ | Alignment | not modelled | 99.6 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**ThiG-like<br>**Family:**ThiG-like |
| 68 | c3gkaB_ | Alignment | not modelled | 99.6 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase;<br>**PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei |
| 69 | d1oyaa_ | Alignment | not modelled | 99.6 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 70 | d1vjia_ | Alignment | not modelled | 99.6 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 71 | c2c3yA_ | Alignment | not modelled | 99.5 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase;<br>**PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus |
| 72 | d1icpa_ | Alignment | not modelled | 99.5 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 73 | c3atyA_ | Alignment | not modelled | 99.5 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**prostaglandin f2a synthase;<br>**PDBTitle:** crystal structure of tcoye |
| 74 | d1ofda2 | Alignment | not modelled | 99.5 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 75 | c3l5aA_ | Alignment | not modelled | 99.5 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase;<br>**PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus |
| 76 | d1ea0a2 | Alignment | not modelled | 99.5 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 77 | d1y0ea_ | Alignment | not modelled | 99.4 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 78 | d1xcfa_ | Alignment | not modelled | 99.4 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 79 | d1qopa_ | Alignment | not modelled | 99.4 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |

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|---|---|---|---|---|---|---|
| 80 | c2gmhA_ | Alignment | not modelled | 99.4 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**electron transfer flavoprotein-ubiquinone<br>**PDBTitle:** structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone |
| 81 | c2vdcF_ | Alignment | not modelled | 99.3 | 19 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**glutamate synthase [nadph] large chain;<br>**PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications. |
| 82 | c3q58A_ | Alignment | not modelled | 99.3 | 18 | **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 |
| 83 | d1q45a_ | Alignment | not modelled | 99.3 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 84 | c2fugG_ | Alignment | not modelled | 99.3 | 33 | **PDB header:**oxidoreductase<br>**Chain:** G: **PDB Molecule:**nadh-quinone oxidoreductase chain 9;<br>**PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 85 | d2fug91 | Alignment | not modelled | 99.3 | 33 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 86 | d1hfel2 | Alignment | not modelled | 99.3 | 23 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 87 | d1yxya1 | Alignment | not modelled | 99.3 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 88 | c1lm1A_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ferredoxin-dependent glutamate synthase;<br>**PDBTitle:** structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme |
| 89 | c3navB_ | Alignment | not modelled | 99.3 | 16 | **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 |
| 90 | d1xera_ | Alignment | not modelled | 99.2 | 25 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Archaeal ferredoxins |
| 91 | c2c3zA_ | Alignment | not modelled | 99.2 | 18 | **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 |
| 92 | d1wa3a1 | Alignment | not modelled | 99.2 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 93 | c2v82A_ | Alignment | not modelled | 99.2 | 18 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase;<br>**PDBTitle:** kdpgal complexed to kdpgal |
| 94 | d2c42a5 | Alignment | not modelled | 99.2 | 28 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 95 | c3gyxJ_ | Alignment | not modelled | 99.2 | 27 | **PDB header:**oxidoreductase<br>**Chain:** J: **PDB Molecule:**adenylylsulfate reductase;<br>**PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas |
| 96 | d7fd1a_ | Alignment | not modelled | 99.2 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**7-Fe ferredoxin |
| 97 | c2ekcA_ | Alignment | not modelled | 99.2 | 16 | **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 |
| 98 | d1wv2a_ | Alignment | not modelled | 99.2 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**ThiG-like<br>**Family:**ThiG-like |
| 99 | c3igsB_ | Alignment | not modelled | 99.2 | 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 |
| 100 | d1jb0c_ | Alignment | not modelled | 99.1 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**7-Fe ferredoxin |
| 101 | c1hfeL_ | Alignment | not modelled | 99.1 | 23 | **PDB header:**hydrogenase<br>**Chain:** L: **PDB Molecule:**protein (fe-only hydrogenase (e.c.1.18.99.1)<br>**PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans |
| 102 | d1rpxa_ | Alignment | not modelled | 99.1 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 103 | d1jnrb_ | Alignment | not modelled | 99.1 | 23 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 104 | c3thaB_ | Alignment | not modelled | 99.1 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain;<br>**PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni. |
| | | | | | | **Fold:**TIM beta/alpha-barrel |

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| 105 | d1ka9f_ | Alignment | not modelled | 99.1 | 21 | **Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 106 | c1gx7A_ | Alignment | not modelled | 99.1 | 28 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**periplasmic [fe] hydrogenase large subunit;<br>**PDBTitle:** best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase |
| 107 | d1dura_ | Alignment | not modelled | 99.1 | 27 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Short-chain ferredoxins |
| 108 | c3qc3B_ | Alignment | not modelled | 99.1 | 10 | **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 |
| 109 | d1bc6a_ | Alignment | not modelled | 99.1 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**7-Fe ferredoxin |
| 110 | d1h98a_ | Alignment | not modelled | 99.1 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**7-Fe ferredoxin |
| 111 | d1h1ya_ | Alignment | not modelled | 99.1 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 112 | d1h5ya_ | Alignment | not modelled | 99.0 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 113 | c3qjaA_ | Alignment | not modelled | 99.0 | 17 | **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 |
| 114 | d2flia1 | Alignment | not modelled | 99.0 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 115 | d1y5ib1 | Alignment | not modelled | 99.0 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 116 | d1wbha1 | Alignment | not modelled | 99.0 | 8 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 117 | d1thfd_ | Alignment | not modelled | 99.0 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 118 | d1a53a_ | Alignment | not modelled | 99.0 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 119 | d2fug34 | Alignment | not modelled | 99.0 | 13 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |
| 120 | d3c8ya3 | Alignment | not modelled | 99.0 | 23 | **Fold:**Ferredoxin-like<br>**Superfamily:**4Fe-4S ferredoxins<br>**Family:**Ferredoxin domains from multidomain proteins |