Junwen Wang

List of Publications by Year
in descending order

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121	7,276	76326	62596
papers	citations	40 h-index	80 g-index

125	125	125	15790
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nature Genetics, 2007, 39, 870-874.	21.4	1,370
2	The support of human genetic evidence for approved drug indications. Nature Genetics, 2015, 47, 856-860.	21.4	1,112
3	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. Nature Genetics, 2012, 44, 1330-1335.	21.4	286
4	Transcriptional Genomics Associates FOX Transcription Factors With Human Heart Failure. Circulation, 2006, 114, 1269-1276.	1.6	210
5	GWASdb: a database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2012, 40, D1047-D1054.	14.5	204
6	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2016, 44, D869-D876.	14.5	184
7	Evaluation of tools for highly variable gene discovery from single-cell RNA-seq data. Briefings in Bioinformatics, 2019, 20, 1583-1589.	6.5	145
8	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. Journal of Clinical Investigation, 2013, 123, 4909-4917.	8.2	126
9	Developments in Blood-Brain Barrier Penetrance and Drug Repurposing for Improved Treatment of Glioblastoma. Frontiers in Oncology, 2018, 8, 462.	2.8	108
10	Vitamin D Inhibits COX-2 Expression and Inflammatory Response by Targeting Thioesterase Superfamily Member 4. Journal of Biological Chemistry, 2014, 289, 11681-11694.	3.4	107
11	Hyperglycemia-Induced Protein Kinase C Î²2 Activation Induces Diastolic Cardiac Dysfunction in Diabetic Rats by Impairing Caveolin-3 Expression and Akt/eNOS Signaling. Diabetes, 2013, 62, 2318-2328.	0.6	106
12	GWAS3D: detecting human regulatory variants by integrative analysis of genome-wide associations, chromosome interactions and histone modifications. Nucleic Acids Research, 2013, 41, W150-W158.	14.5	101
13	Linnorm: improved statistical analysis for single cell RNA-seq expression data. Nucleic Acids Research, 2017, 45, e179-e179.	14.5	100
14	N-Acetylcysteine and allopurinol up-regulated the Jak/STAT3 and PI3K/Akt pathways via adiponectin and attenuated myocardial postischemic injury in diabetes. Free Radical Biology and Medicine, 2013, 63, 291-303.	2.9	92
15	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	2.9	90
16	Lung cancer tumorigenicity and drug resistance are maintained through ALDHhiCD44hi tumor initiating cells. Oncotarget, 2013, 4, 1698-1711.	1.8	90
17	Potent Paracrine Effects of human induced Pluripotent Stem Cell-derived Mesenchymal Stem Cells Attenuate Doxorubicin-induced Cardiomyopathy. Scientific Reports, 2015, 5, 11235.	3.3	86
18	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77

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19	<scp>G</scp>enetic variants associated with longer telomere length are associated with increased lung cancer risk among neverâ€smoking women in Asia: a report from the female lung cancer consortium in Asia. International Journal of Cancer, 2015, 137, 311-319.	5.1	72
20	Improved Cell Survival and Paracrine Capacity of Human Embryonic Stem Cell-Derived Mesenchymal Stem Cells Promote Therapeutic Potential for Pulmonary Arterial Hypertension. Cell Transplantation, 2012, 21, 2225-2239.	2.5	69
21	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. Nucleic Acids Research, 2018, 46, W114-W120.	14.5	69
22	Next generation sequencing has lower sequence coverage and poorer SNP-detection capability in the regulatory regions. Scientific Reports, 2011, 1, 55.	3.3	67
23	Integrative approach for the analysis of the proteome-wide response to bismuth drugs in Helicobacter pylori. Chemical Science, 2017, 8, 4626-4633.	7.4	66
24	Susceptibility to myocardial ischemia reperfusion injury at early stage of type 1 diabetes in rats. Cardiovascular Diabetology, 2013, 12, 133.	6.8	64
25	Predictive models for protein crystallization. Methods, 2004, 34, 390-407.	3.8	63
26	Exploring the function of genetic variants in the non-coding genomic regions: approaches for identifying human regulatory variants affecting gene expression. Briefings in Bioinformatics, 2015, 16, 393-412.	6.5	58
27	A Functional Single-Nucleotide Polymorphism in the Promoter of the Gene Encoding Interleukin 6 Is Associated With Susceptibility to Tuberculosis. Journal of Infectious Diseases, 2012, 205, 1697-1704.	4.0	56
28	YY1 controls IgÎº repertoire and B-cell development, and localizes with condensin on the IgÎº locus. EMBO Journal, 2013, 32, 1168-1182.	7.8	55
29	Mouse Ribosomal RNA Genes Contain Multiple Differentially Regulated Variants. PLoS ONE, 2008, 3, e1843.	2.5	54
30	Long noncoding RNA LINC00305 promotes inflammation by activating the AHRR-NF-ÎºB pathway in human monocytes. Scientific Reports, 2017, 7, 46204.	3.3	53
31	Position and distance specificity are important determinants of cis-regulatory motifs in addition to evolutionary conservation. Nucleic Acids Research, 2007, 35, 3203-3213.	14.5	52
32	An SNP selection strategy identified IL-22 associating with susceptibility to tuberculosis in Chinese. Scientific Reports, 2011, 1, 20.	3.3	52
33	A fast and accurate SNP detection algorithm for next-generation sequencing data. Nature Communications, 2012, 3, 1258.	12.8	51
34	Association between GWAS-identified lung adenocarcinoma susceptibility loci andEGFRmutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	2.9	50
35	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	2.9	50
36	ChIP-Array: combinatory analysis of ChIP-seq/chip and microarray gene expression data to discover direct/indirect targets of a transcription factor. Nucleic Acids Research, 2011, 39, W430-W436.	14.5	49

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37	Predicting disease-associated mutation of metal-binding sites in proteins using a deep learning approach. Nature Machine Intelligence, 2019, 1, 561-567.	16.0	48
38	Exploring the sequence patterns in the Â-helices of proteins. Protein Engineering, Design and Selection, 2003, 16, 799-807.	2.1	46
39	Inhibition of KAP1 Enhances Hypoxia-Induced Kaposi's Sarcoma-Associated Herpesvirus Reactivation through RBP-Jî°. Journal of Virology, 2014, 88, 6873-6884.	3.4	45
40	Inferring gene regulatory networks by integrating ChIP-seq/chip and transcriptome data via LASSO-type regularization methods. Methods, 2014, 67, 294-303.	3.8	44
41	Integrated transcriptomic and regulatory network analyses identify microRNA-200c as a novel repressor of human pluripotent stem cell-derived cardiomyocyte differentiation and maturation. Cardiovascular Research, 2018, 114, 894-906.	3.8	44
42	Acacetin causes a frequency- and use-dependent blockade of hKv1.5 channels by binding to the S6 domain. Journal of Molecular and Cellular Cardiology, 2011, 51, 966-973.	1.9	41
43	Implication of TIGIT+ human memory B cells in immune regulation. Nature Communications, 2021, 12, 1534.	12.8	41
44	Predicting regulatory variants with composite statistic. Bioinformatics, 2016, 32, 2729-2736.	4.1	40
45	Exploring genetic associations with ceRNA regulation in the human genome. Nucleic Acids Research, 2017, 45, 5653-5665.	14.5	39
46	dbPSHP: a database of recent positive selection across human populations. Nucleic Acids Research, 2014, 42, D910-D916.	14.5	36
47	Transcriptional targets of TWIST1 in the cranial mesoderm regulate cell-matrix interactions and mesenchyme maintenance. Developmental Biology, 2016, 418, 189-203.	2.0	36
48	Activation of E-prostanoid 3 receptor in macrophages facilitates cardiac healing after myocardial infarction. Nature Communications, 2017, 8, 14656.	12.8	36
49	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. Nucleic Acids Research, 2017, 45, gkx019.	14.5	36
50	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. Scientific Reports, 2018, 8, 3161.	3.3	35
51	PTHGRN: unraveling post-translational hierarchical gene regulatory networks using PPI, ChIP-seq and gene expression data. Nucleic Acids Research, 2014, 42, W130-W136.	14.5	34
52	Metallochaperone UreG serves as a new target for design of urease inhibitor: A novel strategy for development of antimicrobials. PLoS Biology, 2018, 16, e2003887.	5.6	34
53	The Current Status and Challenges in Computational Analysis of Genomic Big Data. Big Data Research, 2015, 2, 12-18.	4.2	33
54	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. Genome Biology, 2017, 18, 52.	8.8	33

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55	MetaProm: a neural network based meta-predictor for alternative human promoter prediction. BMC Genomics, 2007, 8, 374.	2.8	32
56	A mammalian promoter model links cis elements to genetic networks. Biochemical and Biophysical Research Communications, 2006, 347, 166-177.	2.1	31
57	Genetic variant representation, annotation and prioritization in the post-GWAS era. Cell Research, 2012, 22, 1505-1508.	12.0	31
58	CTCF Controls HOXA Cluster Silencing and Mediates PRC2-Repressive Higher-Order Chromatin Structure in NT2/D1 Cells. Molecular and Cellular Biology, 2014, 34, 3867-3879.	2.3	31
59	Bio-coordination of bismuth in Helicobacter pylori revealed by immobilized metal affinity chromatography. Chemical Communications, 2015, 51, 16479-16482.	4.1	31
60	Search for basonuclin target genes. Biochemical and Biophysical Research Communications, 2006, 348, 1261-1271.	2.1	29
61	CMGRN: a web server for constructing multilevel gene regulatory networks using ChIP-seq and gene expression data. Bioinformatics, 2014, 30, 1190-1192.	4.1	29
62	UClncR: Ultrafast and comprehensive long non-coding RNA detection from RNA-seq. Scientific Reports, 2017, 7, 14196.	3.3	29
63	PU.1 Can Recruit BCL6 to DNA To Repress Gene Expression in Germinal Center B Cells. Molecular and Cellular Biology, 2009, 29, 4612-4622.	2.3	28
64	Colonoscopy surveillance for high risk polyps does not always prevent colorectal cancer. World Journal of Gastroenterology, 2018, 24, 905-916.	3.3	28
65	Histidine-rich proteins in prokaryotes: metal homeostasis and environmental habitat-related occurrence. Metallomics, 2013, 5, 1423.	2.4	26
66	Basonuclin Regulates a Subset of Ribosomal RNA Genes in HaCaT Cells. PLoS ONE, 2007, 2, e902.	2.5	24
67	Correlated evolution of transcription factors and their binding sites. Bioinformatics, 2011, 27, 2972-2978.	4.1	24
68	DDGni: Dynamic delay gene-network inference from high-temporal data using gapped local alignment. Bioinformatics, 2014, 30, 377-383.	4.1	24
69	SpliceNet: recovering splicing isoform-specific differential gene networks from RNA-Seq data of normal and diseased samples. Nucleic Acids Research, 2014, 42, e121-e121.	14.5	22
70	Functional networks of aging markers in the glomeruli of IgA nephropathy: a new therapeutic opportunity. Oncotarget, 2016, 7, 33616-33626.	1.8	22
71	FastPval: a fast and memory efficient program to calculate very low P-values from empirical distribution. Bioinformatics, 2010, 26, 2897-2899.	4.1	21
72	Integration of fluorescence imaging with proteomics enables visualization and identification of metallo-proteomes in living cells. Metallomics, 2017, 9, 38-47.	2.4	21

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73	Hybrid-denovo: a de novo OTU-picking pipeline integrating single-end and paired-end 16S sequence tags. GigaScience, 2018, 7, 1-7.	6.4	21
74	Integrated RNA-seq and ChIP-seq analysis reveals a feed-forward loop regulating H3K9ac and key labor drivers in human placenta. Placenta, 2019, 76, 40-50.	1.5	21
75	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	8.8	20
76	Tissue interactions, cell signaling and transcriptional control in the cranial mesoderm during craniofacial development. AIMS Genetics, 2016, 03, 074-098.	1.9	20
77	EpiRegNet: Constructing epigenetic regulatory network from high throughput gene expression data for humans. Epigenetics, 2011, 6, 1505-1512.	2.7	19
78	ChIP-Array 2: integrating multiple omics data to construct gene regulatory networks. Nucleic Acids Research, 2015, 43, W264-W269.	14.5	19
79	Absence of NUCKS augments paracrine effects of mesenchymal stem cells-mediated cardiac protection. Experimental Cell Research, 2017, 356, 74-84.	2.6	19
80	An integrative method to decode regulatory logics in gene transcription. Nature Communications, 2017, 8, 1044.	12.8	19
81	FaSD-somatic: a fast and accurate somatic SNV detection algorithm for cancer genome sequencing data. Bioinformatics, 2014, 30, 2498-2500.	4.1	18
82	<scp>ADAM10</scp> mediates ectopic proximal tubule development and renal fibrosis through Notch signalling. Journal of Pathology, 2020, 252, 274-289.	4.5	18
83	Rare SNP rs12731181 in the miR-590-3p Target Site of the Prostaglandin F _{2Î±} Receptor Gene Confers Risk for Essential Hypertension in the Han Chinese Population. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1687-1695.	2.4	15
84	Proteomic profiling identifies the SIMâ€associated complex of KSHVâ€encoded LANA. Proteomics, 2015, 15, 2023-2037.	2.2	14
85	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. Genome Research, 2020, 30, 1789-1801.	5.5	14
86	Uncertainty quantification in the radiogenomics modeling of EGFR amplification in glioblastoma. Scientific Reports, 2021, 11, 3932.	3.3	14
87	Human Ocular Epithelial Cells Endogenously Expressing SOX2 and OCT4 Yield High Efficiency of Pluripotency Reprogramming. PLoS ONE, 2015, 10, e0131288.	2.5	13
88	Generalizations of Markov model to characterize biological sequences. BMC Bioinformatics, 2005, 6, 219.	2.6	12
89	Current trend of annotating single nucleotide variation in humans â€“ A case study on SNVrap. Methods, 2015, 79-80, 32-40.	3.8	12
90	mTCTScan: a comprehensive platform for annotation and prioritization of mutations affecting drug sensitivity in cancers. Nucleic Acids Research, 2017, 45, W215-W221.	14.5	12

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91	NdPASA: A novel pairwise protein sequence alignment algorithm that incorporates neighbor-dependent amino acid propensities. Proteins: Structure, Function and Bioinformatics, 2004, 58, 628-637.	2.6	10
92	Chronic Cardiovascular Disease-Associated Gene Network Analysis in Human Umbilical Vein Endothelial Cells Exposed to 2,3,7,8-Tetrachlorodibenzo-p-dioxin. Cardiovascular Toxicology, 2015, 15, 157-171.	2.7	10
93	wKGGSeq: A Comprehensive Strategy-Based and Disease-Targeted Online Framework to Facilitate Exome Sequencing Studies of Inherited Disorders. Human Mutation, 2015, 36, 496-503.	2.5	10
94	MetaMarker: a pipeline for de novo discovery of novel metagenomic biomarkers. Bioinformatics, 2019, 35, 3812-3814.	4.1	10
95	Integrating Convolutional Neural Networks and Multi-Task Dictionary Learning for Cognitive Decline Prediction with Longitudinal Images. Journal of Alzheimer's Disease, 2020, 75, 971-992.	2.6	9
96	Inference of Gene-Phenotype Associations via Protein-Protein Interaction and Orthology. PLoS ONE, 2013, 8, e77478.	2.5	9
97	Inferring RNA sequence preferences for poorly studied RNA-binding proteins based on co-evolution. BMC Bioinformatics, 2018, 19, 96.	2.6	7
98	Tacrolimus dose requirement based on the CYP3A5 genotype in renal transplant patients. Oncotarget, 2017, 8, 81285-81294.	1.8	7
99	Applications of integrative OMICs approaches to gene regulation studies. Quantitative Biology, 2016, 4, 283-301.	0.5	6
100	Accurate Identification of Subclones in Tumor Genomes. Molecular Biology and Evolution, 0, , .	8.9	6
101	A novel neural response algorithm for protein function prediction. BMC Systems Biology, 2012, 6, S19.	3.0	5
102	ProteoMirExpress: Inferring MicroRNA and Protein-centered Regulatory Networks from High-throughput Proteomic and mRNA Expression Data. Molecular and Cellular Proteomics, 2013, 12, 3379-3387.	3.8	5
103	Bayesian detection of embryonic gene expression onset in C. elegans. Annals of Applied Statistics, 2015, 9, .	1.1	5
104	Methods and resources to access mutation-dependent effects on cancer drug treatment. Briefings in Bioinformatics, 2020, 21, 1886-1903.	6.5	5
105	Cell fate conversion prediction by group sparse optimization method utilizing single-cell and bulk OMICs data. Briefings in Bioinformatics, 2021, 22, .	6.5	4
106	NdPASA: a pairwise sequence alignment server for distantly related proteins. Bioinformatics, 2005, 21, 3803-3805.	4.1	2
107	A database of genetic variants in microRNA genes and their putative functional roles in gene regulation. Human Mutation, 2012, 33, vii-vii.	2.5	2
108	Whole-Genome Analysis of an Extensive Drug-Resistant Acinetobacter Baumannii ST195 Isolate from a Recipient After DCD Renal Transplantation in China. Kidney and Blood Pressure Research, 2017, 42, 1247-1257.	2.0	2

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109	Discovery of Surface Target Proteins Linking Drugs, Molecular Markers, Gene Regulation, Protein Networks, and Disease by Using a Web-Based Platform Targets-search. Methods in Molecular Biology, 2018, 1722, 331-344.	0.9	2
110	Novel Neural Network Approach to Predict Drug-Target Interactions Based on Drug Side Effects and Genome-Wide Association Studies. Human Heredity, 2018, 83, 79-91.	0.8	2
111	Phenotype, Function, and Clinical Significance of CD26+ and CD161+Tregs in Splenic Marginal Zone Lymphoma. Clinical Cancer Research, 2022, 28, 4322-4335.	7.0	2
112	NRProF: Neural response based protein function prediction algorithm. , 2011, , .		1
113	Dataset of TWIST1-regulated genes in the cranial mesoderm and a transcriptome comparison of cranial mesoderm and cranial neural crest. Data in Brief, 2016, 9, 372-375.	1.0	1
114	Evolution of Drug-resistant Acinetobacter baumannii After DCD Renal Transplantation. Scientific Reports, 2017, 7, 1968.	3.3	1
115	Assessment of Mapping and SNP-Detection Algorithms for Next-Generation Sequencing Data in Cancer Genomics. , 2013, , 301-317.		1
116	Integrating Transcriptomics, Genomics, and Imaging in Alzheimer's Disease: A Federated Model. Frontiers in Radiology, 2022, 1, .	2.0	1
117	Advanced Computational Approaches for Medical Genetics and Genomics. BioMed Research International, 2015, 2015, 1-2.	1.9	0
118	Next-Generation Sequencing in Human Genetic Studies: Genome Technologies and Applications to Human Genetic Studies. Human Heredity, 2018, 83, 105-106.	0.8	0
119	Abstract 2419: Genome-wide profiling of PAK4 DNA-binding sites and transcriptome reveals its potential transcriptional control on DNA repair-related genes in ovarian cancer cells. , 2017, , .		0
120	Abstract LB-274: Whole-exome sequencing reveals tyrosine kinase-resistant mutations in pretreatment EGFR-mutant lung adenocarcinomas. , 2017, , .		0
121	Translocator. , 2020, , .		0