Liping Wei

List of Publications by Year
in descending order

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58 papers	17,547 citations	117625 34 h-index	138484 58 g-index
62 all docs	62 docs citations	62 times ranked	25862 citing authors

#	Article	IF	Citations
1	KOBAS 2.0: a web server for annotation and identification of enriched pathways and diseases. Nucleic Acids Research, 2011, 39, W316-W322.	14.5	3,897
2	Automated genome annotation and pathway identification using the KEGG Orthology (KO) as a controlled vocabulary. Bioinformatics, 2005, 21, 3787-3793.	4.1	3,124
3	CPC: assess the protein-coding potential of transcripts using sequence features and support vector machine. Nucleic Acids Research, 2007, 35, W345-W349.	14.5	2,525
4	The contribution of de novo coding mutations to autism spectrum disorder. Nature, 2014, 515, 216-221.	27.8	2,188
5	CPC2: a fast and accurate coding potential calculator based on sequence intrinsic features. Nucleic Acids Research, 2017, 45, W12-W16.	14.5	970
6	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	28.9	825
7	KOBAS server: a web-based platform for automated annotation and pathway identification. Nucleic Acids Research, 2006, 34, W720-W724.	14.5	682
8	DATF: a database of Arabidopsis transcription factors. Bioinformatics, 2005, 21, 2568-2569.	4.1	296
9	Genes and (Common) Pathways Underlying Drug Addiction. PLoS Computational Biology, 2008, 4, e2.	3.2	210
10	A large-scale screen for coding variants predisposing to psoriasis. Nature Genetics, 2014, 46, 45-50.	21.4	183
11	CEAS: cis-regulatory element annotation system. Nucleic Acids Research, 2006, 34, W551-W554.	14.5	170
12	Autism prevalence in China is comparable to Western prevalence. Molecular Autism, 2019, 10, 7.	4.9	168
13	AutismKB: an evidence-based knowledgebase of autism genetics. Nucleic Acids Research, 2012, 40, D1016-D1022.	14.5	157
14	Genome-wide in silico identification and analysis of cis natural antisense transcripts (cis-NATs) in ten species. Nucleic Acids Research, 2006, 34, 3465-3475.	14.5	155
15	De Novo Insertions and Deletions of Predominantly Paternal Origin Are Associated with Autism Spectrum Disorder. Cell Reports, 2014, 9, 16-23.	6.4	151
16	DRTF: a database of rice transcription factors. Bioinformatics, 2006, 22, 1286-1287.	4.1	141
17	Hominoid-Specific De Novo Protein-Coding Genes Originating from Long Non-Coding RNAs. PLoS Genetics, 2012, 8, e1002942.	3.5	130
18	Amplicon Resequencing Identified Parental Mosaicism for Approximately 10% of â€œ de novo â€• SCN1A Mutations in Children with Dravet Syndrome. Human Mutation, 2015, 36, 861-872.	2.5	111

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19	A Human-Specific De Novo Protein-Coding Gene Associated with Human Brain Functions. PLoS Computational Biology, 2010, 6, e1000734.	3.2	107
20	DeFine: deep convolutional neural networks accurately quantify intensities of transcription factor-DNA binding and facilitate evaluation of functional non-coding variants. Nucleic Acids Research, 2018, 46, e69-e69.	14.5	89
21	Genome-wide maps of ribosomal occupancy provide insights into adaptive evolution and regulatory roles of uORFs during Drosophila development. PLoS Biology, 2018, 16, e2003903.	5.6	77
22	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. Cell Research, 2007, 17, 357-362.	12.0	72
23	Profiling the RNA editomes of wild-type C. elegans and ADAR mutants. Genome Research, 2015, 25, 66-75.	5.5	70
24	Postzygotic singleâ€nucleotide mosaicisms contribute to the etiology of autism spectrum disorder and autistic traits and the origin of mutations. Human Mutation, 2017, 38, 1002-1013.	2.5	64
25	ATP1A3 Mutations and Genotype-Phenotype Correlation of Alternating Hemiplegia of Childhood in Chinese Patients. PLoS ONE, 2014, 9, e97274.	2.5	60
26	Finding new structural and sequence attributes to predict possible disease association of single amino acid polymorphism (SAP). Bioinformatics, 2007, 23, 1444-1450.	4.1	55
27	NATsDB: Natural Antisense Transcripts DataBase. Nucleic Acids Research, 2007, 35, D156-D161.	14.5	54
28	Postzygotic single-nucleotide mosaicisms in whole-genome sequences of clinically unremarkable individuals. Cell Research, 2014, 24, 1311-1327.	12.0	54
29	MosaicHunter: accurate detection of postzygotic single-nucleotide mosaicism through next-generation sequencing of unpaired, trio, and paired samples. Nucleic Acids Research, 2017, 45, e76-e76.	14.5	51
30	Genomic mosaicism in paternal sperm and multiple parental tissues in a Dravet syndrome cohort. Scientific Reports, 2017, 7, 15677.	3.3	48
31	Somatic LINE-1 retrotransposition in cortical neurons and non-brain tissues of Rett patients and healthy individuals. PLoS Genetics, 2019, 15, e1008043.	3.5	45
32	SynDB: a Synapse protein DataBase based on synapse ontology. Nucleic Acids Research, 2007, 35, D737-D741.	14.5	43
33	Database and analyses of known alternatively spliced genes in plants. Genomics, 2003, 82, 584-595.	2.9	42
34	Optogenetic activation of dorsal raphe neurons rescues the autistic-like social deficits in Shank3 knockout mice. Cell Research, 2017, 27, 950-953.	12.0	41
35	AutismKB 2.0: a knowledgebase for the genetic evidence of autism spectrum disorder. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	37
36	SCN8A mutations in Chinese patients with early onset epileptic encephalopathy and benign infantile seizures. BMC Medical Genetics, 2017, 18, 104.	2.1	36

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37	Mosaicism and incomplete penetrance of PCDH19 mutations. Journal of Medical Genetics, 2019, 56, 81-88.	3.2	35
38	Targeted resequencing of 358 candidate genes for autism spectrum disorder in a Chinese cohort reveals diagnostic potential and genotypeâ€“phenotype correlations. Human Mutation, 2019, 40, 801-815.	2.5	32
39	Distinctive types of postzygotic single-nucleotide mosaicisms in healthy individuals revealed by genome-wide profiling of multiple organs. PLoS Genetics, 2018, 14, e1007395.	3.5	31
40	A model for postzygotic mosaicisms quantifies the allele fraction drift, mutation rate, and contribution to de novo mutations. Genome Research, 2018, 28, 943-951.	5.5	30
41	Identification of EFHD1 as a novel Ca2+ sensor for mitoflash activation. Cell Calcium, 2016, 59, 262-270.	2.4	27
42	iFish: predicting the pathogenicity of human nonsynonymous variants using gene-specific/family-specific attributes and classifiers. Scientific Reports, 2016, 6, 31321.	3.3	24
43	Statistical analysis of twenty years (1993 to 2012) of data from mainland Chinaâ€™s first intervention center for children with autism spectrum disorder. Molecular Autism, 2014, 5, 52.	4.9	23
44	Genomic mosaicism in the pathogenesis and inheritance of a Rett syndrome cohort. Genetics in Medicine, 2019, 21, 1330-1338.	2.4	23
45	Candidate Mycobacterium tuberculosis genes targeted by human microRNAs. Protein and Cell, 2010, 1, 419-421.	11.0	22
46	GBA server: EST-based digital gene expression profiling. Nucleic Acids Research, 2005, 33, W673-W676.	14.5	18
47	Bioinformatics in China: A Personal Perspective. PLoS Computational Biology, 2008, 4, e1000020.	3.2	18
48	Familial cases and male cases with MECP2 mutations. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 451-457.	1.7	17
49	Genome comparison using Gene Ontology (GO) with statistical testing. BMC Bioinformatics, 2006, 7, 374.	2.6	15
50	Development and evaluation of a speech-generating AAC mobile app for minimally verbal children with autism spectrum disorder in Mainland China. Molecular Autism, 2017, 8, 52.	4.9	15
51	Genetic analysis of benign familial epilepsies in the first year of life in a Chinese cohort. Journal of Human Genetics, 2018, 63, 9-18.	2.3	15
52	â€œBioinformatics: Introduction and Methods,â€•a Bilingual Massive Open Online Course (MOOC) as a New Example for Global Bioinformatics Education. PLoS Computational Biology, 2014, 10, e1003955.	3.2	14
53	Recent Adaptive Events in Human Brain Revealed by Meta-Analysis of Positively Selected Genes. PLoS ONE, 2013, 8, e61280.	2.5	12
54	ATP1A3 mosaicism in families with alternating hemiplegia of childhood. Clinical Genetics, 2019, 96, 43-52.	2.0	12

#	Article	IF	Citations
55	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	2.5	10
56	MosaicBase: A Knowledgebase of Postzygotic Mosaic Variants in Noncancer Disease-related and Healthy Human Individuals. Genomics, Proteomics and Bioinformatics, 2020, 18, 140-149.	6.9	10
57	Novel FOXG1 mutations in Chinese patients with Rett syndrome or Rett-like mental retardation. BMC Medical Genetics, 2017, 18, 96.	2.1	8
58	iFish: predicting the pathogenicity of human nonsynonymous variants using gene-specific/family-specific attributes and classifiers. , 0, .		1