

Antônio Jm Ribeiro

List of Publications by Year in descending order

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32
papers

1,345
citations

430442

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414034

32
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docs citations

34
times ranked

2314
citing authors

#	ARTICLE	IF	CITATIONS
1	Conformational Variation in Enzyme Catalysis: A Structural Study on Catalytic Residues. <i>Journal of Molecular Biology</i> , 2022, 434, 167517.	2.0	17
2	GRASP-web: a machine learning strategy to predict binding sites based on residue neighborhood graphs. <i>Nucleic Acids Research</i> , 2022, 50, W392-W397.	6.5	7
3	The Enzyme Portal: an integrative tool for enzyme information and analysis. <i>FEBS Journal</i> , 2021, , .	2.2	2
4	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	6.5	87
5	Identifying pseudoenzymes using functional annotation: pitfalls of common practice. <i>FEBS Journal</i> , 2020, 287, 4128-4140.	2.2	19
6	A global analysis of function and conservation of catalytic residues in enzymes. <i>Journal of Biological Chemistry</i> , 2020, 295, 314-324.	1.6	68
7	GRASP: a graph-based residue neighborhood strategy to predict binding sites. <i>Bioinformatics</i> , 2020, 36, i726-i734.	1.8	10
8	Emerging concepts in pseudoenzyme classification, evolution, and signaling. <i>Science Signaling</i> , 2019, 12, .	1.6	80
9	Exploring Chemical Biosynthetic Design Space with Transform-MinER. <i>ACS Synthetic Biology</i> , 2019, 8, 2494-2506.	1.9	16
10	Mechanism and Catalytic Site Atlas (M-CSA): a database of enzyme reaction mechanisms and active sites. <i>Nucleic Acids Research</i> , 2018, 46, D618-D623.	6.5	151
11	Ranking Enzyme Structures in the PDB by Bound Ligand Similarity to Biological Substrates. <i>Structure</i> , 2018, 26, 565-571.e3.	1.6	23
12	Transform-MinER: transforming molecules in enzyme reactions. <i>Bioinformatics</i> , 2018, 34, 3597-3599.	1.8	10
13	Benchmarking of density functionals for the kinetics and thermodynamics of the hydrolysis of glycosidic bonds catalyzed by glycosidases. <i>International Journal of Quantum Chemistry</i> , 2017, 117, e25409.	1.0	37
14	Unique Triphenylphosphonium Derivatives for Enhanced Mitochondrial Uptake and Photodynamic Therapy. <i>Bioconjugate Chemistry</i> , 2017, 28, 590-599.	1.8	46
15	cuRRBS: simple and robust evaluation of enzyme combinations for reduced representation approaches. <i>Nucleic Acids Research</i> , 2017, 45, 11559-11569.	6.5	14
16	Binding free energy calculations on E-selectin complexes with sL^x oligosaccharide analogs. <i>Chemical Biology and Drug Design</i> , 2017, 89, 114-123.	1.5	8
17	Application of quantum mechanics/molecular mechanics methods in the study of enzymatic reaction mechanisms. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2017, 7, e1281.	6.2	137
18	Improving the Biotransformation of Crude Oil and Derivatives: A QM/MM Investigation of the Catalytic Mechanism of NADH-FMN Oxidoreductase (DszD). <i>Journal of Physical Chemistry A</i> , 2016, 120, 5300-5306.	1.1	24

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19	HMG-CoA Reductase inhibitors: an updated review of patents of novel compounds and formulations (2011-2015). <i>Expert Opinion on Therapeutic Patents</i> , 2016, 26, 1257-1272.	2.4	19
20	Insight into Enzymatic Nitrile Reduction: QM/MM Study of the Catalytic Mechanism of QueF Nitrile Reductase. <i>ACS Catalysis</i> , 2015, 5, 3740-3751.	5.5	28
21	New insights in the catalytic mechanism of tyrosine ammonia-lyase given by QM/MM and QM cluster models. <i>Archives of Biochemistry and Biophysics</i> , 2015, 582, 107-115.	1.4	24
22	Synthesis and Hydrolytic Studies on the Air-Stable [(4-CN-PhO)(E)P($\frac{1}{4}$ -N ^{sup} <i>t</i></sup>Bu)] ₂ (E = O, S, and Se) Cyclodiphosphazanes. <i>Inorganic Chemistry</i> , 2015, 54, 6423-6432.	1.9	25
23	Enzymatic Flexibility and Reaction Rate: A QM/MM Study of HIV-1 Protease. <i>ACS Catalysis</i> , 2015, 5, 5617-5626.	5.5	72
24	Catalytic Mechanism of Retroviral Integrase for the Strand Transfer Reaction Explored by QM/MM Calculations. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 5458-5466.	2.3	6
25	Analyses of cobaltâ€“ligand and potassiumâ€“ligand bond lengths in metalloproteins: trends and patterns. <i>Journal of Molecular Modeling</i> , 2014, 20, 2271.	0.8	4
26	Divalent metal ion-based catalytic mechanism of the Nudix hydrolase Orf153 (YmfB) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1297-1310.	2.5	5
27	Comparative analysis of the performance of commonly available density functionals in the determination of geometrical parameters for copper complexes. <i>Journal of Computational Chemistry</i> , 2013, 34, 2079-2090.	1.5	38
28	A DFT study of the applicability of the charge balance model in two-metal enzymes: The case of cAMP-dependent protein kinase. <i>Chemical Physics Letters</i> , 2013, 571, 66-70.	1.2	7
29	The Catalytic Mechanism of Protein Phosphataseâ€“5 Established by DFT Calculations. <i>Chemistry - A European Journal</i> , 2013, 19, 14081-14089.	1.7	44
30	Protein-Ligand Docking in the New Millennium â€“ A Retrospective of 10 Years in the Field. <i>Current Medicinal Chemistry</i> , 2013, 20, 2296-2314.	1.2	197
31	The Catalytic Mechanism of HIV-1 Integrase for DNA 3â€“End Processing Established by QM/MM Calculations. <i>Journal of the American Chemical Society</i> , 2012, 134, 13436-13447.	6.6	51
32	Benchmarking of DFT Functionals for the Hydrolysis of Phosphodiester Bonds. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 2281-2292.	2.3	69