

# Stefan L Ameres

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

5,000  
citations

331670

21  
h-index

395702

33  
g-index

42  
all docs

42  
docs citations

42  
times ranked

7308  
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversifying microRNA sequence and function. <i>Nature Reviews Molecular Cell Biology</i> , 2013, 14, 475-488.	37.0	1,066
2	Target RNA-directed Trimming and Tailing of Small Silencing RNAs. <i>Science</i> , 2010, 328, 1534-1539.	12.6	514
3	Molecular Basis for Target RNA Recognition and Cleavage by Human RISC. <i>Cell</i> , 2007, 130, 101-112.	28.9	491
4	Thiol-linked alkylation of RNA to assess expression dynamics. <i>Nature Methods</i> , 2017, 14, 1198-1204.	19.0	411
5	Cleavage of the siRNA passenger strand during RISC assembly in human cells. <i>EMBO Reports</i> , 2006, 7, 314-320.	4.5	340
6	Small RNAs Are Trafficked from the Epididymis to Developing Mammalian Sperm. <i>Developmental Cell</i> , 2018, 46, 481-494.e6.	7.0	287
7	SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. <i>Science</i> , 2018, 360, 800-805.	12.6	284
8	The impact of target site accessibility on the design of effective siRNAs. <i>Nature Biotechnology</i> , 2008, 26, 578-583.	17.5	262
9	Long-term, efficient inhibition of microRNA function in mice using rAAV vectors. <i>Nature Methods</i> , 2012, 9, 403-409.	19.0	188
10	The 3'-to-5' Exoribonuclease Nibbler Shapes the 3' Ends of MicroRNAs Bound to Drosophila Argonaute1. <i>Current Biology</i> , 2011, 21, 1878-1887.	3.9	143
11	MicroRNA-regulated, Systemically Delivered rAAV9: A Step Closer to CNS-restricted Transgene Expression. <i>Molecular Therapy</i> , 2011, 19, 526-535.	8.2	143
12	Time-Resolved Small RNA Sequencing Unravels the Molecular Principles of MicroRNA Homeostasis. <i>Molecular Cell</i> , 2019, 75, 756-768.e7.	9.7	116
13	Genetic and mechanistic diversity of piRNA 3'-end formation. <i>Nature</i> , 2016, 539, 588-592.	27.8	115
14	Quantification of experimentally induced nucleotide conversions in high-throughput sequencing datasets. <i>BMC Bioinformatics</i> , 2019, 20, 258.	2.6	86
15	Cell-type specific sequencing of microRNAs from complex animal tissues. <i>Nature Methods</i> , 2018, 15, 283-289.	19.0	68
16	Conformation of sister chromatids in the replicated human genome. <i>Nature</i> , 2020, 586, 139-144.	27.8	68
17	Uridylation of RNA Hairpins by Tailor Confines the Emergence of MicroRNAs in Drosophila. <i>Molecular Cell</i> , 2015, 59, 203-216.	9.7	62
18	Selective Suppression of the Splicing-Mediated MicroRNA Pathway by the Terminal Uridyltransferase Tailor. <i>Molecular Cell</i> , 2015, 59, 217-228.	9.7	58

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19	Target RNA-directed tailing and trimming purifies the sorting of endo-siRNAs between the two <i>Drosophila</i> Argonaute proteins. <i>Rna</i> , 2011, 17, 54-63.	3.5	51
20	Molecular basis for cytoplasmic RNA surveillance by uridylation-triggered decay in <i>Drosophila</i> . <i>EMBO Journal</i> , 2016, 35, 2417-2434.	7.8	50
21	Inducible DNA-loop formation blocks transcriptional activation by an SV40 enhancer. <i>EMBO Journal</i> , 2005, 24, 358-367.	7.8	44
22	SLAM-ITseq: Sequencing cell type-specific transcriptomes without cell sorting. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	29
23	Positioning Europe for the EPITRANSCRIPTOMICS challenge. <i>RNA Biology</i> , 2018, 15, 1-3.	3.1	18
24	NMD is required for timely cell fate transitions by fine-tuning gene expression and regulating translation. <i>Genes and Development</i> , 2022, 36, 348-367.	5.9	17
25	RNA chaperone activity of L1 ribosomal proteins: phylogenetic conservation and splicing inhibition. <i>Nucleic Acids Research</i> , 2007, 35, 3752-3763.	14.5	14
26	Approaching the Golden Fleece a Molecule at a Time: Biophysical Insights into Argonaute-Instructed Nucleic Acid Interactions. <i>Molecular Cell</i> , 2015, 59, 4-7.	9.7	13
27	Structural basis for acceptor RNA substrate selectivity of the 3' terminal uridylyl transferase Tailor. <i>Nucleic Acids Research</i> , 2019, 47, 1030-1042.	14.5	13
28	Sequencing cell-type-specific transcriptomes with SLAM-ITseq. <i>Nature Protocols</i> , 2019, 14, 2261-2278.	12.0	13
29	Structure-function analysis of microRNA 3'-end trimming by Nibbler. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30370-30379.	7.1	9
30	Determining mRNA Stability by Metabolic RNA Labeling and Chemical Nucleoside Conversion. <i>Methods in Molecular Biology</i> , 2020, 2062, 169-189.	0.9	7
31	Riding in silence: a little snowboarding, a lot of small RNAs. <i>Silence: A Journal of RNA Regulation</i> , 2010, 1, 8.	8.1	4
32	Analysis of 3' End Modifications in microRNAs by High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1823, 115-139.	0.9	3
33	Systematic refinement of gene annotations by parsing mRNA 3' end sequencing datasets. <i>Methods in Enzymology</i> , 2021, 655, 205-223.	1.0	2
34	MicroRNome by methylation-dependent sequencing (mime-seq). <i>Protocol Exchange</i> , 0, , .	0.3	1
35	Transcriptome-Wide Profiling of RNA Stability. <i>Methods in Molecular Biology</i> , 2022, 2404, 311-330.	0.9	0