

Wojciech Karlowski

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

4,177
citations

236925

25
h-index

123424

61
g-index

68
all docs

68
docs citations

68
times ranked

6440
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Analysis of the Receptor-Like Kinase Family in Arabidopsis and Rice [W]. <i>Plant Cell</i> , 2004, 16, 1220-1234.	6.6	980
2	Alignment-free sequence comparison: benefits, applications, and tools. <i>Genome Biology</i> , 2017, 18, 186.	8.8	371
3	Sequence composition and genome organization of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14349-14354.	7.1	290
4	Arabidopsis microRNA expression regulation in a wide range of abiotic stress responses. <i>Frontiers in Plant Science</i> , 2015, 6, 410.	3.6	192
5	Complex Regulation of Two Target Genes Encoding SPX-MFS Proteins by Rice miR827 in Response to Phosphate Starvation. <i>Plant and Cell Physiology</i> , 2010, 51, 2119-2131.	3.1	188
6	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	14.5	174
7	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	14.5	160
8	Transcriptionally and post-transcriptionally regulated microRNAs in heat stress response in barley. <i>Journal of Experimental Botany</i> , 2014, 65, 6123-6135.	4.8	153
9	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	14.5	153
10	Benchmarking of alignment-free sequence comparison methods. <i>Genome Biology</i> , 2019, 20, 144.	8.8	147
11	Dual Role of the Histone Variant H2A.Z in Transcriptional Regulation of Stress-Response Genes. <i>Plant Cell</i> , 2017, 29, 791-807.	6.6	145
12	NERD, a Plant-Specific GW Protein, Defines an Additional RNAi-Dependent Chromatin-Based Pathway in Arabidopsis. <i>Molecular Cell</i> , 2012, 48, 121-132.	9.7	134
13	The liverwort <i>Platyneura ovalem</i> shares microtranscriptomic traits that are common to green algae and land plants. <i>New Phytologist</i> , 2015, 206, 352-367.	7.3	84
14	mirEX 2.0 - an integrated environment for expression profiling of plant microRNAs. <i>BMC Plant Biology</i> , 2015, 15, 144.	3.6	68
15	mirEX: a platform for comparative exploration of plant pri-miRNA expression data. <i>Nucleic Acids Research</i> , 2012, 40, D191-D197.	14.5	50
16	Genome-wide computational identification of WG/GW Argonaute-binding proteins in Arabidopsis. <i>Nucleic Acids Research</i> , 2010, 38, 4231-4245.	14.5	47
17	Efficiency of PacBio long read correction by 2nd generation Illumina sequencing. <i>Genomics</i> , 2019, 111, 43-49.	2.9	47
18	Identification of precursor transcripts for 6 novel miRNAs expands the diversity on the genomic organisation and expression of miRNA genes in rice. <i>BMC Plant Biology</i> , 2008, 8, 123.	3.6	46

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19	Developmentally regulated expression and complex processing of barley pri-microRNAs. <i>BMC Genomics</i> , 2013, 14, 34.	2.8	43
20	5SRNadb: an information resource for 5S ribosomal RNAs. <i>Nucleic Acids Research</i> , 2016, 44, D180-D183.	14.5	42
21	Genomewide identification of genes involved in the potato response to drought indicates functional evolutionary conservation with <i>Arabidopsis</i> plants. <i>Plant Biotechnology Journal</i> , 2018, 16, 603-614.	8.3	42
22	TaWAK6 encoding wall-associated kinase is involved in wheat resistance to leaf rust similar to adult plant resistance. <i>PLoS ONE</i> , 2020, 15, e0227713.	2.5	36
23	The over-expression of an alfalfa RING-H2 gene induces pleiotropic effects on plant growth and development. <i>Plant Molecular Biology</i> , 2003, 52, 121-133.	3.9	33
24	The Plant S1-Like Nuclease Family Has Evolved a Highly Diverse Range of Catalytic Capabilities. <i>Plant and Cell Physiology</i> , 2013, 54, 1064-1078.	3.1	33
25	AthCNV: A Map of DNA Copy Number Variations in the Arabidopsis Genome. <i>Plant Cell</i> , 2020, 32, 1797-1819.	6.6	33
26	Defective XRN-mediated transcription termination in Arabidopsis affects the expression of protein-coding genes. <i>Plant Journal</i> , 2018, 93, 1017-1031.	5.7	31
27	Comparison of rice and Arabidopsis annotation. <i>Current Opinion in Plant Biology</i> , 2003, 6, 106-112.	7.1	27
28	MOsDB: an integrated information resource for rice genomics. <i>Nucleic Acids Research</i> , 2003, 31, 190-192.	14.5	27
29	Pathogen-regulated genes in wheat isogenic lines differing in resistance to brown rust <i>Puccinia triticina</i> . <i>BMC Genomics</i> , 2015, 16, 742.	2.8	27
30	tRex: A Web Portal for Exploration of tRNA-Derived Fragments in Arabidopsis thaliana. <i>Plant and Cell Physiology</i> , 2018, 59, e1-e1.	3.1	27
31	Non-Canonical Processing of Arabidopsis pri-miR319a/b/c Generates Additional microRNAs to Target One RAP2.12 mRNA Isoform. <i>Frontiers in Plant Science</i> , 2012, 3, 46.	3.6	26
32	Comparative genomics of Lupinus angustifolius gene-rich regions: BAC library exploration, genetic mapping and cytogenetics. <i>BMC Genomics</i> , 2013, 14, 79.	2.8	25
33	Early origin and adaptive evolution of the GW182 protein family, the key component of RNA silencing in animals. <i>RNA Biology</i> , 2015, 12, 761-770.	3.1	23
34	Promoter-based identification of novel non-coding RNAs reveals the presence of dicistronic snoRNA-miRNA genes in Arabidopsis thaliana. <i>BMC Genomics</i> , 2015, 16, 1009.	2.8	20
35	Remnants of the Legume Ancestral Genome Preserved in Gene-Rich Regions: Insights from Lupinus angustifolius Physical, Genetic, and Comparative Mapping. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 84-101.	1.8	18
36	Taxonomy-aware, sequence similarity ranking reliably predicts phage-host relationships. <i>BMC Biology</i> , 2021, 19, 223.	3.8	16

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37	Biogenesis, conservation, and function of miRNA in liverworts. <i>Journal of Experimental Botany</i> , 2022, 73, 4528-4545.	4.8	16
38	Pi-starvation induced transcriptional changes in barley revealed by a comprehensive RNA-Seq and degradome analyses. <i>BMC Genomics</i> , 2021, 22, 165.	2.8	14
39	Novel genes specifically expressed during the development of the male thalli and antheridia in the dioecious liverwort <i>Pellia endiviifolia</i> . <i>Gene</i> , 2011, 485, 53-62.	2.2	13
40	A stable tRNA-like molecule is generated from the long noncoding RNA <i>GUT15</i> in <i>Arabidopsis</i> . <i>RNA Biology</i> , 2018, 15, 1-13.	3.1	12
41	Local Duplication of TIR-NBS-LRR Gene Marks Clubroot Resistance in <i>Brassica napus</i> cv. Tosca. <i>Frontiers in Plant Science</i> , 2021, 12, 639631.	3.6	12
42	Agos—a universal web tool for GW Argonaute-binding domain prediction. <i>Bioinformatics</i> , 2011, 27, 1318-1319.	4.1	11
43	ORCAN—a web-based meta-server for real-time detection and functional annotation of orthologs. <i>Bioinformatics</i> , 2017, 33, 1224-1226.	4.1	11
44	Annotation and profiling of barley GLYCOGEN SYNTHASE3/Shaggy-like genes indicated shift in organ-preferential expression. <i>PLoS ONE</i> , 2018, 13, e0199364.	2.5	11
45	Silencing of HvGSK1.1—a GSK3/SHAGGY-Like Kinase—Enhances Barley (<i>Hordeum vulgare</i> L.) Growth in Normal and in Salt Stress Conditions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6616.	4.1	11
46	Developmental changes in barley microRNA expression profiles coupled with miRNA targets analysis. <i>Acta Biochimica Polonica</i> , 2017, 63, 799-809.	0.5	11
47	Integrative data analysis indicates an intrinsic disordered domain character of Argonaute-binding motifs. <i>Bioinformatics</i> , 2015, 31, 332-339.	4.1	9
48	Analysis of OPCRIT results indicate the presence of a novel “social functioning” domain and complex structure of other dimensions in the Wielkopolska (Poland) population. <i>Schizophrenia Research</i> , 2012, 138, 223-232.	2.0	8
49	Allele-specific SNP markers for the new low linolenic mutant genotype of winter oilseed rape. <i>Plant Breeding</i> , 2009, 129, 502.	1.9	7
50	Maf1-mediated regulation of yeast RNA polymerase III is correlated with CCA addition at the 3' end of tRNA precursors. <i>Gene</i> , 2017, 612, 12-18.	2.2	7
51	A Role of U12 Intron in Proper Pre-mRNA Splicing of Plant Cap Binding Protein 20 Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 475.	3.6	7
52	Is Polymorphism in the Apoptosis and Inflammatory Pathway Genes Associated With a Primary Response to Anti-TNF Therapy in Crohn's Disease Patients?. <i>Frontiers in Pharmacology</i> , 2020, 11, 1207.	3.5	7
53	Genetic relationships among resynthesized, semi-resynthesized and natural <i>Brassica napus</i> L. genotypes. <i>Euphytica</i> , 2017, 213, 1.	1.2	6
54	A Functional Network of Novel Barley MicroRNAs and Their Targets in Response to Drought. <i>Genes</i> , 2020, 11, 488.	2.4	5

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55	Cold stress-induced miRNA and degradome changes in four soybean varieties differing in chilling resistance. <i>Journal of Agronomy and Crop Science</i> , 2022, 208, 777-794.	3.5	5
56	Nicotine affects protein complex rearrangement in <i>Caenorhabditis elegans</i> cells. <i>Drug and Chemical Toxicology</i> , 2017, 40, 470-483.	2.3	4
57	Identification of Structural Variants in Two Novel Genomes of Maize Inbred Lines Possibly Related to Glyphosate Tolerance. <i>Plants</i> , 2020, 9, 523.	3.5	4
58	Quantitative Analysis of Plant Primary Transcripts. <i>Methods in Molecular Biology</i> , 2021, 2170, 53-77.	0.9	4
59	Expression of miRNAs involved in phosphate homeostasis and senescence is altered in glyphosate-treated maize. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	2.1	3
60	StarSeeker: an automated tool for mature duplex microRNA sequence identification based on secondary structure modeling of precursor molecule. <i>Journal of Biological Research</i> , 2018, 25, 11.	2.1	3
61	The identification of differentially expressed genes in male and female gametophytes of simple thalloid liverwort <i>Pellia endiviifolia</i> sp. B using an RNA-seq approach. <i>Planta</i> , 2020, 252, 21.	3.2	3
62	RESEARCH PAPER Annotating a non-model plant genome – a study on the narrow-leafed lupin. <i>Biotechnologia</i> , 2012, 3, 318-332.	0.9	3
63	Assessing 5S ribosomal RNA heterogeneity in <i>Arabidopsis thaliana</i> using short RNA next generation sequencing data. <i>Acta Biochimica Polonica</i> , 2017, 63, 841-844.	0.5	2
64	Identification and Analysis of WG/GW ARGONAUTE-Binding Domains. <i>Methods in Molecular Biology</i> , 2017, 1640, 241-256.	0.9	0