

Zichen Wang

List of Publications by Citations

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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.

54
papers

9,411
citations

29
h-index

62
g-index

62
ext. papers

14,852
ext. citations

11
avg, IF

5.97
L-index

#	Paper	IF	Citations
54	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , 2016 , 44, W90-7	20.1	3549
53	Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. <i>BMC Bioinformatics</i> , 2013 , 14, 128	3.6	2715
52	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	504
51	Differential cytokine contributions of perivascular haematopoietic stem cell niches. <i>Nature Cell Biology</i> , 2017 , 19, 214-223	23.4	254
50	Single-cell immune landscape of human atherosclerotic plaques. <i>Nature Medicine</i> , 2019 , 25, 1576-1588	50.5	247
49	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018 , 6, 13-24	10.6	199
48	Extraction and analysis of signatures from the Gene Expression Omnibus by the crowd. <i>Nature Communications</i> , 2016 , 7, 12846	17.4	146
47	L1000CDS: LINCS L1000 characteristic direction signatures search engine. <i>Npj Systems Biology and Applications</i> , 2016 , 2,	5	140
46	ChEA3: transcription factor enrichment analysis by orthogonal omics integration. <i>Nucleic Acids Research</i> , 2019 , 47, W212-W224	20.1	134
45	An Integrated Transcriptome Atlas of Embryonic Hair Follicle Progenitors, Their Niche, and the Developing Skin. <i>Developmental Cell</i> , 2015 , 34, 577-91	10.2	109
44	Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. <i>Nature Neuroscience</i> , 2016 , 19, 1321-30	25.5	108
43	Signaling Networks among Stem Cell Precursors, Transit-Amplifying Progenitors, and their Niche in Developing Hair Follicles. <i>Cell Reports</i> , 2016 , 14, 3001-18	10.6	98
42	Drug-induced adverse events prediction with the LINCS L1000 data. <i>Bioinformatics</i> , 2016 , 32, 2338-45	7.2	95
41	Histone H3.3 and its proteolytically processed form drive a cellular senescence programme. <i>Nature Communications</i> , 2014 , 5, 5210	17.4	89
40	Dynamic phosphorylation of CENP-A at Ser68 orchestrates its cell-cycle-dependent deposition at centromeres. <i>Developmental Cell</i> , 2015 , 32, 68-81	10.2	77
39	Lean Big Data integration in systems biology and systems pharmacology. <i>Trends in Pharmacological Sciences</i> , 2014 , 35, 450-60	13.2	67
38	L1000FWD: fireworks visualization of drug-induced transcriptomic signatures. <i>Bioinformatics</i> , 2018 , 34, 2150-2152	7.2	66

37	eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks. <i>Nucleic Acids Research</i> , 2018 , 46, W171-W179	20.1	58
36	SIRT6 haploinsufficiency induces BRAF melanoma cell resistance to MAPK inhibitors via IGF signalling. <i>Nature Communications</i> , 2018 , 9, 3440	17.4	51
35	Arabidopsis CSLD1 and CSLD4 are required for cellulose deposition and normal growth of pollen tubes. <i>Journal of Experimental Botany</i> , 2011 , 62, 5161-77	7	51
34	Habenular TCF7L2 links nicotine addiction to diabetes. <i>Nature</i> , 2019 , 574, 372-377	50.4	47
33	Dermal Condensate Niche Fate Specification Occurs Prior to Formation and Is Placode Progenitor Dependent. <i>Developmental Cell</i> , 2019 , 48, 32-48.e5	10.2	44
32	Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. <i>Nature Cell Biology</i> , 2019 , 21, 560-567	23.4	43
31	Dermal sheath contraction powers stem cell niche relocation during hair cycle regression. <i>Science</i> , 2020 , 367, 161-166	33.3	39
30	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , 2017 , 8, 1186	17.4	38
29	The Signaling Pathways Project, an integrated 'omics knowledgebase for mammalian cellular signaling pathways. <i>Scientific Data</i> , 2019 , 6, 252	8.2	38
28	Predicting opioid dependence from electronic health records with machine learning. <i>BioData Mining</i> , 2019 , 12, 3	4.3	33
27	Integrative Analysis of Sex-Specific microRNA Networks Following Stress in Mouse Nucleus Accumbens. <i>Frontiers in Molecular Neuroscience</i> , 2016 , 9, 144	6.1	31
26	Mining data and metadata from the gene expression omnibus. <i>Biophysical Reviews</i> , 2019 , 11, 103-110	3.7	30
25	Glucocorticoid receptor isoforms direct distinct mitochondrial programs to regulate ATP production. <i>Scientific Reports</i> , 2016 , 6, 26419	4.9	26
24	Connectivity Mapping: Methods and Applications. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 69-92	5.6	23
23	Hospitalised COVID-19 patients of the Mount Sinai Health System: a retrospective observational study using the electronic medical records. <i>BMJ Open</i> , 2020 , 10, e040441	3	23
22	An open RNA-Seq data analysis pipeline tutorial with an example of reprocessing data from a recent Zika virus study. <i>F1000Research</i> , 2016 , 5, 1574	3.6	23
21	Transcriptomic analysis uncovers novel synergistic mechanisms in combination therapy for lupus nephritis. <i>Kidney International</i> , 2018 , 93, 416-429	9.9	21
20	Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. <i>Cell Reports</i> , 2018 , 25, 2821-2835.e7	10.6	21

19	Predicting age by mining electronic medical records with deep learning characterizes differences between chronological and physiological age. <i>Journal of Biomedical Informatics</i> , 2017 , 76, 59-68	10.2	20
18	Podocyte-Specific Induction of Krüppel-Like Factor 15 Restores Differentiation Markers and Attenuates Kidney Injury in Proteinuric Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2018 , 29, 2529-2545	12.7	19
17	Analysis of hospitalized COVID-19 patients in the Mount Sinai Health System using electronic medical records (EMR) reveals important prognostic factors for improved clinical outcomes		15
16	Drug Gene Budger (DGB): an application for ranking drugs to modulate a specific gene based on transcriptomic signatures. <i>Bioinformatics</i> , 2019 , 35, 1247-1248	7.2	15
15	Dynamics of the discovery process of protein-protein interactions from low content studies. <i>BMC Systems Biology</i> , 2015 , 9, 26	3.5	13
14	Integrative radiogenomic analysis for multicentric radiophenotype in glioblastoma. <i>Oncotarget</i> , 2016 , 7, 11526-38	3.3	13
13	Brain microstructural injury occurs in patients with RRMS despite 'no evidence of disease activity'. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2018 , 89, 977-982	5.5	11
12	Cell-specific prediction and application of drug-induced gene expression profiles. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018 , 23, 32-43	1.3	11
11	Temporal proteomic profiling of postnatal human cortical development. <i>Translational Psychiatry</i> , 2018 , 8, 267	8.6	10
10	Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". <i>Computational Biology and Chemistry</i> , 2015 , 59 Pt B, 123-38	3.6	9
9	Principal Angle Enrichment Analysis (PAEA): Dimensionally Reduced Multivariate Gene Set Enrichment Analysis Tool 2015 , 2015, 256-262	0.8	8
8	Datasets2Tools, repository and search engine for bioinformatics datasets, tools and canned analyses. <i>Scientific Data</i> , 2018 , 5, 180023	8.2	7
7	Drug/Cell-line Browser: interactive canvas visualization of cancer drug/cell-line viability assay datasets. <i>Bioinformatics</i> , 2014 , 30, 3289-90	7.2	7
6	Sex differences in viral entry protein expression, host responses to SARS-CoV-2, and in vitro responses to sex steroid hormone treatment in COVID-19 2020 ,		4
5	Connectivity Mapping Identifies BI-2536 as a Potential Drug to Treat Diabetic Kidney Disease. <i>Diabetes</i> , 2021 , 70, 589-602	0.9	4
4	In-hospital use of ACE inhibitors/angiotensin receptor blockers associates with COVID-19 outcomes in African American patients. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	3
3	Publisher's Note: Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction. <i>Computational Biology and Chemistry</i> , 2015 , 58, 104-19	3.6	2
2	Systems Analysis Implicates WAVE2 Complex in the Pathogenesis of Developmental Left-Sided Obstructive Heart Defects. <i>JACC Basic To Translational Science</i> , 2020 , 5, 376-386	8.7	2

- 1 An Esrrb and Nanog Cell Fate Regulatory Module Controlled by Feed Forward Loop Interactions. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 630067 5.7 1