

# 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  
h-index

253896

43  
g-index

74  
all docs

74  
docs citations

74  
times ranked

16840  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. <i>BMC Genomics</i> , 2018, 19, 477.	1.2	1,562
3	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
4	GC-Content Normalization for RNA-Seq Data. <i>BMC Bioinformatics</i> , 2011, 12, 480.	1.2	712
5	A general and flexible method for signal extraction from single-cell RNA-seq data. <i>Nature Communications</i> , 2018, 9, 284.	5.8	540
6	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	9.0	488
7	Normalizing single-cell RNA sequencing data: challenges and opportunities. <i>Nature Methods</i> , 2017, 14, 565-571.	9.0	405
8	Rapid non-uniform adaptation to conformation-specific KRAS(G12C) inhibition. <i>Nature</i> , 2020, 577, 421-425.	13.7	321
9	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316
10	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580.	13.7	195
11	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> , 2018, 19, 24.	3.8	180
12	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
13	Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution. <i>Cell Stem Cell</i> , 2017, 20, 817-830.e8.	5.2	164
14	Deficiency of microRNA <i>miR-34a</i> expands cell fate potential in pluripotent stem cells. <i>Science</i> , 2017, 355, .	6.0	129
15	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. <i>Cell Systems</i> , 2019, 8, 315-328.e8.	2.9	117
16	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
17	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
18	Complementary networks of cortical somatostatin interneurons enforce layer specific control. <i>ELife</i> , 2019, 8, .	2.8	89

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19	Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities. <i>Cell Stem Cell</i> , 2017, 21, 775-790.e9.	5.2	67
20	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
21	Shank3 modulates sleep and expression of circadian transcription factors. <i>ELife</i> , 2019, 8, .	2.8	62
22	A mouse-specific retrotransposon drives a conserved Cdk2ap1 isoform essential for development. <i>Cell</i> , 2021, 184, 5541-5558.e22.	13.5	52
23	A modified LOESS normalization applied to microRNA arrays: a comparative evaluation. <i>Bioinformatics</i> , 2009, 25, 2685-2691.	1.8	49
24	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
25	SpatialExperiment: infrastructure for spatially-resolved transcriptomics data in R using Bioconductor. <i>Bioinformatics</i> , 2022, 38, 3128-3131.	1.8	48
26	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
27	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
28	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
29	A-MADMAN: Annotation-based microarray data meta-analysis tool. <i>BMC Bioinformatics</i> , 2009, 10, 201.	1.2	38
30	mbkmeans: Fast clustering for single cell data using mini-batch k-means. <i>PLoS Computational Biology</i> , 2021, 17, e1008625.	1.5	36
31	Contextual fear conditioning induces differential alternative splicing. <i>Neurobiology of Learning and Memory</i> , 2016, 134, 221-235.	1.0	28
32	Learning-dependent chromatin remodeling highlights noncoding regulatory regions linked to autism. <i>Science Signaling</i> , 2018, 11, .	1.6	25
33	A novel approach to the clustering of microarray data via nonparametric density estimation. <i>BMC Bioinformatics</i> , 2011, 12, 49.	1.2	16
34	A comparison on effects of normalisations in the detection of differentially expressed genes. <i>BMC Bioinformatics</i> , 2009, 10, 61.	1.2	15
35	PsiNorm: a scalable normalization for single-cell RNA-seq data. <i>Bioinformatics</i> , 2021, 38, 164-172.	1.8	14
36	Bioconductor workflow for single-cell RNA sequencing: Normalization, dimensionality reduction, clustering, and lineage inference. <i>F1000Research</i> , 2017, 6, 1158.	0.8	13

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37	The Role of Spike-In Standards in the Normalization of RNA-seq. , 2014, , 169-190.		8
38	Statistical Test of Expression Pattern (STEPath): a new strategy to integrate gene expression data with genomic information in individual and meta-analysis studies. BMC Bioinformatics, 2011, 12, 92.	1.2	4
39	Normalization of Single-Cell RNA-Seq Data. Methods in Molecular Biology, 2021, 2284, 303-329.	0.4	4
40	Per-sample standardization and asymmetric winsorization lead to accurate clustering of RNA-seq expression profiles. Bioinformatics, 2021, 37, 2356-2364.	1.8	4
41	Comparison of computed tomography and magnetic resonance imaging in the discrimination of intraperitoneal and extraperitoneal rectal cancer: initial experience. Clinical Imaging, 2016, 40, 57-62.	0.8	3
42	<i>NewWave</i> : a scalable R/Bioconductor package for the dimensionality reduction and batch effect removal of single-cell RNA-seq data. Bioinformatics, 2022, 38, 2648-2650.	1.8	3
43	Editorial: Multi-omic Data Integration in Oncology. Frontiers in Oncology, 2020, 10, 1768.	1.3	2
44	Abstract LB-A04: Rapid non-uniform adaptation to conformation-specific KRAS G12C inhibition. , 2019, , .		1
45	Abstract 622: Rapid non-uniform adaptation to conformation-specific KRAS G12C inhibition. , 2020, , .		1
46	A Hierarchical Bayesian Model for RNA-Seq Data. Contributions To Statistics, 2013, , 215-227.	0.2	0
47	Multimodal Single-Cell Profiling Defines the Epigenetic Determinants of Chronic Lymphocytic Leukemia Evolution. Blood, 2018, 132, 1312-1312.	0.6	0
48	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