

# Mirosław Kwasniewski

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10997616/publications.pdf>

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	QuantPrime – a flexible tool for reliable high-throughput primer design for quantitative PCR. <i>BMC Bioinformatics</i> , 2008, 9, 465.	2.6	452
2	ORS1, an H <sub>2</sub> O <sub>2</sub> -Responsive NAC Transcription Factor, Controls Senescence in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2011, 4, 346-360.	8.3	281
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	Molecular Cloning and Characterization of Î <sup>2</sup> -Expansin Gene Related to Root Hair Formation in Barley. <i>Plant Physiology</i> , 2006, 141, 1149-1158.	4.8	121
5	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
6	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
7	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
8	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
9	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
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	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
12	Global analysis of the root hair morphogenesis transcriptome reveals new candidate genes involved in root hair formation in barley. <i>Journal of Plant Physiology</i> , 2010, 167, 1076-1083.	3.5	30
13	iRootHair: A Comprehensive Root Hair Genomics Database. <i>Plant Physiology</i> , 2012, 161, 28-35.	4.8	30
14	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
15	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
16	Different recombination frequencies in wheat doubled haploid populations obtained through maize pollination and anther culture. <i>Euphytica</i> , 2007, 156, 173-183.	1.2	17
17	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
18	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

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19	Gut Microbiome in Chronic Coronary Syndrome Patients. <i>Journal of Clinical Medicine</i> , 2021, 10, 5074.	2.4	13
20	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
21	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
22	DNA Methylation Analysis in Barley and Other Species with Large Genomes. <i>Methods in Molecular Biology</i> , 2019, 1900, 253-268.	0.9	1
23	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