

# Junwei Han

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

1,395  
citations

331670

21  
h-index

345221

36  
g-index

46  
all docs

46  
docs citations

46  
times ranked

1223  
citing authors

#	ARTICLE	IF	CITATIONS
1	SubpathwayMiner: a software package for flexible identification of pathways. <i>Nucleic Acids Research</i> , 2009, 37, e131-e131.	14.5	195
2	Subpathway-GM: identification of metabolic subpathways via joint power of interesting genes and metabolites and their topologies within pathways. <i>Nucleic Acids Research</i> , 2013, 41, e101-e101.	14.5	125
3	Computational Methods for Identifying Similar Diseases. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 590-604.	5.1	102
4	LncSEA: a platform for long non-coding RNA related sets and enrichment analysis. <i>Nucleic Acids Research</i> , 2021, 49, D969-D980.	14.5	76
5	Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. <i>Bioinformatics</i> , 2013, 29, 2169-2177.	4.1	60
6	Exposing the Causal Effect of Body Mass Index on the Risk of Type 2 Diabetes Mellitus: A Mendelian Randomization Study. <i>Frontiers in Genetics</i> , 2019, 10, 94.	2.3	55
7	The Implications of Relationships between Human Diseases and Metabolic Subpathways. <i>PLoS ONE</i> , 2011, 6, e21131.	2.5	48
8	psSubpathway: a software package for flexible identification of phenotype-specific subpathways in cancer progression. <i>Bioinformatics</i> , 2020, 36, 2303-2305.	4.1	48
9	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. <i>Scientific Reports</i> , 2015, 5, 17201.	3.3	43
10	Subpathway-GMir: identifying miRNA-mediated metabolic subpathways by integrating condition-specific genes, microRNAs, and pathway topologies. <i>Oncotarget</i> , 2015, 6, 39151-39164.	1.8	33
11	Characterizing the Network of Drugs and Their Affected Metabolic Subpathways. <i>PLoS ONE</i> , 2012, 7, e47326.	2.5	32
12	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. <i>Scientific Reports</i> , 2015, 5, 13044.	3.3	31
13	Subpathway-CorSP: Identification of metabolic subpathways via integrating expression correlations and topological features between metabolites and genes of interest within pathways. <i>Scientific Reports</i> , 2016, 6, 33262.	3.3	29
14	A comprehensive overview of oncogenic pathways in human cancer. <i>Briefings in Bioinformatics</i> , 2020, 21, 957-969.	6.5	29
15	Inference of patient-specific subpathway activities reveals a functional signature associated with the prognosis of patients with breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 4304-4316.	3.6	28
16	Dissection of miRNA-miRNA Interaction in Esophageal Squamous Cell Carcinoma. <i>PLoS ONE</i> , 2013, 8, e73191.	2.5	27
17	Prioritization of candidate cancer drugs based on a drug functional similarity network constructed by integrating pathway activities and drug activities. <i>Molecular Oncology</i> , 2019, 13, 2259-2277.	4.6	27
18	Identification of Cancer Dysfunctional Subpathways by Integrating DNA Methylation, Copy Number Variation, and Gene-Expression Data. <i>Frontiers in Genetics</i> , 2019, 10, 441.	2.3	27

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19	Identification of miRNA-Mediated Core Gene Module for Glioma Patient Prediction by Integrating High-Throughput miRNA, mRNA Expression and Pathway Structure. PLoS ONE, 2014, 9, e96908.	2.5	26
20	Topologically inferring pathway activity toward precise cancer classification via integrating genomic and metabolomic data: prostate cancer as a case. Scientific Reports, 2015, 5, 13192.	3.3	25
21	LncRNAs2Pathways: Identifying the pathways influenced by a set of lncRNAs of interest based on a global network propagation method. Scientific Reports, 2017, 7, 46566.	3.3	24
22	SubtypeDrug: a software package for prioritization of candidate cancer subtype-specific drugs. Bioinformatics, 2021, 37, 2491-2493.	4.1	24
23	Prioritizing Candidate Disease Metabolites Based on Global Functional Relationships between Metabolites in the Context of Metabolic Pathways. PLoS ONE, 2014, 9, e104934.	2.5	23
24	The LncRNA Connectivity Map: Using LncRNA Signatures to Connect Small Molecules, LncRNAs, and Diseases. Scientific Reports, 2017, 7, 6655.	3.3	21
25	A global view of network of lncRNAs and their binding proteins. Molecular BioSystems, 2015, 11, 656-663.	2.9	20
26	A Positive Causal Influence of IL-18 Levels on the Risk of T2DM: A Mendelian Randomization Study. Frontiers in Genetics, 2019, 10, 295.	2.3	19
27	Subpathway-LNCE: Identify dysfunctional subpathways competitively regulated by lncRNAs through integrating lncRNA-mRNA expression profile and pathway topologies. Oncotarget, 2016, 7, 69857-69870.	1.8	18
28	A novel dysregulated pathway-identification analysis based on global influence of within-pathway effects and crosstalk between pathways. Journal of the Royal Society Interface, 2015, 12, 20140937.	3.4	17
29	CNA2Subpathway: identification of dysregulated subpathway driven by copy number alterations in cancer. Briefings in Bioinformatics, 2021, 22, .	6.5	16
30	Identifying disease related sub-pathways for analysis of genome-wide association studies. Gene, 2012, 503, 101-109.	2.2	15
31	Pan-cancer analysis reveals sex-specific signatures in the tumor microenvironment. Molecular Oncology, 2022, 16, 2153-2173.	4.6	13
32	MPINet: Metabolite Pathway Identification via Coupling of Global Metabolite Network Structure and Metabolomic Profile. BioMed Research International, 2014, 2014, 1-14.	1.9	12
33	Identification of novel prognostic indicators for triple-negative breast cancer patients through integrative analysis of cancer genomics data and protein interactome data. Oncotarget, 2016, 7, 71620-71634.	1.8	12
34	Metformin attenuates autoimmune disease of the neuromotor system in animal models of myasthenia gravis. International Immunopharmacology, 2019, 75, 105822.	3.8	11
35	Identifying functions and prognostic biomarkers of network motifs marked by diverse chromatin states in human cell lines. Oncogene, 2020, 39, 677-689.	5.9	11
36	Identification of a lncRNA involved functional module for esophageal cancer subtypes. Molecular BioSystems, 2016, 12, 3312-3323.	2.9	10

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37	MiRSEA: Discovering the pathways regulated by dysfunctional MicroRNAs. <i>Oncotarget</i> , 2016, 7, 55012-55025.	1.8	10
38	The detection of risk pathways, regulated by miRNAs, via the integration of sample-matched miRNA-mRNA profiles and pathway structure. <i>Journal of Biomedical Informatics</i> , 2014, 49, 187-197.	4.3	9
39	Integrative analysis of lung developmentâ€“cancer expression associations reveals the roles of signatures with inverse expression patterns. <i>Molecular BioSystems</i> , 2015, 11, 1271-1284.	2.9	9
40	Integrative Pathway Analysis of Genes and Metabolites Reveals Metabolism Abnormal Subpathway Regions and Modules in Esophageal Squamous Cell Carcinoma. <i>Molecules</i> , 2017, 22, 1599.	3.8	9
41	Prioritization of rheumatoid arthritis risk subpathways based on global immune subpathway interaction network and random walk strategy. <i>Molecular BioSystems</i> , 2015, 11, 2986-2997.	2.9	8
42	System level characterization of small molecule drugs and their affected long noncoding RNAs. <i>Aging</i> , 2019, 11, 12428-12451.	3.1	8
43	Development and Validation of a Three-Gene Prognostic Signature Based on Tumor Microenvironment for Gastric Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 801240.	2.3	5
44	MiRNA-Mediated Subpathway Identification and Network Module Analysis to Reveal Prognostic Markers in Human Pancreatic Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 606940.	2.3	2
45	Identification of Somatic Mutation-Driven Immune Cells by Integrating Genomic and Transcriptome Data. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 715275.	3.7	2
46	Inference of Subpathway Activity Profiles Reveals Metabolism Abnormal Subpathway Regions in Glioblastoma Multiforme. <i>Frontiers in Oncology</i> , 2020, 10, 1549.	2.8	1