Julia Salzman

List of Publications by Year
in descending order

30 papers	**8,317** citations	394286 **19** h-index	501076 **28** g-index
46 all docs	**46** docs citations	**46** times ranked	**8575** citing authors

#	Article	IF	Citations
1	Circular RNAs Are the Predominant Transcript Isoform from Hundreds of Human Genes in Diverse Cell Types. PLoS ONE, 2012, 7, e30733.	1.1	2,088
2	Cell-Type Specific Features of Circular RNA Expression. PLoS Genetics, 2013, 9, e1003777.	1.5	1,544
3	Circular RNAs: analysis, expression and potential functions. Development (Cambridge), 2016, 143, 1838-1847.	1.2	698
4	Circular RNA Expression: Its Potential Regulation and Function. Trends in Genetics, 2016, 32, 309-316.	2.9	678
5	Circular RNA Is Expressed across the Eukaryotic Tree of Life. PLoS ONE, 2014, 9, e90859.	1.1	585
6	Detecting circular RNAs: bioinformatic and experimental challenges. Nature Reviews Genetics, 2016, 17, 679-692.	7.7	554
7	Statistically based splicing detection reveals neural enrichment and tissue-specific induction of circular RNA during human fetal development. Genome Biology, 2015, 16, 126.	3.8	507
8	Circular RNA biogenesis can proceed through an exon-containing lariat precursor. ELife, 2015, 4, e07540.	2.8	377
9	Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome. ISME Journal, 2012, 6, 915-926.	4.4	295
10	Human oral viruses are personal, persistent and gender-consistent. ISME Journal, 2014, 8, 1753-1767.	4.4	159
11	Proteome-Wide Search Reveals Unexpected RNA-Binding Proteins in Saccharomyces cerevisiae. PLoS ONE, 2010, 5, e12671.	1.1	146
12	Association between living environment and human oral viral ecology. ISME Journal, 2013, 7, 1710-1724.	4.4	108
13	Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. Genome Research, 2011, 21, 126-136.	2.4	104
14	ciRS-7 exonic sequence is embedded in a long non-coding RNA locus. PLoS Genetics, 2017, 13, e1007114.	1.5	66
15	Statistical Modeling of RNA-Seq Data. Statistical Science, 2011, 26, .	1.6	64
16	Comparisons of clustered regularly interspaced short palindromic repeats and viromes in human saliva reveal bacterial adaptations to salivary viruses. Environmental Microbiology, 2012, 14, 2564-2576.	1.8	57
17	Extensive site-directed mutagenesis reveals interconnected functional units in the alkaline phosphatase active site. ELife, 2015, 4, .	2.8	57
18	ESRRA-C11orf20 Is a Recurrent Gene Fusion in Serous Ovarian Carcinoma. PLoS Biology, 2011, 9, e1001156.	2.6	50

#	Article	IF	Citations
19	Improved detection of gene fusions by applying statistical methods reveals oncogenic RNA cancer drivers. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15524-15533.	3.3	25
20	RNA splicing programs define tissue compartments and cell types at single-cell resolution. ELife, 2021, 10, .	2.8	24
21	The SpliZ generalizes â€˜percent spliced inâ€™ to reveal regulated splicing at single-cell resolution. Nature Methods, 2022, 19, 307-310.	9.0	16
22	Statistical algorithms improve accuracy of gene fusion detection. Nucleic Acids Research, 2017, 45, e126-e126.	6.5	13
23	Specific splice junction detection in single cells with SICILIAN. Genome Biology, 2021, 22, 219.	3.8	12
24	A penalized likelihood approach for robust estimation of isoform expression. Statistics and Its Interface, 2015, 8, 437-445.	0.2	11
25	Hyperammonemia after capecitabine associated with occult impairment of the urea cycle. Cancer Medicine, 2019, 8, 1996-2004.	1.3	8
26	Ambiguous splice sites distinguish circRNA and linear splicing in the human genome. Bioinformatics, 2019, 35, 1263-1268.	1.8	8
27	Improved Discovery of Molecular Interactions in Genome-Scale Data with Adaptive Model-Based Normalization. PLoS ONE, 2013, 8, e53930.	1.1	2
28	Discovery of gene regulatory elements through a new bioinformatics analysis of haploid genetic screens. PLoS ONE, 2019, 14, e0198463.	1.1	0
29	Molecular sampling at logarithmic rates for next-generation sequencing. PLoS Computational Biology, 2019, 15, e1007537.	1.5	0
30	A novel statistical methodology to detect gene fusions in RNA-Seq data.. Journal of Clinical Oncology, 2016, 34, 11575-11575.	0.8	0