# Florian Buettner

## List of Publications by Year
## in descending order

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|---|---|---|---|
| 46<br>papers | 7,808<br>citations | 159585<br>30<br>h-index | 254184<br>43<br>g-index |
| 57<br>all docs | 57<br>docs citations | 57<br>times ranked | 13067<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | 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 |
| 2 | Diffusion pseudotime robustly reconstructs lineage branching. Nature Methods, 2016, 13, 845-848. | 19.0 | 982 |
| 3 | Multi€Omics Factor Analysis€"a framework for unsupervised integration of multi€omics data sets. Molecular Systems Biology, 2018, 14, e8124. | 7.2 | 659 |
| 4 | Diffusion maps for high-dimensional single-cell analysis of differentiation data. Bioinformatics, 2015, 31, 2989-2998. | 4.1 | 576 |
| 5 | <i>destiny</i>: diffusion maps for large-scale single-cell data in R. Bioinformatics, 2016, 32, 1241-1243. | 4.1 | 518 |
| 6 | Computational assignment of cell-cycle stage from single-cell transcriptome data. Methods, 2015, 85, 54-61. | 3.8 | 381 |
| 7 | Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. Cell Stem Cell, 2015, 16, 712-724. | 11.1 | 376 |
| 8 | Decoding the regulatory network of early blood development from single-cell gene expression measurements. Nature Biotechnology, 2015, 33, 269-276. | 17.5 | 352 |
| 9 | Vitamin A-Retinoic Acid Signaling Regulates Hematopoietic Stem Cell Dormancy. Cell, 2017, 169, 807-823.e19. | 28.9 | 339 |
| 10 | Multi-omics profiling of mouse gastrulation at single-cell resolution. Nature, 2019, 576, 487-491. | 27.8 | 307 |
| 11 | 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 |
| 12 | Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. Nature Communications, 2020, 11, 810. | 12.8 | 235 |
| 13 | Effects of High-Dose Oral Insulin on Immune Responses in Children at High Risk for Type 1 Diabetes. JAMA - Journal of the American Medical Association, 2015, 313, 1541. | 7.4 | 174 |
| 14 | Prospective identification of hematopoietic lineage choice by deep learning. Nature Methods, 2017, 14, 403-406. | 19.0 | 160 |
| 15 | f-scLVM: scalable and versatile factor analysis for single-cell RNA-seq. Genome Biology, 2017, 18, 212. | 8.8 | 119 |
| 16 | Inflammatory fibroblasts mediate resistance to neoadjuvant therapy in rectal cancer. Cancer Cell, 2022, 40, 168-184.e13. | 16.8 | 117 |
| 17 | Design and Selection of Machine Learning Methods Using Radiomics and Dosiomics for Normal Tissue Complication Probability Modeling of Xerostomia. Frontiers in Oncology, 2018, 8, 35. | 2.8 | 115 |
| 18 | Feature ranking of type 1 diabetes susceptibility genes improves prediction of type 1 diabetes. Diabetologia, 2014, 57, 2521-2529. | 6.3 | 112 |

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|---|---------|-----|-----------|
| 19 | Single-cell transcriptomic reconstruction reveals cell cycle and multi-lineage differentiation defects in Bcl11a-deficient hematopoietic stem cells. Genome Biology, 2015, 16, 178. | 8.8 | 86 |
| 20 | 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). Physics in Medicine and Biology, 2009, 54, 6535-6548. | 3.0 | 78 |
| 21 | Metabolic regulation of pluripotency and germ cell fate through α-ketoglutarate. EMBO Journal, 2019, 38, . | 7.8 | 77 |
| 22 | A divergent population of autoantigen-responsive CD4 $^+$ T cells in infants prior to β cell autoimmunity. Science Translational Medicine, 2017, 9, . | 12.4 | 67 |
| 23 | Novel approaches to improve the therapeutic index of head and neck radiotherapy: An analysis of data from the PARSPORT randomised phase III trial. Radiotherapy and Oncology, 2012, 103, 82-87. | 0.6 | 65 |
| 24 | Dosimetric impact of motion in free-breathing and gated lung radiotherapy: A 4D Monte Carlo study of intrafraction and interfraction effects. Medical Physics, 2008, 35, 356-366. | 3.0 | 64 |
| 25 | The dose–response of the anal sphincter region – An analysis of data from the MRC RT01 trial. Radiotherapy and Oncology, 2012, 103, 347-352. | 0.6 | 53 |
| 26 | A novel approach for resolving differences in single-cell gene expression patterns from zygote to blastocyst. Bioinformatics, 2012, 28, i626-i632. | 4.1 | 50 |
| 27 | Using dose-surface maps to predict radiation-induced rectal bleeding: a neural network approach. Physics in Medicine and Biology, 2009, 54, 5139-5153. | 3.0 | 45 |
| 28 | The proteogenomic subtypes of acute myeloid leukemia. Cancer Cell, 2022, 40, 301-317.e12. | 16.8 | 43 |
| 29 | Modeling late rectal toxicities based on a parameterized representation of the 3D dose distribution. Physics in Medicine and Biology, 2011, 56, 2103-2118. | 3.0 | 41 |
| 30 | A modular framework for gene set analysis integrating multilevel omics data. Nucleic Acids Research, 2013, 41, 9622-9633. | 14.5 | 32 |
| 31 | Document Informed Neural Autoregressive Topic Models with Distributional Prior. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 6505-6512. | 4.9 | 27 |
| 32 | Parotid gland mean dose as a xerostomia predictor in low-dose domains. Acta Oncológica, 2017, 56, 1197-1203. | 1.8 | 25 |
| 33 | Probabilistic PCA of censored data: accounting for uncertainties in the visualization of high-throughput single-cell qPCR data. Bioinformatics, 2014, 30, 1867-1875. | 4.1 | 21 |
| 34 | Unbiased Prediction and Feature Selection in High-Dimensional Survival Regression. Journal of Computational Biology, 2016, 23, 279-290. | 1.6 | 21 |
| 35 | Molecular phenotypic profiling of a *Saccharomyces cerevisiae* strain at the single-cell level. Analyst, The, 2014, 139, 5709-5717. | 3.5 | 19 |
| 36 | Single cell analyses identify a highly regenerative and homogenous human CD34+ hematopoietic stem cell population. Nature Communications, 2022, 13, 2048. | 12.8 | 16 |

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|---|---------|-----|-----------|
| 37 | 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 |
| 38 | Ano-rectal wall dose-surface maps localize the dosimetric benefit of hydrogel rectum spacers in prostate cancer radiotherapy. Clinical and Translational Radiation Oncology, 2019, 14, 17-24. | 1.7 | 11 |
| 39 | RAMONA: a Web application for gene set analysis on multilevel omics data. Bioinformatics, 2015, 31, 128-130. | 4.1 | 7 |
| 40 | 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 |
| 41 | Using Bayesian Logistic Regression with High-Order Interactions to Model Radiation-Induced Toxicities Following Radiotherapy. , 2009, , . | | 2 |
| 42 | Non-targeted metabolomic approach reveals two distinct types of metabolic responses to telomerase dysfunction in S. cerevisiae. Metabolomics, 2017, 13, 1. | 3.0 | 2 |
| 43 | No Evidence for Hematopoietic Stem Cell Self-Renewal in-Vivo Following Inflammatory Challenge. Blood, 2019, 134, 456-456. | 1.4 | 1 |
| 44 | Optical trapping dynamics for cell identification. , 2006, , . | | 0 |
| 45 | Decoding the transcriptional program for blood development from whole tissue single-cell gene expression measurements. Experimental Hematology, 2014, 42, S52. | 0.4 | 0 |
| 46 | Exit from HSC dormancy by a continuous upregulation of metabolism is controlled via vitamin A/retinoic acid. Experimental Hematology, 2016, 44, S54. | 0.4 | 0 |