

Rodrigo V Honorato

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/127932/publications.pdf>

Version: 2024-02-01

31
papers

1,302
citations

471509

17
h-index

434195

31
g-index

33
all docs

33
docs citations

33
times ranked

1869
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Biology in the Clouds: The WeNMR-EOSC Ecosystem. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 729513.	3.5	308
2	Molecular Dynamics Simulations in Drug Discovery and Pharmaceutical Development. <i>Processes</i> , 2021, 9, 71.	2.8	162
3	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
4	KVFinder: steered identification of protein cavities as a PyMOL plugin. <i>BMC Bioinformatics</i> , 2014, 15, 197.	2.6	91
5	Active Glutaminase C Self-assembles into a Supratetrameric Oligomer That Can Be Disrupted by an Allosteric Inhibitor. <i>Journal of Biological Chemistry</i> , 2013, 288, 28009-28020.	3.4	74
6	Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1800-1823.	2.6	73
7	Molecular Mechanisms Associated with Xylan Degradation by <i>Xanthomonas</i> Plant Pathogens. <i>Journal of Biological Chemistry</i> , 2014, 289, 32186-32200.	3.4	57
8	Oligomerization as a strategy for cold adaptation: Structure and dynamics of the GH1 β -glucosidase from <i>Exiguobacterium antarcticum</i> B7. <i>Scientific Reports</i> , 2016, 6, 23776.	3.3	57
9	Less Is More: Coarse-Grained Integrative Modeling of Large Biomolecular Assemblies with HADDOCK. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 6358-6367.	5.3	43
10	Identification of Novel Interaction between ADAM17 (a Disintegrin and Metalloprotease 17) and Thioredoxin-1. <i>Journal of Biological Chemistry</i> , 2012, 287, 43071-43082.	3.4	33
11	Structural Insights into Functional Overlapping and Differentiation among Myosin V Motors. <i>Journal of Biological Chemistry</i> , 2013, 288, 34131-34145.	3.4	29
12	The mechanism by which a distinguishing arabinofuranosidase can cope with internal di-substitutions in arabinoxylans. <i>Biotechnology for Biofuels</i> , 2018, 11, 223.	6.2	29
13	MARTINI-Based Protein-DNA Coarse-Grained HADDOCKing. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 102.	3.5	28
14	Kinase Inhibitor Profile for Human Nek1, Nek6, and Nek7 and Analysis of the Structural Basis for Inhibitor Specificity. <i>Molecules</i> , 2015, 20, 1176-1191.	3.8	24
15	Bactericidal Activity Identified in 2S Albumin from Sesame Seeds and In silico Studies of Structure-Function Relations. <i>Protein Journal</i> , 2011, 30, 340-350.	1.6	22
16	Mechanistic Strategies for Catalysis Adopted by Evolutionary Distinct Family 43 Arabinanases. <i>Journal of Biological Chemistry</i> , 2014, 289, 7362-7373.	3.4	21
17	Structural studies of the <i>Trypanosoma cruzi</i> Old Yellow Enzyme: Insights into enzyme dynamics and specificity. <i>Biophysical Chemistry</i> , 2013, 184, 44-53.	2.8	18
18	P-I class metalloproteinase from <i>Bothrops moojeni</i> venom is a post-proline cleaving peptidase with kininogenase activity: Insights into substrate selectivity and kinetic behavior. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 545-552.	2.3	17

#	ARTICLE	IF	CITATIONS
19	Structural basis of exo- β -mannanase activity in the GH2 family. <i>Journal of Biological Chemistry</i> , 2018, 293, 13636-13649.	3.4	16
20	ParKVFinder: A thread-level parallel approach in biomolecular cavity detection. <i>SoftwareX</i> , 2020, 12, 100606.	2.6	14
21	An overview of data-driven HADDOCK strategies in CAPRI rounds 38-45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1029-1036.	2.6	11
22	Information-driven modeling of biomolecular complexes. <i>Current Opinion in Structural Biology</i> , 2021, 70, 70-77.	5.7	11
23	Pyrrole-indolinone SU11652 targets the nucleoside diphosphate kinase from <i>Leishmania</i> parasites. <i>Biochemical and Biophysical Research Communications</i> , 2017, 488, 461-465.	2.1	10
24	Calcium and magnesium ions modulate the oligomeric state and function of mitochondrial 2-Cys peroxiredoxins in <i>Leishmania</i> parasites. <i>Journal of Biological Chemistry</i> , 2017, 292, 7023-7039.	3.4	10
25	Thioredoxin-1 Negatively Modulates ADAM17 Activity Through Direct Binding and Indirect Reductive Activity. <i>Antioxidants and Redox Signaling</i> , 2018, 29, 717-734.	5.4	9
26	Structural Analysis of Intermolecular Interactions in the Kinesin Adaptor Complex Fasciculation and Elongation Protein Zeta 1/ Short Coiled-Coil Protein (FEZ1/SCOCO). <i>PLoS ONE</i> , 2013, 8, e76602.	2.5	8
27	Negative regulation of bacterial killing and inflammation by two novel CD16 ligands. <i>European Journal of Immunology</i> , 2016, 46, 1926-1935.	2.9	7
28	Glutaminase Affects the Transcriptional Activity of Peroxisome Proliferator-Activated Receptor β (PPAR β) via Direct Interaction. <i>Biochemistry</i> , 2018, 57, 6293-6307.	2.5	7
29	Nucleosome binding peptide presents laudable biophysical and in vivo effects. <i>Biomedicine and Pharmacotherapy</i> , 2020, 121, 109678.	5.6	4
30	CAZy-parser a way to extract information from the Carbohydrate-Active enZymes Database. <i>Journal of Open Source Software</i> , 2016, 1, 53.	4.6	4
31	A specific interdomain interaction preserves the structural and binding properties of the ModA protein from the phytopathogen <i>Xanthomonas citri</i> domain interaction and transport in ModA. <i>Archives of Biochemistry and Biophysics</i> , 2013, 539, 20-30.	3.0	3