Christoph Hafemeister

List of Publications by Year
in descending order

16 papers	15,599 citations	759233 12 h-index	940533 16 g-index
23 all docs	23 docs citations	23 times ranked	27567 citing authors

#	Article	IF	Citations
1	Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. MSystems, 2020, 5, .	3.8	14
2	Comprehensive Integration of Single-Cell Data. Cell, 2019, 177, 1888-1902.e21.	28.9	9,755
3	Normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression. Genome Biology, 2019, 20, 296.	8.8	2,460
4	Developmental diversification of cortical inhibitory interneurons. Nature, 2018, 555, 457-462.	27.8	393
5	Simultaneous epitope and transcriptome measurement in single cells. Nature Methods, 2017, 14, 865-868.	19.0	2,124
6	EGRINs (Environmental Gene Regulatory Influence Networks) in Rice That Function in the Response to Water Deficit, High Temperature, and Agricultural Environments. Plant Cell, 2016, 28, 2365-2384.	6.6	139
7	An experimentally supported model of the Bacillus subtilis global transcriptional regulatory network. Molecular Systems Biology, 2015, 11, 839.	7.2	186
8	Multiple abiotic stimuli are integrated in the regulation of rice gene expression under field conditions. ELife, 2015, 4, .	6.0	43
9	Inter-species pathway perturbation prediction via data-driven detection of functional homology. Bioinformatics, 2015, 31, 501-508.	4.1	6
10	Genotet: An Interactive Web-based Visual Exploration Framework to Support Validation of Gene Regulatory Networks. IEEE Transactions on Visualization and Computer Graphics, 2014, 20, 1903-1912.	4.4	11
11	Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks. Bioinformatics, 2013, 29, 1060-1067.	4.1	138
12	Identification of Global Alteration of Translational Regulation in Glioma In Vivo. PLoS ONE, 2012, 7, e46965.	2.5	21
13	Selecting Oligonucleotide Probes for Whole-Genome Tiling Arrays with a Cross-Hybridization Potential. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1642-1652.	3.0	3
14	Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions. Bioinformatics, 2011, 27, 946-952.	4.1	14
15	Constrained mixture estimation for analysis and robust classification of clinical time series. Bioinformatics, 2009, 25, i6-i14.	4.1	30
16	Inferring differentiation pathways from gene expression. Bioinformatics, 2008, 24, i156-i164.	4.1	16