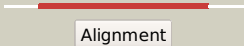

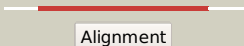

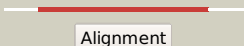







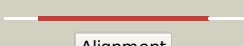











Phyre2

| | |
|------------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3359 (-)_3771515_3772705 |
| Date | Fri Aug 9 18:20:02 BST 2019 |
| Unique Job ID | 1e7a7d53c4565fa7 |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c6qkgB_ |  Alignment |  | 100.0 | 29 | PDB header: flavoprotein Chain: B; PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr) |
| 2 | c1ps9A_ |  Alignment |  | 100.0 | 28 | 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 |
| 3 | c1djnB_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: B; PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1) |
| 4 | c3k30B_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: B; PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiodes simplex |
| 5 | c5ocsB_ |  Alignment |  | 100.0 | 24 | PDB header: flavoprotein Chain: B; PDB Molecule: putative nadh-dependent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans |
| 6 | c6de6B_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: B; PDB Molecule: histamine dehydrogenase; PDBTitle: 2.1 a resolution structure of histamine dehydrogenase from rhizobium2 sp. 4-9 |
| 7 | d1gwja_ |  Alignment |  | 100.0 | 26 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 8 | d1z41a1 |  Alignment |  | 100.0 | 25 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 9 | c3l5aA_ |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: A; PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus |
| 10 | c3kruC_ |  Alignment |  | 100.0 | 25 | 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 |
| 11 | c2h90A_ |  Alignment |  | 100.0 | 28 | PDB header: oxidoreductase Chain: A; PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c4jicB_ | Alignment | | 100.0 | 26 | PDB header: oxidoreductase Chain: B: PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter |
| 13 | d1ps9a1 | Alignment | | 100.0 | 27 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 14 | c3hf3A_ | Alignment | | 100.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01 |
| 15 | d1oyaa_ | Alignment | | 100.0 | 21 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 16 | c5dxxA_ | Alignment | | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: artemisinic aldehyde delta(11(13)) reductase; PDBTitle: crystal structure of dbr2 |
| 17 | c3gkaB_ | Alignment | | 100.0 | 29 | PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei |
| 18 | c3atyA_ | Alignment | | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tcoye |
| 19 | d1vjia_ | Alignment | | 100.0 | 26 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 20 | c4tmcB_ | Alignment | | 100.0 | 21 | PDB header: flavoprotein Chain: B: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from candida macedoniensis2 aku4588 complexed with p-hydroxybenzaldehyde |
| 21 | c2gq8A_ | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone |
| 22 | c4b5nA_ | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sye4) |
| 23 | c4a3uB_ | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadh\flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr) |
| 24 | d1q45a_ | Alignment | not modelled | 100.0 | 24 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 25 | d1djqa1 | Alignment | not modelled | 100.0 | 24 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 26 | d1vyra_ | Alignment | not modelled | 100.0 | 24 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 27 | c3gr7A_ | Alignment | not modelled | 100.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form |
| 28 | c6mywA_ | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: gluconobacter ene-reductase (gluer) mutant - t36a |
| | | | | | | PDB header: oxidoreductase |

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|----|--------------------------|-----------|--------------|-------|----|--|
| 29 | c4qnwA_ | Alignment | not modelled | 100.0 | 25 | Chain: A: PDB Molecule: chanoclavine-i aldehyde reductase; PDBTitle: crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus |
| 30 | d1icpa_ | Alignment | not modelled | 100.0 | 24 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 31 | c6agzA_ | Alignment | not modelled | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from pichia sp. aku4542 |
| 32 | c5epdA_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidorecctase Chain: A: PDB Molecule: glycerol trinitrate reductase; PDBTitle: crystal structure of glycerol trinitrate reductase xdpb from2 agrobacterium sp. r89-1 (apo form) |
| 33 | c4df2A_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: p. stipitis oye2.6 complexed with p-chlorophenol |
| 34 | c4rnvD_ | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase/inhibitor Chain: D: PDB Molecule: nadh dehydrogenase 1; PDBTitle: g303 circular permutation of old yellow enzyme with the inhibitor p-2 hydroxybenzaldehyde |
| 35 | c4ot7A_ | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis |
| 36 | c4rnxA_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase 1; PDBTitle: k154 circular permutation of old yellow enzyme |
| 37 | c6ei9A_ | Alignment | not modelled | 100.0 | 26 | PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb) |
| 38 | c3w9zA_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc |
| 39 | d1gtea2 | Alignment | not modelled | 100.0 | 17 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 40 | c4xp7A_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)-like]; PDBTitle: crystal structure of human trna dihydrouridine synthase 2 |
| 41 | d1ep3a_ | Alignment | not modelled | 100.0 | 19 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 42 | d1vhna_ | Alignment | not modelled | 100.0 | 20 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 43 | c3b0vD_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna |
| 44 | d2b4ga1 | Alignment | not modelled | 99.8 | 14 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 45 | d1f76a_ | Alignment | not modelled | 99.8 | 17 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 46 | d1juba_ | Alignment | not modelled | 99.8 | 15 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 47 | c3oixA_ | Alignment | not modelled | 99.7 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans |
| 48 | c1gthD_ | Alignment | not modelled | 99.7 | 23 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil |
| 49 | d1d3ga_ | Alignment | not modelled | 99.7 | 20 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 50 | c4xq6A_ | Alignment | not modelled | 99.7 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis |
| 51 | c2fptA_ | Alignment | not modelled | 99.7 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors |
| 52 | c6b8sB_ | Alignment | not modelled | 99.6 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn |
| 53 | d1luuma_ | Alignment | not modelled | 99.6 | 22 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 54 | d1tv5a1 | Alignment | not modelled | 99.6 | 15 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 55 | c1tv5A_ | Alignment | not modelled | 99.6 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor |
| 56 | d2gl5a1 | Alignment | not modelled | 99.5 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like |
| 57 | c4n6eA | Alignment | not modelled | 99.5 | 24 | PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex |
| 58 | c3gyeA | Alignment | not modelled | 99.5 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, putative; PDBTitle: didydroorotate dehydrogenase from leishmania major |
| 59 | c5z9yB | Alignment | not modelled | 99.4 | 27 | PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp |
| 60 | c2htmB | Alignment | not modelled | 99.4 | 21 | PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8 |
| 61 | d1vrda1 | Alignment | not modelled | 99.4 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 62 | c4q33F | Alignment | not modelled | 99.3 | 19 | 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 |
| 63 | c4zqrD | Alignment | not modelled | 99.3 | 21 | 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 |
| 64 | c5upxA | Alignment | not modelled | 99.3 | 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 |
| 65 | c4ff0B | Alignment | not modelled | 99.3 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp |
| 66 | c3r2gA | Alignment | not modelled | 99.3 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila |
| 67 | c1jcnA | Alignment | not modelled | 99.3 | 18 | 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 |
| 68 | c1kbiB | Alignment | not modelled | 99.3 | 13 | 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 |
| 69 | d1pvna1 | Alignment | not modelled | 99.3 | 24 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 70 | c4mz1A | Alignment | not modelled | 99.3 | 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 |
| 71 | c1fcbA | Alignment | not modelled | 99.2 | 18 | 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 |
| 72 | d1zfja1 | Alignment | not modelled | 99.2 | 24 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 73 | c4af0B | Alignment | not modelled | 99.2 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase |
| 74 | d1tb3a1 | Alignment | not modelled | 99.2 | 16 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 75 | c2z6jB | Alignment | not modelled | 99.2 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acyl carrier ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor |
| 76 | c3khjE | Alignment | not modelled | 99.2 | 20 | PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64 |
| 77 | d1p0ka | Alignment | not modelled | 99.2 | 25 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 78 | c1ypfB | Alignment | not modelled | 99.2 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 79 | c1vrdA_ | Alignment | not modelled | 99.2 | 19 | 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 |
| 80 | d1kbia1 | Alignment | not modelled | 99.2 | 12 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 81 | d1jcna1 | Alignment | not modelled | 99.2 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 82 | c2rdtA_ | Alignment | not modelled | 99.2 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst |
| 83 | c6a0gA_ | Alignment | not modelled | 99.1 | 25 | PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate |
| 84 | c2zrvC_ | Alignment | not modelled | 99.1 | 19 | PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfolobus shibatae isopentenyl diphosphate2 isomerase in complex with reduced frm. |
| 85 | c2a7nA_ | Alignment | not modelled | 99.1 | 17 | 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 |
| 86 | c1zfa_ | Alignment | not modelled | 99.1 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes |
| 87 | c4mjmD_ | Alignment | not modelled | 99.1 | 19 | 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 |
| 88 | c2gl5A_ | Alignment | not modelled | 99.1 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dehydratase protein; PDBTitle: crystal structure of putative dehydratase from salmonella thymurium |
| 89 | d1goxa_ | Alignment | not modelled | 99.1 | 22 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 90 | d1xm3a_ | Alignment | not modelled | 99.1 | 19 | Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like |
| 91 | c3tdmD_ | Alignment | not modelled | 99.1 | 25 | PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfplr |
| 92 | d1geqa_ | Alignment | not modelled | 99.1 | 21 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |
| 93 | c4xtiA_ | Alignment | not modelled | 99.1 | 20 | 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 |
| 94 | c4n02A_ | Alignment | not modelled | 99.1 | 14 | PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae |
| 95 | d1jr1a1 | Alignment | not modelled | 99.1 | 24 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 96 | d1p4ca_ | Alignment | not modelled | 99.1 | 19 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 97 | c2e77B_ | Alignment | not modelled | 99.1 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex |
| 98 | c4avfD_ | Alignment | not modelled | 99.1 | 27 | PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase |
| 99 | c1me9A_ | Alignment | not modelled | 99.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound |
| 100 | d2cu0a1 | Alignment | not modelled | 99.0 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 101 | d1jpma1 | Alignment | not modelled | 99.0 | 21 | Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like |
| 102 | c5ismF_ | Alignment | not modelled | 99.0 | 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 |
| 103 | c3tda_ | Alignment | not modelled | 99.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 103 | c3b5A_ | Alignment | not modelled | 99.0 | 22 | PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from <i>Bacillus anthracis</i> str. ames complexed with xmp |
| 104 | c4utwB_ | Alignment | not modelled | 99.0 | 16 | PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structural characterisation of nane, mannac6p c2 epimerase,2 from <i>Clostridium perfringens</i> |
| 105 | c5n2pA_ | Alignment | not modelled | 99.0 | 20 | PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: <i>Sulfolobus solfataricus</i> tryptophan synthase a |
| 106 | d1rd5a_ | Alignment | not modelled | 99.0 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 107 | c4z87B_ | Alignment | not modelled | 99.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from <i>Ashbya gossypii</i> bound to gdp |
| 108 | c3bw2A_ | Alignment | not modelled | 99.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from <i>Streptomyces ansiochromogenes</i> |
| 109 | c4iq1B_ | Alignment | not modelled | 99.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of <i>Porphyromonas gingivalis</i> enoyl-acp reductase ii2 (fabk) with cofactors nadph and fmn |
| 110 | c4fxsA_ | Alignment | not modelled | 99.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from <i>Vibrio cholerae</i> complexed2 with imp and mycophenolic acid |
| 111 | c3v3wA_ | Alignment | not modelled | 99.0 | 18 | PDB header: lyase Chain: A: PDB Molecule: starvation sensing protein rspa; PDBTitle: crystal structure of an enolase from the soil bacterium <i>Cellvibrio japonicus</i> (target efi-502161) with bound mg and glycerol |
| 112 | c2o56D_ | Alignment | not modelled | 99.0 | 21 | PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative mandelate racemase; PDBTitle: crystal structure of a member of the enolase superfamily from <i>Salmonella typhimurium</i> |
| 113 | c3ffsC_ | Alignment | not modelled | 98.9 | 22 | PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of <i>Cryptosporidium parvum</i> inosine-5'-2 monophosphate dehydrogenase |
| 114 | c5b69A_ | Alignment | not modelled | 98.9 | 15 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranylgeranyl phosphate synthase; PDBTitle: crystal structure of geranylgeranylgeranyl phosphate synthase2 complexed with an g-1-p from <i>Thermoplasma acidophilum</i> |
| 115 | c6dvhF_ | Alignment | not modelled | 98.9 | 25 | PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from <i>Mycobacterium smegmatis</i> - c203a mutant |
| 116 | d1eepa_ | Alignment | not modelled | 98.9 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 117 | c2ox4E_ | Alignment | not modelled | 98.9 | 22 | PDB header: isomerase Chain: E: PDB Molecule: putative mandelate racemase; PDBTitle: crystal structure of putative dehydratase from <i>Zymomonas mobilis</i> zm4 |
| 118 | c6gk9C_ | Alignment | not modelled | 98.9 | 24 | PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from <i>Pseudomonas aeruginosa</i> |
| 119 | c2rduA_ | Alignment | not modelled | 98.9 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate |
| 120 | c2cdh1_ | Alignment | not modelled | 98.9 | 23 | PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the <i>Thermomyces lanuginosus</i> fungal fatty2 acid synthase at 5 angstrom resolution. |