

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	The consensus molecular subtypes of colorectal cancer. <i>Nature Medicine</i> , 2015, 21, 1350-1356.	30.7	3,596
2	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015, 4, 1521.	1.6	2,612
3	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015, 4, 1521.	1.6	1,848
4	A comparison of methods for differential expression analysis of RNA-seq data. <i>BMC Bioinformatics</i> , 2013, 14, 91.	2.6	743
5	Bias, robustness and scalability in single-cell differential expression analysis. <i>Nature Methods</i> , 2018, 15, 255-261.	19.0	592
6	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
7	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	19.0	488
8	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
9	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
10	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 0, 7, 1141.	1.6	201
11	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> , 2018, 19, 24.	8.8	180
12	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
13	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. <i>PLoS Computational Biology</i> , 2020, 16, e1007664.	3.2	165
14	A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. <i>Nature Communications</i> , 2019, 10, 3359.	12.8	164
15	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. <i>Communications Biology</i> , 2019, 2, 183.	4.4	162
16	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 2018, 7, 1141.	1.6	157
17	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 2018, 7, 1141.	1.6	145
18	Isoform prefiltering improves performance of count-based methods for analysis of differential transcript usage. <i>Genome Biology</i> , 2016, 17, 12.	8.8	116

#	ARTICLE	IF	CITATIONS
19	Essential guidelines for computational method benchmarking. <i>Genome Biology</i> , 2019, 20, 125.	8.8	114
20	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 139-173.	6.5	101
21	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
22	Alignment and mapping methodology influence transcript abundance estimation. <i>Genome Biology</i> , 2020, 21, 239.	8.8	96
23	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
24	Modulation of mTOR Signalling Triggers the Formation of Stem Cell-like Memory T Cells. <i>EBioMedicine</i> , 2016, 4, 50-61.	6.1	89
25	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. <i>F1000Research</i> , 2018, 7, 952.	1.6	87
26	iSEE: Interactive SummarizedExperiment Explorer. <i>F1000Research</i> , 2018, 7, 741.	1.6	83
27	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
28	Origin and differentiation trajectories of fibroblastic reticular cells in the splenic white pulp. <i>Nature Communications</i> , 2019, 10, 1739.	12.8	73
29	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
30	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. <i>F1000Research</i> , 2018, 7, 952.	1.6	63
31	Integrative analysis of gene expression and copy number alterations using canonical correlation analysis. <i>BMC Bioinformatics</i> , 2010, 11, 191.	2.6	53
32	compcodeR—an R package for benchmarking differential expression methods for RNA-seq data. <i>Bioinformatics</i> , 2014, 30, 2517-2518.	4.1	49
33	iCOBRA: open, reproducible, standardized and live method benchmarking. <i>Nature Methods</i> , 2016, 13, 283-283.	19.0	47
34	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
35	Preprocessing choices affect RNA velocity results for droplet scRNA-seq data. <i>PLoS Computational Biology</i> , 2021, 17, e1008585.	3.2	46
36	Batch Effect Confounding Leads to Strong Bias in Performance Estimates Obtained by Cross-Validation. <i>PLoS ONE</i> , 2014, 9, e100335.	2.5	46

#	ARTICLE	IF	CITATIONS
37	Fibroblastic reticular cells initiate immune responses in visceral adipose tissues and secure peritoneal immunity. <i>Science Immunology</i> , 2018, 3, .	11.9	44
38	ARMOR: An Automated Reproducible Modular Workflow for Preprocessing and Differential Analysis of RNA-seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2089-2096.	1.8	44
39	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
40	Towards unified quality verification of synthetic count data with <code>countsQC</code> . <i>Bioinformatics</i> , 2018, 34, 691-692.	4.1	40
41	The projection score - an evaluation criterion for variable subset selection in PCA visualization. <i>BMC Bioinformatics</i> , 2011, 12, 307.	2.6	39
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	monaLisa: an R/Bioconductor package for identifying regulatory motifs. <i>Bioinformatics</i> , 2022, 38, 2624-2625.	4.1	33
44	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
45	CellMixS: quantifying and visualizing batch effects in single-cell RNA-seq data. <i>Life Science Alliance</i> , 2021, 4, e202001004.	2.8	27
46	Fission yeast Cactin restricts telomere transcription and elongation by controlling Rap1 levels. <i>EMBO Journal</i> , 2015, 34, 115-129.	7.8	22
47	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
48	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. <i>Life Science Alliance</i> , 2019, 2, e201800175.	2.8	19
49	The ABCs of viral hepatitis that define biomarker signatures of acute viral hepatitis. <i>Hepatology</i> , 2014, 59, 1273-1282.	7.3	18
50	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
51	Hand2 delineates mesothelium progenitors and is reactivated in mesothelioma. <i>Nature Communications</i> , 2022, 13, 1677.	12.8	17
52	Human Mpn1 promotes post-transcriptional processing and stability of U6atac. <i>FEBS Letters</i> , 2015, 589, 2417-2423.	2.8	16
53	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
54	A unique bipartite Polycomb signature regulates stimulus-response transcription during development. <i>Nature Genetics</i> , 2021, 53, 379-391.	21.4	16

#	ARTICLE	IF	CITATIONS
55	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	1.6	16
56	Optimization of continuous <i>in vivo</i> DOPA production and studies on ectopic DA synthesis using rAAV5 vectors in Parkinsonian rats. Journal of Neurochemistry, 2009, 111, 355-367.	3.9	14
57	Broad and Conserved Immune Regulation by Genetically Heterogeneous Melanoma Cells. Cancer Research, 2017, 77, 1623-1636.	0.9	13
58	HDCytoData: Collection of high-dimensional cytometry benchmark datasets in Bioconductor object formats. F1000Research, 2019, 8, 1459.	1.6	13
59	Genome-wide RNA profiling of long-lasting stem cell-like memory CD8 T cells induced by Yellow Fever vaccination in humans. Genomics Data, 2015, 5, 297-301.	1.3	11
60	Caloric dose-responsive genes in blood cells differentiate the metabolic status of obese men. Journal of Nutritional Biochemistry, 2017, 43, 156-165.	4.2	11
61	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	1.6	11
62	MiR-CLIP reveals <i>iso</i> -miR selective regulation in the miR-124 targetome. Nucleic Acids Research, 2021, 49, 25-37.	14.5	10
63	Faithful mRNA splicing depends on the Prp19 complex subunit <i>faint sausage</i> and is required for tracheal branching morphogenesis in <i>Drosophila</i> . Development (Cambridge), 2017, 144, 657-663.	2.5	9
64	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. Genome Biology, 2021, 22, 157.	8.8	7
65	A framework for list representation, enabling list stabilization through incorporation of gene exchangeabilities. Biostatistics, 2012, 13, 129-141.	1.5	5
66	Mass cytometric and transcriptomic profiling of epithelial-mesenchymal transitions in human mammary cell lines. Scientific Data, 2022, 9, 44.	5.3	5
67	HDCytoData: Collection of high-dimensional cytometry benchmark datasets in Bioconductor object formats. F1000Research, 0, 8, 1459.	1.6	3
68	ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R. F1000Research, 2020, 9, 512.	1.6	3
69	Origin and Differentiation Trajectories of Fibroblastic Reticular Cells in the Splenic White Pulp. SSRN Electronic Journal, 0, , .	0.4	1
70	Incorporation of gene exchangeabilities improves the reproducibility of gene set rankings. Computational Statistics and Data Analysis, 2014, 71, 588-598.	1.2	0
71	ExploreModelMatrix: Interactive exploration for improved understanding of design matrices and linear models in R. F1000Research, 0, 9, 512.	1.6	0
72	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0

#	ARTICLE	IF	CITATIONS
73	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
74	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
75	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0