Zichen Wang

List of Publications by Year in Descending Order

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	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
53	Connectivity Mapping Identifies BI-2536 as a Potential Drug to Treat Diabetic Kidney Disease. *Diabetes*, **2021**, 70, 589-602	0.9	4
52	In-hospital use of ACE inhibitors/angiotensin receptor blockers associates with COVID-19 outcomes in African American patients. *Journal of Clinical Investigation*, **2021**, 131,	15.9	3
51	Systems Analysis Implicates WAVE2 Complex in the Pathogenesis of Developmental Left-Sided Obstructive Heart Defects. *JACC Basic To Translational Science*, **2020**, 5, 376-386	8.7	2
50	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
49	Dermal sheath contraction powers stem cell niche relocation during hair cycle regression. *Science*, **2020**, 367, 161-166	33.3	39
48	Hospitalised COVID-19 patients of the Mount Sinai Health System: a retrospective observational study using the electronic medical records. *BMJ Open*, **2020**, 10, e040441	3	23
47	Predicting opioid dependence from electronic health records with machine learning. *BioData Mining*, **2019**, 12, 3	4.3	33
46	ChEA3: transcription factor enrichment analysis by orthogonal omics integration. *Nucleic Acids Research*, **2019**, 47, W212-W224	20.1	134
45	Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. *Nature Cell Biology*, **2019**, 21, 560-567	23.4	43
44	Connectivity Mapping: Methods and Applications. *Annual Review of Biomedical Data Science*, **2019**, 2, 69-92	5.6	23
43	The Signaling Pathways Project, an integrated 'omics knowledgebase for mammalian cellular signaling pathways. *Scientific Data*, **2019**, 6, 252	8.2	38
42	Habenular TCF7L2 links nicotine addiction to diabetes. *Nature*, **2019**, 574, 372-377	50.4	47
41	Single-cell immune landscape of human atherosclerotic plaques. *Nature Medicine*, **2019**, 25, 1576-1588	50.5	247
40	Drug Gene Budger (DGB): an application for ranking drugs to modulate a specific gene based on transcriptomic signatures. *Bioinformatics*, **2019**, 35, 1247-1248	7.2	15
39	Mining data and metadata from the gene expression omnibus. *Biophysical Reviews*, **2019**, 11, 103-110	3.7	30
38	Dermal Condensate Niche Fate Specification Occurs Prior to Formation and Is Placode Progenitor Dependent. *Developmental Cell*, **2019**, 48, 32-48.e5	10.2	44

37	Datasets2Tools, repository and search engine for bioinformatics datasets, tools and canned analyses. *Scientific Data*, **2018**, 5, 180023	8.2	7
36	L1000FWD: fireworks visualization of drug-induced transcriptomic signatures. *Bioinformatics*, **2018**, 34, 2150-2152	7.2	66
35	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. *Cell Systems*, **2018**, 6, 13-24	10.6	199
34	Brain microstructural injury occurs in patients with RRMS despite 'no evidence of disease activity'. *Journal of Neurology, Neurosurgery and Psychiatry*, **2018**, 89, 977-982	5.5	11
33	SIRT6 haploinsufficiency induces BRAF melanoma cell resistance to MAPK inhibitors via IGF signalling. *Nature Communications*, **2018**, 9, 3440	17.4	51
32	Podocyte-Specific Induction of Krüppel-Like Factor 15 Restores Differentiation Markers and Attenuates Kidney Injury in Proteinuric Kidney Disease. *Journal of the American Society of Nephrology: JASN*, **2018**, 29, 2529-2545	12.7	19
31	Cell-specific prediction and application of drug-induced gene expression profiles. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2018**, 23, 32-43	1.3	11
30	Transcriptomic analysis uncovers novel synergistic mechanisms in combination therapy for lupus nephritis. *Kidney International*, **2018**, 93, 416-429	9.9	21
29	Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. *Cell Reports*, **2018**, 25, 2821-2835.e7	10.6	21
28	Temporal proteomic profiling of postnatal human cortical development. *Translational Psychiatry*, **2018**, 8, 267	8.6	10
27	eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks. *Nucleic Acids Research*, **2018**, 46, W171-W179	20.1	58
26	Differential cytokine contributions of perivascular haematopoietic stem cell niches. *Nature Cell Biology*, **2017**, 19, 214-223	23.4	254
25	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. *Nature Communications*, **2017**, 8, 1186	17.4	38
24	Predicting age by mining electronic medical records with deep learning characterizes differences between chronological and physiological age. *Journal of Biomedical Informatics*, **2017**, 76, 59-68	10.2	20
23	Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. *Nature Neuroscience*, **2016**, 19, 1321-30	25.5	108
22	Extraction and analysis of signatures from the Gene Expression Omnibus by the crowd. *Nature Communications*, **2016**, 7, 12846	17.4	146
21	Glucocorticoid receptor isoforms direct distinct mitochondrial programs to regulate ATP production. *Scientific Reports*, **2016**, 6, 26419	4.9	26
20	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	504

19	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*, **2016**, 44, W90-7	20.1	3549
18	Signaling Networks among Stem Cell Precursors, Transit-Amplifying Progenitors, and their Niche in Developing Hair Follicles. *Cell Reports*, **2016**, 14, 3001-18	10.6	98
17	Integrative radiogenomic analysis for multicentric radiophenotype in glioblastoma. *Oncotarget*, **2016**, 7, 11526-38	3.3	13
16	An open RNA-Seq data analysis pipeline tutorial with an example of reprocessing data from a recent Zika virus study. *F1000Research*, **2016**, 5, 1574	3.6	23
15	Integrative Analysis of Sex-Specific microRNA Networks Following Stress in Mouse Nucleus Accumbens. *Frontiers in Molecular Neuroscience*, **2016**, 9, 144	6.1	31
14	L1000CDS: LINCS L1000 characteristic direction signatures search engine. *Npj Systems Biology and Applications*, **2016**, 2,	5	140
13	Drug-induced adverse events prediction with the LINCS L1000 data. *Bioinformatics*, **2016**, 32, 2338-45	7.2	95
12	Publisher Note:Abstraction for data integration:Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction. *Computational Biology and Chemistry*, **2015**, 58, 104-19	3.6	2
11	An Integrated Transcriptome Atlas of Embryonic Hair Follicle Progenitors, Their Niche, and the Developing Skin. *Developmental Cell*, **2015**, 34, 577-91	10.2	109
10	Dynamics of the discovery process of protein-protein interactions from low content studies. *BMC Systems Biology*, **2015**, 9, 26	3.5	13
9	Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". *Computational Biology and Chemistry*, **2015**, 59 Pt B, 123-38	3.6	9
8	Principal Angle Enrichment Analysis (PAEA): Dimensionally Reduced Multivariate Gene Set Enrichment Analysis Tool **2015**, 2015, 256-262	0.8	8
7	Dynamic phosphorylation of CENP-A at Ser68 orchestrates its cell-cycle-dependent deposition at centromeres. *Developmental Cell*, **2015**, 32, 68-81	10.2	77
6	Histone H3.3 and its proteolytically processed form drive a cellular senescence programme. *Nature Communications*, **2014**, 5, 5210	17.4	89
5	Lean Big Data integration in systems biology and systems pharmacology. *Trends in Pharmacological Sciences*, **2014**, 35, 450-60	13.2	67
4	Drug/Cell-line Browser: interactive canvas visualization of cancer drug/cell-line viability assay datasets. *Bioinformatics*, **2014**, 30, 3289-90	7.2	7
3	Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*, **2013**, 14, 128	3.6	2715
2	Arabidopsis CSLD1 and CSLD4 are required for cellulose deposition and normal growth of pollen tubes. *Journal of Experimental Botany*, **2011**, 62, 5161-77	7	51

List of Publications