

Junwen Wang

List of Publications by Year in descending order

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121
papers

7,276
citations

76326

40
h-index

62596

80
g-index

125
all docs

125
docs citations

125
times ranked

15790
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrating Transcriptomics, Genomics, and Imaging in Alzheimer's Disease: A Federated Model. <i>Frontiers in Radiology</i> , 2022, 1, .	2.0	1
2	Phenotype, Function, and Clinical Significance of CD26+ and CD161+Tregs in Splenic Marginal Zone Lymphoma. <i>Clinical Cancer Research</i> , 2022, 28, 4322-4335.	7.0	2
3	Uncertainty quantification in the radiogenomics modeling of EGFR amplification in glioblastoma. <i>Scientific Reports</i> , 2021, 11, 3932.	3.3	14
4	Implication of TIGIT+ human memory B cells in immune regulation. <i>Nature Communications</i> , 2021, 12, 1534.	12.8	41
5	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	8.8	20
6	Cell fate conversion prediction by group sparse optimization method utilizing single-cell and bulk OMICs data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	4
7	Methods and resources to access mutation-dependent effects on cancer drug treatment. <i>Briefings in Bioinformatics</i> , 2020, 21, 1886-1903.	6.5	5
8	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. <i>Genome Research</i> , 2020, 30, 1789-1801.	5.5	14
9	<sc>ADAM10</sc> mediates ectopic proximal tubule development and renal fibrosis through Notch signalling. <i>Journal of Pathology</i> , 2020, 252, 274-289.	4.5	18
10	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.	2.6	9
11	Translocator. , 2020, , .		0
12	MetaMarker: a pipeline for <i>de novo</i> discovery of novel metagenomic biomarkers. <i>Bioinformatics</i> , 2019, 35, 3812-3814.	4.1	10
13	Predicting disease-associated mutation of metal-binding sites in proteins using a deep learning approach. <i>Nature Machine Intelligence</i> , 2019, 1, 561-567.	16.0	48
14	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.	1.5	21
15	Evaluation of tools for highly variable gene discovery from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2019, 20, 1583-1589.	6.5	145
16	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. <i>Scientific Reports</i> , 2018, 8, 3161.	3.3	35
17	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.	3.8	44
18	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.	0.9	2

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19	Hybrid-denovo: a de novo OTU-picking pipeline integrating single-end and paired-end 16S sequence tags. <i>GigaScience</i> , 2018, 7, 1-7.	6.4	21
20	Developments in Blood-Brain Barrier Penetrance and Drug Repurposing for Improved Treatment of Glioblastoma. <i>Frontiers in Oncology</i> , 2018, 8, 462.	2.8	108
21	Next-Generation Sequencing in Human Genetic Studies: Genome Technologies and Applications to Human Genetic Studies. <i>Human Heredity</i> , 2018, 83, 105-106.	0.8	0
22	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.	0.8	2
23	Colonoscopy surveillance for high risk polyps does not always prevent colorectal cancer. <i>World Journal of Gastroenterology</i> , 2018, 24, 905-916.	3.3	28
24	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. <i>Nucleic Acids Research</i> , 2018, 46, W114-W120.	14.5	69
25	Inferring RNA sequence preferences for poorly studied RNA-binding proteins based on co-evolution. <i>BMC Bioinformatics</i> , 2018, 19, 96.	2.6	7
26	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.	5.6	34
27	Activation of E-prostanoid 3 receptor in macrophages facilitates cardiac healing after myocardial infarction. <i>Nature Communications</i> , 2017, 8, 14656.	12.8	36
28	Long noncoding RNA LINC00305 promotes inflammation by activating the AHRR-NF- κ B pathway in human monocytes. <i>Scientific Reports</i> , 2017, 7, 46204.	3.3	53
29	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. <i>Nucleic Acids Research</i> , 2017, 45, gkx019.	14.5	36
30	Absence of NUCKS augments paracrine effects of mesenchymal stem cells-mediated cardiac protection. <i>Experimental Cell Research</i> , 2017, 356, 74-84.	2.6	19
31	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.	7.4	66
32	mTCTScan: a comprehensive platform for annotation and prioritization of mutations affecting drug sensitivity in cancers. <i>Nucleic Acids Research</i> , 2017, 45, W215-W221.	14.5	12
33	Exploring genetic associations with ceRNA regulation in the human genome. <i>Nucleic Acids Research</i> , 2017, 45, 5653-5665.	14.5	39
34	Evolution of Drug-resistant <i>Acinetobacter baumannii</i> After DCD Renal Transplantation. <i>Scientific Reports</i> , 2017, 7, 1968.	3.3	1
35	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. <i>Genome Biology</i> , 2017, 18, 52.	8.8	33
36	UCLncR: Ultrafast and comprehensive long non-coding RNA detection from RNA-seq. <i>Scientific Reports</i> , 2017, 7, 14196.	3.3	29

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37	An integrative method to decode regulatory logics in gene transcription. <i>Nature Communications</i> , 2017, 8, 1044.	12.8	19
38	Linnorm: improved statistical analysis for single cell RNA-seq expression data. <i>Nucleic Acids Research</i> , 2017, 45, e179-e179.	14.5	100
39	Integration of fluorescence imaging with proteomics enables visualization and identification of metallo-proteomes in living cells. <i>Metalomics</i> , 2017, 9, 38-47.	2.4	21
40	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.	2.0	2
41	Tacrolimus dose requirement based on the CYP3A5 genotype in renal transplant patients. <i>Oncotarget</i> , 2017, 8, 81285-81294.	1.8	7
42	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
43	Abstract LB-274: Whole-exome sequencing reveals tyrosine kinase-resistant mutations in pretreatment EGFR-mutant lung adenocarcinomas. , 2017, , .		0
44	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.	2.9	50
45	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016, 48, 667-674.	21.4	77
46	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.	1.0	1
47	Transcriptional targets of TWIST1 in the cranial mesoderm regulate cell-matrix interactions and mesenchyme maintenance. <i>Developmental Biology</i> , 2016, 418, 189-203.	2.0	36
48	Applications of integrative OMICs approaches to gene regulation studies. <i>Quantitative Biology</i> , 2016, 4, 283-301.	0.5	6
49	Predicting regulatory variants with composite statistic. <i>Bioinformatics</i> , 2016, 32, 2729-2736.	4.1	40
50	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.	2.9	50
51	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. <i>Nucleic Acids Research</i> , 2016, 44, D869-D876.	14.5	184
52	Functional networks of aging markers in the glomeruli of IgA nephropathy: a new therapeutic opportunity. <i>Oncotarget</i> , 2016, 7, 33616-33626.	1.8	22
53	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
54	Bayesian detection of embryonic gene expression onset in <i>C. elegans</i> . <i>Annals of Applied Statistics</i> , 2015, 9, .	1.1	5

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55	<sc>Genetic 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. International Journal of Cancer, 2015, 137, 311-319.	5.1	72
56	Advanced Computational Approaches for Medical Genetics and Genomics. BioMed Research International, 2015, 2015, 1-2.	1.9	0
57	Rare SNP rs12731181 in the miR-590-3p Target Site of the Prostaglandin F ₂ Receptor Gene Confers Risk for Essential Hypertension in the Han Chinese Population. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1687-1695.	2.4	15
58	ChIP-Array 2: integrating multiple omics data to construct gene regulatory networks. Nucleic Acids Research, 2015, 43, W264-W269.	14.5	19
59	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
60	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
61	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
62	The support of human genetic evidence for approved drug indications. Nature Genetics, 2015, 47, 856-860.	21.4	1,112
63	The Current Status and Challenges in Computational Analysis of Genomic Big Data. Big Data Research, 2015, 2, 12-18.	4.2	33
64	Proteomic profiling identifies the SIM-associated complex of KSHV-encoded LANA. Proteomics, 2015, 15, 2023-2037.	2.2	14
65	Bio-coordination of bismuth in Helicobacter pylori revealed by immobilized metal affinity chromatography. Chemical Communications, 2015, 51, 16479-16482.	4.1	31
66	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
67	Current trend of annotating single nucleotide variation in humans – A case study on SNVrap. Methods, 2015, 79-80, 32-40.	3.8	12
68	Human Ocular Epithelial Cells Endogenously Expressing SOX2 and OCT4 Yield High Efficiency of Pluripotency Reprogramming. PLoS ONE, 2015, 10, e0131288.	2.5	13
69	dbPSHP: a database of recent positive selection across human populations. Nucleic Acids Research, 2014, 42, D910-D916.	14.5	36
70	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
71	Inhibition of KAP1 Enhances Hypoxia-Induced Kaposi's Sarcoma-Associated Herpesvirus Reactivation through RBP-J δ . Journal of Virology, 2014, 88, 6873-6884.	3.4	45
72	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

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73	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.	14.5	34
74	DDGni: Dynamic delay gene-network inference from high-temporal data using gapped local alignment. <i>Bioinformatics</i> , 2014, 30, 377-383.	4.1	24
75	CMGRN: a web server for constructing multilevel gene regulatory networks using ChIP-seq and gene expression data. <i>Bioinformatics</i> , 2014, 30, 1190-1192.	4.1	29
76	CTCF Controls <i>HOXA</i> Cluster Silencing and Mediates PRC2-Repressive Higher-Order Chromatin Structure in NT2/D1 Cells. <i>Molecular and Cellular Biology</i> , 2014, 34, 3867-3879.	2.3	31
77	FaSD-somatic: a fast and accurate somatic SNV detection algorithm for cancer genome sequencing data. <i>Bioinformatics</i> , 2014, 30, 2498-2500.	4.1	18
78	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.	3.4	107
79	Inferring gene regulatory networks by integrating ChIP-seq/chip and transcriptome data via LASSO-type regularization methods. <i>Methods</i> , 2014, 67, 294-303.	3.8	44
80	YY1 controls Ig λ repertoire and B-cell development, and localizes with condensin on the Ig λ locus. <i>EMBO Journal</i> , 2013, 32, 1168-1182.	7.8	55
81	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.	0.6	106
82	Susceptibility to myocardial ischemia reperfusion injury at early stage of type 1 diabetes in rats. <i>Cardiovascular Diabetology</i> , 2013, 12, 133.	6.8	64
83	Histidine-rich proteins in prokaryotes: metal homeostasis and environmental habitat-related occurrence. <i>Metalomics</i> , 2013, 5, 1423.	2.4	26
84	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.	2.9	92
85	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.	3.8	5
86	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.	14.5	101
87	Assessment of Mapping and SNP-Detection Algorithms for Next-Generation Sequencing Data in Cancer Genomics. , 2013, , 301-317.		1
88	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. <i>Journal of Clinical Investigation</i> , 2013, 123, 4909-4917.	8.2	126
89	Inference of Gene-Phenotype Associations via Protein-Protein Interaction and Orthology. <i>PLoS ONE</i> , 2013, 8, e77478.	2.5	9
90	Lung cancer tumorigenicity and drug resistance are maintained through ALDH1A1 tumor initiating cells. <i>Oncotarget</i> , 2013, 4, 1698-1711.	1.8	90

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91	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.	4.0	56
92	Genetic variant representation, annotation and prioritization in the post-GWAS era. <i>Cell Research</i> , 2012, 22, 1505-1508.	12.0	31
93	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.	2.5	69
94	GWASdb: a database for human genetic variants identified by genome-wide association studies. <i>Nucleic Acids Research</i> , 2012, 40, D1047-D1054.	14.5	204
95	A fast and accurate SNP detection algorithm for next-generation sequencing data. <i>Nature Communications</i> , 2012, 3, 1258.	12.8	51
96	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. <i>Nature Genetics</i> , 2012, 44, 1330-1335.	21.4	286
97	A novel neural response algorithm for protein function prediction. <i>BMC Systems Biology</i> , 2012, 6, S19.	3.0	5
98	A database of genetic variants in microRNA genes and their putative functional roles in gene regulation. <i>Human Mutation</i> , 2012, 33, vii-vii.	2.5	2
99	NRProF: Neural response based protein function prediction algorithm. , 2011, , .		1
100	Next generation sequencing has lower sequence coverage and poorer SNP-detection capability in the regulatory regions. <i>Scientific Reports</i> , 2011, 1, 55.	3.3	67
101	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.	1.9	41
102	An SNP selection strategy identified IL-22 associating with susceptibility to tuberculosis in Chinese. <i>Scientific Reports</i> , 2011, 1, 20.	3.3	52
103	Correlated evolution of transcription factors and their binding sites. <i>Bioinformatics</i> , 2011, 27, 2972-2978.	4.1	24
104	EpiRegNet: Constructing epigenetic regulatory network from high throughput gene expression data for humans. <i>Epigenetics</i> , 2011, 6, 1505-1512.	2.7	19
105	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.	14.5	49
106	FastPval: a fast and memory efficient program to calculate very low P -values from empirical distribution. <i>Bioinformatics</i> , 2010, 26, 2897-2899.	4.1	21
107	PU.1 Can Recruit BCL6 to DNA To Repress Gene Expression in Germinal Center B Cells. <i>Molecular and Cellular Biology</i> , 2009, 29, 4612-4622.	2.3	28
108	Mouse Ribosomal RNA Genes Contain Multiple Differentially Regulated Variants. <i>PLoS ONE</i> , 2008, 3, e1843.	2.5	54

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109	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.	14.5	52
110	Basonuclin Regulates a Subset of Ribosomal RNA Genes in HaCaT Cells. <i>PLoS ONE</i> , 2007, 2, e902.	2.5	24
111	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. <i>Nature Genetics</i> , 2007, 39, 870-874.	21.4	1,370
112	MetaProm: a neural network based meta-predictor for alternative human promoter prediction. <i>BMC Genomics</i> , 2007, 8, 374.	2.8	32
113	A mammalian promoter model links cis elements to genetic networks. <i>Biochemical and Biophysical Research Communications</i> , 2006, 347, 166-177.	2.1	31
114	Search for basonuclin target genes. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 1261-1271.	2.1	29
115	Transcriptional Genomics Associates FOX Transcription Factors With Human Heart Failure. <i>Circulation</i> , 2006, 114, 1269-1276.	1.6	210
116	Generalizations of Markov model to characterize biological sequences. <i>BMC Bioinformatics</i> , 2005, 6, 219.	2.6	12
117	NdPASA: a pairwise sequence alignment server for distantly related proteins. <i>Bioinformatics</i> , 2005, 21, 3803-3805.	4.1	2
118	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.	2.6	10
119	Predictive models for protein crystallization. <i>Methods</i> , 2004, 34, 390-407.	3.8	63
120	Exploring the sequence patterns in the $\hat{\text{A}}$ -helices of proteins. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 799-807.	2.1	46
121	Accurate Identification of Subclones in Tumor Genomes. <i>Molecular Biology and Evolution</i> , 0, , .	8.9	6