

Johannes Käster

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2307647/publications.pdf>

Version: 2024-02-01

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	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	188
2	Go Get Data (GGD) is a framework that facilitates reproducible access to genomic data. Nature Communications, 2021, 12, 2151.	12.8	9
3	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	642
4	VISPR-online: a web-based interactive tool to visualize CRISPR screening experiments. BMC Bioinformatics, 2021, 22, 344.	2.6	2
5	Accurate and scalable variant calling from single cell DNA sequencing data with ProSolo. Nature Communications, 2021, 12, 6744.	12.8	8
6	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
7	Varlociraptor: enhancing sensitivity and controlling false discovery rate in somatic indel discovery. Genome Biology, 2020, 21, 98.	8.8	12
8	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
9	A Bayesian model for single cell transcript expression analysis on MERFISH data. Bioinformatics, 2019, 35, 995-1001.	4.1	5
10	Full-length <i>de novo</i> viral quasispecies assembly through variation graph construction. Bioinformatics, 2019, 35, 5086-5094.	4.1	31
11	Protein Complex Similarity Based on Weisfeiler-Lehman Labeling. Lecture Notes in Computer Science, 2019, , 308-322.	1.3	1
12	Cancer evolution, mutations, and clonal selection in relapse neuroblastoma. Cell and Tissue Research, 2018, 372, 263-268.	2.9	21
13	Modeling and simulating networks of interdependent protein interactions. Integrative Biology (United Kingdom), 2018, 10, 290-305.	1.3	7
14	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
15	Practical Computational Reproducibility in the Life Sciences. Cell Systems, 2018, 6, 631-635.	6.2	100
16	VIPER: Visualization Pipeline for RNA-seq, a Snakemake workflow for efficient and complete RNA-seq analysis. BMC Bioinformatics, 2018, 19, 135.	2.6	156
17	CRISPR-DO for genome-wide CRISPR design and optimization. Bioinformatics, 2016, 32, 3336-3338.	4.1	46
18	The Public Repository of Xenografts Enables Discovery and Randomized Phase II-like Trials in Mice. Cancer Cell, 2016, 29, 574-586.	16.8	227

#	ARTICLE	IF	CITATIONS
19	SimLoRD: Simulation of Long Read Data. <i>Bioinformatics</i> , 2016, 32, 2704-2706.	4.1	81
20	Rust-Bio: a fast and safe bioinformatics library. <i>Bioinformatics</i> , 2016, 32, 444-446.	4.1	33
21	Quality control, modeling, and visualization of CRISPR screens with MAGECK-VISPR. <i>Genome Biology</i> , 2015, 16, 281.	8.8	330
22	Mutational dynamics between primary and relapse neuroblastomas. <i>Nature Genetics</i> , 2015, 47, 872-877.	21.4	253
23	Proxe: A Public Repository of Xenografts to Facilitate Studies of Biology and Expedite Preclinical Drug Development in Leukemia and Lymphoma. <i>Blood</i> , 2015, 126, 3252-3252.	1.4	2
24	Sensitivity to cdk1-inhibition is modulated by p53 status in preclinical models of embryonal tumors. <i>Oncotarget</i> , 2015, 6, 15425-15435.	1.8	37
25	Massively parallel read mapping on GPUs with the <i>q</i> -group index and PEANUT. <i>PeerJ</i> , 2014, 2, e606.	2.0	3
26	MiR-137 functions as a tumor suppressor in neuroblastoma by downregulating KDM1A. <i>International Journal of Cancer</i> , 2013, 133, 1064-1073.	5.1	91
27	Identifying transcriptional miRNA biomarkers by integrating high-throughput sequencing and real-time PCR data. <i>Methods</i> , 2013, 59, 154-163.	3.8	10
28	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. <i>International Journal of Cancer</i> , 2013, 132, E106-15.	5.1	26
29	Snakemake—a scalable bioinformatics workflow engine. <i>Bioinformatics</i> , 2012, 28, 2520-2522.	4.1	2,041
30	Efficiently mining protein interaction dependencies from large text corpora. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 805.	1.3	8
31	Detection and Validation of Circular DNA Fragments Using Nanopore Sequencing. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3