

# Tobias Jakobi

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/4265853/tobias-jakobi-publications-by-citations.pdf>

**Version:** 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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> , <b>2011</b> , 153, 62-75	3.7	95
22	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. <i>Journal of Biotechnology</i> , <b>2011</b> , 156, 227-35	3.7	88
21	Large-scale compression of genomic sequence databases with the Burrows-Wheeler transform. <i>Bioinformatics</i> , <b>2012</b> , 28, 1415-9	7.2	85
20	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. <i>Bioinformatics</i> , <b>2011</b> , 27, 1351-8	7.2	71
19	Profiling and Validation of the Circular RNA Repertoire in Adult Murine Hearts. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2016</b> , 14, 216-23	6.5	59
18	Integrin-linked kinase regulates the niche of quiescent epidermal stem cells. <i>Nature Communications</i> , <b>2015</b> , 6, 8198	17.4	58
17	ATF6 Regulates Cardiac Hypertrophy by Transcriptional Induction of the mTORC1 Activator, Rheb. <i>Circulation Research</i> , <b>2019</b> , 124, 79-93	15.7	50
16	Computational identification of microRNA gene loci and precursor microRNA sequences in CHO cell lines. <i>Journal of Biotechnology</i> , <b>2012</b> , 158, 151-5	3.7	37
15	Computational approaches for circular RNA analysis. <i>Wiley Interdisciplinary Reviews RNA</i> , <b>2019</b> , 10, e1528	3.3	29
14	circtools-a one-stop software solution for circular RNA research. <i>Bioinformatics</i> , <b>2019</b> , 35, 2326-2328	7.2	20
13	Monitoring Cell-Type-Specific Gene Expression Using Ribosome Profiling In Vivo During Cardiac Hemodynamic Stress. <i>Circulation Research</i> , <b>2019</b> , 125, 431-448	15.7	18
12	Deep Computational Circular RNA Analytics from RNA-seq Data. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1724, 9-25	1.4	15
11	Deep Characterization of Circular RNAs from Human Cardiovascular Cell Models and Cardiac Tissue. <i>Cells</i> , <b>2020</b> , 9,	7.9	14
10	Comparing DNA Sequence Collections by Direct Comparison of Compressed Text Indexes. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 214-224	0.9	11
9	Increased susceptibility of human endothelial cells to infections by SARS-CoV-2 variants. <i>Basic Research in Cardiology</i> , <b>2021</b> , 116, 42	11.8	11
8	Next-generation sequencing of the CHO cell transcriptome. <i>BMC Proceedings</i> , <b>2011</b> , 5 Suppl 8, P6	2.3	10
7	ADAR-deficiency perturbs the global splicing landscape in mouse tissues. <i>Genome Research</i> , <b>2020</b> , 30, 1107-1118	9.7	10

6	Proteomic analysis of the cardiac myocyte secretome reveals extracellular protective functions for the ER stress response. <i>Journal of Molecular and Cellular Cardiology</i> , <b>2020</b> , 143, 132-144	5.8	9
5	TRUNCATULIX--a data warehouse for the legume community. <i>BMC Plant Biology</i> , <b>2009</b> , 9, 19	5.3	9
4	Early Response of to Nutrient Limitation. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 3201	5.7	9
3	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. <i>Journal of Biotechnology</i> , <b>2014</b> , 190, 64-75	3.7	7
2	Identification of Methylated Transcripts Using the TRIBE Approach. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1870, 89-106	1.4	6
1	Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. <i>Frontiers in Genetics</i> , <b>2016</b> , 7, 5	4.5	2