

Davide Risso

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

9,083
citations

185998

28
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253896

43
g-index

74
all docs

74
docs citations

74
times ranked

16840
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | <i>NewWave</i> : a scalable R/Bioconductor package for the dimensionality reduction and batch effect removal of single-cell RNA-seq data. <i>Bioinformatics</i> , 2022, 38, 2648-2650. | 1.8 | 3 |
| 2 | <i>SpatialExperiment</i> : infrastructure for spatially-resolved transcriptomics data in R using Bioconductor. <i>Bioinformatics</i> , 2022, 38, 3128-3131. | 1.8 | 48 |
| 3 | <i>mbkmeans</i> : Fast clustering for single cell data using mini-batch k-means. <i>PLoS Computational Biology</i> , 2021, 17, e1008625. | 1.5 | 36 |
| 4 | A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. <i>Nature Communications</i> , 2021, 12, 463. | 5.8 | 109 |
| 5 | Normalization of Single-Cell RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2021, 2284, 303-329. | 0.4 | 4 |
| 6 | Per-sample standardization and asymmetric winsorization lead to accurate clustering of RNA-seq expression profiles. <i>Bioinformatics</i> , 2021, 37, 2356-2364. | 1.8 | 4 |
| 7 | <i>PsiNorm</i> : a scalable normalization for single-cell RNA-seq data. <i>Bioinformatics</i> , 2021, 38, 164-172. | 1.8 | 14 |
| 8 | A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110. | 13.7 | 166 |
| 9 | A mouse-specific retrotransposon drives a conserved <i>Cdk2ap1</i> isoform essential for development. <i>Cell</i> , 2021, 184, 5541-5558.e22. | 13.5 | 52 |
| 10 | A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102. | 13.7 | 316 |
| 11 | Rapid non-uniform adaptation to conformation-specific KRAS(G12C) inhibition. <i>Nature</i> , 2020, 577, 421-425. | 13.7 | 321 |
| 12 | Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145. | 9.0 | 488 |
| 13 | Editorial: Multi-omic Data Integration in Oncology. <i>Frontiers in Oncology</i> , 2020, 10, 1768. | 1.3 | 2 |
| 14 | Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. <i>Genome Biology</i> , 2020, 21, 191. | 3.8 | 67 |
| 15 | Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. <i>Science Advances</i> , 2020, 6, . | 4.7 | 865 |
| 16 | Abstract 622: Rapid non-uniform adaptation to conformation-specific KRAS G12C inhibition. , 2020, , . | | 1 |
| 17 | Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580. | 13.7 | 195 |
| 18 | Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. <i>Cell Systems</i> , 2019, 8, 315-328.e8. | 2.9 | 117 |

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|----|--|-----|-----------|
| 19 | Shank3 modulates sleep and expression of circadian transcription factors. <i>ELife</i> , 2019, 8, . | 2.8 | 62 |
| 20 | Complementary networks of cortical somatostatin interneurons enforce layer specific control. <i>ELife</i> , 2019, 8, . | 2.8 | 89 |
| 21 | Abstract 909: Single-cell transcriptomic profiling of non-small cell lung cancer uncovers inter- and intracell population structure across TCGA lung adenocarcinoma and lung squamous cancer subtypes. , 2019, , . | | 0 |
| 22 | Abstract LB-A04: Rapid non-uniform adaptation to conformation-specific KRAS G12C inhibition. , 2019, , . | | 1 |
| 23 | Learning-dependent chromatin remodeling highlights noncoding regulatory regions linked to autism. <i>Science Signaling</i> , 2018, 11, . | 1.6 | 25 |
| 24 | A general and flexible method for signal extraction from single-cell RNA-seq data. <i>Nature Communications</i> , 2018, 9, 284. | 5.8 | 540 |
| 25 | Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> , 2018, 19, 24. | 3.8 | 180 |
| 26 | clusterExperiment and RSEC: A Bioconductor package and framework for clustering of single-cell and other large gene expression datasets. <i>PLoS Computational Biology</i> , 2018, 14, e1006378. | 1.5 | 48 |
| 27 | Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. <i>BMC Genomics</i> , 2018, 19, 477. | 1.2 | 1,562 |
| 28 | Combinatorial Expression of <i>Grp</i> and <i>Neurod6</i> Defines Dopamine Neuron Populations with Distinct Projection Patterns and Disease Vulnerability. <i>ENeuro</i> , 2018, 5, ENEURO.0152-18.2018. | 0.9 | 47 |
| 29 | Multimodal Single-Cell Profiling Defines the Epigenetic Determinants of Chronic Lymphocytic Leukemia Evolution. <i>Blood</i> , 2018, 132, 1312-1312. | 0.6 | 0 |
| 30 | Deficiency of microRNA <i>miR-34a</i> expands cell fate potential in pluripotent stem cells. <i>Science</i> , 2017, 355, . | 6.0 | 129 |
| 31 | Normalizing single-cell RNA sequencing data: challenges and opportunities. <i>Nature Methods</i> , 2017, 14, 565-571. | 9.0 | 405 |
| 32 | Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution. <i>Cell Stem Cell</i> , 2017, 20, 817-830.e8. | 5.2 | 164 |
| 33 | Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities. <i>Cell Stem Cell</i> , 2017, 21, 775-790.e9. | 5.2 | 67 |
| 34 | Bioconductor workflow for single-cell RNA sequencing: Normalization, dimensionality reduction, clustering, and lineage inference. <i>F1000Research</i> , 2017, 6, 1158. | 0.8 | 13 |
| 35 | Contextual fear conditioning induces differential alternative splicing. <i>Neurobiology of Learning and Memory</i> , 2016, 134, 221-235. | 1.0 | 28 |
| 36 | Removal of unwanted variation reveals novel patterns of gene expression linked to sleep homeostasis in murine cortex. <i>BMC Genomics</i> , 2016, 17, 727. | 1.2 | 41 |

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|----|--|-----|-----------|
| 37 | Comparison of computed tomography and magnetic resonance imaging in the discrimination of intraperitoneal and extraperitoneal rectal cancer: initial experience. <i>Clinical Imaging</i> , 2016, 40, 57-62. | 0.8 | 3 |
| 38 | How data analysis affects power, reproducibility and biological insight of RNA-seq studies in complex datasets. <i>Nucleic Acids Research</i> , 2015, 43, 7664-7674. | 6.5 | 90 |
| 39 | The Role of Spike-In Standards in the Normalization of RNA-seq. , 2014, , 169-190. | | 8 |
| 40 | Silencing of Odorant Receptor Genes by G Protein $\beta\gamma$ Signaling Ensures the Expression of One Odorant Receptor per Olfactory Sensory Neuron. <i>Neuron</i> , 2014, 81, 847-859. | 3.8 | 47 |
| 41 | Normalization of RNA-seq data using factor analysis of control genes or samples. <i>Nature Biotechnology</i> , 2014, 32, 896-902. | 9.4 | 1,570 |
| 42 | A Hierarchical Bayesian Model for RNA-Seq Data. <i>Contributions To Statistics</i> , 2013, , 215-227. | 0.2 | 0 |
| 43 | GC-Content Normalization for RNA-Seq Data. <i>BMC Bioinformatics</i> , 2011, 12, 480. | 1.2 | 712 |
| 44 | A novel approach to the clustering of microarray data via nonparametric density estimation. <i>BMC Bioinformatics</i> , 2011, 12, 49. | 1.2 | 16 |
| 45 | Statistical Test of Expression Pattern (STEPath): a new strategy to integrate gene expression data with genomic information in individual and meta-analysis studies. <i>BMC Bioinformatics</i> , 2011, 12, 92. | 1.2 | 4 |
| 46 | A modified LOESS normalization applied to microRNA arrays: a comparative evaluation. <i>Bioinformatics</i> , 2009, 25, 2685-2691. | 1.8 | 49 |
| 47 | A-MADMAN: Annotation-based microarray data meta-analysis tool. <i>BMC Bioinformatics</i> , 2009, 10, 201. | 1.2 | 38 |
| 48 | A comparison on effects of normalisations in the detection of differentially expressed genes. <i>BMC Bioinformatics</i> , 2009, 10, 61. | 1.2 | 15 |