

Andrea Rau

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,142
citations

430874

18
h-index

395702

33
g-index

47
all docs

47
docs citations

47
times ranked

4552
citing authors

#	ARTICLE	IF	CITATIONS
1	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2013, 14, 671-683.	6.5	1,064
2	Data-based filtering for replicated high-throughput transcriptome sequencing experiments. <i>Bioinformatics</i> , 2013, 29, 2146-2152.	4.1	193
3	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. <i>BMC Biology</i> , 2019, 17, 108.	3.8	109
4	Differential meta-analysis of RNA-seq data from multiple studies. <i>BMC Bioinformatics</i> , 2014, 15, 91.	2.6	99
5	Contribution of mammary epithelial cells to the immune response during early stages of a bacterial infection to <i>Staphylococcus aureus</i> . <i>Veterinary Research</i> , 2014, 45, 16.	3.0	65
6	Co-expression analysis of high-throughput transcriptome sequencing data with Poisson mixture models. <i>Bioinformatics</i> , 2015, 31, 1420-1427.	4.1	64
7	Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 49-59.	2.0	51
8	Transformation and model choice for RNA-seq co-expression analysis. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw128.	6.5	48
9	An Empirical Bayesian Method for Estimating Biological Networks from Temporal Microarray Data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article 9.	0.6	46
10	Synthetic data sets for the identification of key ingredients for RNA-seq differential analysis. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw092.	6.5	40
11	Domestication rewired gene expression and nucleotide diversity patterns in tomato. <i>Plant Journal</i> , 2017, 91, 631-645.	5.7	34
12	Clustering transformed compositional data using <i>t</i> -means, with applications in gene expression and bicycle sharing system data. <i>Journal of Applied Statistics</i> , 2019, 46, 47-65.	1.3	34
13	Transcriptome profiling of the honeybee parasite <i>Varroa destructor</i> provides new biological insights into the mite adult life cycle. <i>BMC Genomics</i> , 2018, 19, 328.	2.8	33
14	A comprehensive overview of bull sperm-borne small non-coding RNAs and their diversity across breeds. <i>Epigenetics and Chromatin</i> , 2020, 13, 19.	3.9	31
15	Compositional Bias in Na ⁺ -ve and Chemically-modified Phage-Displayed Libraries uncovered by Paired-end Deep Sequencing. <i>Scientific Reports</i> , 2018, 8, 1214.	3.3	28
16	Cellular reprogramming for successful CNS axon regeneration is driven by a temporally changing cast of transcription factors. <i>Scientific Reports</i> , 2019, 9, 14198.	3.3	28
17	A Hierarchical Poisson Log-Normal Model for Network Inference from RNA Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e77503.	2.5	24
18	Joint estimation of causal effects from observational and intervention gene expression data. <i>BMC Systems Biology</i> , 2013, 7, 111.	3.0	22

#	ARTICLE	IF	CITATIONS
19	Exploring drivers of gene expression in the Cancer Genome Atlas. <i>Bioinformatics</i> , 2019, 35, 62-68.	4.1	21
20	Impact of the Genetic Background on the Composition of the Chicken Plasma MiRNome in Response to a Stress. <i>PLoS ONE</i> , 2014, 9, e114598.	2.5	19
21	Genetic and transcriptomic analyses provide new insights on the early antiviral response to VHSV in resistant and susceptible rainbow trout. <i>BMC Genomics</i> , 2018, 19, 482.	2.8	17
22	Reverse engineering gene regulatory networks using approximate Bayesian computation. <i>Statistics and Computing</i> , 2012, 22, 1257-1271.	1.5	15
23	An evaluation of the predictive performance and mapping power of the BayesR model for genomic prediction. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	9
24	Mendelian randomization analysis with survival outcomes. <i>Genetic Epidemiology</i> , 2021, 45, 16-23.	1.3	6
25	Identification of a Rat Mammary Tumor Risk Locus That Is Syntenic with the Commonly Amplified 8q12.1 and 8q22.1 Regions in Human Breast Cancer Patients. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1739-1743.	1.8	5
26	Integrated sRNA-seq and RNA-seq Analyses Reveal a microRNA Regulation Network Involved in Cold Response in <i>Pisum sativum</i> L.. <i>Genes</i> , 2022, 13, 1119.	2.4	4
27	Regeneration Rosetta: An Interactive Web Application To Explore Regeneration-Associated Gene Expression and Chromatin Accessibility. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3953-3959.	1.8	3
28	Individualized multi-omic pathway deviation scores using multiple factor analysis. <i>Biostatistics</i> , 2020, , .	1.5	3
29	A limited sample model to predict area under the drug concentration curve for 17-(allylamino)-17-demethoxygeldanamycin and its active metabolite 17-(amino)-17-demethoxygeldanamycin. <i>Cancer Chemotherapy and Pharmacology</i> , 2007, 61, 39-45.	2.3	2
30	A unified linear mixed model for familial relatedness and population structure in genetic association studies. <i>Genetic Epidemiology</i> , 2021, 45, 305-315.	1.3	1
31	Identification of marginal causal relationships in gene networks from observational and interventional expression data. <i>PLoS ONE</i> , 2017, 12, e0171142.	2.5	1
32	Multiview cluster aggregation and splitting, with an application to multiomic breast cancer data. <i>Annals of Applied Statistics</i> , 2020, 14, .	1.1	1
33	Potential genetic robustness of Prnp and Sprn double knockout mouse embryos towards ShRNA-lentiviral inoculation. <i>Veterinary Research</i> , 2022, 53, .	3.0	1
34	A model selection criterion for model-based clustering of annotated gene expression data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 413-28.	0.6	0
35	32 Functional annotation of livestock genomes: chromatin structure and regulation of gene expression. <i>Journal of Animal Science</i> , 2019, 97, 15-16.	0.5	0
36	APPROXIMATE BAYESIAN APPROACHES FOR REVERSE ENGINEERING BIOLOGICAL NETWORKS. <i>Conference on Applied Statistics in Agriculture</i> , 0, , .	0.0	0

#	ARTICLE	IF	CITATIONS
37	Estimation d'effets causaux dans les réseaux de régulation génique. Vers la grande dimension. Revue D'Intelligence Artificielle, 2015, 29, 205-227.	0.6	0