

Florian Buettner

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

7,808
citations

159585

30
h-index

254184

43
g-index

57
all docs

57
docs citations

57
times ranked

13067
citing authors

#	ARTICLE	IF	CITATIONS
1	Inflammatory fibroblasts mediate resistance to neoadjuvant therapy in rectal cancer. <i>Cancer Cell</i> , 2022, 40, 168-184.e13.	16.8	117
2	The proteogenomic subtypes of acute myeloid leukemia. <i>Cancer Cell</i> , 2022, 40, 301-317.e12.	16.8	43
3	Single cell analyses identify a highly regenerative and homogenous human CD34+ hematopoietic stem cell population. <i>Nature Communications</i> , 2022, 13, 2048.	12.8	16
4	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. <i>Nature Communications</i> , 2020, 11, 810.	12.8	235
5	Document Informed Neural Autoregressive Topic Models with Distributional Prior. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2019, 33, 6505-6512.	4.9	27
6	Ano-rectal wall dose-surface maps localize the dosimetric benefit of hydrogel rectum spacers in prostate cancer radiotherapy. <i>Clinical and Translational Radiation Oncology</i> , 2019, 14, 17-24.	1.7	11
7	Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , 2019, 576, 487-491.	27.8	307
8	Metabolic regulation of pluripotency and germ cell fate through α -ketoglutarate. <i>EMBO Journal</i> , 2019, 38, .	7.8	77
9	No Evidence for Hematopoietic Stem Cell Self-Renewal in-Vivo Following Inflammatory Challenge. <i>Blood</i> , 2019, 134, 456-456.	1.4	1
10	Design and Selection of Machine Learning Methods Using Radiomics and Dosiomics for Normal Tissue Complication Probability Modeling of Xerostomia. <i>Frontiers in Oncology</i> , 2018, 8, 35.	2.8	115
11	Multi-Omics Factor Analysis—a framework for unsupervised integration of multi-omics data sets. <i>Molecular Systems Biology</i> , 2018, 14, e8124.	7.2	659
12	cgCorrect: a method to correct for confounding cell-to-cell variation due to cell growth in single-cell transcriptomics. <i>Physical Biology</i> , 2017, 14, 036001.	1.8	15
13	Prospective identification of hematopoietic lineage choice by deep learning. <i>Nature Methods</i> , 2017, 14, 403-406.	19.0	160
14	A divergent population of autoantigen-responsive CD4 ⁺ T cells in infants prior to H^2 cell autoimmunity. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	67
15	Vitamin A-Retinoic Acid Signaling Regulates Hematopoietic Stem Cell Dormancy. <i>Cell</i> , 2017, 169, 807-823.e19.	28.9	339
16	Parotid gland mean dose as a xerostomia predictor in low-dose domains. <i>Acta Oncologica</i> , 2017, 56, 1197-1203.	1.8	25
17	Non-targeted metabolomic approach reveals two distinct types of metabolic responses to telomerase dysfunction in <i>S. cerevisiae</i> . <i>Metabolomics</i> , 2017, 13, 1.	3.0	2
18	f-sLVM: scalable and versatile factor analysis for single-cell RNA-seq. <i>Genome Biology</i> , 2017, 18, 212.	8.8	119

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19	Exit from HSC dormancy by a continuous upregulation of metabolism is controlled via vitamin A/retinoic acid. <i>Experimental Hematology</i> , 2016, 44, S54.	0.4	0
20	Diffusion pseudotime robustly reconstructs lineage branching. <i>Nature Methods</i> , 2016, 13, 845-848.	19.0	982
21	<i>destiny</i> : diffusion maps for large-scale single-cell data in R. <i>Bioinformatics</i> , 2016, 32, 1241-1243.	4.1	518
22	Unbiased Prediction and Feature Selection in High-Dimensional Survival Regression. <i>Journal of Computational Biology</i> , 2016, 23, 279-290.	1.6	21
23	Diffusion maps for high-dimensional single-cell analysis of differentiation data. <i>Bioinformatics</i> , 2015, 31, 2989-2998.	4.1	576
24	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. <i>Cell Stem Cell</i> , 2015, 16, 712-724.	11.1	376
25	Single-cell transcriptomic reconstruction reveals cell cycle and multi-lineage differentiation defects in <i>Bcl11a</i> -deficient hematopoietic stem cells. <i>Genome Biology</i> , 2015, 16, 178.	8.8	86
26	Decoding the regulatory network of early blood development from single-cell gene expression measurements. <i>Nature Biotechnology</i> , 2015, 33, 269-276.	17.5	352
27	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , 2015, 33, 155-160.	17.5	1,068
28	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , 2015, 85, 54-61.	3.8	381
29	Effects of High-Dose Oral Insulin on Immune Responses in Children at High Risk for Type 1 Diabetes. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1541.	7.4	174
30	RAMONA: a Web application for gene set analysis on multilevel omics data. <i>Bioinformatics</i> , 2015, 31, 128-130.	4.1	7
31	Feature ranking of type 1 diabetes susceptibility genes improves prediction of type 1 diabetes. <i>Diabetologia</i> , 2014, 57, 2521-2529.	6.3	112
32	Probabilistic PCA of censored data: accounting for uncertainties in the visualization of high-throughput single-cell qPCR data. <i>Bioinformatics</i> , 2014, 30, 1867-1875.	4.1	21
33	Decoding the transcriptional program for blood development from whole tissue single-cell gene expression measurements. <i>Experimental Hematology</i> , 2014, 42, S52.	0.4	0
34	Molecular phenotypic profiling of a <i>Saccharomyces cerevisiae</i> strain at the single-cell level. <i>Analyst</i> , 2014, 139, 5709-5717.	3.5	19
35	Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. <i>Nature Cell Biology</i> , 2013, 15, 363-372.	10.3	257
36	A modular framework for gene set analysis integrating multilevel omics data. <i>Nucleic Acids Research</i> , 2013, 41, 9622-9633.	14.5	32

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37	A novel approach for resolving differences in single-cell gene expression patterns from zygote to blastocyst. <i>Bioinformatics</i> , 2012, 28, i626-i632.	4.1	50
38	Novel approaches to improve the therapeutic index of head and neck radiotherapy: An analysis of data from the PARSPORT randomised phase III trial. <i>Radiotherapy and Oncology</i> , 2012, 103, 82-87.	0.6	65
39	The doseâ€“response of the anal sphincter region â€“ An analysis of data from the MRC RT01 trial. <i>Radiotherapy and Oncology</i> , 2012, 103, 347-352.	0.6	53
40	Modeling late rectal toxicities based on a parameterized representation of the 3D dose distribution. <i>Physics in Medicine and Biology</i> , 2011, 56, 2103-2118.	3.0	41
41	Using a Bayesian Feature-selection Algorithm to Identify Dose-response Models Based on the Shape of the 3D Dose-distribution: An Example from a Head-and-neck Cancer Trial. , 2010, , .		3
42	Using dose-surface maps to predict radiation-induced rectal bleeding: a neural network approach. <i>Physics in Medicine and Biology</i> , 2009, 54, 5139-5153.	3.0	45
43	Assessing correlations between the spatial distribution of the dose to the rectal wall and late rectal toxicity after prostate radiotherapy: an analysis of data from the MRC RT01 trial (ISRCTN 47772397). <i>Physics in Medicine and Biology</i> , 2009, 54, 6535-6548.	3.0	78
44	Using Bayesian Logistic Regression with High-Order Interactions to Model Radiation-Induced Toxicities Following Radiotherapy. , 2009, , .		2
45	Dosimetric impact of motion in freeâ€“breathing and gated lung radiotherapy: A 4D Monte Carlo study of intrafraction and interfraction effects. <i>Medical Physics</i> , 2008, 35, 356-366.	3.0	64
46	Optical trapping dynamics for cell identification. , 2006, , .		0