

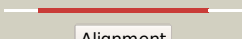













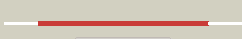







Phyre2

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|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0417_(thiG)_502369_503127 |
| Date | Tue Jul 23 14:50:49 BST 2019 |
| Unique Job ID | 0013a74c62ae9b20 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d1xm3a_ |  Alignment |  | 100.0 | 49 | Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like |
| 2 | c5z9yB_ |  Alignment |  | 100.0 | 100 | PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp |
| 3 | c2htmB_ |  Alignment |  | 100.0 | 46 | PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8 |
| 4 | c4n6eA_ |  Alignment |  | 100.0 | 35 | PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex |
| 5 | d1wv2a_ |  Alignment |  | 100.0 | 55 | Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like |
| 6 | c6ei9A_ |  Alignment |  | 100.0 | 17 | PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb) |
| 7 | c3tsmB_ |  Alignment |  | 100.0 | 15 | PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 bruceella melitensis |
| 8 | c1piiA_ |  Alignment |  | 100.0 | 13 | PDB header: bifunctional(isomerase and synthase) Chain: A: PDB Molecule: n-(5'phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution |
| 9 | c6bmaA_ |  Alignment |  | 99.9 | 14 | PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168 |
| 10 | d1vc4a_ |  Alignment |  | 99.9 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |
| 11 | d1i4na_ |  Alignment |  | 99.9 | 13 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |

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|----|-------------------------|-----------|--------------|------|----|---|
| 12 | c4xp7A_ | Alignment | | 99.9 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2 |
| 13 | c3qjaA_ | Alignment | | 99.9 | 21 | PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form |
| 14 | d1pia2 | Alignment | | 99.9 | 13 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 15 | d1a53a_ | Alignment | | 99.9 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 16 | d1vhna_ | Alignment | | 99.9 | 19 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 17 | c5ismF_ | Alignment | | 99.9 | 17 | PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1 |
| 18 | c3w9za_ | Alignment | | 99.9 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc |
| 19 | c2qjIA_ | Alignment | | 99.9 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase |
| 20 | c4iqIB_ | Alignment | | 99.9 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acp reductase ii2 (fabk) with cofactors nadph and fmn |
| 21 | d1j5ta_ | Alignment | not modelled | 99.9 | 12 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 22 | c1ypfB_ | Alignment | not modelled | 99.9 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution |
| 23 | c2rdtA_ | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst |
| 24 | c2z6jB_ | Alignment | not modelled | 99.9 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acp reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor |
| 25 | c3bo9B_ | Alignment | not modelled | 99.9 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution |
| 26 | d1tb3a1 | Alignment | not modelled | 99.9 | 10 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 27 | c4zqrD_ | Alignment | not modelled | 99.9 | 16 | PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from mycobacterium tuberculosis |
| 28 | c2a7nA_ | Alignment | not modelled | 99.9 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: l(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c6a0gA | Alignment | not modelled | 99.9 | 21 | PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate |
| 30 | d1p4ca | Alignment | not modelled | 99.9 | 21 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 31 | d1goxa | Alignment | not modelled | 99.9 | 16 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 32 | d1ep3a | Alignment | not modelled | 99.9 | 18 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 33 | c3r2gA | Alignment | not modelled | 99.9 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila |
| 34 | d1pvna1 | Alignment | not modelled | 99.9 | 13 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 35 | c3khjE | Alignment | not modelled | 99.9 | 14 | PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64 |
| 36 | c2e77B | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex |
| 37 | d1vrda1 | Alignment | not modelled | 99.9 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 38 | c4q33F | Alignment | not modelled | 99.9 | 14 | PDB header: oxidoreductase Chain: F: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5'-monophosphate dehydrogenase from2 clostridium perfringens complexed with imp and a110 |
| 39 | c3bw2A | Alignment | not modelled | 99.9 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes |
| 40 | c5upxA | Alignment | not modelled | 99.9 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from listeria monocytogenes in the presence of3 xanthosine monophosphate |
| 41 | c3b0vD | Alignment | not modelled | 99.9 | 16 | PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna |
| 42 | c4xtiA | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: structure of imp dehydrogenase of ashbya gossypii with imp bound to2 the active site |
| 43 | c4ff0B | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp |
| 44 | c3oixA | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans |
| 45 | d1juba | Alignment | not modelled | 99.9 | 16 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 46 | c2c3zA | Alignment | not modelled | 99.9 | 16 | PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus |
| 47 | c3nm3D | Alignment | not modelled | 99.9 | 12 | PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes |
| 48 | d1gtea2 | Alignment | not modelled | 99.9 | 15 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 49 | d1zfja1 | Alignment | not modelled | 99.9 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 50 | c4avfD | Alignment | not modelled | 99.9 | 18 | PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase |
| 51 | c5zknA | Alignment | not modelled | 99.9 | 15 | PDB header: isomerase Chain: A: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum |
| 52 | d1kbia1 | Alignment | not modelled | 99.9 | 10 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |

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|----|-------------------------|-----------|--------------|------|----|---|
| 53 | c4af0B_ | Alignment | not modelled | 99.9 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase |
| 54 | c6bkaA_ | Alignment | not modelled | 99.9 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberindnera2 saturnus |
| 55 | c1kbiB_ | Alignment | not modelled | 99.9 | 10 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme |
| 56 | c4n02A_ | Alignment | not modelled | 99.9 | 12 | PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae |
| 57 | c4mz1A_ | Alignment | not modelled | 99.9 | 17 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a internal deletion of cbs domain from campylobacter jejuni complexed3 with inhibitor compound p12 |
| 58 | d1jr1a1 | Alignment | not modelled | 99.9 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 59 | c3ffsC_ | Alignment | not modelled | 99.9 | 13 | PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase |
| 60 | d1p0ka_ | Alignment | not modelled | 99.9 | 18 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 61 | c6dvhF_ | Alignment | not modelled | 99.9 | 19 | PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant |
| 62 | c2zrvC_ | Alignment | not modelled | 99.9 | 14 | PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfolobus shibatae isopentenyl diphosphate2 isomerase in complex with reduced fmn. |
| 63 | d1d3ga_ | Alignment | not modelled | 99.9 | 15 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 64 | c1me9A_ | Alignment | not modelled | 99.9 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound |
| 65 | c3sr7C_ | Alignment | not modelled | 99.9 | 14 | PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase |
| 66 | c2rduA_ | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate |
| 67 | c6gk9C_ | Alignment | not modelled | 99.9 | 21 | PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa |
| 68 | d1eepa_ | Alignment | not modelled | 99.9 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 69 | c1fcbA_ | Alignment | not modelled | 99.9 | 10 | PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution |
| 70 | c1gthD_ | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil |
| 71 | c2a7rD_ | Alignment | not modelled | 99.9 | 11 | PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2) |
| 72 | c2cdh1_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution. |
| 73 | d1zna1 | Alignment | not modelled | 99.9 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: PdxS-like |
| 74 | d1f76a_ | Alignment | not modelled | 99.9 | 15 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 75 | c1jcnA_ | Alignment | not modelled | 99.8 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp |
| 76 | d1jcna1 | Alignment | not modelled | 99.8 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 77 | c4utwB_ | Alignment | not modelled | 99.8 | 16 | PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens |
| 78 | c1znnF_ | Alignment | not modelled | 99.8 | 20 | PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase |
| 79 | c4mjmD_ | Alignment | not modelled | 99.8 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a short internal deletion of cbs domain from bacillus anthracis str.3 ames |
| 80 | c1vrdA_ | Alignment | not modelled | 99.8 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution |
| 81 | c1yadD_ | Alignment | not modelled | 99.8 | 17 | PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis |
| 82 | d1uuma_ | Alignment | not modelled | 99.8 | 16 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 83 | c2qr6A_ | Alignment | not modelled | 99.8 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase; PDBTitle: crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution |
| 84 | c2fptA_ | Alignment | not modelled | 99.8 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors |
| 85 | d1vcfa1 | Alignment | not modelled | 99.8 | 18 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 86 | c4xq6A_ | Alignment | not modelled | 99.8 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis |
| 87 | d1yxya1 | Alignment | not modelled | 99.8 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like |
| 88 | d1tv5a1 | Alignment | not modelled | 99.8 | 12 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 89 | c1tv5A_ | Alignment | not modelled | 99.8 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor |
| 90 | d1xi3a_ | Alignment | not modelled | 99.8 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase |
| 91 | d2b4qa1 | Alignment | not modelled | 99.8 | 14 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 92 | c3gr7A_ | Alignment | not modelled | 99.8 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form |
| 93 | c5zjnB_ | Alignment | not modelled | 99.8 | 16 | PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate |
| 94 | c6b8sB_ | Alignment | not modelled | 99.8 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn |
| 95 | c3q58A_ | Alignment | not modelled | 99.8 | 17 | PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica |
| 96 | d1y0ea_ | Alignment | not modelled | 99.8 | 11 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like |
| 97 | d2tpsa_ | Alignment | not modelled | 99.8 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase |
| 98 | d2cu0a1 | Alignment | not modelled | 99.8 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 99 | c4ot7A_ | Alignment | not modelled | 99.8 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis |
| 100 | c3gyeA_ | Alignment | not modelled | 99.8 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: dihydroorotate dehydrogenase from leishmania major |
| 101 | c4fxsA_ | Alignment | not modelled | 99.8 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio |

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| | | | | | cholerae complexed2 with imp and mycophenolic acid |
| 102 | c3igsB_ | Alignment | not modelled | 99.8 | 14 PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase |
| 103 | c2h90A_ | Alignment | not modelled | 99.8 | 24 PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin |
| 104 | c4z9rA_ | Alignment | not modelled | 99.8 | 16 PDB header: oxidoreductase Chain: A: PDB Molecule: omega-3 polyunsaturated fatty acid synthase subunit pfa2; PDBTitle: crystal structure of pfa2 from shewanella oneidensis in complex with2 nad+ determined by in-situ diffraction. |
| 105 | c2cu0B_ | Alignment | not modelled | 99.8 | 13 PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3 |
| 106 | c3o63B_ | Alignment | not modelled | 99.7 | 17 PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis |
| 107 | c3hf3A_ | Alignment | not modelled | 99.7 | 19 PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01 |
| 108 | c5ocsB_ | Alignment | not modelled | 99.7 | 23 PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-dependent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans |
| 109 | d1ka9f_ | Alignment | not modelled | 99.7 | 15 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes |
| 110 | d1ps9a1 | Alignment | not modelled | 99.7 | 23 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 111 | c3tsdA_ | Alignment | not modelled | 99.7 | 18 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp |
| 112 | c4z38B_ | Alignment | not modelled | 99.7 | 12 PDB header: transferase Chain: B: PDB Molecule: mlna; PDBTitle: crystal structure of enoyl reductase domain of mlna from the2 macrolactin biosynthesis cluster from bacillus amyloliquefaciens |
| 113 | c3kruC_ | Alignment | not modelled | 99.7 | 16 PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39 |
| 114 | c4z87B_ | Alignment | not modelled | 99.7 | 15 PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp |
| 115 | c4dqwb_ | Alignment | not modelled | 99.7 | 22 PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770 |
| 116 | c1zfjA_ | Alignment | not modelled | 99.7 | 18 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes |
| 117 | c1ps9A_ | Alignment | not modelled | 99.7 | 22 PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase |
| 118 | c4x2rA_ | Alignment | not modelled | 99.7 | 17 PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis |
| 119 | c4axkB_ | Alignment | not modelled | 99.7 | 17 PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens |
| 120 | d1djqa1 | Alignment | not modelled | 99.7 | 15 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |