

# Christoph Hafemeister

## List of Publications by Year in descending order

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16  
papers

15,599  
citations

759055

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times ranked

27567  
citing authors

#	ARTICLE	IF	CITATIONS
1	Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. <i>MSystems</i> , 2020, 5, .	1.7	14
2	Comprehensive Integration of Single-Cell Data. <i>Cell</i> , 2019, 177, 1888-1902.e21.	13.5	9,755
3	Normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression. <i>Genome Biology</i> , 2019, 20, 296.	3.8	2,460
4	Developmental diversification of cortical inhibitory interneurons. <i>Nature</i> , 2018, 555, 457-462.	13.7	393
5	Simultaneous epitope and transcriptome measurement in single cells. <i>Nature Methods</i> , 2017, 14, 865-868.	9.0	2,124
6	EGRINs (Environmental Gene Regulatory Influence Networks) in Rice That Function in the Response to Water Deficit, High Temperature, and Agricultural Environments. <i>Plant Cell</i> , 2016, 28, 2365-2384.	3.1	139
7	An experimentally supported model of the <i>Bacillus subtilis</i> global transcriptional regulatory network. <i>Molecular Systems Biology</i> , 2015, 11, 839.	3.2	186
8	Multiple abiotic stimuli are integrated in the regulation of rice gene expression under field conditions. <i>ELife</i> , 2015, 4, .	2.8	43
9	Inter-species pathway perturbation prediction via data-driven detection of functional homology. <i>Bioinformatics</i> , 2015, 31, 501-508.	1.8	6
10	Genotet: An Interactive Web-based Visual Exploration Framework to Support Validation of Gene Regulatory Networks. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2014, 20, 1903-1912.	2.9	11
11	Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks. <i>Bioinformatics</i> , 2013, 29, 1060-1067.	1.8	138
12	Identification of Global Alteration of Translational Regulation in Glioma In Vivo. <i>PLoS ONE</i> , 2012, 7, e46965.	1.1	21
13	Selecting Oligonucleotide Probes for Whole-Genome Tiling Arrays with a Cross-Hybridization Potential. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1642-1652.	1.9	3
14	Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions. <i>Bioinformatics</i> , 2011, 27, 946-952.	1.8	14
15	Constrained mixture estimation for analysis and robust classification of clinical time series. <i>Bioinformatics</i> , 2009, 25, i6-i14.	1.8	30
16	Inferring differentiation pathways from gene expression. <i>Bioinformatics</i> , 2008, 24, i156-i164.	1.8	16