

Izabela MakaÅ,owska

List of Publications by Year in descending order

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94
papers

6,378
citations

109321

35
h-index

69250

77
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104
all docs

104
docs citations

104
times ranked

9348
citing authors

#	ARTICLE	IF	CITATIONS
1	The Mediating Role of the Gut Microbiota in the Physical Growth of Children. <i>Life</i> , 2022, 12, 152.	2.4	8
2	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.	2.4	27
3	lncEvo: automated identification and conservation study of long noncoding RNAs. <i>BMC Bioinformatics</i> , 2021, 22, 59.	2.6	8
4	Promoter switching in response to changing environment and elevated expression of protein-coding genes overlapping at their 5' ends. <i>Scientific Reports</i> , 2021, 11, 8984.	3.3	4
5	Comparative genomics in the search for conserved long noncoding RNAs. <i>Essays in Biochemistry</i> , 2021, 65, 741-749.	4.7	10
6	Not So Dead Genes—Retrocopies as Regulators of Their Disease-Related Progenitors and Hosts. <i>Cells</i> , 2021, 10, 912.	4.1	9
7	Cancer, Retrogenes, and Evolution. <i>Life</i> , 2021, 11, 72.	2.4	7
8	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.	3.1	8
9	Towards a deeper annotation of human lncRNAs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194385.	1.9	12
10	Complex Analysis of Retroposed Genes' Contribution to Human Genome, Proteome and Transcriptome. <i>Genes</i> , 2020, 11, 542.	2.4	8
11	Transposable Elements: Classification, Identification, and Their Use As a Tool For Comparative Genomics. <i>Methods in Molecular Biology</i> , 2019, 1910, 177-207.	0.9	74
12	CANTATAdb 2.0: Expanding the Collection of Plant Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2019, 1933, 415-429.	0.9	71
13	SyntDB: Defining orthologues of human long noncoding RNAs across primates. <i>Nucleic Acids Research</i> , 2019, 48, D238-D245.	14.5	16
14	Overactive BRCA1 Affects Presenilin 1 in Induced Pluripotent Stem Cell-Derived Neurons in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2018, 62, 175-202.	2.6	36
15	Natural antisense transcripts in diseases: From modes of action to targeted therapies. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1461.	6.4	50
16	Transcriptional interference by small transcripts in proximal promoter regions. <i>Nucleic Acids Research</i> , 2018, 46, 1069-1088.	14.5	10
17	OverGeneDB: a database of 5' end protein coding overlapping genes in human and mouse genomes. <i>Nucleic Acids Research</i> , 2018, 46, D186-D193.	14.5	6
18	Comparison of Highly and Weakly Virulent <i>Dickeya solani</i> Strains, With a View on the Pangenome and Panregulon of This Species. <i>Frontiers in Microbiology</i> , 2018, 9, 1940.	3.5	50

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19	Hypermethylation of TRIM59 and KLF14 Influences Cell Death Signaling in Familial Alzheimer's Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2018, 2018, 1-11.	4.0	23
20	Biological Functions of Natural Antisense Transcripts. <i>Acta Biochimica Polonica</i> , 2017, 63, 665-673.	0.5	46
21	Protein-Coding Genes' Retrocopies and Their Functions. <i>Viruses</i> , 2017, 9, 80.	3.3	57
22	RetrogeneDB—a database of plant and animal retrocopies. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	30
23	Retroposition as a source of antisense long non-coding RNAs with possible regulatory functions. <i>Acta Biochimica Polonica</i> , 2017, 63, 825-833.	0.5	10
24	Comparative genomic analysis of retrogene repertoire in two green algae <i>Volvox carteri</i> and <i>Chlamydomonas reinhardtii</i> . <i>Biology Direct</i> , 2016, 11, 35.	4.6	11
25	CANTATadb: A Collection of Plant Long Non-Coding RNAs. <i>Plant and Cell Physiology</i> , 2016, 57, e8-e8.	3.1	142
26	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.	1.9	19
27	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.	1.9	17
28	lncRNA-RNA Interactions across the Human Transcriptome. <i>PLoS ONE</i> , 2016, 11, e0150353.	2.5	77
29	Identification of apple miRNAs and their potential role in fire blight resistance. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	24
30	Inter-population Differences in Retrogene Loss and Expression in Humans. <i>PLoS Genetics</i> , 2015, 11, e1005579.	3.5	12
31	miRNEST 2.0: a database of plant and animal microRNAs. <i>Nucleic Acids Research</i> , 2014, 42, D74-D77.	14.5	68
32	RetrogeneDB—A Database of Animal Retrogenes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1646-1648.	8.9	31
33	Characterization of the mitochondrial genome of <i>Rousettus leschenaulti</i> . <i>Mitochondrial DNA</i> , 2014, 25, 443-444.	0.6	5
34	"Orphan" Retrogenes in the Human Genome. <i>Molecular Biology and Evolution</i> , 2013, 30, 384-396.	8.9	50
35	ERISdb: A Database of Plant Splice Sites and Splicing Signals. <i>Plant and Cell Physiology</i> , 2013, 54, e10-e10.	3.1	55
36	HuntMi: an efficient and taxon-specific approach in pre-miRNA identification. <i>BMC Bioinformatics</i> , 2013, 14, 83.	2.6	67

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37	miRNEST database: an integrative approach in microRNA search and annotation. <i>Nucleic Acids Research</i> , 2012, 40, D198-D204.	14.5	52
38	Transposable Elements and Their Identification. <i>Methods in Molecular Biology</i> , 2012, 855, 337-359.	0.9	26
39	Rootstock-regulated gene expression patterns associated with fire blight resistance in apple. <i>BMC Genomics</i> , 2012, 13, 9.	2.8	84
40	Functional Retrogenes in Animal Genomes. , 2012, , 283-300.		0
41	Application of the Burrows-Wheeler Transform for Searching for Approximate Tandem Repeats. <i>Lecture Notes in Computer Science</i> , 2012, , 255-266.	1.3	3
42	ROOTSTOCK-REGULATED GENE EXPRESSION PROFILING IN APPLE TREES REVEALS GENES WHOSE EXPRESSION LEVELS ARE ASSOCIATED WITH FIRE BLIGHT RESISTANCE. <i>Acta Horticulturae</i> , 2011, , 87-93.	0.2	4
43	Primate and Rodent Specific Intron Gains and the Origin of Retrogenes with Splice Variants. <i>Molecular Biology and Evolution</i> , 2011, 28, 33-37.	8.9	48
44	Rootstock-regulated gene expression patterns in apple tree scions. <i>Tree Genetics and Genomes</i> , 2010, 6, 57-72.	1.6	79
45	Comparative analysis of an unusual gene arrangement in the human chromosome 1. <i>Gene</i> , 2008, 423, 172-179.	2.2	6
46	<i>Phytophthora</i> Database: A Forensic Database Supporting the Identification and Monitoring of <i>Phytophthora</i> . <i>Plant Disease</i> , 2008, 92, 966-972.	1.4	64
47	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	14.5	57
48	Birth and death of gene overlaps in vertebrates. <i>BMC Evolutionary Biology</i> , 2007, 7, 193.	3.2	30
49	Plant Pathogen Culture Collections: It Takes a Village to Preserve These Resources Vital to the Advancement of Agricultural Security and Plant Pathology. <i>Phytopathology</i> , 2006, 96, 920-925.	2.2	26
50	Identification of human tRNA:m5C methyltransferase catalysing intron-dependent m5C formation in the first position of the anticodon of the $\text{pre-tRNA}_{\text{left(CAA)}}^{\text{Leu}}$. <i>Nucleic Acids Research</i> , 2006, 34, 6034-6043.	14.5	162
51	ChloroplastDB: the Chloroplast Genome Database. <i>Nucleic Acids Research</i> , 2006, 34, D692-D696.	14.5	88
52	Overlapping genes in the human genome. , 2005, , .		0
53	Overlapping genes in vertebrate genomes. <i>Computational Biology and Chemistry</i> , 2005, 29, 1-12.	2.3	100
54	SLC24A5, a Putative Cation Exchanger, Affects Pigmentation in Zebrafish and Humans. <i>Science</i> , 2005, 310, 1782-1786.	12.6	925

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55	Origin and evolution of the chicken leukocyte receptor complex. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4057-4062.	7.1	36
56	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
57	FUSARIUM-ID v. 1.0: A DNA Sequence Database for Identifying Fusarium. European Journal of Plant Pathology, 2004, 110, 473-479.	1.7	860
58	Mammalian Overlapping Genes: The Comparative Perspective. Genome Research, 2004, 14, 280-286.	5.5	125
59	Identification and characterization of mouse Rab32 by mRNA and protein expression analysis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1651, 68-75.	2.3	22
60	Melanoma mouse model implicates metabotropic glutamate signaling in melanocytic neoplasia. Nature Genetics, 2003, 34, 108-112.	21.4	260
61	Cloning and characterization of a novel gene, SHPRH, encoding a conserved putative protein with SNF2/helicase and PHD-finger domains from the 6q24 region. Genomics, 2003, 82, 153-161.	2.9	36
62	GALA, a Database for Genomic Sequence Alignments and Annotations. Genome Research, 2003, 13, 732-741.	5.5	45
63	The Histone Database. Nucleic Acids Research, 2002, 30, 341-342.	14.5	58
64	Physical and Transcript Map of the Hereditary Prostate Cancer Region at Xq27. Genomics, 2002, 79, 41-50.	2.9	24
65	Chromosomes and expression mechanisms. Current Opinion in Genetics and Development, 2002, 12, 125-126.	3.3	0
66	Genetics of disease. Current Opinion in Genetics and Development, 2002, 12, 261-262.	3.3	0
67	Pattern formation and developmental mechanisms. Current Opinion in Genetics and Development, 2002, 12, 381-382.	3.3	0
68	Genomes and evolution. Current Opinion in Genetics and Development, 2002, 12, 629.	3.3	0
69	Identification of six novel genes by experimental validation of GeneMachine predicted genes. Gene, 2002, 284, 203-213.	2.2	9
70	Germline mutations in the ribonuclease L gene in families showing linkage with HPC1. Nature Genetics, 2002, 30, 181-184.	21.4	470
71	Mutant deoxynucleotide carrier is associated with congenital microcephaly. Nature Genetics, 2002, 32, 175-179.	21.4	141
72	Cloning and Characterization of 13 Novel Transcripts and the Human RGS8 Gene from the 1q25 Region Encompassing the Hereditary Prostate Cancer (HPC1) Locus. Genomics, 2001, 73, 211-222.	2.9	58

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73	Tissue-Specific Expression of a Splicing Mutation in the Gene Causes Familial Dysautonomia. <i>American Journal of Human Genetics</i> , 2001, 68, 598-605.	6.2	558
74	Oncogenes and cell proliferation. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 9-10.	3.3	0
75	Pattern formation and developmental mechanisms. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 361-362.	3.3	0
76	GeneMachine: gene prediction and sequence annotation. <i>Bioinformatics</i> , 2001, 17, 843-844.	4.1	22
77	The human RGL (RalGDS-like) gene: cloning, expression analysis and genomic organization. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2000, 1491, 285-288.	2.4	11
78	Isolation and characterization of the human homeobox gene HOX D1. <i>Molecular Biology Reports</i> , 2000, 27, 195-201.	2.3	3
79	Cloning, mapping, and expression of a novel brain-specific transcript in the Familial Dysautonomia candidate region on Chromosome 9q31. <i>Mammalian Genome</i> , 2000, 11, 81-83.	2.2	5
80	The Histone Database: a comprehensive WWW resource for histones and histone fold-containing proteins. <i>Nucleic Acids Research</i> , 2000, 28, 320-322.	14.5	32
81	A 6-Mb High-Resolution Physical and Transcription Map Encompassing the Hereditary Prostate Cancer 1 (HPC1) Region. <i>Genomics</i> , 2000, 64, 1-14.	2.9	33
82	Chromosomes and expression mechanisms. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 139-140.	3.3	1
83	Genetics of disease Web alert. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 245-246.	3.3	1
84	Pattern formation and developmental mechanisms. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 345-346.	3.3	0
85	Genomes and evolution. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 591.	3.3	0
86	Oncogenes and cell proliferation. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 11-12.	3.3	0
87	WebBLAST 2.0: an integrated solution for organizing and analyzing sequence data. <i>Bioinformatics</i> , 1999, 15, 422-423.	4.1	13
88	Histone Sequence Database: sequences, structures, post-translational modifications and genetic loci. <i>Nucleic Acids Research</i> , 1999, 27, 323-324.	14.5	10
89	CACP, encoding a secreted proteoglycan, is mutated in camptodactyly-arthropathy-coxa vara-pericarditis syndrome. <i>Nature Genetics</i> , 1999, 23, 319-322.	21.4	286
90	Differentiation and gene regulation. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 495-496.	3.3	0

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91	Genomes and evolution. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 619-620.	3.3	1
92	Cloning, genomic organization and expression of a putative human transmembrane protein related to the <i>Caenorhabditis elegans</i> MO1F1.4 gene. <i>Gene</i> , 1999, 240, 67-73.	2.2	4
93	Cloning, Mapping, and Expression of Two Novel Actin Genes, Actin-like-7A (ACTL7A) and Actin-like-7B (ACTL7B), from the Familial Dysautonomia Candidate Region on 9q31. <i>Genomics</i> , 1999, 58, 302-309.	2.9	34
94	Contig Map of the Parkinson's Disease Region on 4q21-q23. <i>DNA Research</i> , 1998, 5, 19-23.	3.4	9