

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	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	3.8	1,898
2	CANTATAdb: A Collection of Plant Long Non-Coding RNAs. <i>Plant and Cell Physiology</i> , 2016, 57, e8-e8.	1.5	142
3	lncRNA-RNA Interactions across the Human Transcriptome. <i>PLoS ONE</i> , 2016, 11, e0150353.	1.1	77
4	CANTATAdb 2.0: Expanding the Collection of Plant Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2019, 1933, 415-429.	0.4	71
5	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
6	miRNEST 2.0: a database of plant and animal microRNAs. <i>Nucleic Acids Research</i> , 2014, 42, D74-D77.	6.5	68
7	HuntMi: an efficient and taxon-specific approach in pre-miRNA identification. <i>BMC Bioinformatics</i> , 2013, 14, 83.	1.2	67
8	ERISdb: A Database of Plant Splice Sites and Splicing Signals. <i>Plant and Cell Physiology</i> , 2013, 54, e10-e10.	1.5	55
9	miRNEST database: an integrative approach in microRNA search and annotation. <i>Nucleic Acids Research</i> , 2012, 40, D198-D204.	6.5	52
10	mirEX: a platform for comparative exploration of plant pri-miRNA expression data. <i>Nucleic Acids Research</i> , 2012, 40, D191-D197.	6.5	50
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	Primate and Rodent Specific Intron Gains and the Origin of Retrogenes with Splice Variants. <i>Molecular Biology and Evolution</i> , 2011, 28, 33-37.	3.5	48
13	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
14	Identification of apple miRNAs and their potential role in fire blight resistance. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	24
15	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
16	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
17	SyntDB: Defining orthologues of human long noncoding RNAs across primates. <i>Nucleic Acids Research</i> , 2019, 48, D238-D245.	6.5	16
18	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

#	ARTICLE	IF	CITATIONS
19	MEF2C shapes the microtranscriptome during differentiation of skeletal muscles. <i>Scientific Reports</i> , 2021, 11, 3476.	1.6	14
20	Towards a deeper annotation of human lncRNAs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194385.	0.9	12
21	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
22	Comparative genomics in the search for conserved long noncoding RNAs. <i>Essays in Biochemistry</i> , 2021, 65, 741-749.	2.1	10
23	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
24	Complex Analysis of Retroposed Genes'™ Contribution to Human Genome, Proteome and Transcriptome. <i>Genes</i> , 2020, 11, 542.	1.0	8
25	lncEvo: automated identification and conservation study of long noncoding RNAs. <i>BMC Bioinformatics</i> , 2021, 22, 59.	1.2	8
26	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