

Julia Salzman

List of Publications by Year in Descending Order

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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	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
35	Specific splice junction detection in single cells with SICILIAN. <i>Genome Biology</i> , 2021 , 22, 219	18.3	7
34	RNA splicing programs define tissue compartments and cell types at single-cell resolution. <i>ELife</i> , 2021 , 10,	8.9	5
33	High-throughput SARS-CoV-2 and host genome sequencing from single nasopharyngeal swabs 2020 ,		4
32	Hyperammonemia after capecitabine associated with occult impairment of the urea cycle. <i>Cancer Medicine</i> , 2019 , 8, 1996-2004	4.8	6
31	Discovery of gene regulatory elements through a new bioinformatics analysis of haploid genetic screens. <i>PLoS ONE</i> , 2019 , 14, e0198463	3.7	
30	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
29	Molecular sampling at logarithmic rates for next-generation sequencing. <i>PLoS Computational Biology</i> , 2019 , 15, e1007537	5	
28	Ambiguous splice sites distinguish circRNA and linear splicing in the human genome. <i>Bioinformatics</i> , 2019 , 35, 1263-1268	7.2	6
27	Statistical algorithms improve accuracy of gene fusion detection. <i>Nucleic Acids Research</i> , 2017 , 45, e126	20.1	9
26	ciRS-7 exonic sequence is embedded in a long non-coding RNA locus. <i>PLoS Genetics</i> , 2017 , 13, e1007114	6	48
25	Detecting circular RNAs: bioinformatic and experimental challenges. <i>Nature Reviews Genetics</i> , 2016 , 17, 679-692	30.1	381
24	Circular RNAs: analysis, expression and potential functions. <i>Development (Cambridge)</i> , 2016 , 143, 1838-47	47.6	500
23	A novel statistical methodology to detect gene fusions in RNA-Seq data.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 11575-11575	2.2	
22	Circular RNA Expression: Its Potential Regulation and Function. <i>Trends in Genetics</i> , 2016 , 32, 309-316	8.5	471
21	Circular RNA biogenesis can proceed through an exon-containing lariat precursor. <i>ELife</i> , 2015 , 4, e075408	9	276
20	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

19	A penalized likelihood approach for robust estimation of isoform expression. <i>Statistics and Its Interface</i> , 2015 , 8, 437-445	0.4	6
18	Extensive site-directed mutagenesis reveals interconnected functional units in the alkaline phosphatase active site. <i>ELife</i> , 2015 , 4,	8.9	44
17	Author response: Circular RNA biogenesis can proceed through an exon-containing lariat precursor 2015 ,		2
16	Human oral viruses are personal, persistent and gender-consistent. <i>ISME Journal</i> , 2014 , 8, 1753-67	11.9	107
15	Circular RNA is expressed across the eukaryotic tree of life. <i>PLoS ONE</i> , 2014 , 9, e90859	3.7	457
14	Association between living environment and human oral viral ecology. <i>ISME Journal</i> , 2013 , 7, 1710-24	11.9	73
13	Cell-type specific features of circular RNA expression. <i>PLoS Genetics</i> , 2013 , 9, e1003777	6	1155
12	Improved discovery of molecular interactions in genome-scale data with adaptive model-based normalization. <i>PLoS ONE</i> , 2013 , 8, e53930	3.7	2
11	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
10	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
9	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
8	Statistical Modeling of RNA-Seq Data. <i>Statistical Science</i> , 2011 , 26,	2.4	53
7	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
6	ESRRA-C11orf20 is a recurrent gene fusion in serous ovarian carcinoma. <i>PLoS Biology</i> , 2011 , 9, e1001156	9.7	44
5	Proteome-wide search reveals unexpected RNA-binding proteins in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2010 , 5, e12671	3.7	121
4	ciRS-7 exonic sequence is embedded in a long non-coding RNA locus		1
3	Specific splice junction detection in single cells with SICILIAN		5
2	The SpliZ generalizes Percent Spliced In to reveal regulated splicing at single-cell resolution		3

1 RNA splicing programs define tissue compartments and cell types at single cell resolution

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