Andrea Rau

List of Publications by Year in descending order

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	Integrated sRNA-seq and RNA-seq Analyses Reveal a microRNA Regulation Network Involved in Cold Response in Pisum sativum L.. Genes, 2022, 13, 1119.	2.4	4
2	Potential genetic robustness of Prnp and Sprn double knockout mouse embryos towards ShRNA-lentiviral inoculation. Veterinary Research, 2022, 53, .	3.0	1
3	Mendelian randomization analysis with survival outcomes. Genetic Epidemiology, 2021, 45, 16-23.	1.3	6
4	A unified linear mixed model for familial relatedness and population structure in genetic association studies. Genetic Epidemiology, 2021, 45, 305-315.	1.3	1
5	An evaluation of the predictive performance and mapping power of the BayesR model for genomic prediction. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	9
6	Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. Journal of Animal Breeding and Genetics, 2020, 137, 49-59.	2.0	51
7	Individualized multi-omic pathway deviation scores using multiple factor analysis. Biostatistics, 2020, , .	1.5	3
8	A comprehensive overview of bull sperm-borne small non-coding RNAs and their diversity across breeds. Epigenetics and Chromatin, 2020, 13, 19.	3.9	31
9	Multiview cluster aggregation and splitting, with an application to multiomic breast cancer data. Annals of Applied Statistics, 2020, 14, .	1.1	1
10	Exploring drivers of gene expression in the Cancer Genome Atlas. Bioinformatics, 2019, 35, 62-68.	4.1	21
11	Cellular reprogramming for successful CNS axon regeneration is driven by a temporally changing cast of transcription factors. Scientific Reports, 2019, 9, 14198.	3.3	28
12	32 Functional annotation of livestock genomes: chromatin structure and regulation of gene expression. Journal of Animal Science, 2019, 97, 15-16.	0.5	0
13	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. G3: Genes, Genomes, Genetics, 2019, 9, 1739-1743.	1.8	5
14	Regeneration Rosetta: An Interactive Web Application To Explore Regeneration-Associated Gene Expression and Chromatin Accessibility. G3: Genes, Genomes, Genetics, 2019, 9, 3953-3959.	1.8	3
15	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	3.8	109
16	Clustering transformed compositional data using K-means, with applications in gene expression and bicycle sharing system data. Journal of Applied Statistics, 2019, 46, 47-65.	1.3	34
17	Synthetic data sets for the identification of key ingredients for RNA-seq differential analysis. Briefings in Bioinformatics, 2018, 19, bbw092.	6.5	40
18	Transformation and model choice for RNA-seq co-expression analysis. Briefings in Bioinformatics, 2018, 19, bbw128.	6.5	48

#	Article	IF	Citations
19	Compositional Bias in Naïve and Chemically-modified Phage-Displayed Libraries uncovered by Paired-end Deep Sequencing. Scientific Reports, 2018, 8, 1214.	3.3	28
20	Transcriptome profiling of the honeybee parasite Varroa destructor provides new biological insights into the mite adult life cycle. BMC Genomics, 2018, 19, 328.	2.8	33
21	Genetic and transcriptomic analyses provide new insights on the early antiviral response to VHSV in resistant and susceptible rainbow trout. BMC Genomics, 2018, 19, 482.	2.8	17
22	Domestication rewired gene expression and nucleotide diversity patterns in tomato. Plant Journal, 2017, 91, 631-645.	5.7	34
23	Identification of marginal causal relationships in gene networks from observational and interventional expression data. PLoS ONE, 2017, 12, e0171142.	2.5	1
24	A model selection criterion for model-based clustering of annotated gene expression data. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 413-28.	0.6	0
25	Co-expression analysis of high-throughput transcriptome sequencing data with Poisson mixture models. Bioinformatics, 2015, 31, 1420-1427.	4.1	64
26	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
27	Contribution of mammary epithelial cells to the immune response during early stages of a bacterial infection to Staphylococcus aureus. Veterinary Research, 2014, 45, 16.	3.0	65
28	Differential meta-analysis of RNA-seq data from multiple studies. BMC Bioinformatics, 2014, 15, 91.	2.6	99
29	Impact of the Genetic Background on the Composition of the Chicken Plasma MiRNome in Response to a Stress. PLoS ONE, 2014, 9, e114598.	2.5	19
30	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. Briefings in Bioinformatics, 2013, 14, 671-683.	6.5	1,064
31	Data-based filtering for replicated high-throughput transcriptome sequencing experiments. Bioinformatics, 2013, 29, 2146-2152.	4.1	193
32	Joint estimation of causal effects from observational and intervention gene expression data. BMC Systems Biology, 2013, 7, 111.	3.0	22
33	A Hierarchical Poisson Log-Normal Model for Network Inference from RNA Sequencing Data. PLoS ONE, 2013, 8, e77503.	2.5	24
34	Reverse engineering gene regulatory networks using approximate Bayesian computation. Statistics and Computing, 2012, 22, 1257-1271.	1.5	15
35	An Empirical Bayesian Method for Estimating Biological Networks from Temporal Microarray Data. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 9.	0.6	46
36	A limited sample model to predict area under the drug concentration curve for 17-(allylamino)-17-demethoxygeldanamycin and its active metabolite 17-(amino)-17-demethoxygeldanomycin. Cancer Chemotherapy and Pharmacology, 2007, 61, 39-45.	2.3	2

#	ARTICLE	IF	CITATIONS
37	APPROXIMATE BAYESIAN APPROACHES FOR REVERSE ENGINEERING BIOLOGICAL NETWORKS. Conference on Applied Statistics in Agriculture, 0, , .	0.0	0