

# Junwei Han

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

45 papers	889 citations	17 h-index	28 g-index
46 ext. papers	1,225 ext. citations	6.5 avg, IF	3.96 L-index

#	Paper	IF	Citations
45	Development and Validation of a Three-Gene Prognostic Signature Based on Tumor Microenvironment for Gastric Cancer.. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 801240	4.5	0
44	LncSEA: a platform for long non-coding RNA related sets and enrichment analysis. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D969-D980	20.1	15
43	Identification of Somatic Mutation-Driven Immune Cells by Integrating Genomic and Transcriptome Data. <i>Frontiers in Cell and Developmental Biology</i> , <b>2021</b> , 9, 715275	5.7	1
42	SubtypeDrug: a software package for prioritization of candidate cancer subtype-specific drugs. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	12
41	CNA2Subpathway: identification of dysregulated subpathway driven by copy number alterations in cancer. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	8
40	MiRNA-Mediated Subpathway Identification and Network Module Analysis to Reveal Prognostic Markers in Human Pancreatic Cancer. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 606940	4.5	1
39	psSubpathway: a software package for flexible identification of phenotype-specific subpathways in cancer progression. <i>Bioinformatics</i> , <b>2020</b> , 36, 2303-2305	7.2	21
38	Inference of Subpathway Activity Profiles Reveals Metabolism Abnormal Subpathway Regions in Glioblastoma Multiforme. <i>Frontiers in Oncology</i> , <b>2020</b> , 10, 1549	5.3	
37	A comprehensive overview of oncogenic pathways in human cancer. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 957-969	13.4	10
36	Identifying functions and prognostic biomarkers of network motifs marked by diverse chromatin states in human cell lines. <i>Oncogene</i> , <b>2020</b> , 39, 677-689	9.2	5
35	Metformin attenuates autoimmune disease of the neuromotor system in animal models of myasthenia gravis. <i>International Immunopharmacology</i> , <b>2019</b> , 75, 105822	5.8	5
34	Identification of Cancer Dysfunctional Subpathways by Integrating DNA Methylation, Copy Number Variation, and Gene-Expression Data. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 441	4.5	8
33	A Positive Causal Influence of IL-18 Levels on the Risk of T2DM: A Mendelian Randomization Study. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 295	4.5	11
32	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> , <b>2019</b> , 10, 94	4.5	32
31	Prioritization of candidate cancer drugs based on a drug functional similarity network constructed by integrating pathway activities and drug activities. <i>Molecular Oncology</i> , <b>2019</b> , 13, 2259-2277	7.9	11
30	Computational Methods for Identifying Similar Diseases. <i>Molecular Therapy - Nucleic Acids</i> , <b>2019</b> , 18, 590-604	10.7	69
29	System level characterization of small molecule drugs and their affected long noncoding RNAs. <i>Aging</i> , <b>2019</b> , 11, 12428-12451	5.6	6

28	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> , <b>2018</b> , 22, 4304-4316	5.6	8
27	LncRNAs2Pathways: Identifying the pathways influenced by a set of lncRNAs of interest based on a global network propagation method. <i>Scientific Reports</i> , <b>2017</b> , 7, 46566	4.9	13
26	The LncRNA Connectivity Map: Using LncRNA Signatures to Connect Small Molecules, LncRNAs, and Diseases. <i>Scientific Reports</i> , <b>2017</b> , 7, 6655	4.9	19
25	Integrative Pathway Analysis of Genes and Metabolites Reveals Metabolism Abnormal Subpathway Regions and Modules in Esophageal Squamous Cell Carcinoma. <i>Molecules</i> , <b>2017</b> , 22,	4.8	7
24	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> , <b>2016</b> , 6, 33262	4.9	11
23	MiRSEA: Discovering the pathways regulated by dysfunctional MicroRNAs. <i>Oncotarget</i> , <b>2016</b> , 7, 55012-55025	5.0	9
22	Identification of novel prognostic indicators for triple-negative breast cancer patients through integrative analysis of cancer genomics data and protein interactome data. <i>Oncotarget</i> , <b>2016</b> , 7, 71620-71634	5.3	12
21	Subpathway-LNCE: Identify dysfunctional subpathways competitively regulated by lncRNAs through integrating lncRNA-mRNA expression profile and pathway topologies. <i>Oncotarget</i> , <b>2016</b> , 7, 69837-69870	5.7	16
20	Identification of a lncRNA involved functional module for esophageal cancer subtypes. <i>Molecular BioSystems</i> , <b>2016</b> , 12, 3312-3323		9
19	A novel dysregulated pathway-identification analysis based on global influence of within-pathway effects and crosstalk between pathways. <i>Journal of the Royal Society Interface</i> , <b>2015</b> , 12, 20140937	4.1	11
18	Integrative analysis of lung development-cancer expression associations reveals the roles of signatures with inverse expression patterns. <i>Molecular BioSystems</i> , <b>2015</b> , 11, 1271-84		7
17	Prioritization of rheumatoid arthritis risk subpathways based on global immune subpathway interaction network and random walk strategy. <i>Molecular BioSystems</i> , <b>2015</b> , 11, 2986-97		5
16	A global view of network of lncRNAs and their binding proteins. <i>Molecular BioSystems</i> , <b>2015</b> , 11, 656-63		19
15	Topologically inferring pathway activity toward precise cancer classification via integrating genomic and metabolomic data: prostate cancer as a case. <i>Scientific Reports</i> , <b>2015</b> , 5, 13192	4.9	22
14	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. <i>Scientific Reports</i> , <b>2015</b> , 5, 13044	4.9	23
13	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. <i>Scientific Reports</i> , <b>2015</b> , 5, 17201	4.9	29
12	Subpathway-GMir: identifying miRNA-mediated metabolic subpathways by integrating condition-specific genes, microRNAs, and pathway topologies. <i>Oncotarget</i> , <b>2015</b> , 6, 39151-64	3.3	18
11	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> , <b>2014</b> , 49, 187-97	10.2	8

10	MPINet: metabolite pathway identification via coupling of global metabolite network structure and metabolomic profile. <i>BioMed Research International</i> , <b>2014</b> , 2014, 325697	3	10
9	Identification of miRNA-mediated core gene module for glioma patient prediction by integrating high-throughput miRNA, mRNA expression and pathway structure. <i>PLoS ONE</i> , <b>2014</b> , 9, e96908	3.7	23
8	Prioritizing candidate disease metabolites based on global functional relationships between metabolites in the context of metabolic pathways. <i>PLoS ONE</i> , <b>2014</b> , 9, e104934	3.7	17
7	Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. <i>Bioinformatics</i> , <b>2013</b> , 29, 2169-77	7.2	46
6	Subpathway-GM: identification of metabolic subpathways via joint power of interesting genes and metabolites and their topologies within pathways. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e101	20.1	85
5	Dissection of miRNA-miRNA interaction in esophageal squamous cell carcinoma. <i>PLoS ONE</i> , <b>2013</b> , 8, e73191	3.7	24
4	Identifying disease related sub-pathways for analysis of genome-wide association studies. <i>Gene</i> , <b>2012</b> , 503, 101-9	3.8	14
3	Characterizing the network of drugs and their affected metabolic subpathways. <i>PLoS ONE</i> , <b>2012</b> , 7, e47326	3.7	26
2	The implications of relationships between human diseases and metabolic subpathways. <i>PLoS ONE</i> , <b>2011</b> , 6, e21131	3.7	39
1	SubpathwayMiner: a software package for flexible identification of pathways. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, e131	20.1	143