

Miroslaw Kwasniewski

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,589
citations

516710

16
h-index

677142

22
g-index

23
all docs

23
docs citations

23
times ranked

2850
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Demethylation in Response to Heat Stress in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 1555.	4.1	31
2	Gut Microbiome in Chronic Coronary Syndrome Patients. <i>Journal of Clinical Medicine</i> , 2021, 10, 5074.	2.4	13
3	Molecular Signature of Subtypes of Non-Small-Cell Lung Cancer by Large-Scale Transcriptional Profiling: Identification of Key Modules and Genes by Weighted Gene Co-Expression Network Analysis (WGCNA). <i>Cancers</i> , 2020, 12, 37.	3.7	179
4	Systematic Review of Polygenic Risk Scores for Type 1 and Type 2 Diabetes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1703.	4.1	46
5	Insights into Barley Root Transcriptome under Mild Drought Stress with an Emphasis on Gene Expression Regulatory Mechanisms. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6139.	4.1	30
6	DNA Methylation Analysis in Barley and Other Species with Large Genomes. <i>Methods in Molecular Biology</i> , 2019, 1900, 253-268.	0.9	1
7	Evaluation of Genome-Wide Markers and Orthologous Markers in <i>Brachypodium distachyon</i> . <i>Methods in Molecular Biology</i> , 2018, 1667, 195-201.	0.9	0
8	Forward Genetics Approach Reveals a Mutation in bHLH Transcription Factor-Encoding Gene as the Best Candidate for the Root Hairless Phenotype in Barley. <i>Frontiers in Plant Science</i> , 2018, 9, 1229.	3.6	10
9	Systematic biobanking, novel imaging techniques, and advanced molecular analysis for precise tumor diagnosis and therapy: The Polish MOBIT project. <i>Advances in Medical Sciences</i> , 2017, 62, 405-413.	2.1	18
10	Methylation Sensitive Amplification Polymorphism Sequencing (MSAP-Seq) – A Method for High-Throughput Analysis of Differentially Methylated CCGG Sites in Plants with Large Genomes. <i>Frontiers in Plant Science</i> , 2017, 8, 2056.	3.6	32
11	No Time to Waste: Transcriptome Study Reveals that Drought Tolerance in Barley May Be Attributed to Stressed-Like Expression Patterns that Exist before the Occurrence of Stress. <i>Frontiers in Plant Science</i> , 2017, 8, 2212.	3.6	66
12	Cytomolecular Analysis of Ribosomal DNA Evolution in a Natural Allotetraploid <i>Brachypodium hybridum</i> and Its Putative Ancestors – Dissecting Complex Repetitive Structure of Intergenic Spacers. <i>Frontiers in Plant Science</i> , 2016, 7, 1499.	3.6	14
13	Water-deficiency conditions differently modulate the methylome of roots and leaves in barley (<i>Hordeum vulgare</i> L.). <i>Journal of Experimental Botany</i> , 2016, 67, 1109-1121.	4.8	72
14	Transcriptome analysis reveals the role of the root hairs as environmental sensors to maintain plant functions under water-deficiency conditions. <i>Journal of Experimental Botany</i> , 2016, 67, 1079-1094.	4.8	80
15	Comet-FISH for the evaluation of plant DNA damage after mutagenic treatments. <i>Journal of Applied Genetics</i> , 2013, 54, 407-415.	1.9	6
16	Accumulation of peroxidase-related reactive oxygen species in trichoblasts correlates with root hair initiation in barley. <i>Journal of Plant Physiology</i> , 2013, 170, 185-195.	3.5	45
17	iRootHair: A Comprehensive Root Hair Genomics Database. <i>Plant Physiology</i> , 2012, 161, 28-35.	4.8	30
18	Comet-FISH with rDNA probes for the analysis of mutagen-induced DNA damage in plant cells. <i>Environmental and Molecular Mutagenesis</i> , 2012, 53, 369-375.	2.2	15

#	ARTICLE	IF	CITATIONS
19	ORS1, an H ₂ O ₂ -Responsive NAC Transcription Factor, Controls Senescence in Arabidopsis thaliana. Molecular Plant, 2011, 4, 346-360.	8.3	281
20	Global analysis of the root hair morphogenesis transcriptome reveals new candidate genes involved in root hair formation in barley. Journal of Plant Physiology, 2010, 167, 1076-1083.	3.5	30
21	QuantPrime – a flexible tool for reliable high-throughput primer design for quantitative PCR. BMC Bioinformatics, 2008, 9, 465.	2.6	452
22	Different recombination frequencies in wheat doubled haploid populations obtained through maize pollination and anther culture. Euphytica, 2007, 156, 173-183.	1.2	17
23	Molecular Cloning and Characterization of Î²-Expansin Gene Related to Root Hair Formation in Barley. Plant Physiology, 2006, 141, 1149-1158.	4.8	121