Tobias Jakobi

List of Publications by Year in descending order

23 papers	1,032 citations	516710 16 h-index	642732 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 Burrowsâ€“Wheeler transform. Bioinformatics, 2012, 28, 1415-1419.	4.1	118
2	Next-generation sequencing of the Chinese hamster ovary microRNA transcriptome: Identification, annotation and profiling of microRNAs as targets for cellular engineering. Journal of Biotechnology, 2011, 153, 62-75.	3.8	102
3	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. Journal of Biotechnology, 2011, 156, 227-235.	3.8	96
4	Integrin-linked kinase regulates the niche of quiescent epidermal stem cells. Nature Communications, 2015, 6, 8198.	12.8	83
5	ATF6 Regulates Cardiac Hypertrophy by Transcriptional Induction of the mTORC1 Activator, Rheb. Circulation Research, 2019, 124, 79-93.	4.5	80
6	Profiling and Validation of the Circular RNA Repertoire in Adult Murine Hearts. Genomics, Proteomics and Bioinformatics, 2016, 14, 216-223.	6.9	79
7	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. Bioinformatics, 2011, 27, 1351-1358.	4.1	78
8	Monitoring Cell-Typeâ€“Specific Gene Expression Using Ribosome Profiling In Vivo During Cardiac Hemodynamic Stress. Circulation Research, 2019, 125, 431-448.	4.5	56
9	Computational approaches for circular RNA analysis. Wiley Interdisciplinary Reviews RNA, 2019, 10, e1528.	6.4	52
10	Computational identification of microRNA gene loci and precursor microRNA sequences in CHO cell lines. Journal of Biotechnology, 2012, 158, 151-155.	3.8	46
11	circtoolsâ€”a one-stop software solution for circular RNA research. Bioinformatics, 2019, 35, 2326-2328.	4.1	46
12	Increased susceptibility of human endothelial cells to infections by SARS-CoV-2 variants. Basic Research in Cardiology, 2021, 116, 42.	5.9	33
13	ADAR-deficiency perturbs the global splicing landscape in mouse tissues. Genome Research, 2020, 30, 1107-1118.	5.5	32
14	Deep Characterization of Circular RNAs from Human Cardiovascular Cell Models and Cardiac Tissue. Cells, 2020, 9, 1616.	4.1	22
15	Early Response of Sulfolobus acidocaldarius to Nutrient Limitation. Frontiers in Microbiology, 2018, 9, 3201.	3.5	21
16	Deep Computational Circular RNA Analytics from RNA-seq Data. Methods in Molecular Biology, 2018, 1724, 9-25.	0.9	18
17	Proteomic analysis of the cardiac myocyte secretome reveals extracellular protective functions for the ER stress response. Journal of Molecular and Cellular Cardiology, 2020, 143, 132-144.	1.9	14
18	Comparing DNA Sequence Collections by Direct Comparison of Compressed Text Indexes. Lecture Notes in Computer Science, 2012, , 214-224.	1.3	12

#	Article	IF	Citations
19	TRUNCATULIX - a data warehouse for the legume community. BMC Plant Biology, 2009, 9, 19.	3.6	11
20	Next-generation sequencing of the CHO cell transcriptome. BMC Proceedings, 2011, 5, P6.	1.6	11
21	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. Journal of Biotechnology, 2014, 190, 64-75.	3.8	9
22	Identification of Methylated Transcripts Using the TRIBE Approach. Methods in Molecular Biology, 2019, 1870, 89-106.	0.9	8
23	Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. Frontiers in Genetics, 2016, 7, 5.	2.3	4