Daniel Auguin

List of Publications by Year in descending order

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Version: 2024-02-01

34	1,051	17 h-index	31
papers	citations		g-index
39	39	39	1429
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	A Perspective for Ménière's Disease: In Silico Investigations of Dexamethasone as a Direct Modulator of AQP2. Biomolecules, 2022, 12, 511.	4.0	2
2	Noncanonical Function of AGO2 Augments T-cell Receptor Signaling in T-cell Prolymphocytic Leukemia. Cancer Research, 2022, 82, 1818-1831.	0.9	9
3	Voltageâ€gating of aquaporins, a putative conserved safety mechanism during ionic stresses. FEBS Letters, 2021, 595, 41-57.	2.8	18
4	Fungal X-Intrinsic Protein Aquaporin from Trichoderma atroviride: Structural and Functional Considerations. Biomolecules, 2021, 11, 338.	4.0	3
5	The actomyosin interface contains an evolutionary conserved core and an ancillary interface involved in specificity. Nature Communications, 2021, 12, 1892.	12.8	23
6	Crystal structures of N-terminally truncated telomerase reverse transcriptase from fungi. Nucleic Acids Research, 2021, 49, 4768-4781.	14.5	7
7	Full-length Plasmodium falciparum myosin A and essential light chain PfELC structures provide new anti-malarial targets. ELife, 2020, 9, .	6.0	19
8	Plasmodium myosin A drives parasite invasion by an atypical force generating mechanism. Nature Communications, 2019, 10, 3286.	12.8	49
9	Characterization of LuWRKY36, a flax transcription factor promoting secoisolariciresinol biosynthesis in response to Fusarium oxysporum elicitors in Linum usitatissimum L. hairy roots. Planta, 2019, 250, 347-366.	3.2	15
10	Pinoresinol–lariciresinol reductases, key to the lignan synthesis in plants. Planta, 2019, 249, 1695-1714.	3.2	46
11	The control exerted by ABA on lignan biosynthesis in flax (Linum usitatissimum L.) is modulated by a Ca2+ signal transduction involving the calmodulin-like LuCML15b. Journal of Plant Physiology, 2019, 236, 74-87.	3.5	21
12	Aquaporins and water control in drought-stressed poplar leaves: A glimpse into the extraxylem vascular territories. Environmental and Experimental Botany, 2019, 162, 25-37.	4.2	19
13	A genome-wide analysis of the flax (Linum usitatissimum L.) dirigent protein family: from gene identification and evolution to differential regulation. Plant Molecular Biology, 2018, 97, 73-101.	3.9	66
14	Molecular Mechanistic Insights into Drosophila DHX36-Mediated G-Quadruplex Unfolding: A Structure-Based Model. Structure, 2018, 26, 403-415.e4.	3.3	35
15	Hypertrophic cardiomyopathy disease results from disparate impairments of cardiac myosin function and auto-inhibition. Nature Communications, 2018, 9, 4019.	12.8	91
16	MIP diversity from Trichoderma: Structural considerations and transcriptional modulation during mycoparasitic association with Fusarium solani olive trees. PLoS ONE, 2018, 13, e0193760.	2.5	10
17	Beneficial effect of Trichoderma harzianum strain Ths97 in biocontrolling Fusarium solani causal agent of root rot disease in olive trees. Biological Control, 2017, 110, 70-78.	3.0	83
18	Functional characterization of the pinoresinol–lariciresinol reductase-2 gene reveals its roles in yatein biosynthesis and flax defense response. Planta, 2017, 246, 405-420.	3.2	35

#	Article	IF	Citations
19	Functional Divergence of Poplar Histidine-Aspartate Kinase HK1 Paralogs in Response to Osmotic Stress. International Journal of Molecular Sciences, 2016, 17, 2061.	4.1	24
20	The Hevea brasiliensis XIP aquaporin subfamily: genomic, structural and functional characterizations with relevance to intensive latex harvesting. Plant Molecular Biology, 2016, 91, 375-396.	3.9	16
21	Nettle (Urtica dioica L.) as a source of antioxidant and anti-aging phytochemicals for cosmetic applications. Comptes Rendus Chimie, 2016, 19, 1090-1100.	0.5	64
22	Insights into B-type RR members as signaling partners acting downstream of HPt partners of HK1 in the osmotic stress response in Populus. Plant Physiology and Biochemistry, 2015, 94, 244-252.	5.8	11
23	In silico study of wall-associated kinase family reveals large-scale genomic expansion potentially connected with functional diversification in Populus. Tree Genetics and Genomes, 2014, 10, 1135-1147.	1.6	17
24	Role of protein farnesylation events in the ABA-mediated regulation of the Pinoresinol–Lariciresinol Reductase 1 (LuPLR1) gene expression and lignan biosynthesis in flax (Linum usitatissimum L.). Plant Physiology and Biochemistry, 2013, 72, 96-111.	5.8	25
25	Insights into Populus XIP aquaporins: evolutionary expansion, protein functionality, and environmental regulation. Journal of Experimental Botany, 2012, 63, 2217-2230.	4.8	101
26	Structure of the <i>Mycobacterium tuberculosis</i> OmpATb protein: A model of an oligomeric channel in the mycobacterial cell wall. Proteins: Structure, Function and Bioinformatics, 2011, 79, 645-661.	2.6	24
27	Structural Studies of the Complex Between Akt-in and the Akt2-PH Domain Suggest that the Peptide Acts as an Allosteric Inhibitor of the Akt Kinase. The Open Spectroscopy Journal, 2009, 3, 65-76.	1.0	1
28	The Solution Structure of the Adhesion Protein Bd37 from Babesia divergens Reveals Structural Homology with Eukaryotic Proteins Involved in Membrane Trafficking. Journal of Molecular Biology, 2008, 375, 409-424.	4.2	19
29	Unraveling protein dynamics through fast spectral density mapping. Journal of Biomolecular NMR, 2007, 37, 159-177.	2.8	5
30	Structural Basis for the Co-activation of Protein Kinase B by T-cell Leukemia-1 (TCL1) Family Proto-oncoproteins. Journal of Biological Chemistry, 2004, 279, 35890-35902.	3.4	47
31	Inhibition of Akt Kinase Activity by a Peptide Spanning the \hat{l}^2A Strand of the Proto-oncogene TCL1. Journal of Biological Chemistry, 2004, 279, 53407-53418.	3.4	84
32	Solution Structure and Backbone Dynamics of the Pleckstrin Homology Domain of the Human Protein KinaseÂB (PKB/Akt). Interaction with Inositol Phosphates. Journal of Biomolecular NMR, 2004, 28, 137-155.	2.8	47
33	1H, 15N and 13C chemical shift assignments of the Pleckstrin Homology domain of the Human Protein Kinase B (PKB/Akt). Journal of Biomolecular NMR, 2003, 27, 287-288.	2.8	3
34	Superposition of chemical shifts in NMR spectra can be overcome to determine automatically the structure of a protein. Spectroscopy, 2003, 17, 559-568.	0.8	5