

Charlotte Soneson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9016188/publications.pdf>

Version: 2024-02-01

75
papers

14,407
citations

109321

35
h-index

98798

67
g-index

103
all docs

103
docs citations

103
times ranked

25844
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass cytometric and transcriptomic profiling of epithelial-mesenchymal transitions in human mammary cell lines. <i>Scientific Data</i> , 2022, 9, 44.	5.3	5
2	monaLisa: an R/Bioconductor package for identifying regulatory motifs. <i>Bioinformatics</i> , 2022, 38, 2624-2625.	4.1	33
3	Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data. <i>Nature Methods</i> , 2022, 19, 316-322.	19.0	31
4	Hand2 delineates mesothelium progenitors and is reactivated in mesothelioma. <i>Nature Communications</i> , 2022, 13, 1677.	12.8	17
5	A unique bipartite Polycomb signature regulates stimulus-response transcription during development. <i>Nature Genetics</i> , 2021, 53, 379-391.	21.4	16
6	CellMixS: quantifying and visualizing batch effects in single-cell RNA-seq data. <i>Life Science Alliance</i> , 2021, 4, e202001004.	2.8	27
7	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. <i>Genome Biology</i> , 2021, 22, 157.	8.8	7
8	Preprocessing choices affect RNA velocity results for droplet scRNA-seq data. <i>PLoS Computational Biology</i> , 2021, 17, e1008585.	3.2	46
9	MiR-CLIP reveals <i>iso</i>-miR selective regulation in the miR-124 targetome. <i>Nucleic Acids Research</i> , 2021, 49, 25-37.	14.5	10
10	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	19.0	488
11	muscat detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. <i>Nature Communications</i> , 2020, 11, 6077.	12.8	223
12	Alignment and mapping methodology influence transcript abundance estimation. <i>Genome Biology</i> , 2020, 21, 239.	8.8	96
13	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. <i>PLoS Computational Biology</i> , 2020, 16, e1007664.	3.2	165
14	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , 2020, 9, 1246.	1.6	16
15	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , 2020, 9, 1246.	1.6	11
16	ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R. <i>F1000Research</i> , 2020, 9, 512.	1.6	3
17	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
18	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0

#	ARTICLE	IF	CITATIONS
19	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
20	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
21	A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. Nature Communications, 2019, 10, 3359.	12.8	164
22	Essential guidelines for computational method benchmarking. Genome Biology, 2019, 20, 125.	8.8	114
23	ARMOR: An Automated Reproducible Modular Workflow for Preprocessing and Differential Analysis of RNA-seq Data. G3: Genes, Genomes, Genetics, 2019, 9, 2089-2096.	1.8	44
24	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. Communications Biology, 2019, 2, 183.	4.4	162
25	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. Annual Review of Biomedical Data Science, 2019, 2, 139-173.	6.5	101
26	Origin and differentiation trajectories of fibroblastic reticular cells in the splenic white pulp. Nature Communications, 2019, 10, 1739.	12.8	73
27	HDCytoData: Collection of high-dimensional cytometry benchmark datasets in Bioconductor object formats. F1000Research, 2019, 8, 1459.	1.6	13
28	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. Life Science Alliance, 2019, 2, e201800175.	2.8	19
29	Bias, robustness and scalability in single-cell differential expression analysis. Nature Methods, 2018, 15, 255-261.	19.0	592
30	Towards unified quality verification of synthetic count data with <i>countsQC</i> . Bioinformatics, 2018, 34, 691-692.	4.1	40
31	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. Genome Biology, 2018, 19, 24.	8.8	180
32	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	1.6	87
33	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. F1000Research, 2018, 7, 1141.	1.6	157
34	Fibroblastic reticular cells initiate immune responses in visceral adipose tissues and secure peritoneal immunity. Science Immunology, 2018, 3, .	11.9	44
35	iSEE: Interactive SummarizedExperiment Explorer. F1000Research, 2018, 7, 741.	1.6	83
36	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	1.6	63

#	ARTICLE	IF	CITATIONS
37	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 2018, 7, 1141.	1.6	145
38	Broad and Conserved Immune Regulation by Genetically Heterogeneous Melanoma Cells. <i>Cancer Research</i> , 2017, 77, 1623-1636.	0.9	13
39	Human Cactin interacts with DHX8 and SRRM2 to assure efficient pre-mRNA splicing and sister chromatid cohesion. <i>Journal of Cell Science</i> , 2017, 130, 767-778.	2.0	16
40	Faithful mRNA splicing depends on the Prp19 complex subunit <i>faint sausage</i> and is required for tracheal branching morphogenesis in <i>Drosophila</i> . <i>Development (Cambridge)</i> , 2017, 144, 657-663.	2.5	9
41	Caloric dose-responsive genes in blood cells differentiate the metabolic status of obese men. <i>Journal of Nutritional Biochemistry</i> , 2017, 43, 156-165.	4.2	11
42	Increased ex vivo antigen presentation profile of B cells in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2017, 23, 802-809.	3.0	36
43	stageR: a general stage-wise method for controlling the gene-level false discovery rate in differential expression and differential transcript usage. <i>Genome Biology</i> , 2017, 18, 151.	8.8	97
44	A Well-Controlled Experimental System to Study Interactions of Cytotoxic T Lymphocytes with Tumor Cells. <i>Frontiers in Immunology</i> , 2016, 7, 326.	4.8	22
45	iCOBRA: open, reproducible, standardized and live method benchmarking. <i>Nature Methods</i> , 2016, 13, 283-283.	19.0	47
46	Serum neurofilament light chain in early relapsing remitting MS is increased and correlates with CSF levels and with MRI measures of disease severity. <i>Multiple Sclerosis Journal</i> , 2016, 22, 1550-1559.	3.0	202
47	Modulation of mTOR Signalling Triggers the Formation of Stem Cell-like Memory T Cells. <i>EBioMedicine</i> , 2016, 4, 50-61.	6.1	89
48	Isoform prefiltering improves performance of count-based methods for analysis of differential transcript usage. <i>Genome Biology</i> , 2016, 17, 12.	8.8	116
49	A Composite Gene Expression Signature Optimizes Prediction of Colorectal Cancer Metastasis and Outcome. <i>Clinical Cancer Research</i> , 2016, 22, 734-745.	7.0	43
50	Genome-wide RNA profiling of long-lasting stem cell-like memory CD8 T cells induced by Yellow Fever vaccination in humans. <i>Genomics Data</i> , 2015, 5, 297-301.	1.3	11
51	Low Bias Local Intrinsic Dimension Estimation from Expected Simplex Skewness. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2015, 37, 196-202.	13.9	18
52	Long-lasting stem cell-like memory CD8 ⁺ T cells with a naïve-like profile upon yellow fever vaccination. <i>Science Translational Medicine</i> , 2015, 7, 282ra48.	12.4	174
53	Human Mpn1 promotes post-transcriptional processing and stability of U6atac. <i>FEBS Letters</i> , 2015, 589, 2417-2423.	2.8	16
54	The consensus molecular subtypes of colorectal cancer. <i>Nature Medicine</i> , 2015, 21, 1350-1356.	30.7	3,596

#	ARTICLE	IF	CITATIONS
55	Fission yeast Cactin restricts telomere transcription and elongation by controlling Rap1 levels. <i>EMBO Journal</i> , 2015, 34, 115-129.	7.8	22
56	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015, 4, 1521.	1.6	1,848
57	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015, 4, 1521.	1.6	2,612
58	A glioma classification scheme based on coexpression modules of EGFR and PDGFRA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3538-3543.	7.1	93
59	The ABCs of viral hepatitis that define biomarker signatures of acute viral hepatitis. <i>Hepatology</i> , 2014, 59, 1273-1282.	7.3	18
60	Distal and proximal colon cancers differ in terms of molecular, pathological, and clinical features. <i>Annals of Oncology</i> , 2014, 25, 1995-2001.	1.2	498
61	compcodeR – an R package for benchmarking differential expression methods for RNA-seq data. <i>Bioinformatics</i> , 2014, 30, 2517-2518.	4.1	49
62	Incorporation of gene exchangeabilities improves the reproducibility of gene set rankings. <i>Computational Statistics and Data Analysis</i> , 2014, 71, 588-598.	1.2	0
63	Batch Effect Confounding Leads to Strong Bias in Performance Estimates Obtained by Cross-Validation. <i>PLoS ONE</i> , 2014, 9, e100335.	2.5	46
64	A comparison of methods for differential expression analysis of RNA-seq data. <i>BMC Bioinformatics</i> , 2013, 14, 91.	2.6	743
65	A framework for list representation, enabling list stabilization through incorporation of gene exchangeabilities. <i>Biostatistics</i> , 2012, 13, 129-141.	1.5	5
66	Mpn1, Mutated in Poikiloderma with Neutropenia Protein 1, Is a Conserved 3' to-5' RNA Exonuclease Processing U6 Small Nuclear RNA. <i>Cell Reports</i> , 2012, 2, 855-865.	6.4	63
67	The projection score - an evaluation criterion for variable subset selection in PCA visualization. <i>BMC Bioinformatics</i> , 2011, 12, 307.	2.6	39
68	Early changes in the hypothalamic region in prodromal Huntington disease revealed by MRI analysis. <i>Neurobiology of Disease</i> , 2010, 40, 531-543.	4.4	74
69	Integrative analysis of gene expression and copy number alterations using canonical correlation analysis. <i>BMC Bioinformatics</i> , 2010, 11, 191.	2.6	53
70	The correlation pattern of acquired copy number changes in 164 ETV6/RUNX1-positive childhood acute lymphoblastic leukemias. <i>Human Molecular Genetics</i> , 2010, 19, 3150-3158.	2.9	46
71	Optimization of continuous <i>in vivo</i> DOPA production and studies on ectopic DA synthesis using rAAV5 vectors in Parkinsonian rats. <i>Journal of Neurochemistry</i> , 2009, 111, 355-367.	3.9	14
72	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 0, 7, 1141.	1.6	201

#	ARTICLE	IF	CITATIONS
73	HDCytoData: Collection of high-dimensional cytometry benchmark datasets in Bioconductor object formats. F1000Research, 0, 8, 1459.	1.6	3
74	Origin and Differentiation Trajectories of Fibroblastic Reticular Cells in the Splenic White Pulp. SSRN Electronic Journal, 0, , .	0.4	1
75	ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R. F1000Research, 0, 9, 512.	1.6	0