

VÃ-tor G Mendes

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

801
citations

516710

16
h-index

526287

27
g-index

42
all docs

42
docs citations

42
times ranked

1190
citing authors

#	ARTICLE	IF	CITATIONS
1	Arginine-deprivation-induced oxidative damage sterilizes <i>Mycobacterium tuberculosis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9779-9784.	7.1	97
2	<i>Bacillus foraminis</i> sp. nov., isolated from a non-saline alkaline groundwater. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2571-2574.	1.7	55
3	<i>Microcella putealis</i> gen. nov., sp. nov., a Gram-positive alkaliphilic bacterium isolated from a nonsaline alkaline groundwater. Systematic and Applied Microbiology, 2005, 28, 479-487.	2.8	52
4	The molecular biology of mycobacterial trehalose in the quest for advanced tuberculosis therapies. Microbiology (United Kingdom), 2014, 160, 1547-1570.	1.8	50
5	<i>Chimaereicella alkaliphila</i> gen. nov., sp. nov., a Gram-negative alkaliphilic bacterium isolated from a nonsaline alkaline groundwater. Systematic and Applied Microbiology, 2006, 29, 100-108.	2.8	40
6	Structural Biology and the Design of New Therapeutics: From HIV and Cancer to Mycobacterial Infections. Journal of Molecular Biology, 2017, 429, 2677-2693.	4.2	39
7	Organic solutes in <i>Rubrobacter xylanophilus</i> : the first example of di-myo-inositol-phosphate in a thermophile. Extremophiles, 2007, 11, 667-673.	2.3	38
8	Targeting tuberculosis using structure-guided fragment-based drug design. Drug Discovery Today, 2017, 22, 546-554.	6.4	36
9	Identification of the mycobacterial glucosyl-3-phosphoglycerate synthase. FEMS Microbiology Letters, 2008, 280, 195-202.	1.8	33
10	<i>Phenylobacterium falsum</i> sp. nov., an Alphaproteobacterium isolated from a nonsaline alkaline groundwater, and emended description of the genus <i>Phenylobacterium</i> . Systematic and Applied Microbiology, 2005, 28, 295-302.	2.8	32
11	Development of Inhibitors against <i>Mycobacterium abscessus</i> tRNA (m ¹ G37) Methyltransferase (TrmD) Using Fragment-Based Approaches. Journal of Medicinal Chemistry, 2019, 62, 7210-7232.	6.4	32
12	Structure-guided fragment-based drug discovery at the synchrotron: screening binding sites and correlations with hotspot mapping. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2019, 377, 20180422.	3.4	30
13	Biochemical characterization of the maltokinase from <i>Mycobacterium bovis</i> BCG. BMC Biochemistry, 2010, 11, 21.	4.4	29
14	Fragment-Based Design of <i>Mycobacterium tuberculosis</i> InhA Inhibitors. Journal of Medicinal Chemistry, 2020, 63, 4749-4761.	6.4	27
15	Biosynthesis of mycobacterial methylglucose lipopolysaccharides. Natural Product Reports, 2012, 29, 834.	10.3	25
16	Target Identification of <i>Mycobacterium tuberculosis</i> Phenotypic Hits Using a Concerted Chemogenomic, Biophysical, and Structural Approach. Frontiers in Pharmacology, 2017, 8, 681.	3.5	22
17	Fragment-based discovery of a new class of inhibitors targeting mycobacterial tRNA modification. Nucleic Acids Research, 2020, 48, 8099-8112.	14.5	20
18	Two Alternative Pathways for the Synthesis of the Rare Compatible Solute Mannosylglucosylglycerate in <i>Petrogoga mobilis</i> . Journal of Bacteriology, 2010, 192, 1624-1633.	2.2	17

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19	Genome Sequence of <i>Mycobacterium hassiacum</i> DSM 44199, a Rare Source of Heat-Stable Mycobacterial Proteins. <i>Journal of Bacteriology</i> , 2012, 194, 7010-7011.	2.2	17
20	Structural insights into the EthRâ€™DNA interaction using native mass spectrometry. <i>Chemical Communications</i> , 2017, 53, 3527-3530.	4.1	17
21	<i>Mycobacterium tuberculosis</i> Rv2419c, the missing glucosyl-3-phosphoglycerate phosphatase for the second step in methylglucose lipopolysaccharide biosynthesis. <i>Scientific Reports</i> , 2011, 1, 177.	3.3	16
22	A fragment-based approach to assess the ligandability of ArgB, ArgC, ArgD and ArgF in the L-arginine biosynthetic pathway of <i>Mycobacterium tuberculosis</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3491-3506.	4.1	16
23	Fragment Screening against the EthRâ€™DNA Interaction by Native Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 7488-7491.	13.8	12
24	Development of Inhibitors of SAICAR Synthetase (PurC) from <i>Mycobacterium abscessus</i> Using a Fragment-Based Approach. <i>ACS Infectious Diseases</i> , 2022, 8, 296-309.	3.8	10
25	Inhibiting <i>Mycobacterium tuberculosis</i> CoaBC by targeting an allosteric site. <i>Nature Communications</i> , 2021, 12, 143.	12.8	8
26	Mycobacterial OtsA Structures Unveil Substrate Preference Mechanism and Allosteric Regulation by 2-Oxoglutarate and 2-Phosphoglycerate. <i>MBio</i> , 2019, 10, .	4.1	7
27	Crystal structure of <i>Staphylococcus aureus</i> Zn-glyoxalase I: new subfamily of glyoxalase I family. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 376-386.	3.5	5
28	Discovery of Novel Inhibitors of Uridine Diphosphate-N-Acetylenolpyruvylglucosamine Reductase (MurB) from <i>Pseudomonas aeruginosa</i> , an Opportunistic Infectious Agent Causing Death in Cystic Fibrosis Patients. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 2149-2173.	6.4	5
29	Structural insights into <i>Escherichia coli</i> phosphopantothenoylcysteine synthetase by native ion mobilityâ€™mass spectrometry. <i>Biochemical Journal</i> , 2019, 476, 3125-3139.	3.7	4
30	Structure of <i>Mycobacterium thermoresistibile</i> GlgE defines novel conformational states that contribute to the catalytic mechanism. <i>Scientific Reports</i> , 2015, 5, 17144.	3.3	3
31	Targeting <i>Mycobacterium tuberculosis</i> CoaBC through Chemical Inhibition of 4-Phosphopantothenoyl-cysteine Synthetase (CoaB) Activity. <i>ACS Infectious Diseases</i> , 2021, 7, 1666-1679.	3.8	3
32	Fragment Screening against the EthRâ€™DNA Interaction by Native Mass Spectrometry. <i>Angewandte Chemie</i> , 2017, 129, 7596-7599.	2.0	2