

# Fabian J. Theis

## List of Publications by Citations

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452  
papers

24,212  
citations

76  
h-index

147  
g-index

539  
ext. papers

35,548  
ext. citations

9.1  
avg. IF

7.5  
L-index

#	Paper	IF	Citations
452	SCANPY: large-scale single-cell gene expression data analysis. <i>Genome Biology</i> , <b>2018</b> , 19, 15	18.3	1418
451	SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. <i>Cell</i> , <b>2020</b> , 181, 1016-1035.e19	56.2	1326
450	The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,	8.9	937
449	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 155-60	44.5	778
448	An atlas of genetic influences on human blood metabolites. <i>Nature Genetics</i> , <b>2014</b> , 46, 543-550	36.3	695
447	Current best practices in single-cell RNA-seq analysis: a tutorial. <i>Molecular Systems Biology</i> , <b>2019</b> , 15, e8746	12.2	574
446	Diffusion pseudotime robustly reconstructs lineage branching. <i>Nature Methods</i> , <b>2016</b> , 13, 845-8	21.6	566
445	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , <b>2020</b> , 182, 1419-1440.e236.2	36.2	558
444	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , <b>2013</b> , 45, 145-54	36.3	505
443	Generalizing RNA velocity to transient cell states through dynamical modeling. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1408-1414	44.5	383
442	Diffusion maps for high-dimensional single-cell analysis of differentiation data. <i>Bioinformatics</i> , <b>2015</b> , 31, 2989-98	7.2	378
441	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. <i>Genome Biology</i> , <b>2019</b> , 20, 59	18.3	369
440	Deep learning: new computational modelling techniques for genomics. <i>Nature Reviews Genetics</i> , <b>2019</b> , 20, 389-403	30.1	367
439	A cellular census of human lungs identifies novel cell states in health and in asthma. <i>Nature Medicine</i> , <b>2019</b> , 25, 1153-1163	50.5	334
438	Single-cell RNA-seq denoising using a deep count autoencoder. <i>Nature Communications</i> , <b>2019</b> , 10, 390	17.4	314
437	destiny: diffusion maps for large-scale single-cell data in R. <i>Bioinformatics</i> , <b>2016</b> , 32, 1241-3	7.2	301
436	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. <i>Cell Stem Cell</i> , <b>2015</b> , 16, 712-24	18	286

435	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , <b>2020</b> , 21, 31	18.3	274
434	Live imaging of astrocyte responses to acute injury reveals selective juxtavascular proliferation. <i>Nature Neuroscience</i> , <b>2013</b> , 16, 580-6	25.5	271
433	Decoding the regulatory network of early blood development from single-cell gene expression measurements. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 269-276	44.5	268
432	Discovery of sexual dimorphisms in metabolic and genetic biomarkers. <i>PLoS Genetics</i> , <b>2011</b> , 7, e10022156		256
431	MicroRNA loss enhances learning and memory in mice. <i>Journal of Neuroscience</i> , <b>2010</b> , 30, 14835-42	6.6	244
430	Cell type atlas and lineage tree of a whole complex animal by single-cell transcriptomics. <i>Science</i> , <b>2018</b> , 360,	33.3	233
429	The dynamic range of the human metabolome revealed by challenges. <i>FASEB Journal</i> , <b>2012</b> , 26, 2607-19	0.9	226
428	Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 363-72	23.4	221
427	Epigenetic germline inheritance of diet-induced obesity and insulin resistance. <i>Nature Genetics</i> , <b>2016</b> , 48, 497-9	36.3	211
426	Sparse component analysis and blind source separation of underdetermined mixtures. <i>IEEE Transactions on Neural Networks</i> , <b>2005</b> , 16, 992-6		211
425	Hypergraphs and cellular networks. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000385	5	209
424	Gaussian graphical modeling reconstructs pathway reactions from high-throughput metabolomics data. <i>BMC Systems Biology</i> , <b>2011</b> , 5, 21	3.5	207
423	PhenomiR: a knowledgebase for microRNA expression in diseases and biological processes. <i>Genome Biology</i> , <b>2010</b> , 11, R6	18.3	207
422	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. <i>Nature Communications</i> , <b>2019</b> , 10, 963	17.4	186
421	Statistical methods for the analysis of high-throughput metabolomics data. <i>Computational and Structural Biotechnology Journal</i> , <b>2013</b> , 4, e201301009	6.8	176
420	Lessons learned from quantitative dynamical modeling in systems biology. <i>PLoS ONE</i> , <b>2013</b> , 8, e74335	3.7	174
419	Next-generation sequencing reveals novel differentially regulated mRNAs, lncRNAs, miRNAs, sdRNAs and a piRNA in pancreatic cancer. <i>Molecular Cancer</i> , <b>2015</b> , 14, 94	42.1	171
418	Transforming Boolean models to continuous models: methodology and application to T-cell receptor signaling. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 98	3.5	158

417	Label-free cell cycle analysis for high-throughput imaging flow cytometry. <i>Nature Communications</i> , <b>2016</b> , 7, 10256	17.4	156
416	A test metric for assessing single-cell RNA-seq batch correction. <i>Nature Methods</i> , <b>2019</b> , 16, 43-49	21.6	140
415	Fast clonal expansion and limited neural stem cell self-renewal in the adult subependymal zone. <i>Nature Neuroscience</i> , <b>2015</b> , 18, 490-2	25.5	138
414	Early myeloid lineage choice is not initiated by random PU.1 to GATA1 protein ratios. <i>Nature</i> , <b>2016</b> , 535, 299-302	50.4	138
413	Reconstructing cell cycle and disease progression using deep learning. <i>Nature Communications</i> , <b>2017</b> , 8, 463	17.4	136
412	Gender-specific pathway differences in the human serum metabolome. <i>Metabolomics</i> , <b>2015</b> , 11, 1815-1823	13.7	130
411	Intraindividual genome expression analysis reveals a specific molecular signature of psoriasis and eczema. <i>Science Translational Medicine</i> , <b>2014</b> , 6, 244ra90	17.5	128
410	Social transfer of pathogenic fungus promotes active immunisation in ant colonies. <i>PLoS Biology</i> , <b>2012</b> , 10, e1001300	9.7	126
409	Mining the unknown: a systems approach to metabolite identification combining genetic and metabolic information. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003005	6	126
408	Neurodevelopment. Live imaging of adult neural stem cell behavior in the intact and injured zebrafish brain. <i>Science</i> , <b>2015</b> , 348, 789-93	33.3	125
407	Transcriptional Mechanisms of Proneural Factors and REST in Regulating Neuronal Reprogramming of Astrocytes. <i>Cell Stem Cell</i> , <b>2015</b> , 17, 74-88	18	118
406	Stem-cell-like properties and epithelial plasticity arise as stable traits after transient Twist1 activation. <i>Cell Reports</i> , <b>2015</b> , 10, 131-9	10.6	118
405	Software tools for single-cell tracking and quantification of cellular and molecular properties. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 703-6	44.5	108
404	The structure of borders in a small world. <i>PLoS ONE</i> , <b>2010</b> , 5, e15422	3.7	107
403	Reconstructing gene regulatory dynamics from high-dimensional single-cell snapshot data. <i>Bioinformatics</i> , <b>2015</b> , 31, i89-96	7.2	106
402	Evaluation of Deep Learning Strategies for Nucleus Segmentation in Fluorescence Images. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2019</b> , 95, 952-965	4.6	106
401	Intronic microRNAs support their host genes by mediating synergistic and antagonistic regulatory effects. <i>BMC Genomics</i> , <b>2010</b> , 11, 224	4.5	106
400	Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. <i>Nature Communications</i> , <b>2020</b> , 11, 3559	17.4	106

399	Hierarchical differentiation of myeloid progenitors is encoded in the transcription factor network. <i>PLoS ONE</i> , <b>2011</b> , 6, e22649	3.7	103
398	Prospective identification of hematopoietic lineage choice by deep learning. <i>Nature Methods</i> , <b>2017</b> , 14, 403-406	21.6	102
397	Erythropoietin enhances hippocampal long-term potentiation and memory. <i>BMC Biology</i> , <b>2008</b> , 6, 37	7.3	102
396	A BaSiC tool for background and shading correction of optical microscopy images. <i>Nature Communications</i> , <b>2017</b> , 8, 14836	17.4	99
395	The Human Lung Cell Atlas: A High-Resolution Reference Map of the Human Lung in Health and Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2019</b> , 61, 31-41	5.7	98
394	Network plasticity of pluripotency transcription factors in embryonic stem cells. <i>Nature Cell Biology</i> , <b>2015</b> , 17, 1235-46	23.4	98
393	Single cells make big data: New challenges and opportunities in transcriptomics. <i>Current Opinion in Systems Biology</i> , <b>2017</b> , 4, 85-91	3.2	96
392	The signal separation evaluation campaign (2007-2010): Achievements and remaining challenges. <i>Signal Processing</i> , <b>2012</b> , 92, 1928-1936	4.4	95
391	IRE1-XBP1s pathway promotes prostate cancer by activating c-MYC signaling. <i>Nature Communications</i> , <b>2019</b> , 10, 323	17.4	93
390	scGen predicts single-cell perturbation responses. <i>Nature Methods</i> , <b>2019</b> , 16, 715-721	21.6	89
389	Concepts and limitations for learning developmental trajectories from single cell genomics. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	89
388	Swarm Learning for decentralized and confidential clinical machine learning. <i>Nature</i> , <b>2021</b> , 594, 265-270	50.4	89
387	Blind source separation techniques for the decomposition of multiply labeled fluorescence images. <i>Biophysical Journal</i> , <b>2009</b> , 96, 3791-800	2.9	88
386	Scalable Parameter Estimation for Genome-Scale Biochemical Reaction Networks. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005331	5	87
385	Quantification of regenerative potential in primary human mammary epithelial cells. <i>Development (Cambridge)</i> , <b>2015</b> , 142, 3239-51	6.6	86
384	Feature ranking of type 1 diabetes susceptibility genes improves prediction of type 1 diabetes. <i>Diabetologia</i> , <b>2014</b> , 57, 2521-9	10.3	85
383	Odefy--from discrete to continuous models. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 233	3.6	84
382	A unilateral negative feedback loop between miR-200 microRNAs and Sox2/E2F3 controls neural progenitor cell-cycle exit and differentiation. <i>Journal of Neuroscience</i> , <b>2012</b> , 32, 13292-308	6.6	83

381	Vertex centralities in input-output networks reveal the structure of modern economies. <i>Physical Review E</i> , <b>2011</b> , 83, 046127	2.4	82
380	Atrx promotes heterochromatin formation at retrotransposons. <i>EMBO Reports</i> , <b>2015</b> , 16, 836-50	6.5	79
379	scSLAM-seq reveals core features of transcription dynamics in single cells. <i>Nature</i> , <b>2019</b> , 571, 419-423	50.4	77
378	Effects of smoking and smoking cessation on human serum metabolite profile: results from the KORA cohort study. <i>BMC Medicine</i> , <b>2013</b> , 11, 60	11.4	77
377	Body fat free mass is associated with the serum metabolite profile in a population-based study. <i>PLoS ONE</i> , <b>2012</b> , 7, e40009	3.7	77
376	AURKA, DLGAP5, TPX2, KIF11 and CKAP5: Five specific mitosis-associated genes correlate with poor prognosis for non-small cell lung cancer patients. <i>International Journal of Oncology</i> , <b>2017</b> , 50, 365-372	4.4	73
375	Method of conditional moments (MCM) for the Chemical Master Equation: a unified framework for the method of moments and hybrid stochastic-deterministic models. <i>Journal of Mathematical Biology</i> , <b>2014</b> , 69, 687-735	2	72
374	An automatic method for robust and fast cell detection in bright field images from high-throughput microscopy. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 297	3.6	71
373	On the hypothesis-free testing of metabolite ratios in genome-wide and metabolome-wide association studies. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 120	3.6	70
372	The single-cell eQTLGen consortium. <i>ELife</i> , <b>2020</b> , 9,	8.9	68
371	A geometric algorithm for overcomplete linear ICA. <i>Neurocomputing</i> , <b>2004</b> , 56, 381-398	5.4	66
370	Generalizing RNA velocity to transient cell states through dynamical modeling		66
369	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D220-4	20.1	65
368	The Human Blood Metabolome-Transcriptome Interface. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005274	6	65
367	The proteome landscape of the kingdoms of life. <i>Nature</i> , <b>2020</b> , 582, 592-596	50.4	64
366	Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. <i>Metabolomics</i> , <b>2018</b> , 14, 128	4.7	63
365	Joining forces of Bayesian and frequentist methodology: a study for inference in the presence of non-identifiability. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , <b>2013</b> , 371, 20110544	3	62
364	Zebrafish reward mutants reveal novel transcripts mediating the behavioral effects of amphetamine. <i>Genome Biology</i> , <b>2009</b> , 10, R81	18.3	62

363	Stability and multiattractor dynamics of a toggle switch based on a two-stage model of stochastic gene expression. <i>Biophysical Journal</i> , <b>2012</b> , 102, 19-29	2.9	61
362	Dynamic mathematical modeling of IL13-induced signaling in Hodgkin and primary mediastinal B-cell lymphoma allows prediction of therapeutic targets. <i>Cancer Research</i> , <b>2011</b> , 71, 693-704	10.1	61
361	Systematic single-cell analysis provides new insights into heterogeneity and plasticity of the pancreas. <i>Molecular Metabolism</i> , <b>2017</b> , 6, 974-990	8.8	59
360	Integrative genetic and metabolite profiling analysis suggests altered phosphatidylcholine metabolism in asthma. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2013</b> , 68, 629-36	9.3	57
359	GATA2/3-TFAP2A/C transcription factor network couples human pluripotent stem cell differentiation to trophoblast with repression of pluripotency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E9579-E9588	11.5	56
358	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , <b>2020</b> , 587, 377-386	50.4	56
357	Efficient Parameter Estimation Enables the Prediction of Drug Response Using a Mechanistic Pan-Cancer Pathway Model. <i>Cell Systems</i> , <b>2018</b> , 7, 567-579.e6	10.6	56
356	The nature and perception of fluctuations in human musical rhythms. <i>PLoS ONE</i> , <b>2011</b> , 6, e26457	3.7	55
355	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. <i>Nature Communications</i> , <b>2019</b> , 10, 2548	17.4	54
354	A strategy for combining minor genetic susceptibility genes to improve prediction of disease in type 1 diabetes. <i>Genes and Immunity</i> , <b>2012</b> , 13, 549-55	4.4	54
353	Inferring Interaction Networks From Multi-Omics Data. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 535	4.5	52
352	Multi-omic signature of body weight change: results from a population-based cohort study. <i>BMC Medicine</i> , <b>2015</b> , 13, 48	11.4	51
351	Inference for Stochastic Chemical Kinetics Using Moment Equations and System Size Expansion. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005030	5	51
350	PhenomiR: microRNAs in human diseases and biological processes. <i>Methods in Molecular Biology</i> , <b>2012</b> , 822, 249-60	1.4	51
349	Comprehensive single cell mRNA profiling reveals a detailed roadmap for pancreatic endocrinogenesis. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	50
348	Hypothalamic miR-103 protects from hyperphagic obesity in mice. <i>Journal of Neuroscience</i> , <b>2014</b> , 34, 10659-74	6.6	50
347	MicroRNAs coordinately regulate protein complexes. <i>BMC Systems Biology</i> , <b>2011</b> , 5, 136	3.5	48
346	miTALOS v2: Analyzing Tissue Specific microRNA Function. <i>PLoS ONE</i> , <b>2016</b> , 11, e0151771	3.7	47

345	MicroRNA-138 promotes acquired alkylator resistance in glioblastoma by targeting the Bcl-2-interacting mediator BIM. <i>Oncotarget</i> , <b>2016</b> , 7, 12937-50	3.3	47
344	Inferring population dynamics from single-cell RNA-sequencing time series data. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 461-468	44.5	46
343	Proteome-wide analysis reveals an age-associated cellular phenotype of in situ aged human fibroblasts. <i>Aging</i> , <b>2014</b> , 6, 856-78	5.6	46
342	Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation		46
341	Money Circulation, Trackable Items, and the Emergence of Universal Human Mobility Patterns. <i>IEEE Pervasive Computing</i> , <b>2008</b> , 7, 28-35	1.3	45
340	Targeted pharmacological therapy restores $\beta$ cell function for diabetes remission. <i>Nature Metabolism</i> , <b>2020</b> , 2, 192-209	14.6	44
339	Interleukin-4 and interferon- $\gamma$ orchestrate an epithelial polarization in the airways. <i>Mucosal Immunology</i> , <b>2016</b> , 9, 917-26	9.2	44
338	miTALOS: analyzing the tissue-specific regulation of signaling pathways by human and mouse microRNAs. <i>Rna</i> , <b>2011</b> , 17, 809-19	5.8	44
337	A novel approach for resolving differences in single-cell gene expression patterns from zygote to blastocyst. <i>Bioinformatics</i> , <b>2012</b> , 28, i626-i632	7.2	44
336	fastER: a user-friendly tool for ultrafast and robust cell segmentation in large-scale microscopy. <i>Bioinformatics</i> , <b>2017</b> , 33, 2020-2028	7.2	43
335	High-dimensional Bayesian parameter estimation: case study for a model of JAK2/STAT5 signaling. <i>Mathematical Biosciences</i> , <b>2013</b> , 246, 293-304	3.9	43
334	Computational approaches for systems metabolomics. <i>Current Opinion in Biotechnology</i> , <b>2016</b> , 39, 198-206	6.4	42
333	Metabolic regulation of pluripotency and germ cell fate through $\beta$ ketoglutarate. <i>EMBO Journal</i> , <b>2019</b> , 38,	13	41
332	A subset of metastatic pancreatic ductal adenocarcinomas depends quantitatively on oncogenic Kras/Mek/Erk-induced hyperactive mTOR signalling. <i>Gut</i> , <b>2016</b> , 65, 647-57	19.2	40
331	Impulse model-based differential expression analysis of time course sequencing data. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e119	20.1	38
330	Linear geometric ICA: fundamentals and algorithms. <i>Neural Computation</i> , <b>2003</b> , 15, 419-39	2.9	38
329	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , <b>2018</b> , 50, e453	12.8	37
328	Parallelization and High-Performance Computing Enables Automated Statistical Inference of Multi-scale Models. <i>Cell Systems</i> , <b>2017</b> , 4, 194-206.e9	10.6	36



327	Metabolite profiling reveals new insights into the regulation of serum urate in humans. <i>Metabolomics</i> , <b>2014</b> , 10, 141-151	4.7	36
326	Benchmarking atlas-level data integration in single-cell genomics.. <i>Nature Methods</i> , <b>2021</b> ,	21.6	35
325	Identification of a plasma miRNA biomarker signature for allergic asthma: A translational approach. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2017</b> , 72, 1962-1971	9.3	34
324	Meeting the Challenges of High-Dimensional Single-Cell Data Analysis in Immunology. <i>Frontiers in Immunology</i> , <b>2019</b> , 10, 1515	8.4	34
323	Cytokine-regulated GADD45G induces differentiation and lineage selection in hematopoietic stem cells. <i>Stem Cell Reports</i> , <b>2014</b> , 3, 34-43	8	34
322	Network-based approach for analyzing intra- and interfluid metabolite associations in human blood, urine, and saliva. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 1183-94	5.6	33
321	Opposing effects of allogrooming on disease transmission in ant societies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 370,	5.8	33
320	Spatial analysis of expression patterns predicts genetic interactions at the mid-hindbrain boundary. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000569	5	33
319	The HeckscherOhlin model and the network structure of international trade. <i>International Review of Economics and Finance</i> , <b>2011</b> , 20, 135-145	2.8	32
318	ODE constrained mixture modelling: a method for unraveling subpopulation structures and dynamics. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003686	5	31
317	Early IFN- $\gamma$ signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. <i>Immunity</i> , <b>2021</b> , 54, 2650-2669.e14	32.3	31
316	Dynamic landscape of pancreatic carcinogenesis reveals early molecular networks of malignancy. <i>Gut</i> , <b>2018</b> , 67, 146-156	19.2	30
315	The human transcriptome is enriched for miRNA-binding sites located in cooperativity-permitting distance. <i>RNA Biology</i> , <b>2013</b> , 10, 1125-35	4.8	30
314	Knowledge-based gene expression classification via matrix factorization. <i>Bioinformatics</i> , <b>2008</b> , 24, 1688-972	9.2	30
313	Parameterizing cell-to-cell regulatory heterogeneities via stochastic transcriptional profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E626-35	11.5	29
312	Denosing using local projective subspace methods. <i>Neurocomputing</i> , <b>2006</b> , 69, 1485-1501	5.4	29
311	Uniqueness of complex and multidimensional independent component analysis. <i>Signal Processing</i> , <b>2004</b> , 84, 951-956	4.4	29
310	A novel molecular disease classifier for psoriasis and eczema. <i>Experimental Dermatology</i> , <b>2016</b> , 25, 767-74	7.4	29

309	CERENA: ChEmical REaction Network Analyzer--A Toolbox for the Simulation and Analysis of Stochastic Chemical Kinetics. <i>PLoS ONE</i> , <b>2016</b> , 11, e0146732	3.7	28
308	Metabolomics screening identifies reduced L-carnitine to be associated with progressive emphysema. <i>Clinical Science</i> , <b>2016</b> , 130, 273-87	6.5	28
307	MPRAnalyze: statistical framework for massively parallel reporter assays. <i>Genome Biology</i> , <b>2019</b> , 20, 18318.3		27
306	Epigenetically Regulated Chromosome 14q32 miRNA Cluster Induces Metastasis and Predicts Poor Prognosis in Lung Adenocarcinoma Patients. <i>Molecular Cancer Research</i> , <b>2018</b> , 16, 390-402	6.6	27
305	Toll-like receptor 7/8 agonists stimulate plasmacytoid dendritic cells to initiate T17-deviated acute contact dermatitis in human subjects. <i>Journal of Allergy and Clinical Immunology</i> , <b>2018</b> , 141, 1320-1333.e11.5	11.5	27
304	Wound-healing growth factor, basic FGF, induces Erk1/2-dependent mechanical hyperalgesia. <i>Pain</i> , <b>2013</b> , 154, 2216-2226	8	27
303	A modular framework for gene set analysis integrating multilevel omics data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 9622-33	20.1	27
302	A new concept for separability problems in blind source separation. <i>Neural Computation</i> , <b>2004</b> , 16, 1827-50		27
301	Inhibition of LTR signalling activates WNT-induced regeneration in lung. <i>Nature</i> , <b>2020</b> , 588, 151-156	50.4	26
300	Protocol of a population-based prospective COVID-19 cohort study Munich, Germany (KoCo19). <i>BMC Public Health</i> , <b>2020</b> , 20, 1036	4.1	26
299	Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. <i>Nature Communications</i> , <b>2017</b> , 8, 1483	17.4	26
298	Query to reference single-cell integration with transfer learning		26
297	Integrated intra- and intercellular signaling knowledge for multicellular omics analysis. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e9923	12.2	26
296	Squidpy: a scalable framework for spatial single cell analysis		26
295	Aldh1b1 expression defines progenitor cells in the adult pancreas and is required for Kras-induced pancreatic cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 20679-20688	11.5	25
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112	Efficient parameterization of large-scale mechanistic models enables drug response prediction for cancer cell lines		4

111	Integrated single cell analysis of human lung fibrosis resolves cellular origins of predictive protein signatures in body fluids		4
110	Learning interpretable latent autoencoder representations with annotations of feature sets		4
109	FASTGenomics: An analytical ecosystem for single-cell RNA sequencing data		4
108	Predicting antigen-specificity of single T-cells based on TCR CDR3 regions		4
107	Learning cell communication from spatial graphs of cells		4
106	Sparse Nonnegative Matrix Factorization Applied to Microarray Data Sets. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 254-261	0.9	4
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