

Michał, Wojciech Szczęśniak

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5291810/publications.pdf>

Version: 2024-02-01

26
papers

2,848
citations

567144

15
h-index

526166

27
g-index

27
all docs

27
docs citations

27
times ranked

6026
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-Term Waterlogging as Factor Contributing to Hypoxia Stress Tolerance Enhancement in Cucumber: Comparative Transcriptome Analysis of Waterlogging Sensitive and Tolerant Accessions. <i>Genes</i> , 2021, 12, 189.	1.0	27
2	lncEvo: automated identification and conservation study of long noncoding RNAs. <i>BMC Bioinformatics</i> , 2021, 22, 59.	1.2	8
3	MEF2C shapes the microtranscriptome during differentiation of skeletal muscles. <i>Scientific Reports</i> , 2021, 11, 3476.	1.6	14
4	Comparative genomics in the search for conserved long noncoding RNAs. <i>Essays in Biochemistry</i> , 2021, 65, 741-749.	2.1	10
5	Waterlogging-Stress-Responsive LncRNAs, Their Regulatory Relationships with miRNAs and Target Genes in Cucumber (<i>Cucumis sativus</i> L.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 8197.	1.8	12
6	A chromatin-associated splicing isoform of <i>OIP5-AS1</i> acts in <i>cis</i> to regulate the <i>OIP5</i> oncogene. <i>RNA Biology</i> , 2021, 18, 1834-1845.	1.5	8
7	Towards a deeper annotation of human lncRNAs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194385.	0.9	12
8	Complex Analysis of Retroposed Genes™ Contribution to Human Genome, Proteome and Transcriptome. <i>Genes</i> , 2020, 11, 542.	1.0	8
9	CANTATadb 2.0: Expanding the Collection of Plant Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2019, 1933, 415-429.	0.4	71
10	SyntDB: Defining orthologues of human long noncoding RNAs across primates. <i>Nucleic Acids Research</i> , 2019, 48, D238-D245.	6.5	16
11	Natural antisense transcripts in diseases: From modes of action to targeted therapies. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1461.	3.2	50
12	Collagen synthesis disruption and downregulation of core elements of TGF- β^2 , Hippo, and Wnt pathways in keratoconus corneas. <i>European Journal of Human Genetics</i> , 2017, 25, 582-590.	1.4	70
13	KTCNlncDB™ a first platform to investigate lncRNAs expressed in human keratoconus and non-keratoconus corneas. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw168.	1.4	14
14	Retroposition as a source of antisense long non-coding RNAs with possible regulatory functions. <i>Acta Biochimica Polonica</i> , 2017, 63, 825-833.	0.3	10
15	CANTATadb: A Collection of Plant Long Non-Coding RNAs. <i>Plant and Cell Physiology</i> , 2016, 57, e8-e8.	1.5	142
16	Sequence-non-specific effects generated by various types of RNA interference triggers. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 306-314.	0.9	19
17	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	3.8	1,898
18	siRNA release from pri-miRNA scaffolds is controlled by the sequence and structure of RNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 639-649.	0.9	17

#	ARTICLE	IF	CITATIONS
19	lncRNA-RNA Interactions across the Human Transcriptome. PLoS ONE, 2016, 11, e0150353.	1.1	77
20	Identification of apple miRNAs and their potential role in fire blight resistance. Tree Genetics and Genomes, 2015, 11, 1.	0.6	24
21	miRNEST 2.0: a database of plant and animal microRNAs. Nucleic Acids Research, 2014, 42, D74-D77.	6.5	68
22	ERISdb: A Database of Plant Splice Sites and Splicing Signals. Plant and Cell Physiology, 2013, 54, e10-e10.	1.5	55
23	HuntMi: an efficient and taxon-specific approach in pre-miRNA identification. BMC Bioinformatics, 2013, 14, 83.	1.2	67
24	miRNEST database: an integrative approach in microRNA search and annotation. Nucleic Acids Research, 2012, 40, D198-D204.	6.5	52
25	mirEX: a platform for comparative exploration of plant pri-miRNA expression data. Nucleic Acids Research, 2012, 40, D191-D197.	6.5	50
26	Primate and Rodent Specific Intron Gains and the Origin of Retrogenes with Splice Variants. Molecular Biology and Evolution, 2011, 28, 33-37.	3.5	48