# Phyre$^{2}$

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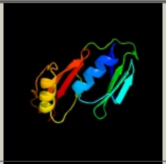
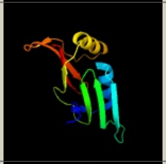
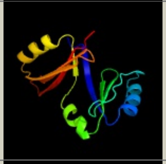
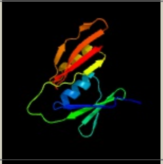
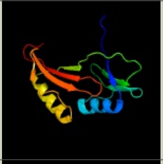
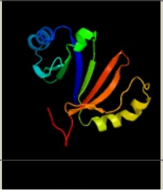
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0546c_(-)_637586_637972 |
| Date | Fri Jul 26 01:50:09 BST 2019 |
| Unique Job ID | 2485e5b114ee3690 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2i7ra1 | Alignment |  | 99.9 | 14 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| 2 | c3bt3B_ | Alignment |  | 99.9 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**glyoxalase-related enzyme, arac type;<br>**PDBTitle:** crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans |
| 3 | c4nvsB_ | Alignment |  | 99.9 | 19 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**putative enzyme, glyoxalase family;<br>**PDBTitle:** crystal structure of the q18cp6_clod6 protein from glyoxalase family.2 northeast structural genomics consortium target cfr3 |
| 4 | c2r6uB_ | Alignment |  | 99.8 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of gene product rha04853 from rhodococcus sp. rha1 |
| 5 | c4hc5A_ | Alignment |  | 99.8 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of member of glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily from sphaerobacter thermophilus dsm3 20745 |
| 6 | c3bqxA_ | Alignment |  | 99.8 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**glyoxalase-related enzyme;<br>**PDBTitle:** high resolution crystal structure of a glyoxalase-related enzyme from2 fulvimarina pelagi |
| 7 | c3r6aB_ | Alignment |  | 99.8 | 24 | **PDB header:**isomerase, lyase<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of an uncharacterized protein (hypothetical protein2 mm_3218) from methanosarcina mazei. |
| 8 | c3g12A_ | Alignment |  | 99.8 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase;<br>**PDBTitle:** crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus |
| 9 | c6a4zA_ | Alignment |  | 99.8 | 16 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**chap protein;<br>**PDBTitle:** oxidase chap |
| 10 | c4mymA_ | Alignment |  | 99.8 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of a glyoxalase/ bleomycin resistance protein/2 dioxygenase from nocardioides |
| 11 | c3fcdB_ | Alignment |  | 99.8 | 18 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**lyase;<br>**PDBTitle:** crystal structure of a putative glyoxalase from an2 environmental bacteria |

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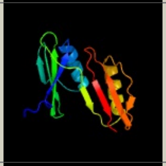
| 12 | c4g6xA_ | Alignment |  | 99.8 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of glyoxalase/bleomycin resistance protein from2 catenulispora acidiphila. |
| 13 | d2pjsa1 | Alignment |  | 99.8 | 17 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| 14 | c3rheA_ | Alignment |  | 99.8 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nad-dependent benzaldehyde dehydrogenase;<br>**PDBTitle:** the crystal structure of nad-dependent benzaldehyde dehydrogenase from2 legionella pneumophila |
| 15 | c3rriB_ | Alignment |  | 99.8 | 16 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from alicyclobacillus acidocaldarius |
| 16 | c5umwA_ | Alignment |  | 99.8 | 20 | **PDB header:**tiancimycin-binding protein<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resisance protein/dioxygenase;<br>**PDBTitle:** crystal structure of tnms2, an antibiotic binding protein from2 streptomyces sp. cb03234 |
| 17 | d1qipa_ | Alignment |  | 99.8 | 17 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Glyoxalase I (lactoylglutathione lyase) |
| 18 | c2kjzA_ | Alignment |  | 99.8 | 14 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**atc0852;<br>**PDBTitle:** solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2. |
| 19 | c3ghjA_ | Alignment |  | 99.8 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative integron gene cassette protein;<br>**PDBTitle:** crystal structure from the mobile metagenome of halifax harbour sewage2 outfall: integron cassette protein hfx_cass4 |
| 20 | c3itwA_ | Alignment |  | 99.8 | 17 | **PDB header:**peptide binding protein<br>**Chain:** A: **PDB Molecule:**protein tiox;<br>**PDBTitle:** crystal structure of tiox from micromonospora sp. ml1 |
| 21 | c3sk1C_ | Alignment | not modelled | 99.8 | 18 | **PDB header:**griseoluteate-binding protein<br>**Chain:** C: **PDB Molecule:**ehpr;<br>**PDBTitle:** crystal structure of phenazine resistance protein ehpr from2 enterobacter agglomerans (erwinia herbicola, pantoea agglomerans)3 eh1087, apo form |
| 22 | c3pkwA_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**toxoflavin lyase (tfla);<br>**PDBTitle:** crystal structure of toxoflavin lyase (tfla) bound to mn(ii) |
| 23 | c3l7tB_ | Alignment | not modelled | 99.8 | 24 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of smu.1112c |
| 24 | c6a4xA_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**bleomycin resistance protein;<br>**PDBTitle:** oxidase chap-h2 |
| 25 | c3zw5A_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**glyoxalase domain-containing protein 5;<br>**PDBTitle:** crystal structure of the human glyoxalase domain-containing protein 5 |
| 26 | c4jh1B_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**metallothiol transferase fosb;<br>**PDBTitle:** crystal structure of fosb from bacillus cereus with zinc and sulfate2 at 1.55 a resolution -sad phasing |
| 27 | c2rk9B_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily member from vibrio splendidus 12b01 |
| 28 | c5ujpB_ | Alignment | not modelled | 99.8 | 20 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resisance protein/dioxygenase;<br>**PDBTitle:** the crystal structure of a glyoxalase/bleomycin resistance |

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| | | | | | | protein2 from streptomyces sp. cb03234 |
| 29 | d1twua_ | Alignment | not modelled | 99.8 | 17 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Hypothetical protein YycE |
| 30 | d1f9za_ | Alignment | not modelled | 99.8 | 21 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Glyoxalase I (lactoylglutathione lyase) |
| 31 | c3m2oB_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein;<br>**PDBTitle:** crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009 |
| 32 | c2zw7A_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**bleomycin acetyltransferase;<br>**PDBTitle:** crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a |
| 33 | d1mpya2 | Alignment | not modelled | 99.8 | 14 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 34 | c4n04B_ | Alignment | not modelled | 99.8 | 23 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** the crystal structure of glyoxalase / bleomycin resistance protein2 from catenulispora acidiphila dsm 44928 |
| 35 | c4nb2B_ | Alignment | not modelled | 99.8 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**metallothiol transferase fosb;<br>**PDBTitle:** crystal structure of fosb from staphylococcus aureus at 1.89 angstrom2 resolution - apo structure |
| 36 | c3huhA_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**virulence protein stm3117;<br>**PDBTitle:** the structure of biphenyl-2,3-diol 1,2-dioxygenase iii-related protein2 from salmonella typhimurium |
| 37 | c4mtsA_ | Alignment | not modelled | 99.8 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**lactoylglutathione lyase;<br>**PDBTitle:** ni- and zn-bound gloa2 at high resolution |
| 38 | d1klla_ | Alignment | not modelled | 99.8 | 20 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| 39 | c2p25A_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glyoxalase family protein;<br>**PDBTitle:** the crystal structure of the glyoxalase family protein from2 enterococcus faecalis |
| 40 | c4rt5A_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase protein from planctomyces limnophilus dsm 3776 |
| 41 | d1ecsa_ | Alignment | not modelled | 99.8 | 23 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| 42 | c2rbbB_ | Alignment | not modelled | 99.8 | 9 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase family enzyme from burkholderia phytofirmans psjn |
| 43 | c5cb9A_ | Alignment | not modelled | 99.8 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of c-as lyase with mercaptoethonal |
| 44 | c6a52A_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**dioxidase chap-h1;<br>**PDBTitle:** oxidase chap-h1 |
| 45 | c4pavA_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**glyoxalase family protein;<br>**PDBTitle:** structure of hypothetical protein sa1046 from s. aureus. |
| 46 | c4gymB_ | Alignment | not modelled | 99.8 | 11 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from conexibacter woesei dsm 14684 |
| 47 | c5uhjA_ | Alignment | not modelled | 99.8 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resisance protein/dioxygenase;<br>**PDBTitle:** the crystal structure of a natural product biosynthetic enzyme from2 streptomyces sp. cb03234 |
| 48 | c2qntA_ | Alignment | not modelled | 99.8 | 26 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein atu1872;<br>**PDBTitle:** crystal structure of protein of unknown function from agrobacterium2 tumefaciens str. c58 |
| 49 | c3ey7B_ | Alignment | not modelled | 99.7 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**biphenyl-2,3-diol 1,2-dioxygenase iii-related<br>**PDBTitle:** structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass1 |
| 50 | c3zi1A_ | Alignment | not modelled | 99.7 | 18 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glyoxalase domain-containing protein 4;<br>**PDBTitle:** crystal structure of human glyoxalase domain-containing protein 42 (glod4) |
| 51 | c6jptB | Alignment | not modelled | 99.7 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**all3014 protein; |

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| | | | | | | **PDBTitle:** crystal structure of a fosfomycin and bleomycin resistant protein from2 anabaena/nostoc cyanobacterium at 1.70 a resolution |
| 52 | d1nkia_ | Alignment | not modelled | 99.7 | 21 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| 53 | c1zswA_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**glyoxalase family protein;<br>**PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family |
| 54 | d1jc4a_ | Alignment | not modelled | 99.7 | 14 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Methylmalonyl-CoA epimerase |
| 55 | c3ct8A_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative glyoxalase;<br>**PDBTitle:** crystal structure of a putative glyoxalase (np_243026.1) from bacillus2 halodurans at 2.10 a resolution |
| 56 | c6bu2A_ | Alignment | not modelled | 99.7 | 25 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glyoxalase;<br>**PDBTitle:** crystal structure of methylmalonyl-coa epimerase from mycobacterium2 tuberculosis |
| 57 | c3uh9B_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**metallothiol transferase fosb 2;<br>**PDBTitle:** crystal structure of metallothiol transferase fosb 2 from bacillus2 anthracis str. ames |
| 58 | c3b59A_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of the mn(ii)-bound glyoxalase from novosphingobium2 aromaticivorans |
| 59 | c4qb5A_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of a glyoxalase/bleomycin resistance protein from2 albidiferax ferrireducens t118 |
| 60 | d1lgta2 | Alignment | not modelled | 99.7 | 13 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 61 | d1kw3b1 | Alignment | not modelled | 99.7 | 18 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 62 | c3e5dA_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative glyoxalase i;<br>**PDBTitle:** crystal structure of a putative glyoxalase i (lmof2365_0426) from2 listeria monocytogenes str. 4b f2365 at 2.70 a resolution |
| 63 | c2qqzB_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**glyoxalase family protein, putative;<br>**PDBTitle:** crystal structure of putative glyoxalase family protein from bacillus2 anthracis |
| 64 | c5znhA_ | Alignment | not modelled | 99.7 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**catechol 2,3-dioxygenase, extradiol protein;<br>**PDBTitle:** catechol 2,3-dioxygenase with 4-methyl catechol from diaphorobacter sp2 ds2 |
| 65 | d1jifa_ | Alignment | not modelled | 99.7 | 18 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| 66 | d1lgta1 | Alignment | not modelled | 99.7 | 17 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 67 | d1ss4a_ | Alignment | not modelled | 99.7 | 15 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Hypothetical protein BC1747 |
| 68 | c3r4qB_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**lactoylglutathione lyase;<br>**PDBTitle:** crystal structure of lactoylglutathione lyase from agrobacterium2 tumefaciens |
| 69 | d1zswa2 | Alignment | not modelled | 99.7 | 11 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**BC1024-like |
| 70 | d1f1ua1 | Alignment | not modelled | 99.7 | 16 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 71 | c4z04A_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance /dioxygenase superfamily<br>**PDBTitle:** crystal structure of a probable lactoylglutathione lyase from brucella2 melitensis in complex with glutathione |
| 72 | d1xrka_ | Alignment | not modelled | 99.7 | 17 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| | | | | | | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**glyoxalase; |

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| | | Alignment | | | | **PDBTitle:** crystal structure of hypothetical protein bh1468 from bacillus2 halodurans c-125 |
| 74 | d1xy7a_ | Alignment | not modelled | 99.7 | 19 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Hypothetical protein At5g48480 |
| 75 | c2q48A_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**protein at5g48480;<br>**PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at5g48480 |
| 76 | d1xqaa_ | Alignment | not modelled | 99.7 | 16 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| 77 | d1mpya1 | Alignment | not modelled | 99.7 | 18 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 78 | c2zi8A_ | Alignment | not modelled | 99.7 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**probable biphenyl-2,3-diol 1,2-dioxygenase bphc;<br>**PDBTitle:** crystal structure of the hsac extradiol dioxygenase from m.2 tuberculosis in complex with 3,4-dihydroxy-9,10-3 seconandrost-1,3,5(10)-triene-9,17-dione (dhsa) |
| 79 | d1f1xa1 | Alignment | not modelled | 99.7 | 15 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 80 | d1zswa1 | Alignment | not modelled | 99.7 | 9 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**BC1024-like |
| 81 | c3rmuD_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**methylmalonyl-coa epimerase, mitochondrial;<br>**PDBTitle:** crystal structure of human methylmalonyl-coa epimerase, mcee |
| 82 | d2c21a1 | Alignment | not modelled | 99.7 | 20 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Glyoxalase I (lactoylglutathione lyase) |
| 83 | c3gm5A_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**lactoylglutathione lyase and related lyases;<br>**PDBTitle:** crystal structure of a putative methylmalonyl-coenzyme a epimerase2 from thermoanaerobacter tengcongensis at 2.0 a resolution |
| 84 | d1npba_ | Alignment | not modelled | 99.7 | 21 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Antibiotic resistance proteins |
| 85 | c2qh0A_ | Alignment | not modelled | 99.7 | 10 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**lactoylglutathione lyase;<br>**PDBTitle:** crystal structure of a glyoxalase from clostridium acetobutylicum |
| 86 | c2p7pB_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**metal binding protein, hydrolase<br>**Chain:** B: **PDB Molecule:**glyoxalase family protein;<br>**PDBTitle:** crystal structure of genomically encoded fosfomycin resistance2 protein, fosx, from listeria monocytogenes complexed with mn(ii) and3 sulfate ion |
| 87 | c3kolA_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance<br>**PDBTitle:** crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme |
| 88 | c5vb0E_ | Alignment | not modelled | 99.7 | 21 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**fosfomycin resistance protein fosa3;<br>**PDBTitle:** crystal structure of fosfomycin resistance protein fosa3 |
| 89 | c6on3C_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**l-dopa extradiol dioxygenase;<br>**PDBTitle:** a substrate bound structure of l-dopa dioxygenase from streptomyces2 sclerotialus |
| 90 | c4lqbA_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of uncharacterized protein kfla3161 |
| 91 | c2wl9A_ | Alignment | not modelled | 99.7 | 9 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**catechol 2,3-dioxygenase;<br>**PDBTitle:** crystal structure of catechol 2,3-dioxygenase |
| 92 | c3oajA_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative ring-cleaving dioxygenase mhqo;<br>**PDBTitle:** crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168 |
| 93 | c2ei2A_ | Alignment | not modelled | 99.7 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**1,2-dihydroxynaphthalene dioxygenase;<br>**PDBTitle:** crystal structure analysis of the 1,2-dihydroxynaphthalene dioxygenase2 from pseudomonas sp. stain c18 |
| 94 | c1knfA_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2,3-dihydroxybiphenyl 1,2-dioxygenase;<br>**PDBTitle:** crystal structure of 2,3-dihydroxybiphenyl 1,2-dioxygenase complexed2 with 3-methyl catechol under anaerobic condition |
| 95 | d1r9ca_ | Alignment | not modelled | 99.7 | 16 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase |

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|---|---|---|---|---|---|---|
| | | | | | | **Family:**Antibiotic resistance proteins |
| 96 | d1kw3b2 | Alignment | not modelled | 99.7 | 14 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 97 | c2rk0B_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase domain;<br>**PDBTitle:** crystal structure of glyoxylase/bleomycin resistance2 protein/dioxygenase domain from frankia sp. ean1pec |
| 98 | c1f1uB_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**homoprotocatechuate 2,3-dioxygenase;<br>**PDBTitle:** crystal structure of homoprotocatechuate 2,3-dioxygenase from2 arthrobacter globiformis (native, low temperature) |
| 99 | c3lm4C_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**catechol 2,3-dioxygenase;<br>**PDBTitle:** crystal structure of 2,3-dihydroxy biphenyl dioxygenase from2 rhodococcus sp. (strain rha1) |
| 100 | c3ecjC_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**protein (homoprotocatechuate 2,3-dioxygenase);<br>**PDBTitle:** structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution |
| 101 | c4iagA_ | Alignment | not modelled | 99.6 | 23 | **PDB header:**zorbamycin binding protein<br>**Chain:** A: **PDB Molecule:**zbm binding protein;<br>**PDBTitle:** crystal structure of zbma, the zorbamycin binding protein from2 streptomyces flavoviridis |
| 102 | d1q0oa2 | Alignment | not modelled | 99.6 | 10 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 103 | c1kw3B_ | Alignment | not modelled | 99.6 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**2,3-dihydroxybiphenyl dioxygenase;<br>**PDBTitle:** crystal structure of 2,3-dihydroxybiphenyal dioxygenase (bphc) at 1.452 a resolution |
| 104 | c1mpyD_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**catechol 2,3-dioxygenase;<br>**PDBTitle:** structure of catechol 2,3-dioxygenase (metapyrocatechase)2 from pseudomonas putida mt-2 |
| 105 | c3vb0D_ | Alignment | not modelled | 99.6 | 12 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase;<br>**PDBTitle:** crystal structure of 2,2',3-trihydroxybiphenyl 1,2-dioxygenase from2 dibenzofuran-degrading sphingomonas wittichii strain rw1 |
| 106 | c4huzA_ | Alignment | not modelled | 99.6 | 8 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2,6-dichloro-p-hydroquinone 1,2-dioxygenase;<br>**PDBTitle:** 2,6-dichloro-p-hydroquinone 1,2-dioxygenase |
| 107 | c3hpyD_ | Alignment | not modelled | 99.6 | 19 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**catechol 2,3-dioxygenase;<br>**PDBTitle:** crystal structure analysis of the 2,3-dioxygenase lapb from2 pseudomonas in the complex with 4-methylcatechol |
| 108 | d1sp8a1 | Alignment | not modelled | 99.6 | 25 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 109 | d1sqda1 | Alignment | not modelled | 99.6 | 16 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 110 | d1f1ua2 | Alignment | not modelled | 99.6 | 11 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 111 | d1f1xa2 | Alignment | not modelled | 99.6 | 12 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 112 | d1t47a1 | Alignment | not modelled | 99.6 | 13 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 113 | c4ro6A_ | Alignment | not modelled | 99.6 | 18 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**lactoylglutathione lyase;<br>**PDBTitle:** crystal structure of glyoxalase i from zea mays |
| 114 | d1sp9a_ | Alignment | not modelled | 99.5 | 13 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 115 | d1u6la_ | Alignment | not modelled | 99.5 | 14 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**3-demethylubiquinone-9 3-methyltransferase |
| 116 | c1tfzA_ | Alignment | not modelled | 99.5 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase;<br>**PDBTitle:** structural basis for herbicidal inhibitor selectivity revealed by2 comparison of crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases |
| 117 | c3l20A_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of a hypothetical protein from |

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|---|---|---|---|---|---|---|
|  |  |  |  |  |  | staphylococcus aureus |
| 118 | c1sp8A_ | Alignment | not modelled | 99.5 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase;<br>**PDBTitle:** 4-hydroxyphenylpyruvate dioxygenase |
| 119 | c3e0rC_ | Alignment | not modelled | 99.5 | 13 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**c3-degrading proteinase (cppa protein);<br>**PDBTitle:** crystal structure of cppa protein from streptococcus pneumoniae tigr4 |
| 120 | d1sqia1 | Alignment | not modelled | 99.5 | 21 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |