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	Mapping single-cell data to reference atlases by transfer learning. Nature Biotechnology, 2022, 40, 121-130.	17.5	236
2	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
3	Toward modeling metabolic state from single-cell transcriptomics. Molecular Metabolism, 2022, 57, 101396.	6.5	27
4	Integration of single-cell transcriptomes and chromatin landscapes reveals regulatory programs driving pharyngeal organ development. Nature Communications, 2022, 13, 457.	12.8	22
5	Squidpy: a scalable framework for spatial omics analysis. Nature Methods, 2022, 19, 171-178.	19.0	308
6	CellRank for directed single-cell fate mapping. Nature Methods, 2022, 19, 159-170.	19.0	286
7	The discovAIR project: a roadmap towards the Human Lung Cell Atlas. European Respiratory Journal, 2022, 60, 2102057.	6.7	15
8	Effect of Atmospheric Aging on Soot Particle Toxicity in Lung Cell Models at the Air–Liquid Interface: Differential Toxicological Impacts of Biogenic and Anthropogenic Secondary Organic Aerosols (SOAs). Environmental Health Perspectives, 2022, 130, 27003.	6.0	44
9	Spatial components of molecular tissue biology. Nature Biotechnology, 2022, 40, 308-318.	17.5	148
10	A Python library for probabilistic analysis of single-cell omics data. Nature Biotechnology, 2022, 40, 163-166.	17.5	216
11	Benchmarking atlas-level data integration in single-cell genomics. Nature Methods, 2022, 19, 41-50.	19.0	403
12	Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation. Molecular Systems Biology, 2022, 18, e10798.	7.2	261
13	Parkinson's disease motor symptoms rescue by CRISPRa-reprogramming astrocytes into GABAergic neurons. EMBO Molecular Medicine, 2022, 14, e14797.	6.9	26
14	Mature neutrophils and a NFκB-to-IFN transition determine the unifying disease recovery dynamics in COVID-19. Cell Reports Medicine, 2022, , 100652.	6.5	9
15	Ketamine exerts its sustained antidepressant effects via cell-type-specific regulation of Kcnq2. Neuron, 2022, 110, 2283-2298.e9.	8.1	40
16	Ly6D+Siglec-H+ precursors contribute to conventional dendritic cells via a Zbtb46+Ly6D+ intermediary stage. Nature Communications, 2022, 13, .	12.8	7
17	Exposure to naphthalene and β-pinene-derived secondary organic aerosol induced divergent changes in transcript levels of BEAS-2B cells. Environment International, 2022, 166, 107366.	10.0	18
18	Heterogeneous Development of β-Cell Populations in Diabetes-Resistant and -Susceptible Mice. Diabetes, 2022, 71, 1962-1978.	0.6	3

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19	Asthma in farm children is more determined by genetic polymorphisms and in non‐farm children by environmental factors. Pediatric Allergy and Immunology, 2021, 32, 295-304.	2.6	17
20	CD23 Levels on B Cells Determine Long-Term Therapeutic Response in Patients with Atopic Eczema Treated with Selective IgE Immune Apheresis. Journal of Investigative Dermatology, 2021, 141, 681-685.e6.	0.7	1
21	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
22	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
23	Deep learning the collisional cross sections of the peptide universe from a million experimental values. Nature Communications, 2021, 12, 1185.	12.8	81
24	Deep Learning-based Propensity Scores for Confounding Control in Comparative Effectiveness Research. Epidemiology, 2021, 32, 378-388.	2.7	15
25	Asc-1 regulates white versus beige adipocyte fate in a subcutaneous stromal cell population. Nature Communications, 2021, 12, 1588.	12.8	17
26	Posterior subcapsular cataracts are a late effect after acute exposure to 0.5‰Gy ionizing radiation in mice. International Journal of Radiation Biology, 2021, 97, 529-540.	1.8	5
27	Integrated intra‐and intercellular signaling knowledge for multicellular omics analysis. Molecular Systems Biology, 2021, 17, e9923.	7.2	152
28	Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. EMBO Molecular Medicine, 2021, 13, e12871.	6.9	53
29	Comparison of genome-wide gene expression profiling by RNA Sequencing *versus* microarray in bronchial biopsies of COPD patients before and after inhaled corticosteroid treatment: does it provide new insights?. ERJ Open Research, 2021, 7, 00104-2021.	2.6	2
30	Graph representation learning for single-cell biology. Current Opinion in Systems Biology, 2021, 28, 100347.	2.6	15
31	Swarm Learning for decentralized and confidential clinical machine learning. Nature, 2021, 594, 265-270.	27.8	375
32	Cellular connectomes as arbiters of local circuit models in the cerebral cortex. Nature Communications, 2021, 12, 2785.	12.8	11
33	Epithelial cell plasticity drives endoderm formation during gastrulation. Nature Cell Biology, 2021, 23, 692-703.	10.3	41
34	Machine learning for perturbational single-cell omics. Cell Systems, 2021, 12, 522-537.	6.2	52
35	Single-cell RNA sequencing reveals ex vivo signatures of SARS-CoV-2-reactive T cells through 'reverse phenotyping'. Nature Communications, 2021, 12, 4515.	12.8	23
36	AutoGeneS: Automatic gene selection using multi-objective optimization for RNA-seq deconvolution. Cell Systems, 2021, 12, 706-715.e4.	6.2	44

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37	CD81 marks immature and dedifferentiated pancreatic β-cells. Molecular Metabolism, 2021, 49, 101188.	6.5	26
38	Sfaira accelerates data and model reuse in single cell genomics. Genome Biology, 2021, 22, 248.	8.8	18
39	Group Testing for SARS-CoV-2 Allows for Up to 10-Fold Efficiency Increase Across Realistic Scenarios and Testing Strategies. Frontiers in Public Health, 2021, 9, 583377.	2.7	25
40	RNA velocity—current challenges and future perspectives. Molecular Systems Biology, 2021, 17, e10282.	7.2	130
41	Early IFN-α signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. Immunity, 2021, 54, 2650-2669.e14.	14.3	145
42	EpiScanpy: integrated single-cell epigenomic analysis. Nature Communications, 2021, 12, 5228.	12.8	59
43	Diet-induced alteration of intestinal stem cell function underlies obesity and prediabetes in mice. Nature Metabolism, 2021, 3, 1202-1216.	11.9	47
44	Current Smoking Alters Gene Expression and DNA Methylation in the Nasal Epithelium of Patients with Asthma. American Journal of Respiratory Cell and Molecular Biology, 2021, 65, 366-377.	2.9	10
45	Vertical sleeve gastrectomy triggers fast β-cell recovery upon overt diabetes. Molecular Metabolism, 2021, 54, 101330.	6.5	10
46	Identification and characterization of distinct brown adipocyte subtypes in C57BL/6J mice. Life Science Alliance, 2021, 4, e202000924.	2.8	14
47	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	5.6	6
48	Over 1000 tools reveal trends in the single-cell RNA-seq analysis landscape. Genome Biology, 2021, 22, 301.	8.8	85
49	scCODA is a Bayesian model for compositional single-cell data analysis. Nature Communications, 2021, 12, 6876.	12.8	98
50	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis. Cell, 2021, 184, 6243-6261.e27.	28.9	277
51	scPower accelerates and optimizes the design of multi-sample single cell transcriptomic studies. Nature Communications, 2021, 12, 6625.	12.8	38
52	Impact of Brain Fatty Acid Signaling on Peripheral Insulin Action in Mice. Experimental and Clinical Endocrinology and Diabetes, 2020, 128, 20-29.	1.2	2
53	Altered relaxation times in MRI indicate bronchopulmonary dysplasia. Thorax, 2020, 75, 184-187.	5.6	22
54	IL-17C amplifies epithelial inflammation in human psoriasis and atopic eczema. Journal of the European Academy of Dermatology and Venereology, 2020, 34, 800-809.	2.4	26

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55	Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. Nature Communications, 2020, 11, 3559.	12.8	378
56	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	27.8	108
57	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. Cell, 2020, 182, 1419-1440.e23.	28.9	1,162
58	Generalizing RNA velocity to transient cell states through dynamical modeling. Nature Biotechnology, 2020, 38, 1408-1414.	17.5	1,460
59	<i>In vivo</i> identification of apoptotic and extracellular vesicle–bound live cells using image–based deep learning. Journal of Extracellular Vesicles, 2020, 9, 1792683.	12.2	18
60	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
61	Predicting single-cell gene expression profiles of imaging flow cytometry data with machine learning. Nucleic Acids Research, 2020, 48, 11335-11346.	14.5	16
62	Inhibition of LTβR signalling activates WNT-induced regeneration in lung. Nature, 2020, 588, 151-156.	27.8	81
63	Post-surgical adhesions are triggered by calcium-dependent membrane bridges between mesothelial surfaces. Nature Communications, 2020, 11, 3068.	12.8	42
64	The proteome landscape of the kingdoms of life. Nature, 2020, 582, 592-596.	27.8	128
65	Automatic identification of relevant genes from low-dimensional embeddings of single-cell RNA-seq data. Bioinformatics, 2020, 36, 4291-4295.	4.1	7
66	Model-based analysis of response and resistance factors of cetuximab treatment in gastric cancer cell lines. PLoS Computational Biology, 2020, 16, e1007147.	3.2	8
67	Protocol of a population-based prospective COVID-19 cohort study Munich, Germany (KoCo19). BMC Public Health, 2020, 20, 1036.	2.9	42
68	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. PLoS Computational Biology, 2020, 16, e1007616.	3.2	54
69	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
70	Targeted pharmacological therapy restores β-cell function for diabetes remission. Nature Metabolism, 2020, 2, 192-209.	11.9	93
71	Epithelial Planar Bipolarity Emerges from Notch-Mediated Asymmetric Inhibition of Emx2. Current Biology, 2020, 30, 1142-1151.e6.	3.9	25
72	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

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73	A sparse deep learning approach for automatic segmentation of human vasculature in multispectral optoacoustic tomography. Photoacoustics, 2020, 20, 100203.	7.8	26
74	Conditional out-of-distribution generation for unpaired data using transfer VAE. Bioinformatics, 2020, 36, i610-i617.	4.1	62
75	Predicting antigen specificity of single T cells based on <scp>TCR CDR</scp> 3 regions. Molecular Systems Biology, 2020, 16, e9416.	7.2	68
76	The single-cell eQTLGen consortium. ELife, 2020, 9, .	6.0	150
77	Is the humoral immunity dispensable for the pathogenesis of psoriasis?. Journal of the European Academy of Dermatology and Venereology, 2019, 33, 115-122.	2.4	10
78	BART-Seq: cost-effective massively parallelized targeted sequencing for genomics, transcriptomics, and single-cell analysis. Genome Biology, 2019, 20, 155.	8.8	19
79	scGen predicts single-cell perturbation responses. Nature Methods, 2019, 16, 715-721.	19.0	290
80	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
81	scSLAM-seq reveals core features of transcription dynamics in single cells. Nature, 2019, 571, 419-423.	27.8	153
82	Meeting the Challenges of High-Dimensional Single-Cell Data Analysis in Immunology. Frontiers in Immunology, 2019, 10, 1515.	4.8	67
83	GENOTYPE, PRENATAL ENVIRONMENT OR BOTHâ€"WHAT SHAPES THE NEWBORN'S EPIGENOME?. European Neuropsychopharmacology, 2019, 29, S1036-S1037.	0.7	0
84	Concepts and limitations for learning developmental trajectories from single cell genomics. Development (Cambridge), 2019, 146, .	2.5	177
85	F96POLYGENIC RISK SCORE ANALYSIS OF TRAJECTORIES OF COGNITIVE PERFORMANCE IN PSYCHIATRIC PATIENTS. European Neuropsychopharmacology, 2019, 29, S1161.	0.7	0
86	Pheno-seq â€" linking visual features and gene expression in 3D cell culture systems. Scientific Reports, 2019, 9, 12367.	3.3	16
87	Current best practices in singleâ€cell RNAâ€seq analysis: a tutorial. Molecular Systems Biology, 2019, 15, e8746.	7.2	1,322
88	MPRAnalyze: statistical framework for massively parallel reporter assays. Genome Biology, 2019, 20, 183.	8.8	58
89	A map of Î²-cell differentiation pathways supports cell therapies for diabetes. Nature, 2019, 569, 342-343.	27.8	8
90	Establishment of a high-resolution 3D modeling system for studying pancreatic epithelial cell biology in vitro. Molecular Metabolism, 2019, 30, 16-29.	6.5	22

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91	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
92	Single-cell RNA-seq denoising using a deep count autoencoder. Nature Communications, 2019, 10, 390.	12.8	668
93	IRE1Î±-XBP1s pathway promotes prostate cancer by activating c-MYC signaling. Nature Communications, 2019, 10, 323.	12.8	158
94	Dynamic modelling of an ACADS genotype in fatty acid oxidation â€" Application of cellular models for the analysis of common genetic variants. PLoS ONE, 2019, 14, e0216110.	2.5	1
95	A cellular census of human lungs identifies novel cell states in health and in asthma. Nature Medicine, 2019, 25, 1153-1163.	30.7	631
96	Inferring Interaction Networks From Multi-Omics Data. Frontiers in Genetics, 2019, 10, 535.	2.3	105
97	Massive single-cell mRNA profiling reveals a detailed roadmap for pancreatic endocrinogenesis. Development (Cambridge), 2019, 146, .	2.5	145
98	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. Nature Communications, 2019, 10, 2548.	12.8	94
99	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. Genome Biology, 2019, 20, 59.	8.8	911
100	Common patterns of gene regulation associated with Cesarean section and the development of islet autoimmunity â€" indications of immune cell activation. Scientific Reports, 2019, 9, 6250.	3.3	4
101	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
102	Deep learning: new computational modelling techniques for genomics. Nature Reviews Genetics, 2019, 20, 389-403.	16.3	717
103	Inferring population dynamics from single-cell RNA-sequencing time series data. Nature Biotechnology, 2019, 37, 461-468.	17.5	85
104	A strategy for highâ€dimensional multivariable analysis classifies childhood asthma phenotypes from genetic, immunological, and environmental factors. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 1364-1373.	5.7	24
105	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. Nature Communications, 2019, 10, 963.	12.8	408
106	SA125POLYGENIC BURDEN ANALYSIS OF LONGITUDINAL CLUSTERS OF PSYCHOPATHOLOGICAL FEATURES IN A CROSS-DIAGNOSTIC GROUP OF INDIVIDUALS WITH SEVERE MENTAL ILLNESS. European Neuropsychopharmacology, 2019, 29, S1257-S1258.	0.7	0
107	Editorial: Integrative Computational Systems Biology Approaches in Immunology and Medicine. Frontiers in Microbiology, 2019, 9, 3338.	3.5	1
108	A test metric for assessing single-cell RNA-seq batch correction. Nature Methods, 2019, 16, 43-49.	19.0	278

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109	Metabolic regulation of pluripotency and germ cell fate through α‑ketoglutarate. EMBO Journal, 2019, 38, .	7.8	77
110	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	7.7	49
111	Cell type atlas and lineage tree of a whole complex animal by single-cell transcriptomics. Science, 2018, 360, .	12.6	381
112	<i>netReg</i>: network-regularized linear models for biological association studies. Bioinformatics, 2018, 34, 896-898.	4.1	12
113	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
114	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
115	Lifetime study in mice after acute low-dose ionizing radiation: a multifactorial study with special focus on cataract risk. Radiation and Environmental Biophysics, 2018, 57, 99-113.	1.4	30
116	Type I Immune Response Induces Keratinocyte Necroptosis and Is Associated with Interface Dermatitis. Journal of Investigative Dermatology, 2018, 138, 1785-1794.	0.7	52
117	Dynamic landscape of pancreatic carcinogenesis reveals early molecular networks of malignancy. Gut, 2018, 67, 146-156.	12.1	43
118	Prediction of type 1 diabetes using a genetic risk model in the Diabetes Autoimmunity Study in the Young. Pediatric Diabetes, 2018, 19, 277-283.	2.9	19
119	Early Identification of Bronchopulmonary Dysplasia Using Novel Biomarkers by Proteomic Screening. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1076-1080.	5.6	26
120	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
121	MicroRNA as an Integral Part of Cell Communication: Regularized Target Prediction and Network Prediction. Lecture Notes in Bioengineering, 2018, , 85-100.	0.4	0
122	Information Theoretic Concepts to Unravel Cell–Cell Communication. Lecture Notes in Bioengineering, 2018, , 115-136.	0.4	0
123	Mechanistic description of spatial processes using integrative modelling of noise-corrupted imaging data. Journal of the Royal Society Interface, 2018, 15, 20180600.	3.4	2
124	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
125	Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. Metabolomics, 2018, 14, 128.	3.0	138
126	Multi-experiment nonlinear mixed effect modeling of single-cell translation kinetics after transfection. Npj Systems Biology and Applications, 2018, 4, 1.	3.0	66

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127	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
128	Copy number aberrations from Affymetrix SNP 6.0 genotyping data—how accurate are commonly used prediction approaches?. Briefings in Bioinformatics, 2018, , .	6.5	3
129	Bayesian parameter estimation for biochemical reaction networks using region-based adaptive parallel tempering. Bioinformatics, 2018, 34, i494-i501.	4.1	14
130	LNA++: Linear Noise Approximation with First and Second Order Sensitivities. Lecture Notes in Computer Science, 2018, , 300-306.	1.3	0
131	Inductive and Selective Effects of GSK3 and MEK Inhibition on Nanog Heterogeneity in Embryonic Stem Cells. Stem Cell Reports, 2018, 11, 58-69.	4.8	25
132	Lineage marker synchrony in hematopoietic genealogies refutes the PU.1/GATA1 toggle switch paradigm. Nature Communications, 2018, 9, 2697.	12.8	24
133	SCANPY: large-scale single-cell gene expression data analysis. Genome Biology, 2018, 19, 15.	8.8	3,958
134	Impulse model-based differential expression analysis of time course sequencing data. Nucleic Acids Research, 2018, 46, e119.	14.5	81
135	MetaMap: an atlas of metatranscriptomic reads in human disease-related RNA-seq data. GigaScience, 2018, 7, .	6.4	22
136	Data Driven Computational Modeling of Hematopoiesis in Myelodysplastic Syndromes Unveils Differences in Hematopoietic Stem Cell Kinetics Compared to Age-Matched Healthy Controls. Blood, 2018, 132, 4354-4354.	1.4	0
137	Parameter estimation for dynamical systems with discrete events and logical operations. Bioinformatics, 2017, 33, 1049-1056.	4.1	36
138	Inhibition of fat cell differentiation in 3T3-L1 pre-adipocytes by all-trans retinoic acid: Integrative analysis of transcriptomic and phenotypic data. Biomolecular Detection and Quantification, 2017, 11, 31-44.	7.0	9
139	Parallelization and High-Performance Computing Enables Automated Statistical Inference of Multi-scale Models. Cell Systems, 2017, 4, 194-206.e9.	6.2	62
140	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
141	cgCorrect: a method to correct for confounding cell–cell variation due to cell growth in single-cell transcriptomics. Physical Biology, 2017, 14, 036001.	1.8	15
142	Prospective identification of hematopoietic lineage choice by deep learning. Nature Methods, 2017, 14, 403-406.	19.0	160
143	Pulmonary microRNA profiles identify involvement of Creb1 and Sec14l3 in bronchial epithelial changes in allergic asthma. Scientific Reports, 2017, 7, 46026.	3.3	29
144	fastER: a user-friendly tool for ultrafast and robust cell segmentation in large-scale microscopy. Bioinformatics, 2017, 33, 2020-2028.	4.1	58

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145	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
146	Model-based branching point detection in single-cell data by K-branches clustering. Bioinformatics, 2017, 33, 3211-3219.	4.1	13
147	A BaSiC tool for background and shading correction of optical microscopy images. Nature Communications, 2017, 8, 14836.	12.8	213
148	Label Free Identification of Peripheral Blood Eosinophils Using High-Throughput Imaging Flow Cytometry. Journal of Allergy and Clinical Immunology, 2017, 139, AB163.	2.9	0
149	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
150	Integrating Polygenic Allele Burden Information And Phenomic Data To Characterize Complex Disease Trajectories In Severe Mental Illness. European Neuropsychopharmacology, 2017, 27, S406.	0.7	0
151	POLYGENIC BURDEN ANALYSIS OF LONGITUDINAL CLUSTERS OF QUALITY OF LIFE AND FUNCTIONING IN PATIENTS WITH SEVERE MENTAL ILLNESS. European Neuropsychopharmacology, 2017, 27, S408-S409.	0.7	0
152	The Role Of Micrornas In The Course Of Severe Mental Disorders. European Neuropsychopharmacology, 2017, 27, S456-S457.	0.7	0
153	Reconstructing cell cycle and disease progression using deep learning. Nature Communications, 2017, 8, 463.	12.8	210
154	Single cells make big data: New challenges and opportunities in transcriptomics. Current Opinion in Systems Biology, 2017, 4, 85-91.	2.6	171
155	Systematic single-cell analysis provides new insights into heterogeneity and plasticity of the pancreas. Molecular Metabolism, 2017, 6, 974-990.	6.5	95
156	Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. Nature Communications, 2017, 8, 1483.	12.8	67
157	Comprehensive benchmarking of Markov chain Monte Carlo methods for dynamical systems. BMC Systems Biology, 2017, 11, 63.	3.0	34
158	Peptide serum markers in islet autoantibody-positive children. Diabetologia, 2017, 60, 287-295.	6.3	24
159	TALEN/CRISPR-mediated engineering of a promoterless anti-viral RNAi hairpin into an endogenous miRNA locus. Nucleic Acids Research, 2017, 45, e3-e3.	14.5	8
160	pulver: an R package for parallel ultra-rapid p-value computation for linear regression interaction terms. BMC Bioinformatics, 2017, 18, 429.	2.6	1
161	A scalable moment-closure approximation for large-scale biochemical reaction networks. Bioinformatics, 2017, 33, i293-i300.	4.1	2
162	Model Based Targeting of IL-6-Induced Inflammatory Responses in Cultured Primary Hepatocytes to Improve Application of the JAK Inhibitor Ruxolitinib. Frontiers in Physiology, 2017, 8, 775.	2.8	19

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163	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
164	Correcting Classifiers for Sample Selection Bias in Two-Phase Case-Control Studies. Computational and Mathematical Methods in Medicine, 2017, 2017, 1-18.	1.3	8
165	Scalable Parameter Estimation for Genome-Scale Biochemical Reaction Networks. PLoS Computational Biology, 2017, 13, e1005331.	3.2	125
166	Calcium-regulatory proteins as modulators of chemotherapy in human neuroblastoma. Oncotarget, 2017, 8, 22876-22893.	1.8	27
167	2D cross-omics integrated enrichment analysis reveals insights into COPD pathogenesis. , 2017, , .		0
168	CERENA: ChEmical REaction Network Analyzerâ€"A Toolbox for the Simulation and Analysis of Stochastic Chemical Kinetics. PLoS ONE, 2016, 11, e0146732.	2.5	35
169	A novel molecular disease classifier for psoriasis and eczema. Experimental Dermatology, 2016, 25, 767-774.	2.9	54
170	Software tools for single-cell tracking and quantification of cellular and molecular properties. Nature Biotechnology, 2016, 34, 703-706.	17.5	162
171	Separation of Uncorrelated Stationary time series using Autocovariance Matrices. Journal of Time Series Analysis, 2016, 37, 337-354.	1.2	36
172	Quantitative comparison of competing PDE models for Pom1p dynamics in fission yeast * *The authors acknowledge financial support from the Postdoctoral Fellowship Program (PFP) of the Helmholtz Zentrum Munchen.. IFAC-PapersOnLine, 2016, 49, 264-269.	0.9	2
173	Metabolomics reveals effects of maternal smoking on endogenous metabolites from lipid metabolism in cord blood of newborns. Metabolomics, 2016, 12, 76.	3.0	18
174	Computational approaches for systems metabolomics. Current Opinion in Biotechnology, 2016, 39, 198-206.	6.6	53
175	Editorial overview: Systems biology-the intersection of experiments and computation, underpinning biotechnology. Current Opinion in Biotechnology, 2016, 39, iv-vi.	6.6	0
176	Metabolomics screening identifies reduced<scp>L</scp>-carnitine to be associated with progressive emphysema. Clinical Science, 2016, 130, 273-287.	4.3	39
177	Diffusion pseudotime robustly reconstructs lineage branching. Nature Methods, 2016, 13, 845-848.	19.0	982
178	Analysis of Cell Lineage Trees by Exact Bayesian Inference Identifies Negative Autoregulation of Nanog in Mouse Embryonic Stem Cells. Cell Systems, 2016, 3, 480-490.e13.	6.2	30
179	Lactation is associated with altered metabolomic signatures in women with gestational diabetes. Diabetologia, 2016, 59, 2193-2202.	6.3	20
180	Early myeloid lineage choice is not initiated by random PU.1 to GATA1 protein ratios. Nature, 2016, 535, 299-302.	27.8	180

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181	Tailored parameter optimization methods for ordinary differential equation models with steady-state constraints. BMC Systems Biology, 2016, 10, 80.	3.0	30
182	MEMO: multi-experiment mixture model analysis of censored data. Bioinformatics, 2016, 32, 2464-2472.	4.1	7
183	A computational model to predict severity of atopic eczema from 30 serum proteins. Journal of Allergy and Clinical Immunology, 2016, 138, 1207-1210.e2.	2.9	13
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