

Liping Wei

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

17,547
citations

134610

34
h-index

156644

58
g-index

62
all docs

62
docs citations

62
times ranked

28200
citing authors

#	ARTICLE	IF	CITATIONS
1	MosaicBase: A Knowledgebase of Postzygotic Mosaic Variants in Noncancer Disease-related and Healthy Human Individuals. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 140-149.	3.0	10
2	Assessment of predicted enzymatic activity of N-acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , 2019, 40, 1519-1529.	1.1	10
3	Somatic LINE-1 retrotransposition in cortical neurons and non-brain tissues of Rett patients and healthy individuals. <i>PLoS Genetics</i> , 2019, 15, e1008043.	1.5	45
4	ATP1A3 mosaicism in families with alternating hemiplegia of childhood. <i>Clinical Genetics</i> , 2019, 96, 43-52.	1.0	12
5	Autism prevalence in China is comparable to Western prevalence. <i>Molecular Autism</i> , 2019, 10, 7.	2.6	168
6	Targeted resequencing of 358 candidate genes for autism spectrum disorder in a Chinese cohort reveals diagnostic potential and genotype-phenotype correlations. <i>Human Mutation</i> , 2019, 40, 801-815.	1.1	32
7	Genomic mosaicism in the pathogenesis and inheritance of a Rett syndrome cohort. <i>Genetics in Medicine</i> , 2019, 21, 1330-1338.	1.1	23
8	Mosaicism and incomplete penetrance of PCDH19 mutations. <i>Journal of Medical Genetics</i> , 2019, 56, 81-88.	1.5	35
9	DeFine: deep convolutional neural networks accurately quantify intensities of transcription factor-DNA binding and facilitate evaluation of functional non-coding variants. <i>Nucleic Acids Research</i> , 2018, 46, e69-e69.	6.5	89
10	Genetic analysis of benign familial epilepsies in the first year of life in a Chinese cohort. <i>Journal of Human Genetics</i> , 2018, 63, 9-18.	1.1	15
11	Distinctive types of postzygotic single-nucleotide mosaicisms in healthy individuals revealed by genome-wide profiling of multiple organs. <i>PLoS Genetics</i> , 2018, 14, e1007395.	1.5	31
12	AutismKB 2.0: a knowledgebase for the genetic evidence of autism spectrum disorder. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	37
13	Genome-wide maps of ribosomal occupancy provide insights into adaptive evolution and regulatory roles of uORFs during <i>Drosophila</i> development. <i>PLoS Biology</i> , 2018, 16, e2003903.	2.6	77
14	A model for postzygotic mosaicisms quantifies the allele fraction drift, mutation rate, and contribution to de novo mutations. <i>Genome Research</i> , 2018, 28, 943-951.	2.4	30
15	Familial cases and male cases with MECP2 mutations. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 451-457.	1.1	17
16	Postzygotic single-nucleotide mosaicisms contribute to the etiology of autism spectrum disorder and autistic traits and the origin of mutations. <i>Human Mutation</i> , 2017, 38, 1002-1013.	1.1	64
17	CPC2: a fast and accurate coding potential calculator based on sequence intrinsic features. <i>Nucleic Acids Research</i> , 2017, 45, W12-W16.	6.5	970
18	Optogenetic activation of dorsal raphe neurons rescues the autistic-like social deficits in Shank3 knockout mice. <i>Cell Research</i> , 2017, 27, 950-953.	5.7	41

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19	Genomic mosaicism in paternal sperm and multiple parental tissues in a Dravet syndrome cohort. <i>Scientific Reports</i> , 2017, 7, 15677.	1.6	48
20	Novel FOXP1 mutations in Chinese patients with Rett syndrome or Rett-like mental retardation. <i>BMC Medical Genetics</i> , 2017, 18, 96.	2.1	8
21	SCN8A mutations in Chinese patients with early onset epileptic encephalopathy and benign infantile seizures. <i>BMC Medical Genetics</i> , 2017, 18, 104.	2.1	36
22	Development and evaluation of a speech-generating AAC mobile app for minimally verbal children with autism spectrum disorder in Mainland China. <i>Molecular Autism</i> , 2017, 8, 52.	2.6	15
23	MosaicHunter: accurate detection of postzygotic single-nucleotide mosaicism through next-generation sequencing of unpaired, trio, and paired samples. <i>Nucleic Acids Research</i> , 2017, 45, e76-e76.	6.5	51
24	iFish: predicting the pathogenicity of human nonsynonymous variants using gene-specific/family-specific attributes and classifiers. <i>Scientific Reports</i> , 2016, 6, 31321.	1.6	24
25	Identification of EFHD1 as a novel Ca ²⁺ sensor for mitoflash activation. <i>Cell Calcium</i> , 2016, 59, 262-270.	1.1	27
26	Amplicon Resequencing Identified Parental Mosaicism for Approximately 10% of <i>de novo</i> SCN1A Mutations in Children with Dravet Syndrome. <i>Human Mutation</i> , 2015, 36, 861-872.	1.1	111
27	Profiling the RNA editomes of wild-type <i>C. elegans</i> and ADAR mutants. <i>Genome Research</i> , 2015, 25, 66-75.	2.4	70
28	Postzygotic single-nucleotide mosaicism in whole-genome sequences of clinically unremarkable individuals. <i>Cell Research</i> , 2014, 24, 1311-1327.	5.7	54
29	Bioinformatics: Introduction and Methods, a Bilingual Massive Open Online Course (MOOC) as a New Example for Global Bioinformatics Education. <i>PLoS Computational Biology</i> , 2014, 10, e1003955.	1.5	14
30	Statistical analysis of twenty years (1993 to 2012) of data from mainland China's first intervention center for children with autism spectrum disorder. <i>Molecular Autism</i> , 2014, 5, 52.	2.6	23
31	De Novo Insertions and Deletions of Predominantly Paternal Origin Are Associated with Autism Spectrum Disorder. <i>Cell Reports</i> , 2014, 9, 16-23.	2.9	151
32	A large-scale screen for coding variants predisposing to psoriasis. <i>Nature Genetics</i> , 2014, 46, 45-50.	9.4	183
33	The contribution of de novo coding mutations to autism spectrum disorder. <i>Nature</i> , 2014, 515, 216-221.	13.7	2,188
34	ATP1A3 Mutations and Genotype-Phenotype Correlation of Alternating Hemiplegia of Childhood in Chinese Patients. <i>PLoS ONE</i> , 2014, 9, e97274.	1.1	60
35	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. <i>Cell</i> , 2013, 155, 997-1007.	13.5	825
36	Recent Adaptive Events in Human Brain Revealed by Meta-Analysis of Positively Selected Genes. <i>PLoS ONE</i> , 2013, 8, e61280.	1.1	12

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37	Hominoid-Specific De Novo Protein-Coding Genes Originating from Long Non-Coding RNAs. <i>PLoS Genetics</i> , 2012, 8, e1002942.	1.5	130
38	AutismKB: an evidence-based knowledgebase of autism genetics. <i>Nucleic Acids Research</i> , 2012, 40, D1016-D1022.	6.5	157
39	KOBAS 2.0: a web server for annotation and identification of enriched pathways and diseases. <i>Nucleic Acids Research</i> , 2011, 39, W316-W322.	6.5	3,897
40	Candidate <i>Mycobacterium tuberculosis</i> genes targeted by human microRNAs. <i>Protein and Cell</i> , 2010, 1, 419-421.	4.8	22
41	A Human-Specific De Novo Protein-Coding Gene Associated with Human Brain Functions. <i>PLoS Computational Biology</i> , 2010, 6, e1000734.	1.5	107
42	Bioinformatics in China: A Personal Perspective. <i>PLoS Computational Biology</i> , 2008, 4, e1000020.	1.5	18
43	Genes and (Common) Pathways Underlying Drug Addiction. <i>PLoS Computational Biology</i> , 2008, 4, e2.	1.5	210
44	NATsDB: Natural Antisense Transcripts DataBase. <i>Nucleic Acids Research</i> , 2007, 35, D156-D161.	6.5	54
45	Finding new structural and sequence attributes to predict possible disease association of single amino acid polymorphism (SAP). <i>Bioinformatics</i> , 2007, 23, 1444-1450.	1.8	55
46	SynDB: a Synapse protein DataBase based on synapse ontology. <i>Nucleic Acids Research</i> , 2007, 35, D737-D741.	6.5	43
47	CPC: assess the protein-coding potential of transcripts using sequence features and support vector machine. <i>Nucleic Acids Research</i> , 2007, 35, W345-W349.	6.5	2,525
48	A nonsynonymous SNP in human cytosolic sialidase in a small Asian population results in reduced enzyme activity: potential link with severe adverse reactions to oseltamivir. <i>Cell Research</i> , 2007, 17, 357-362.	5.7	72
49	DRTF: a database of rice transcription factors. <i>Bioinformatics</i> , 2006, 22, 1286-1287.	1.8	141
50	Genome comparison using Gene Ontology (GO) with statistical testing. <i>BMC Bioinformatics</i> , 2006, 7, 374.	1.2	15
51	CEAS: cis-regulatory element annotation system. <i>Nucleic Acids Research</i> , 2006, 34, W551-W554.	6.5	170
52	Genome-wide in silico identification and analysis of cis natural antisense transcripts (cis-NATs) in ten species. <i>Nucleic Acids Research</i> , 2006, 34, 3465-3475.	6.5	155
53	KOBAS server: a web-based platform for automated annotation and pathway identification. <i>Nucleic Acids Research</i> , 2006, 34, W720-W724.	6.5	682
54	DATF: a database of Arabidopsis transcription factors. <i>Bioinformatics</i> , 2005, 21, 2568-2569.	1.8	296

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55	Automated genome annotation and pathway identification using the KEGG Orthology (KO) as a controlled vocabulary. <i>Bioinformatics</i> , 2005, 21, 3787-3793.	1.8	3,124
56	GBA server: EST-based digital gene expression profiling. <i>Nucleic Acids Research</i> , 2005, 33, W673-W676.	6.5	18
57	Database and analyses of known alternatively spliced genes in plants. <i>Genomics</i> , 2003, 82, 584-595.	1.3	42
58	iFish: predicting the pathogenicity of human nonsynonymous variants using gene-specific/family-specific attributes and classifiers. , 0, .		1