

Julia Salzman

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1259349/julia-salzman-publications-by-citations.pdf>

Version: 2024-04-27

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.

36

papers

6,065

citations

18

h-index

46

g-index

46

ext. papers

7,531

ext. citations

8.9

avg, IF

6.52

L-index

#	Paper	IF	Citations
36	Circular RNAs are the predominant transcript isoform from hundreds of human genes in diverse cell types. <i>PLoS ONE</i> , 2012 , 7, e30733	3.7	1531
35	Cell-type specific features of circular RNA expression. <i>PLoS Genetics</i> , 2013 , 9, e1003777	6	1155
34	Circular RNAs: analysis, expression and potential functions. <i>Development (Cambridge)</i> , 2016 , 143, 1838-47.6	4.6	500
33	Circular RNA Expression: Its Potential Regulation and Function. <i>Trends in Genetics</i> , 2016 , 32, 309-316	8.5	471
32	Circular RNA is expressed across the eukaryotic tree of life. <i>PLoS ONE</i> , 2014 , 9, e90859	3.7	457
31	Detecting circular RNAs: bioinformatic and experimental challenges. <i>Nature Reviews Genetics</i> , 2016 , 17, 679-692	30.1	381
30	Statistically based splicing detection reveals neural enrichment and tissue-specific induction of circular RNA during human fetal development. <i>Genome Biology</i> , 2015 , 16, 126	18.3	363
29	Circular RNA biogenesis can proceed through an exon-containing lariat precursor. <i>ELife</i> , 2015 , 4, e075408.9	9	276
28	Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome. <i>ISME Journal</i> , 2012 , 6, 915-26	11.9	211
27	Proteome-wide search reveals unexpected RNA-binding proteins in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2010 , 5, e12671	3.7	121
26	Human oral viruses are personal, persistent and gender-consistent. <i>ISME Journal</i> , 2014 , 8, 1753-67	11.9	107
25	Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. <i>Genome Research</i> , 2011 , 21, 126-36	9.7	90
24	Association between living environment and human oral viral ecology. <i>ISME Journal</i> , 2013 , 7, 1710-24	11.9	73
23	Statistical Modeling of RNA-Seq Data. <i>Statistical Science</i> , 2011 , 26,	2.4	53
22	Comparisons of clustered regularly interspaced short palindromic repeats and viromes in human saliva reveal bacterial adaptations to salivary viruses. <i>Environmental Microbiology</i> , 2012 , 14, 2564-76	5.2	51
21	ciRS-7 exonic sequence is embedded in a long non-coding RNA locus. <i>PLoS Genetics</i> , 2017 , 13, e1007114.6	6	48
20	ESRRA-C11orf20 is a recurrent gene fusion in serous ovarian carcinoma. <i>PLoS Biology</i> , 2011 , 9, e1001156.9.7	9.7	44

19	Extensive site-directed mutagenesis reveals interconnected functional units in the alkaline phosphatase active site. <i>ELife</i> , 2015 , 4,	8.9	44
18	Improved detection of gene fusions by applying statistical methods reveals oncogenic RNA cancer drivers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 15524-15533 ¹⁶	11.5	16
17	Statistical algorithms improve accuracy of gene fusion detection. <i>Nucleic Acids Research</i> , 2017 , 45, e126	20.1	9
16	Specific splice junction detection in single cells with SICILIAN. <i>Genome Biology</i> , 2021 , 22, 219	18.3	7
15	Hyperammonemia after capecitabine associated with occult impairment of the urea cycle. <i>Cancer Medicine</i> , 2019 , 8, 1996-2004	4.8	6
14	A penalized likelihood approach for robust estimation of isoform expression. <i>Statistics and Its Interface</i> , 2015 , 8, 437-445	0.4	6
13	Ambiguous splice sites distinguish circRNA and linear splicing in the human genome. <i>Bioinformatics</i> , 2019 , 35, 1263-1268	7.2	6
12	Specific splice junction detection in single cells with SICILIAN		5
11	RNA splicing programs define tissue compartments and cell types at single-cell resolution. <i>ELife</i> , 2021 , 10,	8.9	5
10	High-throughput SARS-CoV-2 and host genome sequencing from single nasopharyngeal swabs 2020 ,		4
9	The SpliZ generalizes Percent Spliced In to reveal regulated splicing at single-cell resolution		3
8	Improved discovery of molecular interactions in genome-scale data with adaptive model-based normalization. <i>PLoS ONE</i> , 2013 , 8, e53930	3.7	2
7	Author response: Circular RNA biogenesis can proceed through an exon-containing lariat precursor 2015 ,		2
6	ciRS-7 exonic sequence is embedded in a long non-coding RNA locus		1
5	RNA splicing programs define tissue compartments and cell types at single cell resolution		1
4	The SpliZ generalizes 'percent spliced in' to reveal regulated splicing at single-cell resolution.. <i>Nature Methods</i> , 2022 , 19, 307-310	21.6	1
3	Discovery of gene regulatory elements through a new bioinformatics analysis of haploid genetic screens. <i>PLoS ONE</i> , 2019 , 14, e0198463	3.7	
2	A novel statistical methodology to detect gene fusions in RNA-Seq data.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 11575-11575	2.2	

1

Molecular sampling at logarithmic rates for next-generation sequencing. *PLoS Computational Biology*, **2019**, 15, e1007537

5