

Lana X Garmire

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

3,562
citations

218677

26
h-index

206112

48
g-index

69
all docs

69
docs citations

69
times ranked

6458
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep Learning-Based Multi-Omics Integration Robustly Predicts Survival in Liver Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 1248-1259.	7.0	670
2	More Is Better: Recent Progress in Multi-Omics Data Integration Methods. <i>Frontiers in Genetics</i> , 2017, 8, 84.	2.3	517
3	Cox-nnet: An artificial neural network method for prognosis prediction of high-throughput omics data. <i>PLoS Computational Biology</i> , 2018, 14, e1006076.	3.2	241
4	Power analysis and sample size estimation for RNA-Seq differential expression. <i>Rna</i> , 2014, 20, 1684-1696.	3.5	204
5	DeepImpute: an accurate, fast, and scalable deep neural network method to impute single-cell RNA-seq data. <i>Genome Biology</i> , 2019, 20, 211.	8.8	185
6	Deep Learning Accurately Predicts Estrogen Receptor Status in Breast Cancer Metabolomics Data. <i>Journal of Proteome Research</i> , 2018, 17, 337-347.	3.7	176
7	Novel personalized pathway-based metabolomics models reveal key metabolic pathways for breast cancer diagnosis. <i>Genome Medicine</i> , 2016, 8, 34.	8.2	122
8	DeepProg: an ensemble of deep-learning and machine-learning models for prognosis prediction using multi-omics data. <i>Genome Medicine</i> , 2021, 13, 112.	8.2	90
9	Recommendations to enhance rigor and reproducibility in biomedical research. <i>GigaScience</i> , 2020, 9, .	6.4	83
10	Time Series miRNA-mRNA integrated analysis reveals critical miRNAs and targets in macrophage polarization. <i>Scientific Reports</i> , 2016, 6, 37446.	3.3	79
11	Using single-cell multiple omics approaches to resolve tumor heterogeneity. <i>Clinical and Translational Medicine</i> , 2017, 6, 46.	4.0	73
12	Evaluation of Cell Type Annotation R Packages on Single-cell RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 267-281.	6.9	68
13	Co-detection and sequencing of genes and transcripts from the same single cells facilitated by a microfluidics platform. <i>Scientific Reports</i> , 2014, 4, 6485.	3.3	65
14	A Novel Model to Combine Clinical and Pathway-Based Transcriptomic Information for the Prognosis Prediction of Breast Cancer. <i>PLoS Computational Biology</i> , 2014, 10, e1003851.	3.2	64
15	Granatum: a graphical single-cell RNA-Seq analysis pipeline for genomics scientists. <i>Genome Medicine</i> , 2017, 9, 108.	8.2	63
16	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	7.0	57
17	Genome-wide hypermethylation coupled with promoter hypomethylation in the chorioamniotic membranes of early onset pre-eclampsia. <i>Molecular Human Reproduction</i> , 2014, 20, 885-904.	2.8	54
18	Using single nucleotide variations in single-cell RNA-seq to identify subpopulations and genotype-phenotype linkage. <i>Nature Communications</i> , 2018, 9, 4892.	12.8	51

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19	Blood-derived lncRNAs as biomarkers for cancer diagnosis: the Good, the Bad and the Beauty. <i>Npj Precision Oncology</i> , 2022, 6, .	5.4	50
20	A review of omics approaches to study preeclampsia. <i>Placenta</i> , 2020, 92, 17-27.	1.5	48
21	Single cell transcriptome research in human placenta. <i>Reproduction</i> , 2020, 160, R155-R167.	2.6	46
22	Genome-scale hypomethylation in the cord blood DNAs associated with early onset preeclampsia. <i>Clinical Epigenetics</i> , 2015, 7, 21.	4.1	41
23	Multimodal Meta-Analysis of 1,494 Hepatocellular Carcinoma Samples Reveals Significant Impact of Consensus Driver Genes on Phenotypes. <i>Clinical Cancer Research</i> , 2019, 25, 463-472.	7.0	41
24	mirMark: a site-level and UTR-level classifier for miRNA target prediction. <i>Genome Biology</i> , 2014, 15, 500.	8.8	40
25	Computational reconstruction of the signalling networks surrounding implanted biomaterials from single-cell transcriptomics. <i>Nature Biomedical Engineering</i> , 2021, 5, 1228-1238.	22.5	40
26	Evaluation of STAR and Kallisto on Single Cell RNA-Seq Data Alignment. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1775-1783.	1.8	34
27	Pan-Cancer Analyses Reveal Long Intergenic Non-Coding RNAs Relevant to Tumor Diagnosis, Subtyping and Prognosis. <i>EBioMedicine</i> , 2016, 7, 62-72.	6.1	33
28	A Global Clustering Algorithm to Identify Long Intergenic Non-Coding RNA - with Applications in Mouse Macrophages. <i>PLoS ONE</i> , 2011, 6, e24051.	2.5	27
29	Celebrating parasites. <i>Nature Genetics</i> , 2017, 49, 483-484.	21.4	25
30	Lilikoï: an R package for personalized pathway-based classification modeling using metabolomics data. <i>GigaScience</i> , 2018, 7, .	6.4	25
31	Non-coding yet non-trivial: a review on the computational genomics of lincRNAs. <i>BioData Mining</i> , 2015, 8, 44.	4.0	20
32	Two-stage Cox-nnet: biologically interpretable neural-network model for prognosis prediction and its application in liver cancer survival using histopathology and transcriptomic data. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab015.	3.2	18
33	Deep Learning data integration for better risk stratification models of bladder cancer. <i>AMIA Summits on Translational Science Proceedings</i> , 2018, 2017, 197-206.	0.4	18
34	The maternal blood lipidome is indicative of the pathogenesis of severe preeclampsia. <i>Journal of Lipid Research</i> , 2021, 62, 100118.	4.2	17
35	Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer. <i>Oncotarget</i> , 2016, 7, 55249-55263.	1.8	14
36	Placentas delivered by preëpregnant obese women have reduced abundance and diversity in the microbiome. <i>FASEB Journal</i> , 2021, 35, e21524.	0.5	14

#	ARTICLE	IF	CITATIONS
37	Lilikoï V2.0: a deep learning-enabled, personalized pathway-based R package for diagnosis and prognosis predictions using metabolomics data. <i>GigaScience</i> , 2021, 10, .	6.4	12
38	Cox-nnet v2.0: improved neural-network-based survival prediction extended to large-scale EMR data. <i>Bioinformatics</i> , 2021, 37, 2772-2774.	4.1	10
39	THE TRAINING OF NEXT GENERATION DATA SCIENTISTS IN BIOMEDICINE. , 2017, 22, 640-645.		9
40	A Novel FGFR3 Splice Variant Preferentially Expressed in African American Prostate Cancer Drives Aggressive Phenotypes and Docetaxel Resistance. <i>Molecular Cancer Research</i> , 2019, 17, 2115-2125.	3.4	9
41	Maternal plasma lipids are involved in the pathogenesis of preterm birth. <i>GigaScience</i> , 2022, 11, .	6.4	8
42	The poor performance of TMM on microRNA-Seq. <i>Rna</i> , 2013, 19, 735-736.	3.5	7
43	Prepregnant Obesity of Mothers in a Multiethnic Cohort Is Associated with Cord Blood Metabolomic Changes in Offspring. <i>Journal of Proteome Research</i> , 2020, 19, 1361-1374.	3.7	7
44	Maternal cardiovascular-related single nucleotide polymorphisms, genes, and pathways associated with early-onset preeclampsia. <i>PLoS ONE</i> , 2019, 14, e0222672.	2.5	6
45	A Dual-Filtration System for Single-Cell Sequencing of Circulating Tumor Cells and Clusters in HCC. <i>Hepatology Communications</i> , 2022, 6, 1482-1491.	4.3	6
46	Mentorship is not co-authorship: a revisit to mentorship. <i>Genome Biology</i> , 2021, 22, 2.	8.8	5
47	GranatumX: A Community-engaging, Modularized, and Flexible Webtool for Single-cell Data Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 452-460.	6.9	3
48	SINGLE CELL ANALYSIS, WHAT IS IN THE FUTURE?. , 2018, , .		1
49	Pan-cancer analysis of expressed somatic nucleotide variants in long intergenic non-coding RNA. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 512-523.	0.7	1
50	Data Analysis in Single-Cell RNA-Seq. , 2019, , 419-432.		0
51	BML: a versatile web server for bipartite motif discovery. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	0