

Irene Papatheodorou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1086616/publications.pdf>

Version: 2024-02-01

44
papers

10,560
citations

279798

23
h-index

243625

44
g-index

55
all docs

55
docs citations

55
times ranked

21927
citing authors

#	ARTICLE	IF	CITATIONS
1	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2022, 50, D129-D140.	14.5	78
2	The discovAIR project: a roadmap towards the Human Lung Cell Atlas. <i>European Respiratory Journal</i> , 2022, 60, 2102057.	6.7	15
3	Fly Cell Atlas: A single-nucleus transcriptomic atlas of the adult fruit fly. <i>Science</i> , 2022, 375, eabk2432.	12.6	295
4	Integrated view and comparative analysis of baseline protein expression in mouse and rat tissues. <i>PLoS Computational Biology</i> , 2022, 18, e1010174.	3.2	11
5	Implementing the reuse of public DIA proteomics datasets: from the PRIDE database to Expression Atlas. <i>Scientific Data</i> , 2022, 9, .	5.3	13
6	From ArrayExpress to BioStudies. <i>Nucleic Acids Research</i> , 2021, 49, D1502-D1506.	14.5	53
7	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. <i>Nucleic Acids Research</i> , 2021, 49, D1452-D1463.	14.5	83
8	PathExNET: A tool for extracting pathway expression networks from gene expression statistics. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4336-4344.	4.1	2
9	DRscDB: A single-cell RNA-seq resource for data mining and data comparison across species. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2018-2026.	4.1	17
10	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , 2021, 18, 327-328.	19.0	26
11	An integrated landscape of protein expression in human cancer. <i>Scientific Data</i> , 2021, 8, 115.	5.3	38
12	UCSC Cell Browser: visualize your single-cell data. <i>Bioinformatics</i> , 2021, 37, 4578-4580.	4.1	105
13	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. <i>Nature Genetics</i> , 2021, 53, 1290-1299.	21.4	193
14	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	12.8	45
15	Meta-analysis of COVID-19 single-cell studies confirms eight key immune responses. <i>Scientific Reports</i> , 2021, 11, 20833.	3.3	11
16	Single-Cell Analysis Reveals the Immune Characteristics of Myeloid Cells and Memory T Cells in Recovered COVID-19 Patients With Different Severities. <i>Frontiers in Immunology</i> , 2021, 12, 781432.	4.8	13
17	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020, 48, D77-D83.	14.5	363
18	Plant Reactome: a knowledgebase and resource for comparative pathway analysis. <i>Nucleic Acids Research</i> , 2020, 48, D1093-D1103.	14.5	44

#	ARTICLE	IF	CITATIONS
19	Ensembl Genomes 2020“enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	14.5	416
20	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020, 38, 1384-1386.	17.5	27
21	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. <i>GigaScience</i> , 2020, 9, .	6.4	14
22	Comparative Transcriptome Analysis of the Regenerating Zebrafish Telencephalon Unravels a Resource With Key Pathways During Two Early Stages and Activation of Wnt/ β -Catenin Signaling at the Early Wound Healing Stage. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 584604.	3.7	18
23	Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , 2020, 17, 621-628.	19.0	91
24	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020, 11, 3400.	12.8	23
25	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
26	Common and distinct transcriptional signatures of mammalian embryonic lethality. <i>Nature Communications</i> , 2019, 10, 2792.	12.8	16
27	ArrayExpress update “ from bulk to single-cell expression data. <i>Nucleic Acids Research</i> , 2019, 47, D711-D715.	14.5	497
28	Gramene 2018: unifying comparative genomics and pathway resources for plant research. <i>Nucleic Acids Research</i> , 2018, 46, D1181-D1189.	14.5	147
29	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018, 46, D246-D251.	14.5	365
30	Open Targets: a platform for therapeutic target identification and validation. <i>Nucleic Acids Research</i> , 2017, 45, D985-D994.	14.5	355
31	Tools for exploring mouse models of human disease. <i>Drug Discovery Today: Disease Models</i> , 2016, 20, 21-26.	1.2	0
32	Linking gene expression to phenotypes via pathway information. <i>Journal of Biomedical Semantics</i> , 2015, 6, 17.	1.6	26
33	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015, 9, 115-127.	4.6	38
34	Interplay of dFOXO and Two ETS-Family Transcription Factors Determines Lifespan in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2014, 10, e1004619.	3.5	60
35	DAF-16/FoxO Directly Regulates an Atypical AMP-Activated Protein Kinase Gamma Isoform to Mediate the Effects of Insulin/IGF-1 Signaling on Aging in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2014, 10, e1004109.	3.5	55
36	Comparison of the mammalian insulin signalling pathway to invertebrates in the context of FOXO-mediated ageing. <i>Bioinformatics</i> , 2014, 30, 2999-3003.	4.1	15

#	ARTICLE	IF	CITATIONS
37	Using association rule mining to determine promising secondary phenotyping hypotheses. <i>Bioinformatics</i> , 2014, 30, i52-i59.	4.1	9
38	Transcriptional feedback in the insulin signalling pathway modulates ageing in both <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> . <i>Molecular BioSystems</i> , 2013, 9, 1756.	2.9	4
39	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. <i>Nature</i> , 2012, 486, 346-352.	27.8	4,708
40	Using Answer Set Programming to Integrate RNA Expression with Signalling Pathway Information to Infer How Mutations Affect Ageing. <i>PLoS ONE</i> , 2012, 7, e50881.	2.5	13
41	Genome-wide dFOXO targets and topology of the transcriptomic response to stress and insulin signalling. <i>Molecular Systems Biology</i> , 2011, 7, 502.	7.2	112
42	Computational biology for ageing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 51-63.	4.0	35
43	A metadata approach for clinical data management in translational genomics studies in breast cancer. <i>BMC Medical Genomics</i> , 2009, 2, 66.	1.5	26
44	Visualization of microarray results to assist interpretation. <i>Tuberculosis</i> , 2004, 84, 275-281.	1.9	2