Zofia Szweykowska-KuliÅ„ska

List of Publications by Year
in descending order

98 papers	3,969 citations	117453 34 h-index	138251 58 g-index
107 all docs	107 docs citations	107 times ranked	4283 citing authors

#	Article	IF	Citations
1	MicroRNA biogenesis and activity in plant cell dedifferentiation stimulated by cell wall removal. BMC Plant Biology, 2022, 22, 9.	1.6	3
2	Biogenesis, conservation, and function of miRNA in liverworts. Journal of Experimental Botany, 2022, 73, 4528-4545.	2.4	16
3	R-loops at microRNA encoding loci promote co-transcriptional processing of pri-miRNAs in plants. Nature Plants, 2022, 8, 402-418.	4.7	47
4	Pi-starvation induced transcriptional changes in barley revealed by a comprehensive RNA-Seq and degradome analyses. BMC Genomics, 2021, 22, 165.	1.2	14
5	Quantitative Analysis of Plant Primary Transcripts. Methods in Molecular Biology, 2021, 2170, 53-77.	0.4	4
6	Arabidopsis Spliceosome Factor SmD3 Modulates Immunity to Pseudomonas syringae Infection. Frontiers in Plant Science, 2021, 12, 765003.	1.7	5
7	Identification of transcription factors that bind to the 5â€²-UTR of the barley PHO2 gene. Plant Molecular Biology, 2020, 102, 73-88.	2.0	15
8	Barley microRNAs as metabolic sensors for soil nitrogen availability. Plant Science, 2020, 299, 110608.	1.7	9
9	The identification of differentially expressed genes in male and female gametophytes of simple thalloid liverwort Pellia endiviifolia sp. B using an RNA-seq approach. Planta, 2020, 252, 21.	1.6	3
10	mRNA adenosine methylase (MTA) deposits m ⁶ A on pri-miRNAs to modulate miRNA biogenesis in <i>Arabidopsis thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21785-21795.	3.3	83
11	SERRATE interacts with the nuclear exosome targeting (NEXT) complex to degrade primary miRNA precursors in Arabidopsis. Nucleic Acids Research, 2020, 48, 6839-6854.	6.5	32
12	A Functional Network of Novel Barley MicroRNAs and Their Targets in Response to Drought. Genes, 2020, 11, 488.	1.0	5
13	Regulation of Plant microRNA Biogenesis. Concepts and Strategies in Plant Sciences, 2020, , 3-24.	0.6	3
14	miRNA Detection by Stem-Loop RT-qPCR in Studying microRNA Biogenesis and microRNA Responsiveness to Abiotic Stresses. Methods in Molecular Biology, 2019, 1932, 131-150.	0.4	11
15	Micromanagement of Developmental and Stress-Induced Senescence: The Emerging Role of MicroRNAs. Genes, 2019, 10, 210.	1.0	9
16	A comparative proteomic analysis of the PVY-induced hypersensitive response in leaves of potato (Solanum tuberosum L.) plants that differ in Ny-1 gene dosage. European Journal of Plant Pathology, 2019, 153, 385-396.	0.8	2
17	Novel Nuclear Functions of Arabidopsis ARGONAUTE1: Beyond RNA Interference. Plant Physiology, 2019, 179, 1030-1039.	2.3	24
18	A stable tRNA-like molecule is generated from the long noncoding RNA <i>GUT15</i> in <i>Arabidopsis</i>. RNA Biology, 2018, 15, 1-13.	1.5	12

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19	tRex: A Web Portal for Exploration of tRNA-Derived Fragments in Arabidopsis thaliana. Plant and Cell Physiology, 2018, 59, e1-e1.	1.5	27
20	Genomewide identification of genes involved in the potato response to drought indicates functional evolutionary conservation with <i>Arabidopsis</i> plants. Plant Biotechnology Journal, 2018, 16, 603-614.	4.1	42
21	Divergent strategies displayed by potato (<i>Solanum tuberosum</i> L.) cultivars to cope with soil drought. Journal of Agronomy and Crop Science, 2018, 204, 13-30.	1.7	36
22	N6-methyladenosine (m6A): Revisiting the Old with Focus on New, an Arabidopsis thaliana Centered Review. Genes, 2018, 9, 596.	1.0	30
23	The plastid-nucleus located DNA/RNA binding protein WHIRLY1 regulates microRNA-levels during stress in barley (<i>Hordeum vulgare</i> L.). RNA Biology, 2018, 15, 886-891.	1.5	25
24	A Role of U12 Intron in Proper Pre-mRNA Splicing of Plant Cap Binding Protein 20 Genes. Frontiers in Plant Science, 2018, 9, 475.	1.7	7
25	Regulation of Plant Microprocessor Function in Shaping microRNA Landscape. Frontiers in Plant Science, 2018, 9, 753.	1.7	28
26	Post-transcriptional Regulation of MicroRNA Accumulation and Function: New Insights fromÂPlants. Molecular Plant, 2018, 11, 1006-1007.	3.9	14
27	Active 5â€² splice sites regulate the biogenesis efficiency of Arabidopsis microRNAs derived from intron-containing genes. Nucleic Acids Research, 2017, 45, gkw895.	6.5	47
28	Posttranscriptional coordination of splicing and <scp>miRNA</scp> biogenesis in plants. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1403.	3.2	72
29	MicroRNAs Are Intensively Regulated during Induction of Somatic Embryogenesis in Arabidopsis. Frontiers in Plant Science, 2017, 8, 18.	1.7	62
30	Mutation in HvCBP20 (Cap Binding Protein 20) Adapts Barley to Drought Stress at Phenotypic and Transcriptomic Levels. Frontiers in Plant Science, 2017, 8, 942.	1.7	48
31	MicroRNA-mediated regulation of flower development in grasses. Acta Biochimica Polonica, 2017, 63, 687-692.	0.3	18
32	MicroRNA biogenesis: Epigenetic modifications as another layer of complexity to the microRNA expression regulation. Acta Biochimica Polonica, 2017, 63, 717-723.	0.3	25
33	Developmental changes in barley microRNA expression profiles coupled with miRNA targets analysis.. Acta Biochimica Polonica, 2017, 63, 799-809.	0.3	11
34	Arabidopsis thaliana microRNA162 level is posttranscriptionally regulated via splicing and polyadenylation site selection.. Acta Biochimica Polonica, 2017, 63, 811-816.	0.3	12
35	Barley primary microRNA expression pattern is affected by soil water availability. Acta Biochimica Polonica, 2017, 63, 817-824.	0.3	3
36	Heat Stress Affects Pi-related Genes Expression and Inorganic Phosphate Deposition/Accumulation in Barley. Frontiers in Plant Science, 2016, 7, 926.	1.7	42

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37	Salt Stress Reveals a New Role for ARGONAUTE1 in miRNA Biogenesis at the Transcriptional and Posttranscriptional Levels. Plant Physiology, 2016, 172, 297-312.	2.3	72
38	Construction of Artificial miRNAs to Prevent Drought Stress in Solanum tuberosum. Methods in Molecular Biology, 2016, 1398, 271-290.	0.4	11
39	Promoter-based identification of novel non-coding RNAs reveals the presence of dicistronic snoRNA-miRNA genes in Arabidopsis thaliana. BMC Genomics, 2015, 16, 1009.	1.2	20
40	The Non-Coding RNA Journal Club: Highlights on Recent Papers. Non-coding RNA, 2015, 1, 87-93.	1.3	3
41	The Non-Coding RNA Journal Club: Highlights on Recent Papersâ€"2. Non-coding RNA, 2015, 1, 167-169.	1.3	0
42	Arabidopsis microRNA expression regulation in a wide range of abiotic stress responses. Frontiers in Plant Science, 2015, 6, 410.	1.7	192
43	Novel candidate genes AuxRP and Hsp90 influence the chip color of potato tubers. Molecular Breeding, 2015, 35, 224.	1.0	28
44	FUS/TLS contributes to replication-dependent histone gene expression by interaction with U7 snRNPs and histone-specific transcription factors. Nucleic Acids Research, 2015, 43, gkv794.	6.5	32
45	The liverwort <i><scp>P</scp>ellia endiviifolia</i> shares microtranscriptomic traits that are common to green algae and land plants. New Phytologist, 2015, 206, 352-367.	3.5	84
46	mirEX 2.0 - an integrated environment for expression profiling of plant microRNAs. BMC Plant Biology, 2015, 15, 144.	1.6	68
47	Transcriptionally and post-transcriptionally regulated microRNAs in heat stress response in barley. Journal of Experimental Botany, 2014, 65, 6123-6135.	2.4	153
48	The SERRATE protein is involved in alternative splicing in Arabidopsis thaliana. Nucleic Acids Research, 2014, 42, 1224-1244.	6.5	94
49	The Old and New RNA World. Acta Societatis Botanicorum Poloniae, 2014, 83, 441-448.	0.8	2
50	Female-specific gene expression in dioecious liverwort Pellia endiviifolia is developmentally regulated and connected to archegonia production. BMC Plant Biology, 2014, 14, 168.	1.6	5
51	miR393 Is Required for Production of Proper Auxin Signalling Outputs. PLoS ONE, 2014, 9, e95972.	1.1	43
52	High-throughput sequencing identification of novel and conserved miRNAs in the Brassica oleracea leaves. BMC Genomics, 2013, 14, 801.	1.2	42
53	Arabidopsis suppressor mutant of abh1 shows a new face of the already known players: ABH1 (CBP80) and ABI4â€"in response to ABA and abiotic stresses during seed germination. Plant Molecular Biology, 2013, 81, 189-209.	2.0	32
54	Developmentally regulated expression and complex processing of barley pri-microRNAs. BMC Genomics, 2013, 14, 34.	1.2	43

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55	Downâ€regulation of <i><scp>CBP</scp>80</i> gene expression as a strategy to engineer a droughtâ€tolerant potato. Plant Biotechnology Journal, 2013, 11, 459-469.	4.1	114
56	Introns of plant priâ€miRNAs enhance miRNA biogenesis. EMBO Reports, 2013, 14, 622-628.	2.0	115
57	The crosstalk between plant microRNA biogenesis factors and the spliceosome. Plant Signaling and Behavior, 2013, 8, e26955.	1.2	29
58	mirEX: a platform for comparative exploration of plant pri-miRNA expression data. Nucleic Acids Research, 2012, 40, D191-D197.	6.5	50
59	Role of microRNAs and other sRNAs of plants in their changing environments. Journal of Plant Physiology, 2012, 169, 1664-1672.	1.6	126
60	The human tRNA m⁵C methyltransferase Misu is multisite-specific. RNA Biology, 2012, 9, 1331-1338.	1.5	56
61	Non-Canonical Processing of Arabidopsis pri-miR319a/b/c Generates Additional microRNAs to Target One RAP2.12 mRNA Isoform. Frontiers in Plant Science, 2012, 3, 46.	1.7	26
62	The Role of the P1BS Element Containing Promoter-Driven Genes in Pi Transport and Homeostasis in Plants. Frontiers in Plant Science, 2012, 3, 58.	1.7	32
63	Novel genes specifically expressed during the development of the male thalli and antheridia in the dioecious liverwort Pellia endiviifolia. Gene, 2011, 485, 53-62.	1.0	13
64	Regulation of plant gene expression by alternative splicing. Biochemical Society Transactions, 2010, 38, 667-671.	1.6	27
65	The brome mosaic virus-based recombination vector triggers a limited gene silencing response depending on the orientation of the inserted sequence. Archives of Virology, 2010, 155, 169-179.	0.9	18
66	Involvement of the nuclear cap-binding protein complex in alternative splicing in Arabidopsis thaliana. Nucleic Acids Research, 2010, 38, 265-278.	6.5	99
67	Gene structures and processing of Arabidopsis thaliana HYL1-dependent pri-miRNAs. Nucleic Acids Research, 2009, 37, 3083-3093.	6.5	130
68	Selective recruitment of proteins to 5â€² cap complexes during the growth cycle in Arabidopsis. Plant Journal, 2009, 59, 400-412.	2.8	53
69	The Arabidopsis CBP20 targets the capâ€binding complex to the nucleus, and is stabilized by CBP80. Plant Journal, 2009, 59, 814-825.	2.8	51
70	Alternative splicing in plants. Biochemical Society Transactions, 2008, 36, 508-510.	1.6	32
71	The nuclear cap-binding protein complex is not essential for nonsense-mediated mRNA decay (NMD) in plants.. Acta Biochimica Polonica, 2008, 55, 825-828.	0.3	11
72	Abscisic acid does not influence the subcellular distribution of the HYL1 protein from Arabidopsis thaliana.. Acta Biochimica Polonica, 2008, 55, 517-524.	0.3	4

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73	Abscisic acid does not influence the subcellular distribution of the HYL1 protein from Arabidopsis thaliana. Acta Biochimica Polonica, 2008, 55, 517-24.	0.3	1
74	The nuclear cap-binding protein complex is not essential for nonsense-mediated mRNA decay (NMD) in plants. Acta Biochimica Polonica, 2008, 55, 825-8.	0.3	7
75	STAT activation and differential complex formation dictate selectivity of interferon responses. Acta Biochimica Polonica, 2007, 54, 27-38.	0.3	43
76	Identification of human tRNA:m5C methyltransferase catalysing intron-dependent m5C formation in the first position of the anticodon of the ${hbox{ pre-tRNA }}_{left(hbox{ CAA }ight)}^{hbox{ Leu }}$. Nucleic Acids Research, 2006, 34, 6034-6043.	6.5	162
77	Virus-Induced Gene Silencing-Based Functional Characterization of Genes Associated with Powdery Mildew Resistance in Barley. Plant Physiology, 2005, 138, 2155-2164.	2.3	245
78	Successful extraction of DNA from 100â€yearâ€old herbarium specimens of the liverwort Bazzania trilobata. Taxon, 2005, 54, 335-336.	0.4	34
79	Organellar inheritance in the allopolyploid mossRhizomnium pseudopunctatum. Taxon, 2005, 54, 383-388.	0.4	21
80	Determinants of Plant U12-Dependent Intron Splicing Efficiency. Plant Cell, 2004, 16, 1340-1352.	3.1	54
81	A comparison of group II introns of plastid tRNALysUUU genes encoding maturase protein. Cellular and Molecular Biology Letters, 2004, 9, 239-51.	2.7	4
82	Organellar Inheritance in Liverworts: An Example of Pellia borealis. Journal of Molecular Evolution, 2003, 56, 11-17.	0.8	32
83	RNA interference and its role in the regulation of eucaryotic gene expression.. Acta Biochimica Polonica, 2003, 50, 217-229.	0.3	26
84	Cloning and characterization of two subunits of Arabidopsis thaliana nuclear cap-binding complex. Gene, 2002, 283, 171-183.	1.0	48
85	Pseudouridylation of U35 in the anticodon of Arabidopsis thaliana pre-tRNATyr depends on length rather than structure of an intron. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1574, 137-144.	2.4	4
86	New DNA markers for discrimination between closely-related species and for the reconstruction of historical events; an example using liverworts. Cellular and Molecular Biology Letters, 2002, 7, 403-16.	2.7	9
87	RNAi and viral vectors as useful tools in the functional genomics of plants. Construction of BMV-based vectors for RNA delivery into plant cells. Cellular and Molecular Biology Letters, 2002, 7, 511-22.	2.7	5
88	Phylogeny of the European species of the genus Pellia (Hepaticae; Metzgeriales) based on the molecular data from nuclear tRNA Leu CAA intergenic sequences. Gene, 2001, 262, 309-315.	1.0	27
89	Intergenic sequences of clustered tRNA genes: new type of genetic marker for phylogenetic studies, with application to the taxonomy of liverworts. , 1998, 38, 1257-1261.		8
90	RAPD technique for taxonomic studies of Pellia epiphylla-complex (Hepaticae, Metzgeriales). Genetica, 1998, 104, 179-187.	0.5	16

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91	Intron-dependent enzymatic formation of modified nucleosides in eukaryotic tRNAs: A review. Biochimie, 1997, 79, 293-302.	1.3	78
92	Specific guanylation of Lupinus luteus 5S rRNA at its 3' end in HeLa cell extract. IUBMB Life, 1996, 39, 1221-1227.	1.5	1
93	A cap-binding protein complex mediating U snRNA export. Nature, 1995, 376, 709-712.	13.7	320
94	Mutations of Arabidopsis thaliana pre-tRNATyr affecting pseudouridylation of U35. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1995, 1264, 87-92.	2.4	11
95	Nucleotide sequence of a nuclear tRNATyr gene from Triticum aestivum. Plant Molecular Biology, 1992, 18, 1207-1208.	2.0	5
96	Plant nonsense suppressor tRNATyrgenes are expressed at very low levesin vitrodue to inefficient splicing of the intron-containing pre-tRNAS. Nucleic Acids Research, 1991, 19, 707-712.	6.5	23
97	Nucleotide sequences of two nuclear tRNATyrgenes fromTriticum aestivum. Nucleic Acids Research, 1990, 18, 1894-1894.	6.5	13
98	A nuclear tRNA UGASer gene from the wheat Triticum vulgare var. Aria. Gene, 1989, 77, 163-167.	1.0	7