Yue Wang

List of Publications by Year
in descending order

44 papers	2,959 citations	331670 21 h-index	276875 41 g-index
50 all docs	50 docs citations	50 times ranked	4778 citing authors

#	Article	IF	Citations
1	Comparative assessment and novel strategy on methods for imputing proteomics data. Scientific Reports, 2022, 12, 1067.	3.3	8
2	swCAM: estimation of subtype-specific expressions in individual samples with unsupervised sample-wise deconvolution. Bioinformatics, 2022, 38, 1403-1410.	4.1	5
3	COT: an efficient and accurate method for detecting marker genes among many subtypes. Bioinformatics Advances, 2022, 2, .	2.4	5
4	Data-driven detection of subtype-specific differentially expressed genes. Scientific Reports, 2021, 11, 332.	3.3	9
5	Machine intelligence enabled radiomics. Nature Machine Intelligence, 2021, 3, 838-839.	16.0	3
6	A deep matrix completion method for imputing missing histological data in breast cancer by integrating DCEâ€MRI radiomics. Medical Physics, 2021, 48, 7685-7697.	3.0	2
7	Biomedical image characterization and radiogenomics. , 2020, , 585-613.		1
8	Radiogenomic signatures reveal multiscale intratumour heterogeneity associated with biological functions and survival in breast cancer. Nature Communications, 2020, 11, 4861.	12.8	57
9	Identification of Putative Early Atherosclerosis Biomarkers by Unsupervised Deconvolution of Heterogeneous Vascular Proteomes. Journal of Proteome Research, 2020, 19, 2794-2806.	3.7	16
10	debCAM: a bioconductor R package for fully unsupervised deconvolution of complex tissues. Bioinformatics, 2020, 36, 3927-3929.	4.1	14
11	Tumour heterogeneity revealed by unsupervised decomposition of dynamic contrast-enhanced magnetic resonance imaging is associated with underlying gene expression patterns and poor survival in breast cancer patients. Breast Cancer Research, 2019, 21, 112.	5.0	21
12	Radiomic analysis of imaging heterogeneity in tumours and the surrounding parenchyma based on unsupervised decomposition of DCE-MRI for predicting molecular subtypes of breast cancer. European Radiology, 2019, 29, 4456-4467.	4.5	51
13	Systems biology: perspectives on multiscale modeling in research on endocrine-related cancers. Endocrine-Related Cancer, 2019, 26, R345-R368.	3.1	14
14	Mathematical Modeling and Deconvolution of Molecular Heterogeneity Identifies Novel Subpopulations in Complex Tissues. Methods in Molecular Biology, 2018, 1751, 223-236.	0.9	0
15	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. Circulation, 2018, 137, 2741-2756.	1.6	100
16	Mathematical modelling of transcriptional heterogeneity identifies novel markers and subpopulations in complex tissues. Scientific Reports, 2016, 6, 18909.	3.3	57
17	SIMAT: GC-SIM-MS data analysis tool. BMC Bioinformatics, 2015, 16, 259.	2.6	8
18	UNDO: a Bioconductor R package for unsupervised deconvolution of mixed gene expressions in tumor samples. Bioinformatics, 2015, 31, 137-139.	4.1	60

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19	Unsupervised Deconvolution of Dynamic Imaging Reveals Intratumor Vascular Heterogeneity and Repopulation Dynamics. PLoS ONE, 2014, 9, e112143.	2.5	15
20	An Overview of Population Genetic Data Simulation. Journal of Computational Biology, 2012, 19, 42-54.	1.6	72
21	Identification of Molecular Pathway Aberrations in Uterine Serous Carcinoma by Genome-wide Analyses. Journal of the National Cancer Institute, 2012, 104, 1503-1513.	6.3	231
22	Genome-wide identification of significant aberrations in cancer genome. BMC Genomics, 2012, 13, 342.	2.8	34
23	Comparative Analysis of Methods for Identifying Recurrent Copy Number Alterations in Cancer. PLoS ONE, 2012, 7, e52516.	2.5	11
24	Computational analysis of muscular dystrophy sub-types using a novel integrative scheme. Neurocomputing, 2012, 92, 9-17.	5.9	3
25	TAGCNA: A Method to Identify Significant Consensus Events of Copy Number Alterations in Cancer. PLoS ONE, 2012, 7, e41082.	2.5	3
26	Tissue-Specific Compartmental Analysis for Dynamic Contrast-Enhanced MR Imaging of Complex Tumors. IEEE Transactions on Medical Imaging, 2011, 30, 2044-2058.	8.9	58
27	Simulating Linkage Disequilibrium Structures in a Human Population for SNP Association Studies. Biochemical Genetics, 2011, 49, 395-409.	1.7	16
28	Comparative analysis of methods for detecting interacting loci. BMC Genomics, 2011, 12, 344.	2.8	31
29	BACOM: in silico detection of genomic deletion types and correction of normal cell contamination in copy number data. Bioinformatics, 2011, 27, 1473-1480.	4.1	30
30	PUGSVM: a caBIGTM analytical tool for multiclass gene selection and predictive classification. Bioinformatics, 2011, 27, 736-738.	4.1	19
31	Knowledge-guided gene ranking by coordinative component analysis. BMC Bioinformatics, 2010, 11, 162.	2.6	8
32	Nonnegative Least-Correlated Component Analysis for Separation of Dependent Sources by Volume Maximization. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2010, 32, 875-888.	13.9	64
33	Analysis of DNA Copy Number Alterations in Ovarian Serous Tumors Identifies New Molecular Genetic Changes in Low-Grade and High-Grade Carcinomas. Cancer Research, 2009, 69, 4036-4042.	0.9	166
34	Differential dependency network analysis to identify condition-specific topological changes in biological networks. Bioinformatics, 2009, 25, 526-532.	4.1	127
35	Copy number analysis indicates monoclonal origin of lethal metastatic prostate cancer. Nature Medicine, 2009, 15, 559-565.	30.7	596
36	Approaches to working in high-dimensional data spaces: gene expression microarrays. British Journal of Cancer, 2008, 98, 1023-1028.	6.4	57

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37	The properties of high-dimensional data spaces: implications for exploring gene and protein expression data. Nature Reviews Cancer, 2008, 8, 37-49.	28.4	483
38	caBIGâ„¢ VISDA: Modeling, visualization, and discovery for cluster analysis of genomic data. BMC Bioinformatics, 2008, 9, 383.	2.6	12
39	Motif-directed network component analysis for regulatory network inference. BMC Bioinformatics, 2008, 9, S21.	2.6	22
40	A Convex Analysis Framework for Blind Separation of Non-Negative Sources. IEEE Transactions on Signal Processing, 2008, 56, 5120-5134.	5.3	106
41	Nuclear envelope dystrophies show a transcriptional fingerprint suggesting disruption of Rbâ€“MyoD pathways in muscle regeneration. Brain, 2006, 129, 996-1013.	7.6	288
42	Iterative normalization of cDNA microarray data. IEEE Transactions on Information Technology in Biomedicine, 2002, 6, 29-37.	3.2	43
43	Magnetic resonance image analysis by information theoretic criteria and stochastic site models. IEEE Transactions on Information Technology in Biomedicine, 2001, 5, 150-158.	3.2	24
44	Independent component imaging of disease signatures. , 0, , .		4