

Tobias Jakobi

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,032
citations

516215

16
h-index

642321

23
g-index

24
all docs

24
docs citations

24
times ranked

1744
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-scale compression of genomic sequence databases with the Burrows-Wheeler transform. <i>Bioinformatics</i> , 2012, 28, 1415-1419.	1.8	118
2	Next-generation sequencing of the Chinese hamster ovary microRNA transcriptome: Identification, annotation and profiling of microRNAs as targets for cellular engineering. <i>Journal of Biotechnology</i> , 2011, 153, 62-75.	1.9	102
3	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. <i>Journal of Biotechnology</i> , 2011, 156, 227-235.	1.9	96
4	Integrin-linked kinase regulates the niche of quiescent epidermal stem cells. <i>Nature Communications</i> , 2015, 6, 8198.	5.8	83
5	ATF6 Regulates Cardiac Hypertrophy by Transcriptional Induction of the mTORC1 Activator, Rheb. <i>Circulation Research</i> , 2019, 124, 79-93.	2.0	80
6	Profiling and Validation of the Circular RNA Repertoire in Adult Murine Hearts. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 216-223.	3.0	79
7	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. <i>Bioinformatics</i> , 2011, 27, 1351-1358.	1.8	78
8	Monitoring Cell-Type-Specific Gene Expression Using Ribosome Profiling In Vivo During Cardiac Hemodynamic Stress. <i>Circulation Research</i> , 2019, 125, 431-448.	2.0	56
9	Computational approaches for circular RNA analysis. <i>Wiley Interdisciplinary Reviews RNA</i> , 2019, 10, e1528.	3.2	52
10	Computational identification of microRNA gene loci and precursor microRNA sequences in CHO cell lines. <i>Journal of Biotechnology</i> , 2012, 158, 151-155.	1.9	46
11	circtools—a one-stop software solution for circular RNA research. <i>Bioinformatics</i> , 2019, 35, 2326-2328.	1.8	46
12	Increased susceptibility of human endothelial cells to infections by SARS-CoV-2 variants. <i>Basic Research in Cardiology</i> , 2021, 116, 42.	2.5	33
13	ADAR-deficiency perturbs the global splicing landscape in mouse tissues. <i>Genome Research</i> , 2020, 30, 1107-1118.	2.4	32
14	Deep Characterization of Circular RNAs from Human Cardiovascular Cell Models and Cardiac Tissue. <i>Cells</i> , 2020, 9, 1616.	1.8	22
15	Early Response of <i>Sulfolobus acidocaldarius</i> to Nutrient Limitation. <i>Frontiers in Microbiology</i> , 2018, 9, 3201.	1.5	21
16	Deep Computational Circular RNA Analytics from RNA-seq Data. <i>Methods in Molecular Biology</i> , 2018, 1724, 9-25.	0.4	18
17	Proteomic analysis of the cardiac myocyte secretome reveals extracellular protective functions for the ER stress response. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 143, 132-144.	0.9	14
18	Comparing DNA Sequence Collections by Direct Comparison of Compressed Text Indexes. <i>Lecture Notes in Computer Science</i> , 2012, , 214-224.	1.0	12

#	ARTICLE	IF	CITATIONS
19	TRUNCATULIX - a data warehouse for the legume community. BMC Plant Biology, 2009, 9, 19.	1.6	11
20	Next-generation sequencing of the CHO cell transcriptome. BMC Proceedings, 2011, 5, P6.	1.8	11
21	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. Journal of Biotechnology, 2014, 190, 64-75.	1.9	9
22	Identification of Methylated Transcripts Using the TRIBE Approach. Methods in Molecular Biology, 2019, 1870, 89-106.	0.4	8
23	Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. Frontiers in Genetics, 2016, 7, 5.	1.1	4