Tobias Jakobi

List of Publications by Year in Descending Order

23 papers	723 citations	13 h-index	24 g-index
24 ext. papers	902 ext. citations	6.5 avg, IF	4.07 L-index

#	Paper	IF	Citations
23	Increased susceptibility of human endothelial cells to infections by SARS-CoV-2 variants. *Basic Research in Cardiology*, **2021**, 116, 42	11.8	11
22	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	5.8	9
21	Deep Characterization of Circular RNAs from Human Cardiovascular Cell Models and Cardiac Tissue. *Cells*, **2020**, 9,	7.9	14
20	ADAR-deficiency perturbs the global splicing landscape in mouse tissues. *Genome Research*, **2020**, 30, 1107-1118	9.7	10
19	Computational approaches for circular RNA analysis. *Wiley Interdisciplinary Reviews RNA*, **2019**, 10, e1528	9.3	29
18	Monitoring Cell-Type-Specific Gene Expression Using Ribosome Profiling In Vivo During Cardiac Hemodynamic Stress. *Circulation Research*, **2019**, 125, 431-448	15.7	18
17	circtools-a one-stop software solution for circular RNA research. *Bioinformatics*, **2019**, 35, 2326-2328	7.2	20
16	ATF6 Regulates Cardiac Hypertrophy by Transcriptional Induction of the mTORC1 Activator, Rheb. *Circulation Research*, **2019**, 124, 79-93	15.7	50
15	Identification of Methylated Transcripts Using the TRIBE Approach. *Methods in Molecular Biology*, **2019**, 1870, 89-106	1.4	6
14	Deep Computational Circular RNA Analytics from RNA-seq Data. *Methods in Molecular Biology*, **2018**, 1724, 9-25	1.4	15
13	Early Response of to Nutrient Limitation. *Frontiers in Microbiology*, **2018**, 9, 3201	5.7	9
12	Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. *Frontiers in Genetics*, **2016**, 7, 5	4.5	2
11	Profiling and Validation of the Circular RNA Repertoire in Adult Murine Hearts. *Genomics, Proteomics and Bioinformatics*, **2016**, 14, 216-23	6.5	59
10	Integrin-linked kinase regulates the niche of quiescent epidermal stem cells. *Nature Communications*, **2015**, 6, 8198	17.4	58
9	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. *Journal of Biotechnology*, **2014**, 190, 64-75	3.7	7
8	Computational identification of microRNA gene loci and precursor microRNA sequences in CHO cell lines. *Journal of Biotechnology*, **2012**, 158, 151-5	3.7	37
7	Comparing DNA Sequence Collections by Direct Comparison of Compressed Text Indexes. *Lecture Notes in Computer Science*, **2012**, 214-224	0.9	11

LIST OF PUBLICATIONS

6	Large-scale compression of genomic sequence databases with the Burrows-Wheeler transform. *Bioinformatics*, **2012**, 28, 1415-9	7.2	85
5	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. *Journal of Biotechnology*, **2011**, 156, 227-35	3.7	88
4	Next-generation sequencing of the CHO cell transcriptome. *BMC Proceedings*, **2011**, 5 Suppl 8, P6	2.3	10
3	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	3.7	95
2	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. *Bioinformatics*, **2011**, 27, 1351-8	7.2	71
1	TRUNCATULIX--a data warehouse for the legume community. *BMC Plant Biology*, **2009**, 9, 19	5.3	9