Junwei Han

List of Publications by Citations

Source: https://exaly.com/author-pdf/3964218/junwei-han-publications-by-citations.pdf

Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

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

#	Paper	IF	Citations
45	SubpathwayMiner: a software package for flexible identification of pathways. <i>Nucleic Acids Research</i> , 2009 , 37, e131	20.1	143
44	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	20.1	85
43	Computational Methods for Identifying Similar Diseases. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 18, 590-604	10.7	69
42	Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. <i>Bioinformatics</i> , 2013 , 29, 2169-77	7.2	46
41	The implications of relationships between human diseases and metabolic subpathways. <i>PLoS ONE</i> , 2011 , 6, e21131	3.7	39
40	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	4.5	32
39	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. <i>Scientific Reports</i> , 2015 , 5, 17201	4.9	29
38	Characterizing the network of drugs and their affected metabolic subpathways. PLoS ONE, 2012, 7, e47	′3 2,6	26
37	Dissection of miRNA-miRNA interaction in esophageal squamous cell carcinoma. <i>PLoS ONE</i> , 2013 , 8, e7:	33 <i>9/</i> 1	24
36	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. <i>Scientific Reports</i> , 2015 , 5, 13044	4.9	23
35	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> , 2014 , 9, e96908	3.7	23
34	Topologically inferring pathway activity toward precise cancer classification via integrating genomic and metabolomic data: prostate cancer as a case. <i>Scientific Reports</i> , 2015 , 5, 13192	4.9	22
33	psSubpathway: a software package for flexible identification of phenotype-specific subpathways in cancer progression. <i>Bioinformatics</i> , 2020 , 36, 2303-2305	7.2	21
32	A global view of network of lncRNAs and their binding proteins. <i>Molecular BioSystems</i> , 2015 , 11, 656-63	3	19
31	The LncRNA Connectivity Map: Using LncRNA Signatures to Connect Small Molecules, LncRNAs, and Diseases. <i>Scientific Reports</i> , 2017 , 7, 6655	4.9	19
30	Subpathway-GMir: identifying miRNA-mediated metabolic subpathways by integrating condition-specific genes, microRNAs, and pathway topologies. <i>Oncotarget</i> , 2015 , 6, 39151-64	3.3	18
29	Prioritizing candidate disease metabolites based on global functional relationships between metabolites in the context of metabolic pathways. <i>PLoS ONE</i> , 2014 , 9, e104934	3.7	17

Subpathway-LNCE: Identify dysfunctional subpathways competitively regulated by lncRNAs 28 through integrating lncRNA-mRNA expression profile and pathway topologies. Oncotarget, **2016**, 7, $698\overline{97}^{2}$ - $698\overline{70}$ LncSEA: a platform for long non-coding RNA related sets and enrichment analysis. Nucleic Acids 27 20.1 15 Research, 2021, 49, D969-D980 Identifying disease related sub-pathways for analysis of genome-wide association studies. Gene, 26 3.8 14 2012, 503, 101-9 LncRNAs2Pathways: Identifying the pathways influenced by a set of lncRNAs of interest based on a 25 4.9 13 global network propagation method. Scientific Reports, 2017, 7, 46566 Identification of novel prognostic indicators for triple-negative breast cancer patients through 24 integrative analysis of cancer genomics data and protein interactome data. Oncotarget, 2016, 7, 71620-71634 SubtypeDrug: a software package for prioritization of candidate cancer subtype-specific drugs. 23 7.2 12 Bioinformatics, 2021, A Positive Causal Influence of IL-18 Levels on the Risk of T2DM: A Mendelian Randomization Study. 22 4.5 11 Frontiers in Genetics, **2019**, 10, 295 A novel dysregulated pathway-identification analysis based on global influence of within-pathway 21 4.1 11 effects and crosstalk between pathways. Journal of the Royal Society Interface, 2015, 12, 20140937 Subpathway-CorSP: Identification of metabolic subpathways via integrating expression correlations and topological features between metabolites and genes of interest within pathways. Scientific 20 4.9 11 Reports, 2016, 6, 33262 Prioritization of candidate cancer drugs based on a drug functional similarity network constructed 19 7.9 by integrating pathway activities and drug activities. Molecular Oncology, 2019, 13, 2259-2277 MPINet: metabolite pathway identification via coupling of global metabolite network structure and 18 3 10 metabolomic profile. BioMed Research International, 2014, 2014, 325697 A comprehensive overview of oncogenic pathways in human cancer. Briefings in Bioinformatics, 17 13.4 10 **2020**, 21, 957-969 16 MiRSEA: Discovering the pathways regulated by dysfunctional MicroRNAs. Oncotarget, 2016, 7, 55012-55025 9 Identification of a lncRNA involved functional module for esophageal cancer subtypes. *Molecular* 15 9 BioSystems, 2016, 12, 3312-3323 Identification of Cancer Dysfunctional Subpathways by Integrating DNA Methylation, Copy Number 8 14 4.5 Variation, and Gene-Expression Data. Frontiers in Genetics, 2019, 10, 441 The detection of risk pathways, regulated by miRNAs, via the integration of sample-matched 8 10.2 13 miRNA-mRNA profiles and pathway structure. Journal of Biomedical Informatics, 2014, 49, 187-97 Inference of patient-specific subpathway activities reveals a functional signature associated with 12 the prognosis of patients with breast cancer. Journal of Cellular and Molecular Medicine, 2018, 22, 4304-4316 CNA2Subpathway: identification of dysregulated subpathway driven by copy number alterations in 8 11 13.4 cancer. Briefings in Bioinformatics, 2021, 22,

10	Integrative analysis of lung development-cancer expression associations reveals the roles of signatures with inverse expression patterns. <i>Molecular BioSystems</i> , 2015 , 11, 1271-84		7
9	Integrative Pathway Analysis of Genes and Metabolites Reveals Metabolism Abnormal Subpathway Regions and Modules in Esophageal Squamous Cell Carcinoma. <i>Molecules</i> , 2017 , 22,	4.8	7
8	System level characterization of small molecule drugs and their affected long noncoding RNAs. <i>Aging</i> , 2019 , 11, 12428-12451	5.6	6
7	Metformin attenuates autoimmune disease of the neuromotor system in animal models of myasthenia gravis. <i>International Immunopharmacology</i> , 2019 , 75, 105822	5.8	5
6	Prioritization of rheumatoid arthritis risk subpathways based on global immune subpathway interaction network and random walk strategy. <i>Molecular BioSystems</i> , 2015 , 11, 2986-97		5
5	Identifying functions and prognostic biomarkers of network motifs marked by diverse chromatin states in human cell lines. <i>Oncogene</i> , 2020 , 39, 677-689	9.2	5
4	MiRNA-Mediated Subpathway Identification and Network Module Analysis to Reveal Prognostic Markers in Human Pancreatic Cancer. <i>Frontiers in Genetics</i> , 2020 , 11, 606940	4.5	1
3	Identification of Somatic Mutation-Driven Immune Cells by Integrating Genomic and Transcriptome Data. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 715275	5.7	1
2	Development and Validation of a Three-Gene Prognostic Signature Based on Tumor Microenvironment for Gastric Cancer <i>Frontiers in Genetics</i> , 2021 , 12, 801240	4.5	O
1	Inference of Subpathway Activity Profiles Reveals Metabolism Abnormal Subpathway Regions in Glioblastoma Multiforme. <i>Frontiers in Oncology</i> , 2020 , 10, 1549	5.3	