Jing Wang

List of Publications by Year
in descending order

32	7,167	331670	434195
papers	citations	21	31
		h-index	g-index

34	34	34	16853
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs. Nucleic Acids Research, 2019, 47, W199-W205.	14.5	2,234
2	Genetic Dissection of Femoral and Tibial Microarchitecture. JBMR Plus, 2019, 3, e10241.	2.7	6
3	The Glial Cell-Derived Neurotrophic Factor (GDNF)-responsive Phosphoprotein Landscape Identifies Raptor Phosphorylation Required for Spermatogonial Progenitor Cell Proliferation. Molecular and Cellular Proteomics, 2017, 16, 982-997.	3.8	33
4	WebGestalt 2017: a more comprehensive, powerful, flexible and interactive gene set enrichment analysis toolkit. Nucleic Acids Research, 2017, 45, W130-W137.	14.5	1,071
5	Methods, Tools and Current Perspectives in Proteogenomics. Molecular and Cellular Proteomics, 2017, 16, 959-981.	3.8	130
6	Colorectal Cancer Cell Line Proteomes Are Representative of Primary Tumors and Predict Drug Sensitivity. Gastroenterology, 2017, 153, 1082-1095.	1.3	55
7	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. Molecular and Cellular Proteomics, 2017, 16, 121-134.	3.8	111
8	Disrupted cooperation between transcription factors across diverse cancer types. BMC Genomics, 2016, 17, 560.	2.8	4
9	Dissecting the Origin of Breast Cancer Subtype Stem Cell and the Potential Mechanism of Malignant Transformation. PLoS ONE, 2016, 11, e0165001.	2.5	11
10	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. Journal of Proteome Research, 2016, 15, 691-706.	3.7	44
11	Transcriptome Sequencing to Identify Transcription Factor Regulatory Network and Alternative Splicing in Endothelial Cells Under VEGF Stimulation. Journal of Molecular Neuroscience, 2016, 58, 170-177.	2.3	18
12	The RNA binding protein FXR1 is a new driver in the 3q26-29 amplicon and predicts poor prognosis in human cancers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3469-3474.	7.1	84
13	Global gene expression profiling reveals a suppressed immune response pathway associated with 3q amplification in squamous carcinoma of the lung. Genomics Data, 2015, 5, 272-274.	1.3	6
14	Empowering biologists with multi-omics data: colorectal cancer as a paradigm. Bioinformatics, 2015, 31, 1436-1443.	4.1	22
15	Proteogenomic Analysis Reveals Unanticipated Adaptations of Colorectal Tumor Cells to Deficiencies in DNA Mismatch Repair. Cancer Research, 2014, 74, 387-397.	0.9	46
16	Proteogenomic characterization of human colon and rectal cancer. Nature, 2014, 513, 382-387.	27.8	1,219
17	NetGestalt: integrating multidimensional omics data over biological networks. Nature Methods, 2013, 10, 597-598.	19.0	52
18	Integrative Genomics Analysis Identifies Candidate Drivers at 3q26-29 Amplicon in Squamous Cell Carcinoma of the Lung. Clinical Cancer Research, 2013, 19, 5580-5590.	7.0	56

#	Article	IF	Citations
19	WEB-based GEne SeT AnaLysis Toolkit (WebGestalt): update 2013. Nucleic Acids Research, 2013, 41, W77-W83.	14.5	1,458
20	Evaluating FDR and stratified FDR control approaches for high-throughput biological studies. , 2012, , .		1
21	GO-function: deriving biologically relevant functions from statistically significant functions. Briefings in Bioinformatics, 2012, 13, 216-227.	6.5	71
22	Finding co-mutated genes and candidate cancer genes in cancer genomes by stratified false discovery rate control. Molecular BioSystems, 2011, 7, 1158.	2.9	9
23	Reproducible Cancer Biomarker Discovery in SELDI-TOF MS Using Different Pre-Processing Algorithms. PLoS ONE, 2011, 6, e26294.	2.5	9
24	Revealing and avoiding bias in semantic similarity scores for protein pairs. BMC Bioinformatics, 2010, 11, 290.	2.6	38
25	Extracting consistent knowledge from highly inconsistent cancer gene data sources. BMC Bioinformatics, 2010, 11, 76.	2.6	46
26	Viewing cancer genes from co-evolving gene modules. Bioinformatics, 2010, 26, 919-924.	4.1	3
27	Evaluating reproducibility of differential expression discoveries in microarray studies by considering correlated molecular changes. Bioinformatics, 2009, 25, 1662-1668.	4.1	100
28	Gaining confidence in biological interpretation of the microarray data: the functional consistence of the significant GO categories. Bioinformatics, 2008, 24, 265-271.	4.1	49
29	Edge-based scoring and searching method for identifying condition-responsive protein protein interaction sub-network. Bioinformatics, 2007, 23, 2121-2128.	4.1	139
30	Globally predicting protein functions based on co-expressed protein–protein interaction networks and ontology taxonomy similarities. Gene, 2007, 391, 113-119.	2.2	26
31	GO-2D: identifying 2-dimensional cellular-localized functional modules in Gene Ontology. BMC Genomics, 2007, 8, 30.	2.8	15
32	Finding finer functions for partially characterized proteins by protein-protein interaction networks. Science Bulletin, 2007, 52, 3363-3370.	1.7	1