

Junwen Wang

List of Publications by Year in descending order

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Version: 2024-02-01

121
papers

7,276
citations

76196

40
h-index

62479

80
g-index

125
all docs

125
docs citations

125
times ranked

15790
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide association study identifies alleles in FCGR2 associated with risk of sporadic postmenopausal breast cancer. <i>Nature Genetics</i> , 2007, 39, 870-874.	9.4	1,370
2	The support of human genetic evidence for approved drug indications. <i>Nature Genetics</i> , 2015, 47, 856-860.	9.4	1,112
3	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. <i>Nature Genetics</i> , 2012, 44, 1330-1335.	9.4	286
4	Transcriptional Genomics Associates FOX Transcription Factors With Human Heart Failure. <i>Circulation</i> , 2006, 114, 1269-1276.	1.6	210
5	GWASdb: a database for human genetic variants identified by genome-wide association studies. <i>Nucleic Acids Research</i> , 2012, 40, D1047-D1054.	6.5	204
6	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. <i>Nucleic Acids Research</i> , 2016, 44, D869-D876.	6.5	184
7	Evaluation of tools for highly variable gene discovery from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2019, 20, 1583-1589.	3.2	145
8	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. <i>Journal of Clinical Investigation</i> , 2013, 123, 4909-4917.	3.9	126
9	Developments in Blood-Brain Barrier Penetrance and Drug Repurposing for Improved Treatment of Glioblastoma. <i>Frontiers in Oncology</i> , 2018, 8, 462.	1.3	108
10	Vitamin D Inhibits COX-2 Expression and Inflammatory Response by Targeting Thioesterase Superfamily Member 4. <i>Journal of Biological Chemistry</i> , 2014, 289, 11681-11694.	1.6	107
11	Hyperglycemia-Induced Protein Kinase C β 2 Activation Induces Diastolic Cardiac Dysfunction in Diabetic Rats by Impairing Caveolin-3 Expression and Akt/eNOS Signaling. <i>Diabetes</i> , 2013, 62, 2318-2328.	0.3	106
12	GWAS3D: detecting human regulatory variants by integrative analysis of genome-wide associations, chromosome interactions and histone modifications. <i>Nucleic Acids Research</i> , 2013, 41, W150-W158.	6.5	101
13	Linnorm: improved statistical analysis for single cell RNA-seq expression data. <i>Nucleic Acids Research</i> , 2017, 45, e179-e179.	6.5	100
14	N-Acetylcysteine and allopurinol up-regulated the Jak/STAT3 and PI3K/Akt pathways via adiponectin and attenuated myocardial postischemic injury in diabetes. <i>Free Radical Biology and Medicine</i> , 2013, 63, 291-303.	1.3	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. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	1.4	90
16	Lung cancer tumorigenicity and drug resistance are maintained through ALDHhiCD44hi tumor initiating cells. <i>Oncotarget</i> , 2013, 4, 1698-1711.	0.8	90
17	Potent Paracrine Effects of human induced Pluripotent Stem Cell-derived Mesenchymal Stem Cells Attenuate Doxorubicin-induced Cardiomyopathy. <i>Scientific Reports</i> , 2015, 5, 11235.	1.6	86
18	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016, 48, 667-674.	9.4	77

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19	<scp>G</scp>enetic variants associated with longer telomere length are associated with increased lung cancer risk among never-smoking women in Asia: a report from the female lung cancer consortium in Asia. <i>International Journal of Cancer</i> , 2015, 137, 311-319.	2.3	72
20	Improved Cell Survival and Paracrine Capacity of Human Embryonic Stem Cell-Derived Mesenchymal Stem Cells Promote Therapeutic Potential for Pulmonary Arterial Hypertension. <i>Cell Transplantation</i> , 2012, 21, 2225-2239.	1.2	69
21	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. <i>Nucleic Acids Research</i> , 2018, 46, W114-W120.	6.5	69
22	Next generation sequencing has lower sequence coverage and poorer SNP-detection capability in the regulatory regions. <i>Scientific Reports</i> , 2011, 1, 55.	1.6	67
23	Integrative approach for the analysis of the proteome-wide response to bismuth drugs in <i>Helicobacter pylori</i> . <i>Chemical Science</i> , 2017, 8, 4626-4633.	3.7	66
24	Susceptibility to myocardial ischemia reperfusion injury at early stage of type 1 diabetes in rats. <i>Cardiovascular Diabetology</i> , 2013, 12, 133.	2.7	64
25	Predictive models for protein crystallization. <i>Methods</i> , 2004, 34, 390-407.	1.9	63
26	Exploring the function of genetic variants in the non-coding genomic regions: approaches for identifying human regulatory variants affecting gene expression. <i>Briefings in Bioinformatics</i> , 2015, 16, 393-412.	3.2	58
27	A Functional Single-Nucleotide Polymorphism in the Promoter of the Gene Encoding Interleukin 6 Is Associated With Susceptibility to Tuberculosis. <i>Journal of Infectious Diseases</i> , 2012, 205, 1697-1704.	1.9	56
28	YY1 controls Ig γ repertoire and B-cell development, and localizes with condensin on the Ig γ locus. <i>EMBO Journal</i> , 2013, 32, 1168-1182.	3.5	55
29	Mouse Ribosomal RNA Genes Contain Multiple Differentially Regulated Variants. <i>PLoS ONE</i> , 2008, 3, e1843.	1.1	54
30	Long noncoding RNA LINC00305 promotes inflammation by activating the AHRR-NF- κ B pathway in human monocytes. <i>Scientific Reports</i> , 2017, 7, 46204.	1.6	53
31	Position and distance specificity are important determinants of cis-regulatory motifs in addition to evolutionary conservation. <i>Nucleic Acids Research</i> , 2007, 35, 3203-3213.	6.5	52
32	An SNP selection strategy identified IL-22 associating with susceptibility to tuberculosis in Chinese. <i>Scientific Reports</i> , 2011, 1, 20.	1.6	52
33	A fast and accurate SNP detection algorithm for next-generation sequencing data. <i>Nature Communications</i> , 2012, 3, 1258.	5.8	51
34	Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. <i>Human Molecular Genetics</i> , 2016, 26, ddw414.	1.4	50
35	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. <i>Human Molecular Genetics</i> , 2016, 25, 620-629.	1.4	50
36	ChIP-Array: combinatory analysis of ChIP-seq/chip and microarray gene expression data to discover direct/indirect targets of a transcription factor. <i>Nucleic Acids Research</i> , 2011, 39, W430-W436.	6.5	49

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37	Predicting disease-associated mutation of metal-binding sites in proteins using a deep learning approach. <i>Nature Machine Intelligence</i> , 2019, 1, 561-567.	8.3	48
38	Exploring the sequence patterns in the α -helices of proteins. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 799-807.	1.0	46
39	Inhibition of KAP1 Enhances Hypoxia-Induced Kaposi's Sarcoma-Associated Herpesvirus Reactivation through RBP-J δ . <i>Journal of Virology</i> , 2014, 88, 6873-6884.	1.5	45
40	Inferring gene regulatory networks by integrating ChIP-seq/chip and transcriptome data via LASSO-type regularization methods. <i>Methods</i> , 2014, 67, 294-303.	1.9	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. <i>Cardiovascular Research</i> , 2018, 114, 894-906.	1.8	44
42	Acacetin causes a frequency- and use-dependent blockade of hKv1.5 channels by binding to the S6 domain. <i>Journal of Molecular and Cellular Cardiology</i> , 2011, 51, 966-973.	0.9	41
43	Implication of TICIT+ human memory B cells in immune regulation. <i>Nature Communications</i> , 2021, 12, 1534.	5.8	41
44	Predicting regulatory variants with composite statistic. <i>Bioinformatics</i> , 2016, 32, 2729-2736.	1.8	40
45	Exploring genetic associations with ceRNA regulation in the human genome. <i>Nucleic Acids Research</i> , 2017, 45, 5653-5665.	6.5	39
46	dbPSHP: a database of recent positive selection across human populations. <i>Nucleic Acids Research</i> , 2014, 42, D910-D916.	6.5	36
47	Transcriptional targets of TWIST1 in the cranial mesoderm regulate cell-matrix interactions and mesenchyme maintenance. <i>Developmental Biology</i> , 2016, 418, 189-203.	0.9	36
48	Activation of E-prostanoid 3 receptor in macrophages facilitates cardiac healing after myocardial infarction. <i>Nature Communications</i> , 2017, 8, 14656.	5.8	36
49	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. <i>Nucleic Acids Research</i> , 2017, 45, gkx019.	6.5	36
50	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. <i>Scientific Reports</i> , 2018, 8, 3161.	1.6	35
51	PTHGRN: unraveling post-translational hierarchical gene regulatory networks using PPI, ChIP-seq and gene expression data. <i>Nucleic Acids Research</i> , 2014, 42, W130-W136.	6.5	34
52	Metallochaperone UreG serves as a new target for design of urease inhibitor: A novel strategy for development of antimicrobials. <i>PLoS Biology</i> , 2018, 16, e2003887.	2.6	34
53	The Current Status and Challenges in Computational Analysis of Genomic Big Data. <i>Big Data Research</i> , 2015, 2, 12-18.	2.6	33
54	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. <i>Genome Biology</i> , 2017, 18, 52.	3.8	33

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55	MetaProm: a neural network based meta-predictor for alternative human promoter prediction. BMC Genomics, 2007, 8, 374.	1.2	32
56	A mammalian promoter model links cis elements to genetic networks. Biochemical and Biophysical Research Communications, 2006, 347, 166-177.	1.0	31
57	Genetic variant representation, annotation and prioritization in the post-GWAS era. Cell Research, 2012, 22, 1505-1508.	5.7	31
58	CTCF Controls <i>HOXA</i> Cluster Silencing and Mediates PRC2-Repressive Higher-Order Chromatin Structure in NT2/D1 Cells. Molecular and Cellular Biology, 2014, 34, 3867-3879.	1.1	31
59	Bio-coordination of bismuth in <i>Helicobacter pylori</i> revealed by immobilized metal affinity chromatography. Chemical Communications, 2015, 51, 16479-16482.	2.2	31
60	Search for basonuclin target genes. Biochemical and Biophysical Research Communications, 2006, 348, 1261-1271.	1.0	29
61	CMGRN: a web server for constructing multilevel gene regulatory networks using ChIP-seq and gene expression data. Bioinformatics, 2014, 30, 1190-1192.	1.8	29
62	UCLncR: Ultrafast and comprehensive long non-coding RNA detection from RNA-seq. Scientific Reports, 2017, 7, 14196.	1.6	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.	1.1	28
64	Colonoscopy surveillance for high risk polyps does not always prevent colorectal cancer. World Journal of Gastroenterology, 2018, 24, 905-916.	1.4	28
65	Histidine-rich proteins in prokaryotes: metal homeostasis and environmental habitat-related occurrence. Metallomics, 2013, 5, 1423.	1.0	26
66	Basonuclin Regulates a Subset of Ribosomal RNA Genes in HaCaT Cells. PLoS ONE, 2007, 2, e902.	1.1	24
67	Correlated evolution of transcription factors and their binding sites. Bioinformatics, 2011, 27, 2972-2978.	1.8	24
68	DDGni: Dynamic delay gene-network inference from high-temporal data using gapped local alignment. Bioinformatics, 2014, 30, 377-383.	1.8	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.	6.5	22
70	Functional networks of aging markers in the glomeruli of IgA nephropathy: a new therapeutic opportunity. Oncotarget, 2016, 7, 33616-33626.	0.8	22
71	FastPval: a fast and memory efficient program to calculate very low <i>P</i> -values from empirical distribution. Bioinformatics, 2010, 26, 2897-2899.	1.8	21
72	Integration of fluorescence imaging with proteomics enables visualization and identification of metallo-proteomes in living cells. Metallomics, 2017, 9, 38-47.	1.0	21

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73	Hybrid-denovo: a de novo OTU-picking pipeline integrating single-end and paired-end 16S sequence tags. <i>GigaScience</i> , 2018, 7, 1-7.	3.3	21
74	Integrated RNA-seq and ChIP-seq analysis reveals a feed-forward loop regulating H3K9ac and key labor drivers in human placenta. <i>Placenta</i> , 2019, 76, 40-50.	0.7	21
75	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	3.8	20
76	Tissue interactions, cell signaling and transcriptional control in the cranial mesoderm during craniofacial development. <i>AIMS Genetics</i> , 2016, 03, 074-098.	1.9	20
77	EpiRegNet: Constructing epigenetic regulatory network from high throughput gene expression data for humans. <i>Epigenetics</i> , 2011, 6, 1505-1512.	1.3	19
78	ChIP-Array 2: integrating multiple omics data to construct gene regulatory networks. <i>Nucleic Acids Research</i> , 2015, 43, W264-W269.	6.5	19
79	Absence of NUCKS augments paracrine effects of mesenchymal stem cells-mediated cardiac protection. <i>Experimental Cell Research</i> , 2017, 356, 74-84.	1.2	19
80	An integrative method to decode regulatory logics in gene transcription. <i>Nature Communications</i> , 2017, 8, 1044.	5.8	19
81	FaSD-somatic: a fast and accurate somatic SNV detection algorithm for cancer genome sequencing data. <i>Bioinformatics</i> , 2014, 30, 2498-2500.	1.8	18
82	<scp>ADAM10</scp> mediates ectopic proximal tubule development and renal fibrosis through Notch signalling. <i>Journal of Pathology</i> , 2020, 252, 274-289.	2.1	18
83	Rare SNP rs12731181 in the miR-590-3p Target Site of the Prostaglandin F $2\pm$ Receptor Gene Confers Risk for Essential Hypertension in the Han Chinese Population. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1687-1695.	1.1	15
84	Proteomic profiling identifies the SIM-associated complex of KSHV-encoded LANA. <i>Proteomics</i> , 2015, 15, 2023-2037.	1.3	14
85	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. <i>Genome Research</i> , 2020, 30, 1789-1801.	2.4	14
86	Uncertainty quantification in the radiogenomics modeling of EGFR amplification in glioblastoma. <i>Scientific Reports</i> , 2021, 11, 3932.	1.6	14
87	Human Ocular Epithelial Cells Endogenously Expressing SOX2 and OCT4 Yield High Efficiency of Pluripotency Reprogramming. <i>PLoS ONE</i> , 2015, 10, e0131288.	1.1	13
88	Generalizations of Markov model to characterize biological sequences. <i>BMC Bioinformatics</i> , 2005, 6, 219.	1.2	12
89	Current trend of annotating single nucleotide variation in humans – A case study on SNVrap. <i>Methods</i> , 2015, 79-80, 32-40.	1.9	12
90	mTCTScan: a comprehensive platform for annotation and prioritization of mutations affecting drug sensitivity in cancers. <i>Nucleic Acids Research</i> , 2017, 45, W215-W221.	6.5	12

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91	NdPASA: A novel pairwise protein sequence alignment algorithm that incorporates neighbor-dependent amino acid propensities. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 628-637.	1.5	10
92	Chronic Cardiovascular Disease-Associated Gene Network Analysis in Human Umbilical Vein Endothelial Cells Exposed to 2,3,7,8-Tetrachlorodibenzo-p-dioxin. <i>Cardiovascular Toxicology</i> , 2015, 15, 157-171.	1.1	10
93	wKGSSeq: A Comprehensive Strategy-Based and Disease-Targeted Online Framework to Facilitate Exome Sequencing Studies of Inherited Disorders. <i>Human Mutation</i> , 2015, 36, 496-503.	1.1	10
94	MetaMarker: a pipeline for <i>de novo</i> discovery of novel metagenomic biomarkers. <i>Bioinformatics</i> , 2019, 35, 3812-3814.	1.8	10
95	Integrating Convolutional Neural Networks and Multi-Task Dictionary Learning for Cognitive Decline Prediction with Longitudinal Images. <i>Journal of Alzheimer's Disease</i> , 2020, 75, 971-992.	1.2	9
96	Inference of Gene-Phenotype Associations via Protein-Protein Interaction and Orthology. <i>PLoS ONE</i> , 2013, 8, e77478.	1.1	9
97	Inferring RNA sequence preferences for poorly studied RNA-binding proteins based on co-evolution. <i>BMC Bioinformatics</i> , 2018, 19, 96.	1.2	7
98	Tacrolimus dose requirement based on the CYP3A5 genotype in renal transplant patients. <i>Oncotarget</i> , 2017, 8, 81285-81294.	0.8	7
99	Applications of integrative OMICs approaches to gene regulation studies. <i>Quantitative Biology</i> , 2016, 4, 283-301.	0.3	6
100	Accurate Identification of Subclones in Tumor Genomes. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	6
101	A novel neural response algorithm for protein function prediction. <i>BMC Systems Biology</i> , 2012, 6, S19.	3.0	5
102	ProteoMirExpress: Inferring MicroRNA and Protein-centered Regulatory Networks from High-throughput Proteomic and mRNA Expression Data. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3379-3387.	2.5	5
103	Bayesian detection of embryonic gene expression onset in <i>C. elegans</i> . <i>Annals of Applied Statistics</i> , 2015, 9, .	0.5	5
104	Methods and resources to access mutation-dependent effects on cancer drug treatment. <i>Briefings in Bioinformatics</i> , 2020, 21, 1886-1903.	3.2	5
105	Cell fate conversion prediction by group sparse optimization method utilizing single-cell and bulk OMICs data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
106	NdPASA: a pairwise sequence alignment server for distantly related proteins. <i>Bioinformatics</i> , 2005, 21, 3803-3805.	1.8	2
107	A database of genetic variants in microRNA genes and their putative functional roles in gene regulation. <i>Human Mutation</i> , 2012, 33, vii-vii.	1.1	2
108	Whole-Genome Analysis of an Extensive Drug-Resistant <i>Acinetobacter Baumannii</i> ST195 Isolate from a Recipient After DCD Renal Transplantation in China. <i>Kidney and Blood Pressure Research</i> , 2017, 42, 1247-1257.	0.9	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. <i>Methods in Molecular Biology</i> , 2018, 1722, 331-344.	0.4	2
110	Novel Neural Network Approach to Predict Drug-Target Interactions Based on Drug Side Effects and Genome-Wide Association Studies. <i>Human Heredity</i> , 2018, 83, 79-91.	0.4	2
111	Phenotype, Function, and Clinical Significance of CD26+ and CD161+Tregs in Splenic Marginal Zone Lymphoma. <i>Clinical Cancer Research</i> , 2022, 28, 4322-4335.	3.2	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. <i>Data in Brief</i> , 2016, 9, 372-375.	0.5	1
114	Evolution of Drug-resistant <i>Acinetobacter baumannii</i> After DCD Renal Transplantation. <i>Scientific Reports</i> , 2017, 7, 1968.	1.6	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. <i>Frontiers in Radiology</i> , 2022, 1, .	1.2	1
117	Advanced Computational Approaches for Medical Genetics and Genomics. <i>BioMed Research International</i> , 2015, 2015, 1-2.	0.9	0
118	Next-Generation Sequencing in Human Genetic Studies: Genome Technologies and Applications to Human Genetic Studies. <i>Human Heredity</i> , 2018, 83, 105-106.	0.4	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