Johannes Käster

List of Publications by Year
in descending order

31 papers	5,890 citations	394421 19 h-index	477307 29 g-index
42 all docs	42 docs citations	42 times ranked	12556 citing authors

#	Article	IF	Citations
1	Snakemake—a scalable bioinformatics workflow engine. Bioinformatics, 2012, 28, 2520-2522.	4.1	2,041
2	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
3	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
4	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	642
5	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. Genome Biology, 2015, 16, 281.	8.8	330
6	Mutational dynamics between primary and relapse neuroblastomas. Nature Genetics, 2015, 47, 872-877.	21.4	253
7	The Public Repository of Xenografts Enables Discovery and Randomized Phase II-like Trials in Mice. Cancer Cell, 2016, 29, 574-586.	16.8	227
8	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	188
9	VIPER: Visualization Pipeline for RNA-seq, a Snakemake workflow for efficient and complete RNA-seq analysis. BMC Bioinformatics, 2018, 19, 135.	2.6	156
10	Practical Computational Reproducibility in the Life Sciences. Cell Systems, 2018, 6, 631-635.	6.2	100
11	MiR-137 functions as a tumor suppressor in neuroblastoma by downregulating KDM1A. International Journal of Cancer, 2013, 133, 1064-1073.	5.1	91
12	SimLoRD: Simulation of Long Read Data. Bioinformatics, 2016, 32, 2704-2706.	4.1	81
13	CRISPR-DO for genome-wide CRISPR design and optimization. Bioinformatics, 2016, 32, 3336-3338.	4.1	46
14	Sensitivity to cdk1-inhibition is modulated by p53 status in preclinical models of embryonal tumors. Oncotarget, 2015, 6, 15425-15435.	1.8	37
15	Rust-Bio: a fast and safe bioinformatics library. Bioinformatics, 2016, 32, 444-446.	4.1	33
16	Full-length *de novo* viral quasispecies assembly through variation graph construction. Bioinformatics, 2019, 35, 5086-5094.	4.1	31
17	Targeting the innate immunoreceptor RIG-I overcomes melanoma-intrinsic resistance to T cell immunotherapy. Journal of Clinical Investigation, 2020, 130, 4266-4281.	8.2	27
18	Next-generation RNA sequencing reveals differential expression of MYCN target genes and suggests the mTOR pathway as a promising therapy target in *MYCN*-amplified neuroblastoma. International Journal of Cancer, 2013, 132, E106-15.	5.1	26

#	ARTICLE	IF	CITATIONS
19	Cancer evolution, mutations, and clonal selection in relapse neuroblastoma. Cell and Tissue Research, 2018, 372, 263-268.	2.9	21
20	Varlociraptor: enhancing sensitivity and controlling false discovery rate in somatic indel discovery. Genome Biology, 2020, 21, 98.	8.8	12
21	Identifying transcriptional miRNA biomarkers by integrating high-throughput sequencing and real-time PCR data. Methods, 2013, 59, 154-163.	3.8	10
22	Go Get Data (GGD) is a framework that facilitates reproducible access to genomic data. Nature Communications, 2021, 12, 2151.	12.8	9
23	Efficiently mining protein interaction dependencies from large text corpora. Integrative Biology (United Kingdom), 2012, 4, 805.	1.3	8
24	Accurate and scalable variant calling from single cell DNA sequencing data with ProSolo. Nature Communications, 2021, 12, 6744.	12.8	8
25	Modeling and simulating networks of interdependent protein interactions. Integrative Biology (United Kingdom), 2018, 10, 290-305.	1.3	7
26	A Bayesian model for single cell transcript expression analysis on MERFISH data. Bioinformatics, 2019, 35, 995-1001.	4.1	5
27	Massively parallel read mapping on GPUs with the q-group index and PEANUT. PeerJ, 2014, 2, e606.	2.0	3
28	Detection and Validation of Circular DNA Fragments Using Nanopore Sequencing. Frontiers in Genetics, 0, 13, .	2.3	3
29	VISPR-online: a web-based interactive tool to visualize CRISPR screening experiments. BMC Bioinformatics, 2021, 22, 344.	2.6	2
30	Proxe: A Public Repository of Xenografts to Facilitate Studies of Biology and Expedite Preclinical Drug Development in Leukemia and Lymphoma. Blood, 2015, 126, 3252-3252.	1.4	2
31	Protein Complex Similarity Based on Weisfeiler-Lehman Labeling. Lecture Notes in Computer Science, 2019, , 308-322.	1.3	1