Fabian J. Theis

List of Publications by Year
in descending order

428 papers	44,935 citations	3334 91 h-index	3915 177 g-index
539 all docs	539 docs citations	539 times ranked	56846 citing authors

#	Article	IF	Citations
1	SCANPY: large-scale single-cell gene expression data analysis. Genome Biology, 2018, 19, 15.	8.8	3,958
2	SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. Cell, 2020, 181, 1016-1035.e19.	28.9	1,956
3	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
4	Generalizing RNA velocity to transient cell states through dynamical modeling. Nature Biotechnology, 2020, 38, 1408-1414.	17.5	1,460
5	Current best practices in single‐cell RNA‐seq analysis: a tutorial. Molecular Systems Biology, 2019, 15, e8746.	7.2	1,322
6	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. Cell, 2020, 182, 1419-1440.e23.	28.9	1,162
7	An atlas of genetic influences on human blood metabolites. Nature Genetics, 2014, 46, 543-550.	21.4	1,084
8	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. Nature Biotechnology, 2015, 33, 155-160.	17.5	1,068
9	Diffusion pseudotime robustly reconstructs lineage branching. Nature Methods, 2016, 13, 845-848.	19.0	982
10	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. Genome Biology, 2019, 20, 59.	8.8	911
11	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
12	Deep learning: new computational modelling techniques for genomics. Nature Reviews Genetics, 2019, 20, 389-403.	16.3	717
13	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
14	Single-cell RNA-seq denoising using a deep count autoencoder. Nature Communications, 2019, 10, 390.	12.8	668
15	A cellular census of human lungs identifies novel cell states in health and in asthma. Nature Medicine, 2019, 25, 1153-1163.	30.7	631
16	Diffusion maps for high-dimensional single-cell analysis of differentiation data. Bioinformatics, 2015, 31, 2989-2998.	4.1	576
17	<i>destiny</i>: diffusion maps for large-scale single-cell data in R. Bioinformatics, 2016, 32, 1241-1243.	4.1	518
18	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. Nature Communications, 2019, 10, 963.	12.8	408

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19	Benchmarking atlas-level data integration in single-cell genomics. Nature Methods, 2022, 19, 41-50.	19.0	403
20	Cell type atlas and lineage tree of a whole complex animal by single-cell transcriptomics. Science, 2018, 360, .	12.6	381
21	Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. Nature Communications, 2020, 11, 3559.	12.8	378
22	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. Cell Stem Cell, 2015, 16, 712-724.	11.1	376
23	Swarm Learning for decentralized and confidential clinical machine learning. Nature, 2021, 594, 265-270.	27.8	375
24	Decoding the regulatory network of early blood development from single-cell gene expression measurements. Nature Biotechnology, 2015, 33, 269-276.	17.5	352
25	Live imaging of astrocyte responses to acute injury reveals selective juxtavascular proliferation. Nature Neuroscience, 2013, 16, 580-586.	14.8	340
26	Discovery of Sexual Dimorphisms in Metabolic and Genetic Biomarkers. PLoS Genetics, 2011, 7, e1002215.	3.5	328
27	Hypergraphs and Cellular Networks. PLoS Computational Biology, 2009, 5, e1000385.	3.2	316
28	Squidpy: a scalable framework for spatial omics analysis. Nature Methods, 2022, 19, 171-178.	19.0	308
29	scGen predicts single-cell perturbation responses. Nature Methods, 2019, 16, 715-721.	19.0	290
30	Epigenetic germline inheritance of diet-induced obesity and insulin resistance. Nature Genetics, 2016, 48, 497-499.	21.4	287
31	CellRank for directed single-cell fate mapping. Nature Methods, 2022, 19, 159-170.	19.0	286
32	Sparse Component Analysis and Blind Source Separation of Underdetermined Mixtures. IEEE Transactions on Neural Networks, 2005, 16, 992-996.	4.2	280
33	A test metric for assessing single-cell RNA-seq batch correction. Nature Methods, 2019, 16, 43-49.	19.0	278
34	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis. Cell, 2021, 184, 6243-6261.e27.	28.9	277
35	MicroRNA Loss Enhances Learning and Memory in Mice. Journal of Neuroscience, 2010, 30, 14835-14842.	3.6	276
36	Lessons Learned from Quantitative Dynamical Modeling in Systems Biology. PLoS ONE, 2013, 8, e74335.	2.5	275

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37	The dynamic range of the human metabolome revealed by challenges. FASEB Journal, 2012, 26, 2607-2619.	0.5	268
38	Gaussian graphical modeling reconstructs pathway reactions from high-throughput metabolomics data. BMC Systems Biology, 2011, 5, 21.	3.0	262
39	Ultra‐high sensitivity mass spectrometry quantifies single‐cell proteome changes upon perturbation. Molecular Systems Biology, 2022, 18, e10798.	7.2	261
40	Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. Nature Cell Biology, 2013, 15, 363-372.	10.3	257
41	PhenomiR: a knowledgebase for microRNA expression in diseases and biological processes. Genome Biology, 2010, 11, R6.	9.6	247
42	Label-free cell cycle analysis for high-throughput imaging flow cytometry. Nature Communications, 2016, 7, 10256.	12.8	237
43	Mapping single-cell data to reference atlases by transfer learning. Nature Biotechnology, 2022, 40, 121-130.	17.5	236
44	STATISTICAL METHODS FOR THE ANALYSIS OF HIGH-THROUGHPUT METABOLOMICS DATA. Computational and Structural Biotechnology Journal, 2013, 4, e201301009.	4.1	228
45	Gender-specific pathway differences in the human serum metabolome. Metabolomics, 2015, 11, 1815-1833.	3.0	218
46	A Python library for probabilistic analysis of single-cell omics data. Nature Biotechnology, 2022, 40, 163-166.	17.5	216
47	A BaSiC tool for background and shading correction of optical microscopy images. Nature Communications, 2017, 8, 14836.	12.8	213
48	Transforming Boolean models to continuous models: methodology and application to T-cell receptor signaling. BMC Systems Biology, 2009, 3, 98.	3.0	212
49	Next-generation sequencing reveals novel differentially regulated mRNAs, lncRNAs, miRNAs, sdRNAs and a piRNA in pancreatic cancer. Molecular Cancer, 2015, 14, 94.	19.2	210
50	Reconstructing cell cycle and disease progression using deep learning. Nature Communications, 2017, 8, 463.	12.8	210
51	Evaluation of Deep Learning Strategies for Nucleus Segmentation in Fluorescence Images. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 952-965.	1.5	205
52	Transcriptional Mechanisms of Proneural Factors and REST in Regulating Neuronal Reprogramming of Astrocytes. Cell Stem Cell, 2015, 17, 74-88.	11.1	187
53	Early myeloid lineage choice is not initiated by random PU.1 to GATA1 protein ratios. Nature, 2016, 535, 299-302.	27.8	180
54	The Human Lung Cell Atlas: A High-Resolution Reference Map of the Human Lung in Health and Disease. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 31-41.	2.9	178

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55	Concepts and limitations for learning developmental trajectories from single cell genomics. Development (Cambridge), 2019, 146, .	2.5	177
56	Single cells make big data: New challenges and opportunities in transcriptomics. Current Opinion in Systems Biology, 2017, 4, 85-91.	2.6	171
57	Mining the Unknown: A Systems Approach to Metabolite Identification Combining Genetic and Metabolic Information. PLoS Genetics, 2012, 8, e1003005.	3.5	170
58	Intraindividual genome expression analysis reveals a specific molecular signature of psoriasis and eczema. Science Translational Medicine, 2014, 6, 244ra90.	12.4	170
59	Software tools for single-cell tracking and quantification of cellular and molecular properties. Nature Biotechnology, 2016, 34, 703-706.	17.5	162
60	Fast clonal expansion and limited neural stem cell self-renewal in the adult subependymal zone. Nature Neuroscience, 2015, 18, 490-492.	14.8	160
61	Prospective identification of hematopoietic lineage choice by deep learning. Nature Methods, 2017, 14, 403-406.	19.0	160
62	Social Transfer of Pathogenic Fungus Promotes Active Immunisation in Ant Colonies. PLoS Biology, 2012, 10, e1001300.	5.6	158
63	IRE1Î±-XBP1s pathway promotes prostate cancer by activating c-MYC signaling. Nature Communications, 2019, 10, 323.	12.8	158
64	Live imaging of adult neural stem cell behavior in the intact and injured zebrafish brain. Science, 2015, 348, 789-793.	12.6	156
65	Stem-Cell-like Properties and Epithelial Plasticity Arise as Stable Traits after Transient Twist1 Activation. Cell Reports, 2015, 10, 131-139.	6.4	155
66	scSLAM-seq reveals core features of transcription dynamics in single cells. Nature, 2019, 571, 419-423.	27.8	153
67	Integrated intraâ€•and intercellular signaling knowledge for multicellular omics analysis. Molecular Systems Biology, 2021, 17, e9923.	7.2	152
68	The single-cell eQTLGen consortium. ELife, 2020, 9, .	6.0	150
69	Spatial components of molecular tissue biology. Nature Biotechnology, 2022, 40, 308-318.	17.5	148
70	Massive single-cell mRNA profiling reveals a detailed roadmap for pancreatic endocrinogenesis. Development (Cambridge), 2019, 146, .	2.5	145
71	Early IFN-Î± signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. Immunity, 2021, 54, 2650-2669.e14.	14.3	145
72	Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. Metabolomics, 2018, 14, 128.	3.0	138

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73	Hierarchical Differentiation of Myeloid Progenitors Is Encoded in the Transcription Factor Network. PLoS ONE, 2011, 6, e22649.	2.5	137
74	Reconstructing gene regulatory dynamics from high-dimensional single-cell snapshot data. Bioinformatics, 2015, 31, i89-i96.	4.1	134
75	Network plasticity of pluripotency transcription factors in embryonic stem cells. Nature Cell Biology, 2015, 17, 1235-1246.	10.3	130
76	GATA2/3-TFAP2A/C transcription factor network couples human pluripotent stem cell differentiation to trophectoderm with repression of pluripotency. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9579-E9588.	7.1	130
77	RNA velocityâ€"current challenges and future perspectives. Molecular Systems Biology, 2021, 17, e10282.	7.2	130
78	Erythropoietin enhances hippocampal long-term potentiation and memory. BMC Biology, 2008, 6, 37.	3.8	129
79	The signal separation evaluation campaign (2007â€"2010): Achievements and remaining challenges. Signal Processing, 2012, 92, 1928-1936.	3.7	128
80	The proteome landscape of the kingdoms of life. Nature, 2020, 582, 592-596.	27.8	128
81	Intronic microRNAs support their host genes by mediating synergistic and antagonistic regulatory effects. BMC Genomics, 2010, 11, 224.	2.8	126
82	Atrx promotes heterochromatin formation atÂretrotransposons. EMBO Reports, 2015, 16, 836-850.	4.5	126
83	Scalable Parameter Estimation for Genome-Scale Biochemical Reaction Networks. PLoS Computational Biology, 2017, 13, e1005331.	3.2	125
84	The Structure of Borders in a Small World. PLoS ONE, 2010, 5, e15422.	2.5	122
85	On the hypothesis-free testing of metabolite ratios in genome-wide and metabolome-wide association studies. BMC Bioinformatics, 2012, 13, 120.	2.6	121
86	An automatic method for robust and fast cell detection in bright field images from high-throughput microscopy. BMC Bioinformatics, 2013, 14, 297.	2.6	117
87	Blind Source Separation Techniques for the Decomposition of Multiply Labeled Fluorescence Images. Biophysical Journal, 2009, 96, 3791-3800.	0.5	113
88	Feature ranking of type 1 diabetes susceptibility genes improves prediction of type 1 diabetes. Diabetologia, 2014, 57, 2521-2529.	6.3	112
89	Vertex centralities in input-output networks reveal the structure of modern economies. Physical Review E, 2011, 83, 046127.	2.1	110
90	AURKA, DLGAP5, TPX2, KIF11 and CKAP5: Five specific mitosis-associated genes correlate with poor prognosis for non-small cell lung cancer patients. International Journal of Oncology, 2017, 50, 365-372.	3.3	110

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91	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	27.8	108
92	Quantification of regenerative potential in primary human mammary epithelial cells. Development (Cambridge), 2015, 142, 3239-51.	2.5	105
93	Inferring Interaction Networks From Multi-Omics Data. Frontiers in Genetics, 2019, 10, 535.	2.3	105
94	Effects of smoking and smoking cessation on human serum metabolite profile: results from the KORA cohort study. BMC Medicine, 2013, 11, 60.	5.5	103
95	Odefy - From discrete to continuous models. BMC Bioinformatics, 2010, 11, 233.	2.6	102
96	Efficient Parameter Estimation Enables the Prediction of Drug Response Using a Mechanistic Pan-Cancer Pathway Model. Cell Systems, 2018, 7, 567-579.e6.	6.2	99
97	The Human Blood Metabolome-Transcriptome Interface. PLoS Genetics, 2015, 11, e1005274.	3.5	99
98	A Unilateral Negative Feedback Loop Between<i>miR-200</i>microRNAs and Sox2/E2F3 Controls Neural Progenitor Cell-Cycle Exit and Differentiation. Journal of Neuroscience, 2012, 32, 13292-13308.	3.6	98
99	scCODA is a Bayesian model for compositional single-cell data analysis. Nature Communications, 2021, 12, 6876.	12.8	98
100	Body Fat Free Mass Is Associated with the Serum Metabolite Profile in a Population-Based Study. PLoS ONE, 2012, 7, e40009.	2.5	95
101	Systematic single-cell analysis provides new insights into heterogeneity and plasticity of the pancreas. Molecular Metabolism, 2017, 6, 974-990.	6.5	95
102	Joining forces of Bayesian and frequentist methodology: a study for inference in the presence of non-identifiability. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2013, 371, 20110544.	3.4	94
103	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. Nature Communications, 2019, 10, 2548.	12.8	94
104	Targeted pharmacological therapy restores Î²-cell function for diabetes remission. Nature Metabolism, 2020, 2, 192-209.	11.9	93
105	A geometric algorithm for overcomplete linear ICA. Neurocomputing, 2004, 56, 381-398.	5.9	89
106	Method of conditional moments (MCM) for the Chemical Master Equation. Journal of Mathematical Biology, 2014, 69, 687-735.	1.9	86
107	Inferring population dynamics from single-cell RNA-sequencing time series data. Nature Biotechnology, 2019, 37, 461-468.	17.5	85
108	Over 1000 tools reveal trends in the single-cell RNA-seq analysis landscape. Genome Biology, 2021, 22, 301.	8.8	85

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109	Dynamic Mathematical Modeling of IL13-Induced Signaling in Hodgkin and Primary Mediastinal B-Cell Lymphoma Allows Prediction of Therapeutic Targets. Cancer Research, 2011, 71, 693-704.	0.9	82
110	Interleukin-4 and interferon-Î³ orchestrate an epithelial polarization in the airways. Mucosal Immunology, 2016, 9, 917-926.	6.0	81
111	Impulse model-based differential expression analysis of time course sequencing data. Nucleic Acids Research, 2018, 46, e119.	14.5	81
112	Inhibition of LTÎ²R signalling activates WNT-induced regeneration in lung. Nature, 2020, 588, 151-156.	27.8	81
113	Deep learning the collisional cross sections of the peptide universe from a million experimental values. Nature Communications, 2021, 12, 1185.	12.8	81
114	MIPS: curated databases and comprehensive secondary data resources in 2010. Nucleic Acids Research, 2011, 39, D220-D224.	14.5	77
115	Metabolic regulation of pluripotency and germ cell fate through Î±â€ketoglutarate. EMBO Journal, 2019, 38, .	7.8	77
116	Inference for Stochastic Chemical Kinetics Using Moment Equations and System Size Expansion. PLoS Computational Biology, 2016, 12, e1005030.	3.2	77
117	Stability and Multiattractor Dynamics of a Toggle Switch Based on a Two-Stage Model of Stochastic Gene Expression. Biophysical Journal, 2012, 102, 19-29.	0.5	76
118	Hypothalamic miR-103 Protects from Hyperphagic Obesity in Mice. Journal of Neuroscience, 2014, 34, 10659-10674.	3.6	76
119	Zebrafish reward mutants reveal novel transcripts mediating the behavioral effects of amphetamine. Genome Biology, 2009, 10, R81.	9.6	71
120	Integrative genetic and metabolite profiling analysis suggests altered phosphatidylcholine metabolism in asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2013, 68, 629-636.	5.7	70
121	Multi-omic signature of body weight change: results from a population-based cohort study. BMC Medicine, 2015, 13, 48.	5.5	69
122	Predicting antigen specificity of single T cells basedÂon <scp>TCR CDR</scp> 3 regions. Molecular Systems Biology, 2020, 16, e9416.	7.2	68
123	Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. Nature Communications, 2017, 8, 1483.	12.8	67
124	Meeting the Challenges of High-Dimensional Single-Cell Data Analysis in Immunology. Frontiers in Immunology, 2019, 10, 1515.	4.8	67
125	Multi-experiment nonlinear mixed effect modeling of single-cell translation kinetics after transfection. Npj Systems Biology and Applications, 2018, 4, 1.	3.0	66
126	Proteome-wide analysis reveals an age-associated cellular phenotype of in situ aged human fibroblasts. Aging, 2014, 6, 856-872.	3.1	65

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127	The Nature and Perception of Fluctuations in Human Musical Rhythms. PLoS ONE, 2011, 6, e26457.	2.5	63
128	A strategy for combining minor genetic susceptibility genes to improve prediction of disease in type 1 diabetes. Genes and Immunity, 2012, 13, 549-555.	4.1	63
129	Epigenetically Regulated Chromosome 14q32 miRNA Cluster Induces Metastasis and Predicts Poor Prognosis in Lung Adenocarcinoma Patients. Molecular Cancer Research, 2018, 16, 390-402.	3.4	63
130	Parallelization and High-Performance Computing Enables Automated Statistical Inference of Multi-scale Models. Cell Systems, 2017, 4, 194-206.e9.	6.2	62
131	Conditional out-of-distribution generation for unpaired data using transfer VAE. Bioinformatics, 2020, 36, i610-i617.	4.1	62
132	miTALOS v2: Analyzing Tissue Specific microRNA Function. PLoS ONE, 2016, 11, e0151771.	2.5	60
133	EpiScanpy: integrated single-cell epigenomic analysis. Nature Communications, 2021, 12, 5228.	12.8	59
134	fastER: a user-friendly tool for ultrafast and robust cell segmentation in large-scale microscopy. Bioinformatics, 2017, 33, 2020-2028.	4.1	58
135	MPRAnalyze: statistical framework for massively parallel reporter assays. Genome Biology, 2019, 20, 183.	8.8	58
136	MicroRNA-138 promotes acquired alkylator resistance in glioblastoma by targeting the Bcl-2-interacting mediator BIM. Oncotarget, 2016, 7, 12937-12950.	1.8	58
137	Money Circulation, Trackable Items, and the Emergence of Universal Human Mobility Patterns. IEEE Pervasive Computing, 2008, 7, 28-35.	1.3	57
138	A subset of metastatic pancreatic ductal adenocarcinomas depends quantitatively on oncogenic Kras/Mek/Erk-induced hyperactive mTOR signalling. Gut, 2016, 65, 647-657.	12.1	57
139	PhenomiR: MicroRNAs in Human Diseases and Biological Processes. Methods in Molecular Biology, 2012, 822, 249-260.	0.9	57
140	High-dimensional Bayesian parameter estimation: Case study for a model of JAK2/STAT5 signaling. Mathematical Biosciences, 2013, 246, 293-304.	1.9	56
141	Linear Geometric ICA: Fundamentals and Algorithms. Neural Computation, 2003, 15, 419-439.	2.2	54
142	A novel molecular disease classifier for psoriasis and eczema. Experimental Dermatology, 2016, 25, 767-774.	2.9	54
143	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. PLoS Computational Biology, 2020, 16, e1007616.	3.2	54
144	Computational approaches for systems metabolomics. Current Opinion in Biotechnology, 2016, 39, 198-206.	6.6	53

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145	Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. EMBO Molecular Medicine, 2021, 13, e12871.	6.9	53
146	miTALOS: Analyzing the tissue-specific regulation of signaling pathways by human and mouse microRNAs. Rna, 2011, 17, 809-819.	3.5	52
147	Type I Immune Response Induces Keratinocyte Necroptosis and Is Associated with Interface Dermatitis. Journal of Investigative Dermatology, 2018, 138, 1785-1794.	0.7	52
148	Machine learning for perturbational single-cell omics. Cell Systems, 2021, 12, 522-537.	6.2	52
149	Metabolite profiling reveals new insights into the regulation of serum urate in humans. Metabolomics, 2014, 10, 141-151.	3.0	51
150	Identification of a plasma mi<scp>RNA</scp> biomarker signature for allergic asthma: A translational approach. Allergy: European Journal of Allergy and Clinical Immunology, 2017, 72, 1962-1971.	5.7	51
151	A novel approach for resolving differences in single-cell gene expression patterns from zygote to blastocyst. Bioinformatics, 2012, 28, i626-i632.	4.1	50
152	MicroRNAs coordinately regulate protein complexes. BMC Systems Biology, 2011, 5, 136.	3.0	49
153	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	7.7	49
154	Self-supervised retinal thickness prediction enables deep learning from unlabelled data to boost classification of diabetic retinopathy. Nature Machine Intelligence, 2020, 2, 719-726.	16.0	48
155	Diet-induced alteration of intestinal stem cell function underlies obesity and prediabetes in mice. Nature Metabolism, 2021, 3, 1202-1216.	11.9	47
156	Non-canonical Wnt/PCP signalling regulates intestinal stem cell lineage priming towards enteroendocrine and Paneth cell fates. Nature Cell Biology, 2021, 23, 23-31.	10.3	46
157	The Heckscherâ€"Ohlin model and the network structure of international trade. International Review of Economics and Finance, 2011, 20, 135-145.	4.5	44
158	ODE Constrained Mixture Modelling: A Method for Unraveling Subpopulation Structures and Dynamics. PLoS Computational Biology, 2014, 10, e1003686.	3.2	44
159	Toll-like receptor 7/8 agonists stimulate plasmacytoid dendritic cells to initiate TH17-deviated acute contact dermatitis in human subjects. Journal of Allergy and Clinical Immunology, 2018, 141, 1320-1333.e11.	2.9	44
160	AutoGeneS: Automatic gene selection using multi-objective optimization for RNA-seq deconvolution. Cell Systems, 2021, 12, 706-715.e4.	6.2	44
161	Effect of Atmospheric Aging on Soot Particle Toxicity in Lung Cell Models at the Airâ€"Liquid Interface: Differential Toxicological Impacts of Biogenic and Anthropogenic Secondary Organic Aerosols (SOAs). Environmental Health Perspectives, 2022, 130, 27003.	6.0	44
162	Uniqueness of complex and multidimensional independent component analysis. Signal Processing, 2004, 84, 951-956.	3.7	43

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163	Opposing effects of allogrooming on disease transmission in ant societies. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140108.	4.0	43
164	Dynamic landscape of pancreatic carcinogenesis reveals early molecular networks of malignancy. Gut, 2018, 67, 146-156.	12.1	43
165	Post-surgical adhesions are triggered by calcium-dependent membrane bridges between mesothelial surfaces. Nature Communications, 2020, 11, 3068.	12.8	42
166	Protocol of a population-based prospective COVID-19 cohort study Munich, Germany (KoCo19). BMC Public Health, 2020, 20, 1036.	2.9	42
167	Single-cell molecular profiling of all three components of the HPA axis reveals adrenal ABCB1 as a regulator of stress adaptation. Science Advances, 2021, 7, .	10.3	42
168	Wound-healing growth factor, basic FGF, induces Erk1/2-dependent mechanical hyperalgesia. Pain, 2013, 154, 2216-2226.	4.2	41
169	Aldh1b1 expression defines progenitor cells in the adult pancreas and is required for Kras-induced pancreatic cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20679-20688.	7.1	41
170	Epithelial cell plasticity drives endoderm formation during gastrulation. Nature Cell Biology, 2021, 23, 692-703.	10.3	41
171	Cytokine-Regulated GADD45G Induces Differentiation and Lineage Selection in Hematopoietic Stem Cells. Stem Cell Reports, 2014, 3, 34-43.	4.8	40
172	Network-Based Approach for Analyzing Intra- and Interfluid Metabolite Associations in Human Blood, Urine, and Saliva. Journal of Proteome Research, 2015, 14, 1183-1194.	3.7	40
173	Ketamine exerts its sustained antidepressant effects via cell-type-specific regulation of Kcnq2. Neuron, 2022, 110, 2283-2298.e9.	8.1	40
174	Metabolomics screening identifies reduced<scp>L</scp>-carnitine to be associated with progressive emphysema. Clinical Science, 2016, 130, 273-287.	4.3	39
175	The human transcriptome is enriched for miRNA-binding sites located in cooperativity-permitting distance. RNA Biology, 2013, 10, 1125-1135.	3.1	38
176	Maternal whole blood cell miRNA-340 is elevated in gestational diabetes and inversely regulated by glucose and insulin. Scientific Reports, 2018, 8, 1366.	3.3	38
177	scPower accelerates and optimizes the design of multi-sample single cell transcriptomic studies. Nature Communications, 2021, 12, 6625.	12.8	38
178	The Sox17â€mCherry fusion mouse line allows visualization of endoderm and vascular endothelial development. Genesis, 2012, 50, 496-505.	1.6	37
179	Metabolomic profiles in individuals with negative affectivity and social inhibition: A population-based study of Type D personality. Psychoneuroendocrinology, 2013, 38, 1299-1309.	2.7	37
180	Parameterizing cell-to-cell regulatory heterogeneities via stochastic transcriptional profiles. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E626-35.	7.1	37

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181	Data-Driven Modelling of Biological Multi-Scale Processes. Journal of Coupled Systems and Multiscale Dynamics, 2015, 3, 101-121.	0.2	37
182	Knowledge-based gene expression classification via matrix factorization. Bioinformatics, 2008, 24, 1688-1697.	4.1	36
183	Spatial Analysis of Expression Patterns Predicts Genetic Interactions at the Mid-Hindbrain Boundary. PLoS Computational Biology, 2009, 5, e1000569.	3.2	36
184	Separation of Uncorrelated Stationary time series using Autocovariance Matrices. Journal of Time Series Analysis, 2016, 37, 337-354.	1.2	36
185	Parameter estimation for dynamical systems with discrete events and logical operations. Bioinformatics, 2017, 33, 1049-1056.	4.1	36
186	CERENA: ChEmical REaction Network Analyzerâ€"A Toolbox for the Simulation and Analysis of Stochastic Chemical Kinetics. PLoS ONE, 2016, 11, e0146732.	2.5	35
187	Increasing Neural Stem Cell Division Asymmetry and Quiescence Are Predicted to Contribute to the Age-Related Decline in Neurogenesis. Cell Reports, 2018, 25, 3231-3240.e8.	6.4	35
188	Denoising using local projective subspace methods. Neurocomputing, 2006, 69, 1485-1501.	5.9	34
189	Comprehensive benchmarking of Markov chain Monte Carlo methods for dynamical systems. BMC Systems Biology, 2017, 11, 63.	3.0	34
190	ICA over finite fieldsâ€"Separability and algorithms. Signal Processing, 2012, 92, 1796-1808.	3.7	33
191	Uncertainty Analysis for Non-identifiable Dynamical Systems: Profile Likelihoods, Bootstrapping and More. Lecture Notes in Computer Science, 2014, , 61-72.	1.3	33
192	Cell-Type-Specific Impact of Glucocorticoid Receptor Activation on the Developing Brain: A Cerebral Organoid Study. American Journal of Psychiatry, 2022, 179, 375-387.	7.2	33
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