Lana X Garmire

List of Publications by Year
in descending order

51 papers	3,562 citations	218592 26 h-index	206029 48 g-index
69 all docs	69 docs citations	69 times ranked	6458 citing authors

#	Article	IF	Citations
1	A Dual‐Filtration System for Single‐Cell Sequencing of Circulating Tumor Cells and Clusters in HCC. Hepatology Communications, 2022, 6, 1482-1491.	2.0	6
2	Maternal plasma lipids are involved in the pathogenesis of preterm birth. GigaScience, 2022, 11, .	3.3	8
3	BML: a versatile web server for bipartite motif discovery. Briefings in Bioinformatics, 2022, 23, .	3.2	0
4	Blood-derived lncRNAs as biomarkers for cancer diagnosis: the Good, the Bad and the Beauty. Npj Precision Oncology, 2022, 6, .	2.3	50
5	Cox-nnet v2.0: improved neural-network-based survival prediction extended to large-scale EMR data. Bioinformatics, 2021, 37, 2772-2774.	1.8	10
6	Mentorship is not co-authorship: a revisit to mentorship. Genome Biology, 2021, 22, 2.	3.8	5
7	Lilikoi V2.0: a deep learning–enabled, personalized pathway-based R package for diagnosis and prognosis predictions using metabolomics data. GigaScience, 2021, 10, .	3.3	12
8	Placentas delivered by pre‐pregnant obese women have reduced abundance and diversity in the microbiome. FASEB Journal, 2021, 35, e21524.	0.2	14
9	DeepProg: an ensemble of deep-learning and machine-learning models for prognosis prediction using multi-omics data. Genome Medicine, 2021, 13, 112.	3.6	90
10	Computational reconstruction of the signalling networks surrounding implanted biomaterials from single-cell transcriptomics. Nature Biomedical Engineering, 2021, 5, 1228-1238.	11.6	40
11	The maternal blood lipidome is indicative of the pathogenesis of severe preeclampsia. Journal of Lipid Research, 2021, 62, 100118.	2.0	17
12	Two-stage Cox-nnet: biologically interpretable neural-network model for prognosis prediction and its application in liver cancer survival using histopathology and transcriptomic data. NAR Genomics and Bioinformatics, 2021, 3, lqab015.	1.5	18
13	Evaluation of Cell Type Annotation R Packages on Single-cell RNA-seq Data. Genomics, Proteomics and Bioinformatics, 2021, 19, 267-281.	3.0	68
14	GranatumX: A Community-engaging, Modularized, and Flexible Webtool for Single-cell Data Analysis. Genomics, Proteomics and Bioinformatics, 2021, 19, 452-460.	3.0	3
15	Recommendations to enhance rigor and reproducibility in biomedical research. GigaScience, 2020, 9, .	3.3	83
16	A review of omics approaches to study preeclampsia. Placenta, 2020, 92, 17-27.	0.7	48
17	Prepregnant Obesity of Mothers in a Multiethnic Cohort Is Associated with Cord Blood Metabolomic Changes in Offspring. Journal of Proteome Research, 2020, 19, 1361-1374.	1.8	7
18	Evaluation of STAR and Kallisto on Single Cell RNA-Seq Data Alignment. G3: Genes, Genomes, Genetics, 2020, 10, 1775-1783.	0.8	34

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19	Single cell transcriptome research in human placenta. Reproduction, 2020, 160, R155-R167.	1.1	46
20	Multimodal Meta-Analysis of 1,494 Hepatocellular Carcinoma Samples Reveals Significant Impact of Consensus Driver Genes on Phenotypes. Clinical Cancer Research, 2019, 25, 463-472.	3.2	41
21	Data Analysis in Single-Cell RNA-Seq. , 2019, , 419-432.		0
22	A Novel FGFR3 Splice Variant Preferentially Expressed in African American Prostate Cancer Drives Aggressive Phenotypes and Docetaxel Resistance. Molecular Cancer Research, 2019, 17, 2115-2125.	1.5	9
23	DeepImpute: an accurate, fast, and scalable deep neural network method to impute single-cell RNA-seq data. Genome Biology, 2019, 20, 211.	3.8	185
24	Maternal cardiovascular-related single nucleotide polymorphisms, genes, and pathways associated with early-onset preeclampsia. PLoS ONE, 2019, 14, e0222672.	1.1	6
25	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	3.1	57
26	Deep Learning Accurately Predicts Estrogen Receptor Status in Breast Cancer Metabolomics Data. Journal of Proteome Research, 2018, 17, 337-347.	1.8	176
27	Lilikoi: an R package for personalized pathway-based classification modeling using metabolomics data. GigaScience, 2018, 7, .	3.3	25
28	Using single nucleotide variations in single-cell RNA-seq to identify subpopulations and genotype-phenotype linkage. Nature Communications, 2018, 9, 4892.	5.8	51
29	Cox-nnet: An artificial neural network method for prognosis prediction of high-throughput omics data. PLoS Computational Biology, 2018, 14, e1006076.	1.5	241
30	Deep Learningâ€"Based Multi-Omics Integration Robustly Predicts Survival in Liver Cancer. Clinical Cancer Research, 2018, 24, 1248-1259.	3.2	670
31	SINGLE CELL ANALYSIS, WHAT IS IN THE FUTURE?. , 2018, , .		1
32	Deep Learning data integration for better risk stratification models of bladder cancer. AMIA Summits on Translational Science Proceedings, 2018, 2017, 197-206.	0.4	18
33	Pan-cancer analysis of expressed somatic nucleotide variants in long intergenic non-coding RNA. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 512-523.	0.7	1
34	THE TRAINING OF NEXT GENERATION DATA SCIENTISTS IN BIOMEDICINE. , 2017, 22, 640-645.		9
35	Celebrating parasites. Nature Genetics, 2017, 49, 483-484.	9.4	25
36	More Is Better: Recent Progress in Multi-Omics Data Integration Methods. Frontiers in Genetics, 2017, 8, 84.	1.1	517

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37	Granatum: a graphical single-cell RNA-Seq analysis pipeline for genomics scientists. Genome Medicine, 2017, 9, 108.	3.6	63
38	Using single‑cell multiple omics approaches to resolve tumor heterogeneity. Clinical and Translational Medicine, 2017, 6, 46.	1.7	73
39	Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer. Oncotarget, 2016, 7, 55249-55263.	0.8	14
40	Time Series miRNA-mRNA integrated analysis reveals critical miRNAs and targets in macrophage polarization. Scientific Reports, 2016, 6, 37446.	1.6	79
41	Novel personalized pathway-based metabolomics models reveal key metabolic pathways for breast cancer diagnosis. Genome Medicine, 2016, 8, 34.	3.6	122
42	Pan-Cancer Analyses Reveal Long Intergenic Non-Coding RNAs Relevant to Tumor Diagnosis, Subtyping and Prognosis. EBioMedicine, 2016, 7, 62-72.	2.7	33
43	Non-coding yet non-trivial: a review on the computational genomics of lincRNAs. BioData Mining, 2015, 8, 44.	2.2	20
44	Genome-scale hypomethylation in the cord blood DNAs associated with early onset preeclampsia. Clinical Epigenetics, 2015, 7, 21.	1.8	41
45	mirMark: a site-level and UTR-level classifier for miRNA target prediction. Genome Biology, 2014, 15, 500.	3.8	40
46	A Novel Model to Combine Clinical and Pathway-Based Transcriptomic Information for the Prognosis Prediction of Breast Cancer. PLoS Computational Biology, 2014, 10, e1003851.	1.5	64
47	Genome-wide hypermethylation coupled with promoter hypomethylation in the chorioamniotic membranes of early onset pre-eclampsia. Molecular Human Reproduction, 2014, 20, 885-904.	1.3	54
48	Power analysis and sample size estimation for RNA-Seq differential expression. Rna, 2014, 20, 1684-1696.	1.6	204
49	Co-detection and sequencing of genes and transcripts from the same single cells facilitated by a microfluidics platform. Scientific Reports, 2014, 4, 6485.	1.6	65
50	The poor performance of TMM on microRNA-Seq. Rna, 2013, 19, 735-736.	1.6	7
51	A Global Clustering Algorithm to Identify Long Intergenic Non-Coding RNA - with Applications in Mouse Macrophages. PLoS ONE, 2011, 6, e24051.	1.1	27