






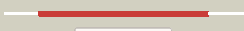















Phyre2

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| Email | mdejesus@rockefeller.edu |
| Description | RVBD2606c (-) _2933181_2934080 |
| Date | Wed Aug 7 12:50:24 BST 2019 |
| Unique Job ID | 06073e41f7677b3b |

Detailed template information


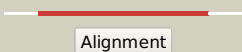


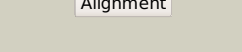
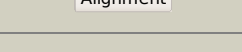
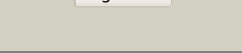


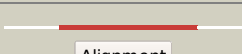

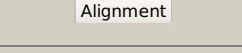
| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c4firB_ |  Alignment |  | 100.0 | 60 | PDB header: lyase Chain: B; PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus |
| 2 | c2zbtB_ |  Alignment |  | 100.0 | 71 | PDB header: lyase Chain: B; PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8 |
| 3 | c3femB_ |  Alignment |  | 100.0 | 64 | PDB header: biosynthetic protein, transferase Chain: B; PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae |
| 4 | c4adsF_ |  Alignment |  | 100.0 | 58 | PDB header: transferase/transferase Chain: F; PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex |
| 5 | c2nv2U_ |  Alignment |  | 100.0 | 65 | PDB header: lyase/transferase Chain: U; PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis |
| 6 | c6hyeF_ |  Alignment |  | 100.0 | 68 | PDB header: plant protein Chain: F; PDB Molecule: pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a) |
| 7 | c6hxgE_ |  Alignment |  | 100.0 | 52 | PDB header: plant protein Chain: E; PDB Molecule: pyridoxal 5'-phosphate synthase-like subunit pdx1.2; PDBTitle: pdx1.2/pdx1.3 complex (intermediate) |
| 8 | c2yztB_ |  Alignment |  | 100.0 | 65 | PDB header: lyase Chain: B; PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii |
| 9 | d1znna1 |  Alignment |  | 100.0 | 66 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like |
| 10 | c1znnF_ |  Alignment |  | 100.0 | 66 | PDB header: biosynthetic protein Chain: F; PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase |
| 11 | d1xm3a_ |  Alignment |  | 99.7 | 24 | Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like |

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|----|-------------------------|-----------|--------------|------|----|---|
| 12 | c3qjaA_ | Alignment | | 99.6 | 27 | 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 |
| 13 | c5zjnB_ | Alignment | | 99.6 | 24 | 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 |
| 14 | c5zknA_ | Alignment | | 99.6 | 24 | 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 |
| 15 | d1yxya1 | Alignment | | 99.5 | 26 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like |
| 16 | c3q58A_ | Alignment | | 99.4 | 25 | PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica |
| 17 | d1y0ea_ | Alignment | | 99.4 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like |
| 18 | c5z9yB_ | Alignment | | 99.4 | 25 | PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp |
| 19 | c3tsmB_ | Alignment | | 99.3 | 15 | PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis |
| 20 | d1wv2a_ | Alignment | | 99.3 | 24 | Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like |
| 21 | d1a53a_ | Alignment | not modelled | 99.3 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |
| 22 | c6bmaA_ | Alignment | not modelled | 99.3 | 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 |
| 23 | d1vc4a_ | Alignment | not modelled | 99.2 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |
| 24 | c4n6eA_ | Alignment | not modelled | 99.1 | 23 | PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex |
| 25 | c4utwB_ | Alignment | not modelled | 99.1 | 23 | 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 |
| 26 | c3igsB_ | Alignment | not modelled | 99.1 | 24 | 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 |
| 27 | d1piia2 | Alignment | not modelled | 99.1 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |
| 28 | d1w0ma_ | Alignment | not modelled | 99.1 | 22 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c2htmB | Alignment | not modelled | 99.0 | 27 | PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8 |
| 30 | c2c3zA | Alignment | not modelled | 99.0 | 17 | 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 |
| 31 | d1ka9f | Alignment | not modelled | 99.0 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes |
| 32 | d1h5ya | Alignment | not modelled | 98.9 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes |
| 33 | d1thfd | Alignment | not modelled | 98.9 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes |
| 34 | c6nkeA | Alignment | not modelled | 98.8 | 18 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranylglycerol phosphate synthase; PDBTitle: wild-type gggps from thermoplasma volcanium |
| 35 | d1hg3a | Alignment | not modelled | 98.8 | 21 | Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) |
| 36 | c5umfB | Alignment | not modelled | 98.8 | 17 | PDB header: isomerase Chain: B: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate |
| 37 | d2flia1 | Alignment | not modelled | 98.8 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase |
| 38 | c3f4wA | Alignment | not modelled | 98.7 | 22 | PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium |
| 39 | c5aheA | Alignment | not modelled | 98.7 | 18 | PDB header: isomerase Chain: A: PDB Molecule: PDBTitle: crystal structure of salmonella enterica hisa |
| 40 | d1j5ta | Alignment | not modelled | 98.7 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 41 | d1i4na | Alignment | not modelled | 98.7 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 42 | c4e38A | Alignment | not modelled | 98.6 | 18 | 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) |
| 43 | d1tqja | Alignment | not modelled | 98.6 | 13 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase |
| 44 | c4wd0A | Alignment | not modelled | 98.6 | 18 | PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of hisap form arthrobacter aureescens |
| 45 | d1wa3a1 | Alignment | not modelled | 98.6 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 46 | d1rpxa | Alignment | not modelled | 98.5 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase |
| 47 | d1h1ya | Alignment | not modelled | 98.5 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase |
| 48 | c5n2pA | Alignment | not modelled | 98.5 | 15 | PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a |
| 49 | c6oviA | Alignment | not modelled | 98.4 | 17 | PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpd aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate |
| 50 | d2tpsa | Alignment | not modelled | 98.4 | 22 | Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase |
| 51 | d1wbha1 | Alignment | not modelled | 98.4 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 52 | c4qccA | Alignment | not modelled | 98.3 | 25 | PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains |
| 53 | c2v82A | Alignment | not modelled | 98.3 | 21 | PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal |
| 54 | c2w6rA | Alignment | not modelled | 98.3 | 19 | PDB header: lyase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit PDBTitle: crystal structure of an artificial (ba)8-barrel protein2 |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | designed from identical half barrels |
| 55 | d1vhna | Alignment | not modelled | 98.3 | 28 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 56 | d1q6oa | Alignment | not modelled | 98.2 | 12 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase |
| 57 | d1xcfa | Alignment | not modelled | 98.2 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 58 | c5b69A | Alignment | not modelled | 98.2 | 26 | PDB header: transferase Chain: A: PDB Molecule: geranylgeranylgeranyl phosphate synthase; PDBTitle: crystal structure of geranylgeranylgeranyl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum |
| 59 | c3inpA | Alignment | not modelled | 98.2 | 13 | PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis. |
| 60 | c3w9zA | Alignment | not modelled | 98.2 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc |
| 61 | c6ei9A | Alignment | not modelled | 98.1 | 26 | PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb) |
| 62 | c2y85D | Alignment | not modelled | 98.1 | 16 | PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp |
| 63 | c4x2rA | Alignment | not modelled | 98.1 | 24 | PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis |
| 64 | c2h6rG | Alignment | not modelled | 98.0 | 27 | PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii |
| 65 | d1vzwa1 | Alignment | not modelled | 98.0 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes |
| 66 | c3o63B | Alignment | not modelled | 98.0 | 17 | PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis |
| 67 | c3tr2A | Alignment | not modelled | 98.0 | 18 | PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: structure of a orotidine 5'-phosphate decarboxylase (pyrf) from2 coxiella burnetii |
| 68 | d1gtea2 | Alignment | not modelled | 98.0 | 14 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 69 | d1vhca | Alignment | not modelled | 97.9 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 70 | c4xp7A | Alignment | not modelled | 97.9 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)-like]; PDBTitle: crystal structure of human trna dihydrouridine synthase 2 |
| 71 | c3b0vD | Alignment | not modelled | 97.9 | 25 | PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna |
| 72 | c4bk9B | Alignment | not modelled | 97.9 | 20 | 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 |
| 73 | c1piiA | Alignment | not modelled | 97.9 | 20 | 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 |
| 74 | c3tdnB | Alignment | not modelled | 97.9 | 20 | PDB header: de novo protein Chain: B: PDB Molecule: flr symmetric alpha-beta tim barrel; PDBTitle: computationally designed two-fold symmetric tim-barrel protein, flr |
| 75 | c2gjlA | Alignment | not modelled | 97.9 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase |
| 76 | c3qc3B | Alignment | not modelled | 97.8 | 14 | PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution |
| 77 | c4axkB | Alignment | not modelled | 97.8 | 23 | PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens |
| 78 | d1juba | Alignment | not modelled | 97.8 | 25 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 79 | d1rd5a | Alignment | not modelled | 97.8 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel |

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|-----|------------------------|-----------|--------------|------|----|---|
| | | | | | | Family: Tryptophan biosynthesis enzymes |
| 80 | c3vndD | Alignment | not modelled | 97.8 | 21 | PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2 |
| 81 | c4xq6A | Alignment | not modelled | 97.8 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis |
| 82 | c5cssA | Alignment | not modelled | 97.8 | 26 | PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from thermoplasma2 acidophilum with glycerol 3-phosphate |
| 83 | c6b8sB | Alignment | not modelled | 97.8 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn |
| 84 | c3khjE | Alignment | not modelled | 97.8 | 21 | PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64 |
| 85 | d1mxsa | Alignment | not modelled | 97.7 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 86 | c2rdtA | Alignment | not modelled | 97.7 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst |
| 87 | d1ep3a | Alignment | not modelled | 97.7 | 28 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 88 | c3ajxA | Alignment | not modelled | 97.7 | 18 | PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase |
| 89 | c2fptA | Alignment | not modelled | 97.7 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors |
| 90 | d1dvja | Alignment | not modelled | 97.7 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase |
| 91 | c6a0gA | Alignment | not modelled | 97.6 | 29 | PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate |
| 92 | c2cdh1 | Alignment | not modelled | 97.6 | 25 | PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution. |
| 93 | d1d3ga | Alignment | not modelled | 97.6 | 22 | Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases |
| 94 | c4nu7C | Alignment | not modelled | 97.6 | 15 | PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii. |
| 95 | c4muzA | Alignment | not modelled | 97.6 | 19 | PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 archaeoglobus fulgidus complexed with inhibitor bmp |
| 96 | c2z6jB | Alignment | not modelled | 97.6 | 23 | 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 |
| 97 | d1qopa | Alignment | not modelled | 97.6 | 24 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 98 | d1tqxa | Alignment | not modelled | 97.5 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase |
| 99 | c4zqrD | Alignment | not modelled | 97.5 | 19 | 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 |
| 100 | c3tfxB | Alignment | not modelled | 97.5 | 23 | PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus |
| 101 | c3ct7E | Alignment | not modelled | 97.5 | 18 | PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12 |
| 102 | d1geqa | Alignment | not modelled | 97.5 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 103 | c3exsB | Alignment | not modelled | 97.4 | 14 | PDB header: lyase Chain: B: PDB Molecule: rrmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p |
| 104 | c4mz1A | Alignment | not modelled | 97.4 | 18 | 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 |

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|-----|-------------------------|---|--------------|------|----|--|
| 105 | c3r2gA_ |  | not modelled | 97.4 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila |
| 106 | c4gj1A_ |  | not modelled | 97.4 | 16 | PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa). |
| 107 | d1ojxa_ |  | not modelled | 97.4 | 25 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 108 | d1xi3a_ |  | not modelled | 97.4 | 22 | Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase |
| 109 | c4mjmD_ |  | not modelled | 97.4 | 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 |
| 110 | c1yadD_ |  | not modelled | 97.4 | 32 | PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis |
| 111 | c1vrdA_ |  | not modelled | 97.4 | 32 | 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 |
| 112 | c2vytA_ |  | not modelled | 97.4 | 16 | PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus |
| 113 | c3bo9B_ |  | not modelled | 97.4 | 22 | 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 |
| 114 | c3ru6C_ |  | not modelled | 97.3 | 20 | PDB header: lyase Chain: C: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168 |
| 115 | c3oixA_ |  | not modelled | 97.2 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans |
| 116 | c4ff0B_ |  | not modelled | 97.2 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp |
| 117 | d1km4a_ |  | not modelled | 97.2 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase |
| 118 | c2qr6A_ |  | not modelled | 97.2 | 20 | 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 |
| 119 | d1pvna1 |  | not modelled | 97.2 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH) |
| 120 | c4avfD_ |  | not modelled | 97.2 | 18 | PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase |