VÃ-tor G Mendes

List of Publications by Year
in descending order

32	801	516710 16	526287 27
papers	citations	h-index	g-index

42	42	42	1190
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Development of Inhibitors of SAICAR Synthetase (PurC) from Mycobacterium abscessus Using a Fragment-Based Approach. ACS Infectious Diseases, 2022, 8, 296-309.	3.8	10
2	Discovery of Novel Inhibitors of Uridine Diphosphate-N-Acetylenolpyruvylglucosamine Reductase (MurB) from Pseudomonas aeruginosa, an Opportunistic Infectious Agent Causing Death in Cystic Fibrosis Patients. Journal of Medicinal Chemistry, 2022, 65, 2149-2173.	6.4	5
3	Targeting Mycobacterium tuberculosis CoaBC through Chemical Inhibition of 4â€²-Phosphopantothenoyl-<scp>l</scp>-cysteine Synthetase (CoaB) Activity. ACS Infectious Diseases, 2021, 7, 1666-1679.	3.8	3
4	A fragment-based approach to assess the ligandability of ArgB, ArgC, ArgD and ArgF in the L-arginine biosynthetic pathway of Mycobacterium tuberculosis. Computational and Structural Biotechnology Journal, 2021, 19, 3491-3506.	4.1	16
5	Inhibiting Mycobacterium tuberculosis CoaBC by targeting an allosteric site. Nature Communications, 2021, 12, 143.	12.8	8
6	Fragment-Based Design of Mycobacterium tuberculosis InhA Inhibitors. Journal of Medicinal Chemistry, 2020, 63, 4749-4761.	6.4	27
7	Fragment-based discovery of a new class of inhibitors targeting mycobacterial tRNA modification. Nucleic Acids Research, 2020, 48, 8099-8112.	14.5	20
8	Development of Inhibitors against Mycobacterium abscessus tRNA (m¹G37) Methyltransferase (TrmD) Using Fragment-Based Approaches. Journal of Medicinal Chemistry, 2019, 62, 7210-7232.	6.4	32
9	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
10	Mycobacterial OtsA Structures Unveil Substrate Preference Mechanism and Allosteric Regulation by 2-Oxoglutarate and 2-Phosphoglycerate. MBio, 2019, 10, .	4.1	7
11	Structural insights into Escherichia coli phosphopantothenoylcysteine synthetase by native ion mobilityâ€“mass spectrometry. Biochemical Journal, 2019, 476, 3125-3139.	3.7	4
12	Crystal structure ofStaphylococcus aureusZn-glyoxalase I: new subfamily of glyoxalase I family. Journal of Biomolecular Structure and Dynamics, 2018, 36, 376-386.	3.5	5
13	Arginine-deprivationâ€“induced oxidative damage sterilizes Mycobacterium tuberculosis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9779-9784.	7.1	97
14	Structural insights into the EthRâ€“DNA interaction using native mass spectrometry. Chemical Communications, 2017, 53, 3527-3530.	4.1	17
15	Fragment Screening against the EthRâ€“DNA Interaction by Native Mass Spectrometry. Angewandte Chemie - International Edition, 2017, 56, 7488-7491.	13.8	12
16	Fragment Screening against the EthRâ€“DNA Interaction by Native Mass Spectrometry. Angewandte Chemie, 2017, 129, 7596-7599.	2.0	2
17	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
18	Targeting tuberculosis using structure-guided fragment-based drug design. Drug Discovery Today, 2017, 22, 546-554.	6.4	36

#	Article	IF	Citations
19	Target Identification of Mycobacterium tuberculosis Phenotypic Hits Using a Concerted Chemogenomic, Biophysical, and Structural Approach. Frontiers in Pharmacology, 2017, 8, 681.	3.5	22
20	Structure of Mycobacterium thermoresistibile GlgE defines novel conformational states that contribute to the catalytic mechanism. Scientific Reports, 2015, 5, 17144.	3.3	3
21	The molecular biology of mycobacterial trehalose in the quest for advanced tuberculosis therapies. Microbiology (United Kingdom), 2014, 160, 1547-1570.	1.8	50
22	Genome Sequence of Mycobacterium hassiacum DSM 44199, a Rare Source of Heat-Stable Mycobacterial Proteins. Journal of Bacteriology, 2012, 194, 7010-7011.	2.2	17
23	Biosynthesis of mycobacterial methylglucose lipopolysaccharides. Natural Product Reports, 2012, 29, 834.	10.3	25
24	Mycobacterium tuberculosis Rv2419c, the missing glucosyl-3-phosphoglycerate phosphatase for the second step in methylglucose lipopolysaccharide biosynthesis. Scientific Reports, 2011, 1, 177.	3.3	16
25	Biochemical characterization of the maltokinase from Mycobacterium bovis BCG. BMC Biochemistry, 2010, 11, 21.	4.4	29
26	Two Alternative Pathways for the Synthesis of the Rare Compatible Solute Mannosylglucosylglycerate inPetrotoga mobilis. Journal of Bacteriology, 2010, 192, 1624-1633.	2.2	17
27	Identification of the mycobacterial glucosyl-3-phosphoglycerate synthase. FEMS Microbiology Letters, 2008, 280, 195-202.	1.8	33
28	Organic solutes in Rubrobacter xylanophilus: the first example of di-myo-inositol-phosphate in a thermophile. Extremophiles, 2007, 11, 667-673.	2.3	38
29	Chimaereicella alkaliphila 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
30	Bacillus foraminis sp. nov., isolated from a non-saline alkaline groundwater. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2571-2574.	1.7	55
31	Phenylobacterium falsum sp. nov., an Alphaproteobacterium isolated from a nonsaline alkaline groundwater, and emended description of the genus Phenylobacterium. Systematic and Applied Microbiology, 2005, 28, 295-302.	2.8	32
32	Microcella putealis 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