

Ludwig Geistlinger

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

2,574
citations

430874

18
h-index

610901

24
g-index

34
all docs

34
docs citations

34
times ranked

5365
citing authors

#	ARTICLE	IF	CITATIONS
1	Toward a gold standard for benchmarking gene set enrichment analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, 545-556.	6.5	83
2	SIMON: Open-Source Knowledge Discovery Platform. <i>Patterns</i> , 2021, 2, 100178.	5.9	15
3	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. <i>Nature Medicine</i> , 2021, 27, 321-332.	30.7	477
4	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
5	CNVranger: association analysis of CNVs with gene expression and quantitative phenotypes. <i>Bioinformatics</i> , 2020, 36, 972-973.	4.1	17
6	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	19.0	488
7	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma. <i>Cancer Research</i> , 2020, 80, 4335-4345.	0.9	57
8	Multiomic Integration of Public Oncology Databases in Bioconductor. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 958-971.	2.1	42
9	Reliable Analysis of Clinical Tumor-Only Whole-Exome Sequencing Data. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 321-335.	2.1	20
10	Waldron et al. Reply to "Commentary on the HMP16SData Bioconductor Package". <i>American Journal of Epidemiology</i> , 2019, 188, 1031-1032.	3.4	0
11	Tobacco exposure associated with oral microbiota oxygen utilization in the New York City Health and Nutrition Examination Study. <i>Annals of Epidemiology</i> , 2019, 34, 18-25.e3.	1.9	27
12	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 210.	2.3	27
13	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. <i>American Journal of Epidemiology</i> , 2019, 188, 1023-1026.	3.4	30
14	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	3.3	25
15	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. <i>Clinical Cancer Research</i> , 2018, 24, 5037-5047.	7.0	93
16	Micropatterning as a tool to identify regulatory triggers and kinetics of actin-mediated endothelial mechanosensing. <i>Journal of Cell Science</i> , 2018, 131, .	2.0	23
17	Orchestrating a community-developed computational workshop and accompanying training materials. <i>F1000Research</i> , 2018, 7, 1656.	1.6	1
18	Genome-Wide Detection of CNVs and Their Association with Meat Tenderness in Nelore Cattle. <i>PLoS ONE</i> , 2016, 11, e0157711.	2.5	59

#	ARTICLE	IF	CITATIONS
19	Bioconductor's EnrichmentBrowser: seamless navigation through combined results of set- & network-based enrichment analysis. BMC Bioinformatics, 2016, 17, 45.	2.6	79
20	A comprehensive gene regulatory network for the diauxic shift in <i>Saccharomyces cerevisiae</i> . Nucleic Acids Research, 2013, 41, 8452-8463.	14.5	26
21	From sets to graphs: towards a realistic enrichment analysis of transcriptomic systems. Bioinformatics, 2011, 27, i366-i373.	4.1	64
22	Evolution of Protein Phosphorylation for Distinct Functional Modules in Vertebrate Genomes. Molecular Biology and Evolution, 2011, 28, 1131-1140.	8.9	22
23	Genome-Wide Association Study Identifies Two Novel Regions at 11p15.5-p13 and 1p31 with Major Impact on Acute-Phase Serum Amyloid A. PLoS Genetics, 2010, 6, e1001213.	3.5	24
24	Genetics Meets Metabolomics: A Genome-Wide Association Study of Metabolite Profiles in Human Serum. PLoS Genetics, 2008, 4, e1000282.	3.5	660