

Marcio Vinicius Bertacine Dias

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

841
citations

471509
17
h-index

501196
28
g-index

49
all docs

49
docs citations

49
times ranked

1017
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Crystal structure of human purine nucleoside phosphorylase complexed with acyclovir. <i>Biochemical and Biophysical Research Communications</i> , 2003, 308, 553-559. | 2.1 | 58 |
| 2 | Crystallographic studies on the binding of isonicotinyl-NAD adduct to wild-type and isoniazid resistant 2-trans-enoyl-ACP (CoA) reductase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural Biology</i> , 2007, 159, 369-380. | 2.8 | 52 |
| 3 | Chimeric Glycosyltransferases for the Generation of Hybrid Glycopeptides. <i>Chemistry and Biology</i> , 2009, 16, 676-685. | 6.0 | 50 |
| 4 | Chorismate Synthase: An Attractive Target For Drug Development Against Orphan Diseases. <i>Current Drug Targets</i> , 2007, 8, 437-444. | 2.1 | 49 |
| 5 | Structure of shikimate kinase from <i>Mycobacterium tuberculosis</i> reveals the binding of shikimic acid. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2310-2319. | 2.5 | 48 |
| 6 | Structural basis for inhibition of human PNP by immucillin-H. <i>Biochemical and Biophysical Research Communications</i> , 2003, 309, 917-922. | 2.1 | 47 |
| 7 | Folate biosynthesis pathway: mechanisms and insights into drug design for infectious diseases. <i>Future Medicinal Chemistry</i> , 2018, 10, 935-959. | 2.3 | 43 |
| 8 | Structure of chorismate synthase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural Biology</i> , 2006, 154, 130-143. | 2.8 | 41 |
| 9 | Enzymology of Pyran Ring...A Formation in Salinomycin Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 13622-13625. | 13.8 | 40 |
| 10 | Crystal structure of human PNP complexed with guanine. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 767-772. | 2.1 | 39 |
| 11 | Structural investigation of inhibitor designs targeting 3-dehydroquinate dehydratase from the shikimate pathway of <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 2011, 436, 729-739. | 3.7 | 39 |
| 12 | Crystal structure of human PNP complexed with hypoxanthine and sulfate ion. <i>Biochemical and Biophysical Research Communications</i> , 2005, 326, 335-338. | 2.1 | 33 |
| 13 | Effects of the magnesium and chloride ions and shikimate on the structure of shikimate kinase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 1-6. | 0.7 | 31 |
| 14 | <i>Mycobacterium tuberculosis</i> Dihydrofolate Reductase Reveals Two Conformational States and a Possible Low Affinity Mechanism to Antifolate Drugs. <i>Structure</i> , 2014, 22, 94-103. | 3.3 | 30 |
| 15 | Structural Basis for the Activity and Substrate Specificity of Fluoroacetyl-CoA Thioesterase Fk. <i>Journal of Biological Chemistry</i> , 2010, 285, 22495-22504. | 3.4 | 24 |
| 16 | Unexpected enzyme-catalysed [4+2] cycloaddition and rearrangement in polyether antibiotic biosynthesis. <i>Nature Catalysis</i> , 2019, 2, 1045-1054. | 34.4 | 20 |
| 17 | Unsaturated fatty acids as high-affinity ligands of the C-terminal Per-ARNT-Sim domain from the Hypoxia-inducible factor 3. <i>Scientific Reports</i> , 2015, 5, 12698. | 3.3 | 17 |
| 18 | Structural Basis of the Selectivity of GenN, an Aminoglycoside N-Methyltransferase Involved in Gentamicin Biosynthesis. <i>ACS Chemical Biology</i> , 2017, 12, 2779-2787. | 3.4 | 16 |

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|----|--|------|-----------|
| 19 | Molecular Models of Tryptophan Synthase From <i>Mycobacterium tuberculosis</i> Complexed With Inhibitors. <i>Cell Biochemistry and Biophysics</i> , 2006, 44, 375-384. | 1.8 | 14 |
| 20 | Using a Fragment-Based Approach to Identify Alternative Chemical Scaffolds Targeting Dihydrofolate Reductase from <i>Mycobacterium tuberculosis</i> . <i>ACS Infectious Diseases</i> , 2020, 6, 2192-2201. | 3.8 | 13 |
| 21 | Discovery of Schaeffer's Acid Analogues as Lead Structures of <i>Mycobacterium tuberculosis</i> Type II Dehydroquinase Using a Rational Drug Design Approach. <i>ChemMedChem</i> , 2013, 8, 54-58. | 3.2 | 11 |
| 22 | Enzymology of Pyran Ring A Formation in Salinomycin Biosynthesis. <i>Angewandte Chemie</i> , 2015, 127, 13826-13829. | 2.0 | 11 |
| 23 | Design and Structural Analysis of Aromatic Inhibitors of Type II Dehydroquinase from <i>Mycobacterium tuberculosis</i> . <i>ChemMedChem</i> , 2015, 10, 116-133. | 3.2 | 10 |
| 24 | Structure of a soluble epoxide hydrolase identified in <i>Trichoderma reesei</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1039-1045. | 2.3 | 10 |
| 25 | Crystal structures of the closed form of <i>Mycobacterium tuberculosis</i> dihydrofolate reductase in complex with dihydrofolate and antifolates. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 682-693. | 2.3 | 10 |
| 26 | Crystal Structure of GenD2, an NAD-Dependent Oxidoreductase Involved in the Biosynthesis of Gentamicin. <i>ACS Chemical Biology</i> , 2019, 14, 925-933. | 3.4 | 10 |
| 27 | Crystallization and preliminary X-ray crystallographic analysis of chorismate synthase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2003-2005. | 2.5 | 8 |
| 28 | Structural Basis for the Interaction and Processing of β -Lactam Antibiotics by L,d-Transpeptidase 3 (LdtMt3) from <i>Mycobacterium tuberculosis</i> . <i>ACS Infectious Diseases</i> , 2019, 5, 260-271. | 3.8 | 8 |
| 29 | Structural and functional characterization of the glutathione peroxidase-like thioredoxin peroxidase from the fungus <i>Trichoderma reesei</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 167, 93-100. | 7.5 | 8 |
| 30 | <i>Mycobacterium</i> OtsA Structures Unveil Substrate Preference Mechanism and Allosteric Regulation by 2-Oxoglutarate and 2-Phosphoglycerate. <i>MBio</i> , 2019, 10, . | 4.1 | 7 |
| 31 | Design, synthesis and biological activity of novel substituted 3-benzoic acid derivatives as MtDHFR inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2020, 28, 115600. | 3.0 | 7 |
| 32 | Trypanosomatid selenophosphate synthetase structure, function and interaction with selenocysteine lyase. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008091. | 3.0 | 5 |
| 33 | Mechanistic Insights into Dideoxygenation in Gentamicin Biosynthesis. <i>ACS Catalysis</i> , 2021, 11, 12274-12283. | 11.2 | 5 |
| 34 | Fragment-Based Drug Discovery in Academia: Experiences From a Tuberculosis Programme. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2009, , 21-36. | 0.5 | 4 |
| 35 | Crystallization and preliminary X-ray diffraction analysis of selenophosphate synthetases from <i>Trypanosoma brucei</i> and <i>Leishmania major</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 864-867. | 0.7 | 4 |
| 36 | Cloning, expression, purification and biophysical analysis of two putative halogenases from the glycopeptide A47,934 gene cluster of <i>Streptomyces toyocaensis</i> . <i>Protein Expression and Purification</i> , 2017, 132, 9-18. | 1.3 | 4 |

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|----|--|-----|-----------|
| 37 | Structural insights into <i>Escherichia coli</i> phosphopantothienoylcysteine synthetase by native ion mobility-mass spectrometry. <i>Biochemical Journal</i> , 2019, 476, 3125-3139. | 3.7 | 4 |
| 38 | The crystal structure of AjiA1 reveals a novel structural motion mechanism in the adenylate-forming enzyme family. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1201-1210. | 2.3 | 2 |
| 39 | An epoxide hydrolase from endophytic <i>Streptomyces</i> shows unique structural features and wide biocatalytic activity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 868-875. | 2.3 | 2 |
| 40 | Title is missing!. , 2020, 14, e0008091. | | 0 |
| 41 | Title is missing!. , 2020, 14, e0008091. | | 0 |
| 42 | Title is missing!. , 2020, 14, e0008091. | | 0 |
| 43 | Title is missing!. , 2020, 14, e0008091. | | 0 |