



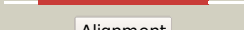

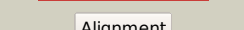





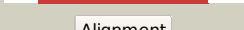



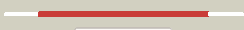


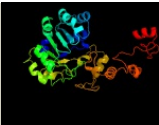

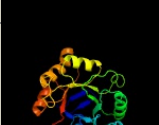








Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0021c_(-)_25913_26881 |
| Date | Tue Jul 23 14:50:05 BST 2019 |
| Unique Job ID | 324c119848ea2478 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3bo9B_ |  Alignment |  | 100.0 | 32 | 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 |
| 2 | c2gjlA_ |  Alignment |  | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase |
| 3 | c4iqjB_ |  Alignment |  | 100.0 | 31 | PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acyl reductase ii2 (fabk) with cofactors nadph and fmn |
| 4 | c2z6jB_ |  Alignment |  | 100.0 | 35 | PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acyl reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor |
| 5 | c3bw2A_ |  Alignment |  | 100.0 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces anschromogenes |
| 6 | c5lsmF_ |  Alignment |  | 100.0 | 28 | PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1 |
| 7 | c6bkaA_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus |
| 8 | c4z9rA_ |  Alignment |  | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: omega-3 polyunsaturated fatty acid synthase subunit pfad; PDBTitle: crystal structure of pfad from shewanella oneidensis in complex with2 nad+ determined by in-situ diffraction. |
| 9 | c4z38B_ |  Alignment |  | 100.0 | 21 | 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 |
| 10 | c4cw5B_ |  Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens |
| 11 | c4xtiA_ |  Alignment |  | 100.0 | 22 | 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 |
| | | | | | | PDB header: transferase |

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|----|-------------------------|-----------|---|-------|----|---|
| 12 | c2uval | Alignment |  | 100.0 | 18 | Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400 |
| 13 | c4af0B | Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase |
| 14 | c3tsdA | Alignment |  | 100.0 | 24 | 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 |
| 15 | d1zfja1 | Alignment |  | 100.0 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 16 | c2vkzH | Alignment |  | 100.0 | 17 | PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex |
| 17 | d1vrda1 | Alignment |  | 100.0 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 18 | c4b3yB | Alignment |  | 100.0 | 22 | PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase |
| 19 | d1pvna1 | Alignment |  | 100.0 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 20 | d1jcnA1 | Alignment |  | 100.0 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 21 | c4ff0B | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp |
| 22 | c1jcnA | Alignment | not modelled | 100.0 | 25 | 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 |
| 23 | c4zqrD | Alignment | not modelled | 100.0 | 17 | 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 |
| 24 | c3r2gA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila |
| 25 | c3khjE | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64 |
| 26 | c5upxA | Alignment | not modelled | 100.0 | 18 | 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 |
| 27 | c4q33F | Alignment | not modelled | 100.0 | 20 | 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 |

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|----|-------------------------|-----------|--------------|-------|----|---|
| | | | | | | and a110 |
| 28 | d1jr1a1 | Alignment | not modelled | 100.0 | 25 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 29 | c4mz1A | Alignment | not modelled | 100.0 | 22 | 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 |
| 30 | c4avfD | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase |
| 31 | c1vrdA | Alignment | not modelled | 100.0 | 24 | 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 |
| 32 | c4z87B | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp |
| 33 | c6gk9C | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa |
| 34 | d1lepa | Alignment | not modelled | 100.0 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 35 | c4mjmD | Alignment | not modelled | 100.0 | 23 | 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 |
| 36 | c2cdh1 | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution. |
| 37 | c3ffsC | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase |
| 38 | c1me9A | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound |
| 39 | d2cu0a1 | Alignment | not modelled | 100.0 | 21 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 40 | c4fxsA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid |
| 41 | c2qr6A | Alignment | not modelled | 100.0 | 18 | 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 |
| 42 | c2cu0B | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3 |
| 43 | c2a7rD | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2) |
| 44 | c4dqwB | Alignment | not modelled | 100.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770 |
| 45 | c1ypfB | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution |
| 46 | d1tb3a1 | Alignment | not modelled | 100.0 | 18 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 47 | c2rdtA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst |
| 48 | c5x8oA | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate |
| 49 | c1zjfA | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes |
| | | | | | | PDB header: flavoprotein |

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|----|-------------------------|-----------|--------------|------|----|---|
| 50 | c6a0gA | Alignment | not modelled | 99.9 | 25 | Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate |
| 51 | d1p4ca | Alignment | not modelled | 99.9 | 20 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 52 | c2a7nA | Alignment | not modelled | 99.9 | 20 | 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 |
| 53 | d1goxa | Alignment | not modelled | 99.9 | 24 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 54 | c2e77B | Alignment | not modelled | 99.9 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex |
| 55 | c1fcbA | Alignment | not modelled | 99.9 | 16 | 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 |
| 56 | c2rduA | Alignment | not modelled | 99.9 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate |
| 57 | d1kbia1 | Alignment | not modelled | 99.9 | 16 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 58 | c3sr7C | Alignment | not modelled | 99.9 | 17 | PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase |
| 59 | c1kbiB | Alignment | not modelled | 99.9 | 16 | 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 |
| 60 | c6dvhF | Alignment | not modelled | 99.9 | 23 | PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant |
| 61 | c2htmB | Alignment | not modelled | 99.9 | 15 | PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8 |
| 62 | d1juba | Alignment | not modelled | 99.9 | 21 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 63 | d1p0ka | Alignment | not modelled | 99.9 | 16 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 64 | c3w9zA | Alignment | not modelled | 99.9 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc |
| 65 | c4n02A | Alignment | not modelled | 99.9 | 16 | PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae |
| 66 | c2zrvC | Alignment | not modelled | 99.9 | 18 | 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. |
| 67 | c3oixA | Alignment | not modelled | 99.9 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans |
| 68 | c4n6eA | Alignment | not modelled | 99.8 | 19 | PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex |
| 69 | d1xm3a | Alignment | not modelled | 99.8 | 15 | Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like |
| 70 | d1vcfa1 | Alignment | not modelled | 99.8 | 20 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 71 | d2b4ga1 | Alignment | not modelled | 99.8 | 20 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 72 | c5z9yB | Alignment | not modelled | 99.8 | 17 | PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp |
| 73 | c3b0vD | Alignment | not modelled | 99.8 | 14 | PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna |
| 74 | d1vhna | Alignment | not modelled | 99.8 | 12 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 75 | d1y0ea | Alignment | not modelled | 99.8 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like |
| | | | | | | PDB header: oxidoreductase |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 76 | c3gyeA | Alignment | not modelled | 99.8 | 15 | Chain: A; PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: didydroorotate dehydrogenase from leishmania major |
| 77 | d1wv2a | Alignment | not modelled | 99.8 | 13 | Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like |
| 78 | c5zknA | Alignment | not modelled | 99.8 | 18 | PDB header: isomerase Chain: A; PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from <i>2</i> fusobacterium nucleatum |
| 79 | c6ei9A | Alignment | not modelled | 99.7 | 19 | PDB header: flavoprotein Chain: A; PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (<i>dusB</i>) |
| 80 | d1ep3a | Alignment | not modelled | 99.7 | 24 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 81 | c4utwB | Alignment | not modelled | 99.7 | 19 | PDB header: isomerase Chain: B; PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens |
| 82 | d1gtea2 | Alignment | not modelled | 99.7 | 21 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 83 | c4xp7A | Alignment | not modelled | 99.7 | 17 | PDB header: oxidoreductase Chain: A; PDB Molecule: trna-dihydrouridine(20) synthase [nad(p)+]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2 |
| 84 | c3igsB | Alignment | not modelled | 99.7 | 19 | 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 |
| 85 | d1d3ga | Alignment | not modelled | 99.7 | 18 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 86 | c6b8sB | Alignment | not modelled | 99.7 | 19 | PDB header: oxidoreductase Chain: B; PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn |
| 87 | d1ofda2 | Alignment | not modelled | 99.7 | 20 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 88 | c4xq6A | Alignment | not modelled | 99.7 | 19 | PDB header: oxidoreductase Chain: A; PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis |
| 89 | d1uuma | Alignment | not modelled | 99.7 | 20 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 90 | c3q58A | Alignment | not modelled | 99.7 | 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 |
| 91 | d1tv5a1 | Alignment | not modelled | 99.7 | 22 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 92 | c1tv5A | Alignment | not modelled | 99.7 | 22 | PDB header: oxidoreductase Chain: A; PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor |
| 93 | d1ea0a2 | Alignment | not modelled | 99.7 | 22 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 94 | c5zjnB | Alignment | not modelled | 99.7 | 15 | 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 |
| 95 | c2fptA | Alignment | not modelled | 99.7 | 19 | PDB header: oxidoreductase Chain: A; PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors |
| 96 | d1f76a | Alignment | not modelled | 99.7 | 22 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 97 | c5n2pA | Alignment | not modelled | 99.6 | 18 | PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a |
| 98 | d1wbha1 | Alignment | not modelled | 99.6 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 99 | d1wa3a1 | Alignment | not modelled | 99.5 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 100 | d1yxya1 | Alignment | not modelled | 99.5 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like |
| | | | | | | PDB header: oxidoreductase Chain: F; PDB Molecule: glutamate synthase [nadph] large chain; |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 101 | c2vdcF_ | Alignment | not modelled | 99.5 | 22 | PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications. PDB header: oxidoreductase |
| 102 | c1lm1A_ | Alignment | not modelled | 99.5 | 22 | Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme |
| 103 | c3qjaA_ | Alignment | not modelled | 99.5 | 20 | 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 |
| 104 | c3tsmB_ | Alignment | not modelled | 99.5 | 14 | PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis |
| 105 | c4e38A_ | Alignment | not modelled | 99.4 | 19 | PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156) |
| 106 | c6bmaA_ | Alignment | not modelled | 99.4 | 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 |
| 107 | c2c3zA_ | Alignment | not modelled | 99.4 | 15 | 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 |
| 108 | d1a53a_ | Alignment | not modelled | 99.4 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 109 | d1vc4a_ | Alignment | not modelled | 99.4 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 110 | d1w0ma_ | Alignment | not modelled | 99.4 | 26 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |
| 111 | c6oviA_ | Alignment | not modelled | 99.3 | 15 | PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate |
| 112 | d1vhca_ | Alignment | not modelled | 99.3 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 113 | d1hg3a_ | Alignment | not modelled | 99.3 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |
| 114 | c1gthD_ | Alignment | not modelled | 99.3 | 22 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpg) from pig, ternary complex with2 nadph and 5-iodouracil |
| 115 | d1ka9f_ | Alignment | not modelled | 99.2 | 22 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes |
| 116 | d1qopa_ | Alignment | not modelled | 99.2 | 12 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 117 | c4bk9B_ | Alignment | not modelled | 99.2 | 16 | PDB header: lyase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo PDBTitle: crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191 |
| 118 | d1h5ya_ | Alignment | not modelled | 99.2 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes |
| 119 | c2v82A_ | Alignment | not modelled | 99.2 | 19 | PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal |
| 120 | d1mxsa_ | Alignment | not modelled | 99.2 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |