

Jing Wang

List of Publications by Year in descending order

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32
papers

7,167
citations

331670

21
h-index

434195

31
g-index

34
all docs

34
docs citations

34
times ranked

16853
citing authors

#	ARTICLE	IF	CITATIONS
1	WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs. <i>Nucleic Acids Research</i> , 2019, 47, W199-W205.	14.5	2,234
2	WEB-based GENE SeT Analysis Toolkit (WebGestalt): update 2013. <i>Nucleic Acids Research</i> , 2013, 41, W77-W83.	14.5	1,458
3	Proteogenomic characterization of human colon and rectal cancer. <i>Nature</i> , 2014, 513, 382-387.	27.8	1,219
4	WebGestalt 2017: a more comprehensive, powerful, flexible and interactive gene set enrichment analysis toolkit. <i>Nucleic Acids Research</i> , 2017, 45, W130-W137.	14.5	1,071
5	Edge-based scoring and searching method for identifying condition-responsive protein protein interaction sub-network. <i>Bioinformatics</i> , 2007, 23, 2121-2128.	4.1	139
6	Methods, Tools and Current Perspectives in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 959-981.	3.8	130
7	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 121-134.	3.8	111
8	Evaluating reproducibility of differential expression discoveries in microarray studies by considering correlated molecular changes. <i>Bioinformatics</i> , 2009, 25, 1662-1668.	4.1	100
9	The RNA binding protein FXR1 is a new driver in the 3q26-29 amplicon and predicts poor prognosis in human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3469-3474.	7.1	84
10	GO-function: deriving biologically relevant functions from statistically significant functions. <i>Briefings in Bioinformatics</i> , 2012, 13, 216-227.	6.5	71
11	Integrative Genomics Analysis Identifies Candidate Drivers at 3q26-29 Amplicon in Squamous Cell Carcinoma of the Lung. <i>Clinical Cancer Research</i> , 2013, 19, 5580-5590.	7.0	56
12	Colorectal Cancer Cell Line Proteomes Are Representative of Primary Tumors and Predict Drug Sensitivity. <i>Gastroenterology</i> , 2017, 153, 1082-1095.	1.3	55
13	NetGestalt: integrating multidimensional omics data over biological networks. <i>Nature Methods</i> , 2013, 10, 597-598.	19.0	52
14	Gaining confidence in biological interpretation of the microarray data: the functional consistence of the significant GO categories. <i>Bioinformatics</i> , 2008, 24, 265-271.	4.1	49
15	Extracting consistent knowledge from highly inconsistent cancer gene data sources. <i>BMC Bioinformatics</i> , 2010, 11, 76.	2.6	46
16	Proteogenomic Analysis Reveals Unanticipated Adaptations of Colorectal Tumor Cells to Deficiencies in DNA Mismatch Repair. <i>Cancer Research</i> , 2014, 74, 387-397.	0.9	46
17	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706.	3.7	44
18	Revealing and avoiding bias in semantic similarity scores for protein pairs. <i>BMC Bioinformatics</i> , 2010, 11, 290.	2.6	38

#	ARTICLE	IF	CITATIONS
19	The Glial Cell-Derived Neurotrophic Factor (GDNF)-responsive Phosphoprotein Landscape Identifies Raptor Phosphorylation Required for Spermatogonial Progenitor Cell Proliferation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 982-997.	3.8	33
20	Globally predicting protein functions based on co-expressed protein-protein interaction networks and ontology taxonomy similarities. <i>Gene</i> , 2007, 391, 113-119.	2.2	26
21	Empowering biologists with multi-omics data: colorectal cancer as a paradigm. <i>Bioinformatics</i> , 2015, 31, 1436-1443.	4.1	22
22	Transcriptome Sequencing to Identify Transcription Factor Regulatory Network and Alternative Splicing in Endothelial Cells Under VEGF Stimulation. <i>Journal of Molecular Neuroscience</i> , 2016, 58, 170-177.	2.3	18
23	GO-2D: identifying 2-dimensional cellular-localized functional modules in Gene Ontology. <i>BMC Genomics</i> , 2007, 8, 30.	2.8	15
24	Dissecting the Origin of Breast Cancer Subtype Stem Cell and the Potential Mechanism of Malignant Transformation. <i>PLoS ONE</i> , 2016, 11, e0165001.	2.5	11
25	Finding co-mutated genes and candidate cancer genes in cancer genomes by stratified false discovery rate control. <i>Molecular BioSystems</i> , 2011, 7, 1158.	2.9	9
26	Reproducible Cancer Biomarker Discovery in SELDI-TOF MS Using Different Pre-Processing Algorithms. <i>PLoS ONE</i> , 2011, 6, e26294.	2.5	9
27	Global gene expression profiling reveals a suppressed immune response pathway associated with 3q amplification in squamous carcinoma of the lung. <i>Genomics Data</i> , 2015, 5, 272-274.	1.3	6
28	Genetic Dissection of Femoral and Tibial Microarchitecture. <i>JBMR Plus</i> , 2019, 3, e10241.	2.7	6
29	Disrupted cooperation between transcription factors across diverse cancer types. <i>BMC Genomics</i> , 2016, 17, 560.	2.8	4
30	Viewing cancer genes from co-evolving gene modules. <i>Bioinformatics</i> , 2010, 26, 919-924.	4.1	3
31	Finding finer functions for partially characterized proteins by protein-protein interaction networks. <i>Science Bulletin</i> , 2007, 52, 3363-3370.	1.7	1
32	Evaluating FDR and stratified FDR control approaches for high-throughput biological studies. , 2012, , .		1