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List of Publications by Year in descending order

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1040056 888059 18 291 9 17 citations g-index h-index papers 18 18 18 611 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Genomic and structural features of the yellow fever virus from the 2016–2017 Brazilian outbreak. Journal of General Virology, 2018, 99, 536-548.	2.9	50
2	Structural modelling and comparative analysis of homologous, analogous and specific proteins from Trypanosoma cruzi versus Homo sapiens: putative drug targets for chagas' disease treatment. BMC Genomics, 2010, 11, 610.	2.8	45
3	The Essential Role of Cholesterol Metabolism in the Intracellular Survival of Mycobacterium leprae Is Not Coupled to Central Carbon Metabolism and Energy Production. Journal of Bacteriology, 2015, 197, 3698-3707.	2.2	33
4	AnEnPi: identification and annotation of analogous enzymes. BMC Bioinformatics, 2008, 9, 544.	2.6	28
5	A new approach for potential drug target discovery through in silico metabolic pathway analysis using Trypanosoma cruzi genome information. Memorias Do Instituto Oswaldo Cruz, 2009, 104, 1100-1110.	1.6	27
6	ESTs from Seeds to Assist the Selective Breeding of <i>Jatropha curcas</i> L. for Oil and Active Compounds. Genomics Insights, 2010, 3, GEI.S4340.	3.0	26
7	In silico identification of inhibitors of ribose 5-phosphate isomerase from Trypanosoma cruzi using ligand and structure based approaches. Journal of Molecular Graphics and Modelling, 2017, 77, 168-180.	2.4	17
8	MamMiBase: a mitochondrial genome database for mammalian phylogenetic studies. Bioinformatics, 2005, 21, 2566-2567.	4.1	15
9	In silico reconstruction of the amino acid metabolic pathways of Trypanosoma cruzi. Genetics and Molecular Research, 2008, 7, 872-882.	0.2	12
10	Functional Analogy in Human Metabolism: Enzymes with Different Biological Roles or Functional Redundancy?. Genome Biology and Evolution, 2017, 9, 1624-1636.	2.5	10
11	In silico structural characterization of protein targets for drug development against Trypanosoma cruzi. Journal of Molecular Modeling, 2016, 22, 244.	1.8	7
12	Proteomics reveals major components of oogenesis in the reproductive tract of sugar-fed Anopheles aquasalis. Parasitology Research, 2016, 115, 1977-1989.	1.6	7
13	Insights into the Mechanism of Ethionamide Resistance in Mycobacterium tuberculosis through an in silico Structural Evaluation of EthA and Mutants Identified in Clinical Isolates. Catalysts, 2020, 10, 543.	3.5	4
14	Specific and Nonhomologous Isofunctional Enzymes of the Genetic Information Processing Pathways as Potential Therapeutical Targets for Tritryps. Enzyme Research, 2011, 2011, 1-8.	1.8	3
15	A Computational Methodology to Overcome the Challenges Associated With the Search for Specific Enzyme Targets to Develop Drugs Against Leishmania major. Bioinformatics and Biology Insights, 2017, 11, 117793221771247.	2.0	3
16	<i>In silico</i> investigation of riboswitches in fungi: structural and dynamical insights into TPP riboswitches in <i>Aspergillus oryzae</i> . RNA Biology, 2022, 19, 90-103.	3.1	2
17	Computational evaluation of natural compounds as potential inhibitors of human PEPCK-M: an alternative for lung cancer therapy. Advances and Applications in Bioinformatics and Chemistry, 2019, Volume 12, 15-32.	2.6	1
18	Differences in Charge Distribution in Leishmania tarentolae Leishmanolysin Result in a Reduced Enzymatic Activity. International Journal of Molecular Sciences, 2022, 23, 7660.	4.1	1