Phyre$^2$

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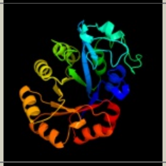
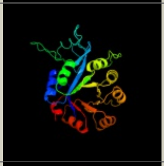
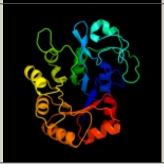
| Description | P10908 |
| Date | Thu Jan 5 11:32:27 GMT 2012 |
| Unique Job ID | a7452211ef412286 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2otdC_ | Alignment |  | 100.0 | 96 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**glycerophosphodiester phosphodiesterase;<br>**PDBTitle:** the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a |
| 2 | c3qvqB_ | Alignment |  | 100.0 | 32 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**phosphodiesterase olei02445;<br>**PDBTitle:** the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate |
| 3 | c2pz0B_ | Alignment |  | 100.0 | 28 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis |
| 4 | c2p76H_ | Alignment |  | 100.0 | 24 | **PDB header:**hydrolase<br>**Chain:** H: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus |
| 5 | d1zcca1 | Alignment |  | 100.0 | 28 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Glycerophosphoryl diester phosphodiesterase |
| 6 | c3l12A_ | Alignment |  | 100.0 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution |
| 7 | c3ks6A_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens3 str. c58 (dupont) at 1.80 a resolution |
| 8 | d1vd6a1 | Alignment |  | 100.0 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Glycerophosphoryl diester phosphodiesterase |
| 9 | c2o55A_ | Alignment |  | 100.0 | 26 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative glycerophosphodiester phosphodiesterase;<br>**PDBTitle:** crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria |
| 10 | c3no3A_ | Alignment |  | 100.0 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**glycerophosphodiester phosphodiesterase;<br>**PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase2 (bdi_0402) from parabacteroides distasonis atcc 8503 at 1.89 a3 resolution |
| 11 | c3mz2A_ | Alignment |  | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of a glycerophosphoryl diester phosphodiesterase2 (bdi_3922) from parabacteroides distasonis atcc 8503 at 1.55 a3 resolution |

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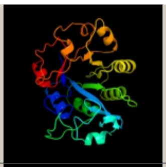
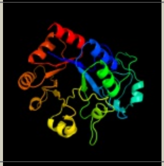
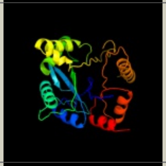
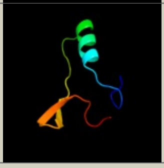
| 12 | d1ydya1 | Alignment |  | 100.0 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Glycerophosphoryl diester phosphodiesterase |
| 13 | c1ydyA_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of periplasmic glycerophosphodiester2 phosphodiesterase from escherichia coli |
| 14 | d1o1za_ | Alignment |  | 100.0 | 23 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Glycerophosphoryl diester phosphodiesterase |
| 15 | c3ch0A_ | Alignment |  | 100.0 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**glycerophosphodiester phosphodiesterase;<br>**PDBTitle:** crystal structure of glycerophosphoryl diester phosphodiesterase2 (yp_677622.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution |
| 16 | c3i10A_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution |
| 17 | c3rlhA_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a;<br>**PDBTitle:** crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom |
| 18 | c3rlgA_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a;<br>**PDBTitle:** crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant |
| 19 | c2f9rC_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**sphingomyelinase d 1;<br>**PDBTitle:** crystal structure of the inactive state of the smase i, a2 sphingomyelinase d from loxosceles laeta venom |
| 20 | c1djyB_ | Alignment |  | 97.5 | 14 | **PDB header:**lipid degradation<br>**Chain:** B: **PDB Molecule:**phosphoinositide-specific phospholipase c,<br>**PDBTitle:** phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate |
| 21 | d1qasa3 | Alignment | not modelled | 97.4 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Mammalian PLC |
| 22 | d2zkmx4 | Alignment | not modelled | 97.4 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Mammalian PLC |
| 23 | c3qr0A_ | Alignment | not modelled | 97.3 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phospholipase c-beta (plc-beta);<br>**PDBTitle:** crystal structure of s. officinalis plc21 |
| 24 | c2fjuB_ | Alignment | not modelled | 97.3 | 16 | **PDB header:**signaling protein,apoptosis/hydrolase<br>**Chain:** B: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate<br>**PDBTitle:** activated rac1 bound to its effector phospholipase c beta 2 |
| 25 | c3ohmB_ | Alignment | not modelled | 97.2 | 16 | **PDB header:**signaling protein / hydrolase<br>**Chain:** B: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase<br>**PDBTitle:** crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3 |
| 26 | c3ktsA_ | Alignment | not modelled | 95.8 | 11 | **PDB header:**transcriptional regulator<br>**Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein;<br>**PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365 |
| 27 | d1qopa_ | Alignment | not modelled | 95.8 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 28 | c3navB_ | Alignment | not modelled | 95.0 | 16 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain;<br>**PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961 |

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| 29 | c3pjwA_ | Alignment | not modelled | 93.9 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein;<br>**PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23 |
| 30 | d1vhca_ | Alignment | not modelled | 93.6 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 31 | c3pfmA_ | Alignment | not modelled | 93.3 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ggdef domain protein;<br>**PDBTitle:** crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf |
| 32 | d1a53a_ | Alignment | not modelled | 92.3 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 33 | d1wbha1 | Alignment | not modelled | 92.2 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 34 | d1vkfa_ | Alignment | not modelled | 92.2 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**GlpP-like<br>**Family:**GlpP-like |
| 35 | c3a24A_ | Alignment | not modelled | 91.5 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-galactosidase;<br>**PDBTitle:** crystal structure of bt1871 retaining glycosidase |
| 36 | c2c3zA_ | Alignment | not modelled | 91.3 | 13 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase;<br>**PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus |
| 37 | d1geqa_ | Alignment | not modelled | 91.2 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 38 | c2zq0B_ | Alignment | not modelled | 90.3 | 10 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb);<br>**PDBTitle:** crystal structure of susb complexed with acarbose |
| 39 | c3gfzB_ | Alignment | not modelled | 89.7 | 17 | **PDB header:**hydrolase, signaling protein<br>**Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1;<br>**PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex |
| 40 | d1rd5a_ | Alignment | not modelled | 89.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 41 | c3h4wA_ | Alignment | not modelled | 89.1 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphatidylinositol-specific phospholipase c1;<br>**PDBTitle:** structure of a ca+2 dependent phosphatidylinositol-specific2 phospholipase c (pi-plc) enzyme from streptomyces antibioticus |
| 42 | d1vc4a_ | Alignment | not modelled | 89.1 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 43 | c3hvbB_ | Alignment | not modelled | 88.5 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protein fimx;<br>**PDBTitle:** crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa |
| 44 | c2yw3E_ | Alignment | not modelled | 88.2 | 13 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-<br>**PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1 |
| 45 | d1mxsa_ | Alignment | not modelled | 88.2 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 46 | d1i4na_ | Alignment | not modelled | 85.6 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 47 | d1piia2 | Alignment | not modelled | 84.5 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 48 | c3kzpA_ | Alignment | not modelled | 83.1 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase;<br>**PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes |
| 49 | c3labA_ | Alignment | not modelled | 82.4 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate)<br>**PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica |
| 50 | c2p10D_ | Alignment | not modelled | 81.3 | 17 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**mll9387 protein;<br>**PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution |
| 51 | c3bo9B_ | Alignment | not modelled | 80.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative nitroalkan dioxygenase;<br>**PDBTitle:** crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution |
| 52 | c3qjaA_ | Alignment | not modelled | 80.3 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase;<br>**PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form |
| 53 | d2p10a1 | Alignment | not modelled | 79.7 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Mll9387-like |

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| 54 | c2htmB_ | Alignment | not modelled | 76.3 | 17 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig;<br>**PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8 |
| 55 | d1ujpa_ | Alignment | not modelled | 76.2 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 56 | d2basa1 | Alignment | not modelled | 76.2 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**EAL domain-like<br>**Family:**EAL domain |
| 57 | c3s83A_ | Alignment | not modelled | 75.8 | 22 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ggdef family protein;<br>**PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15 |
| 58 | c3ct7E_ | Alignment | not modelled | 75.7 | 14 | **PDB header:**isomerase<br>**Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase;<br>**PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12 |
| 59 | c2r6oB_ | Alignment | not modelled | 73.7 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase (ggdef & eal<br>**PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans |
| 60 | d1xm3a_ | Alignment | not modelled | 73.4 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**ThiG-like<br>**Family:**ThiG-like |
| 61 | c2v82A_ | Alignment | not modelled | 72.9 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase;<br>**PDBTitle:** kdpgal complexed to kdpgal |
| 62 | c3igsB_ | Alignment | not modelled | 68.8 | 17 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2;<br>**PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase |
| 63 | c2zbtB_ | Alignment | not modelled | 68.7 | 23 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs;<br>**PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8 |
| 64 | d1j5ta_ | Alignment | not modelled | 68.6 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 65 | c2gjlA_ | Alignment | not modelled | 68.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hypothetical protein pa1024;<br>**PDBTitle:** crystal structure of 2-nitropropane dioxygenase |
| 66 | c3femB_ | Alignment | not modelled | 65.8 | 23 | **PDB header:**biosynthetic protein, transferase<br>**Chain:** B: **PDB Molecule:**pyridoxine biosynthesis protein snz1;<br>**PDBTitle:** structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae |
| 67 | c3gkaB_ | Alignment | not modelled | 65.6 | 21 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase;<br>**PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei |
| 68 | c3nhzA_ | Alignment | not modelled | 65.1 | 14 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra;<br>**PDBTitle:** structure of n-terminal domain of mtra |
| 69 | d1wv2a_ | Alignment | not modelled | 64.8 | 28 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**ThiG-like<br>**Family:**ThiG-like |
| 70 | c2nv2U_ | Alignment | not modelled | 64.6 | 26 | **PDB header:**lyase/transferase<br>**Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs;<br>**PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis |
| 71 | d1wa3a1 | Alignment | not modelled | 64.0 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 72 | d7reqa2 | Alignment | not modelled | 63.8 | 20 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 73 | c3ffsC_ | Alignment | not modelled | 63.7 | 22 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase;<br>**PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase |
| 74 | c3bw2A_ | Alignment | not modelled | 63.1 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase;<br>**PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes |
| 75 | d2ptda_ | Alignment | not modelled | 62.6 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Bacterial PLC |
| 76 | c3jr2D_ | Alignment | not modelled | 62.1 | 11 | **PDB header:**biosynthetic protein<br>**Chain:** D: **PDB Molecule:**hexulose-6-phosphate synthase sgbh;<br>**PDBTitle:** x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961 |
| 77 | c1piiA_ | Alignment | not modelled | 61.3 | 13 | **PDB header:**bifunctional(isomerase and synthase)<br>**Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase;<br>**PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution |
| 78 | c2z6jB_ | Alignment | not modelled | 60.5 | 11 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**trans-2-enoyl-acp reductase ii;<br>**PDBTitle:** crystal structure of s. pneumoniae enoyl-acyl carrier2 |

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| | | | | | | protein reductase (fabk) in complex with an inhibitor |
| 79 | c3gndC_ | Alignment | not modelled | 59.1 | 18 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**aldolase lsrf;<br>**PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate |
| 80 | c3hv9A_ | Alignment | not modelled | 57.7 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**protein fimx;<br>**PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa |
| 81 | c3gk0H_ | Alignment | not modelled | 55.4 | 25 | **PDB header:**transferase<br>**Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase;<br>**PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei |
| 82 | c2ekcA_ | Alignment | not modelled | 55.1 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain;<br>**PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5 |
| 83 | c3qz6A_ | Alignment | not modelled | 52.8 | 12 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**hpch/hpai aldolase;<br>**PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2 |
| 84 | d1h7na_ | Alignment | not modelled | 52.3 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) |
| 85 | d2flia1 | Alignment | not modelled | 51.4 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 86 | d1m5wa_ | Alignment | not modelled | 51.4 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Pyridoxine 5'-phosphate synthase<br>**Family:**Pyridoxine 5'-phosphate synthase |
| 87 | c2vwtA_ | Alignment | not modelled | 51.1 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase;<br>**PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex |
| 88 | c2qjhH_ | Alignment | not modelled | 49.9 | 15 | **PDB header:**lyase<br>**Chain:** H: **PDB Molecule:**putative aldolase mj0400;<br>**PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate |
| 89 | c3inpA_ | Alignment | not modelled | 47.9 | 16 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase;<br>**PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis. |
| 90 | d1nsja_ | Alignment | not modelled | 47.4 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 91 | d2obba1 | Alignment | not modelled | 45.0 | 17 | **Fold:**HAD-like<br>**Superfamily:**HAD-like<br>**Family:**BT0820-like |
| 92 | d2c1ha1 | Alignment | not modelled | 43.8 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) |
| 93 | c3qc3B_ | Alignment | not modelled | 43.4 | 10 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase;<br>**PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution |
| 94 | d1pv8a_ | Alignment | not modelled | 43.1 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) |
| 95 | c2rbgB_ | Alignment | not modelled | 42.1 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein st0493;<br>**PDBTitle:** crystal structure of hypothetical protein(st0493) from2 sulfolobus tokodaii |
| 96 | c1yadD_ | Alignment | not modelled | 41.8 | 13 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**regulatory protein teni;<br>**PDBTitle:** structure of teni from bacillus subtilis |
| 97 | c3thaB_ | Alignment | not modelled | 41.4 | 14 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain;<br>**PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni. |
| 98 | c2w27A_ | Alignment | not modelled | 41.3 | 10 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ykui protein;<br>**PDBTitle:** crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium |
| 99 | c3hf3A_ | Alignment | not modelled | 39.9 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**chromate reductase;<br>**PDBTitle:** old yellow enzyme from thermus scotoductus sa-01 |
| 100 | d1gzga_ | Alignment | not modelled | 39.0 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) |
| 101 | c2h6rG_ | Alignment | not modelled | 37.9 | 12 | **PDB header:**isomerase<br>**Chain:** G: **PDB Molecule:**triosephosphate isomerase;<br>**PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii |
| 102 | d1rpxa_ | Alignment | not modelled | 37.5 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**D-ribulose-5-phosphate 3-epimerase |
| 103 | d1ru8a_ | Alignment | not modelled | 37.3 | 18 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 104 | c3obkH_ | Alignment | not modelled | 35.5 | 15 | **PDB header:**lyase<br>**Chain:** H: **PDB Molecule:**delta-aminolevulinic acid dehydratase;<br>**PDBTitle:** crystal structure of delta-aminolevulinic acid |

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|---|---|---|---|---|---|---|
|  |  |  |  |  |  | dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen |
| 105 | d1mvoa_ | Alignment | not modelled | 35.3 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 106 | c3tdmD_ | Alignment | not modelled | 35.2 | 19 | **PDB header:**de novo protein<br>**Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel<br>**PDBTitle:** computationally designed tim-barrel protein, halfflr |
| 107 | d1yxya1 | Alignment | not modelled | 35.2 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 108 | d1a77a2 | Alignment | not modelled | 34.8 | 14 | **Fold:**PIN domain-like<br>**Superfamily:**PIN domain-like<br>**Family:**5' to 3' exonuclease catalytic domain |
| 109 | d1b43a2 | Alignment | not modelled | 34.4 | 18 | **Fold:**PIN domain-like<br>**Superfamily:**PIN domain-like<br>**Family:**5' to 3' exonuclease catalytic domain |
| 110 | d7odca2 | Alignment | not modelled | 34.2 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLP-binding barrel<br>**Family:**Alanine racemase-like, N-terminal domain |
| 111 | c3rysA_ | Alignment | not modelled | 33.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**adenosine deaminase 1;<br>**PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens |
| 112 | c1jcnA_ | Alignment | not modelled | 32.1 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase i;<br>**PDBTitle:** binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp |
| 113 | c3c85A_ | Alignment | not modelled | 32.1 | 17 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**putative glutathione-regulated potassium-efflux system<br>**PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus |
| 114 | d1p3da1 | Alignment | not modelled | 32.0 | 16 | **Fold:**MurCD N-terminal domain<br>**Superfamily:**MurCD N-terminal domain<br>**Family:**MurCD N-terminal domain |
| 115 | d1oy0a_ | Alignment | not modelled | 31.8 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Ketopantoate hydroxymethyltransferase PanB |
| 116 | d1zesa1 | Alignment | not modelled | 31.7 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 117 | d2d13a1 | Alignment | not modelled | 31.4 | 15 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 118 | c3o63B_ | Alignment | not modelled | 30.9 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase;<br>**PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis |
| 119 | d1qpoa1 | Alignment | not modelled | 30.8 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like<br>**Family:**NadC C-terminal domain-like |
| 120 | c2qr6A_ | Alignment | not modelled | 30.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**imp dehydrogenase/gmp reductase;<br>**PDBTitle:** crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution |