

Marcio Vinicius Bertacine Dias

List of Publications by Year in descending order

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papers

841
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471509
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1017
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Mechanistic Insights into Dideoxygenation in Gentamicin Biosynthesis. <i>ACS Catalysis</i> , 2021, 11, 12274-12283.	11.2	5
3	Trypanosomatid selenophosphate synthetase structure, function and interaction with selenocysteine lyase. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008091.	3.0	5
4	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
5	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
6	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
7	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
8	Title is missing!. , 2020, 14, e0008091.		0
9	Title is missing!. , 2020, 14, e0008091.		0
10	Title is missing!. , 2020, 14, e0008091.		0
11	Title is missing!. , 2020, 14, e0008091.		0
12	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
13	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
14	Mycobacterial OtsA Structures Unveil Substrate Preference Mechanism and Allosteric Regulation by 2-Oxoglutarate and 2-Phosphoglycerate. <i>MBio</i> , 2019, 10, .	4.1	7
15	Unexpected enzyme-catalysed [4+2] cycloaddition and rearrangement in polyether antibiotic biosynthesis. <i>Nature Catalysis</i> , 2019, 2, 1045-1054.	34.4	20
16	Structural Basis for the Interaction and Processing of Î²-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
17	Structural insights into <i>Escherichia coli</i> phosphopantothenoylcysteine synthetase by native ion mobility mass spectrometry. <i>Biochemical Journal</i> , 2019, 476, 3125-3139.	3.7	4
18	Folate biosynthesis pathway: mechanisms and insights into drug design for infectious diseases. <i>Future Medicinal Chemistry</i> , 2018, 10, 935-959.	2.3	43

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19	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
20	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
21	Structural Basis of the Selectivity of GenN, an Aminoglycoside <i>N</i> -Methyltransferase Involved in Gentamicin Biosynthesis. <i>ACS Chemical Biology</i> , 2017, 12, 2779-2787.	3.4	16
22	Enzymology of Pyran Ring A Formation in Salinomycin Biosynthesis. <i>Angewandte Chemie</i> , 2015, 127, 13826-13829.	2.0	11
23	Enzymology of Pyran Ring A Formation in Salinomycin Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 13622-13625.	13.8	40
24	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
25	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
26	<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
27	Discovery of Schaeffer's Acid Analogues as Lead Structures of Type II Dehydroquinase Using a Rational Drug Design Approach. <i>ChemMedChem</i> , 2013, 8, 54-58.	3.2	11
28	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
29	Structural investigation of inhibitor designs targeting 3-dehydroquinase dehydratase from the shikimate pathway of <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 2011, 436, 729-739.	3.7	39
30	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
31	Chimeric Glycosyltransferases for the Generation of Hybrid Glycopeptides. <i>Chemistry and Biology</i> , 2009, 16, 676-685.	6.0	50
32	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
33	Chorismate Synthase: An Attractive Target For Drug Development Against Orphan Diseases. <i>Current Drug Targets</i> , 2007, 8, 437-444.	2.1	49
34	Crystallographic studies on the binding of isonicotinylnad 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
35	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
36	Structure of chorismate synthase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural Biology</i> , 2006, 154, 130-143.	2.8	41

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37	Molecular Models of Tryptophan Synthase From Mycobacterium tuberculosis Complexed With Inhibitors. Cell Biochemistry and Biophysics, 2006, 44, 375-384.	1.8	14
38	Crystal structure of human PNP complexed with hypoxanthine and sulfate ion. Biochemical and Biophysical Research Communications, 2005, 326, 335-338.	2.1	33
39	Crystallization and preliminary X-ray crystallographic analysis of chorismate synthase from Mycobacterium tuberculosis. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2003-2005.	2.5	8
40	Structure of shikimate kinase from Mycobacterium tuberculosis reveals the binding of shikimic acid. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2310-2319.	2.5	48
41	Structural basis for inhibition of human PNP by immucillin-H. Biochemical and Biophysical Research Communications, 2003, 309, 917-922.	2.1	47
42	Crystal structure of human PNP complexed with guanine. Biochemical and Biophysical Research Communications, 2003, 312, 767-772.	2.1	39
43	Crystal structure of human purine nucleoside phosphorylase complexed with acyclovir. Biochemical and Biophysical Research Communications, 2003, 308, 553-559.	2.1	58