

Andreas R Gruber

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

5,158
citations

257101

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580395

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all docs

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docs citations

27
times ranked

8709
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of physiological and cancer-related regulators of 3' UTR processing with KAPAC. <i>Genome Biology</i> , 2018, 19, 44.	3.8	54
2	A comprehensive analysis of 3' end sequencing data sets reveals novel polyadenylation signals and the repressive role of heterogeneous ribonucleoprotein C on cleavage and polyadenylation. <i>Genome Research</i> , 2016, 26, 1145-1159.	2.4	196
3	Roquin recognizes a non-canonical hexaloop structure in the 3'-UTR of Ox40. <i>Nature Communications</i> , 2016, 7, 11032.	5.8	38
4	An updated human snoRNAome. <i>Nucleic Acids Research</i> , 2016, 44, 5068-5082.	6.5	216
5	Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. <i>Genome Biology</i> , 2015, 16, 150.	13.9	126
6	The ViennaRNA Web Services. <i>Methods in Molecular Biology</i> , 2015, 1269, 307-326.	0.4	135
7	Means to an end: mechanisms of alternative polyadenylation of messenger <i>scn</i> RNA precursors. <i>Wiley Interdisciplinary Reviews RNA</i> , 2014, 5, 183-196.	3.2	68
8	Reconstitution of CPSF active in polyadenylation: recognition of the polyadenylation signal by WDR33. <i>Genes and Development</i> , 2014, 28, 2381-2393.	2.7	201
9	Global 3' UTR shortening has a limited effect on protein abundance in proliferating T cells. <i>Nature Communications</i> , 2014, 5, 5465.	5.8	164
10	RNA Polymerase III promoter screen uncovers a novel noncoding RNA family conserved in <i>Caenorhabditis</i> and other clade V nematodes. <i>Gene</i> , 2014, 544, 236-240.	1.0	2
11	Translation-dependent displacement of UPF1 from coding sequences causes its enrichment in 3' UTRs. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 936-943.	3.6	155
12	Insights into snoRNA biogenesis and processing from PAR-CLIP of snoRNA core proteins and small RNA sequencing. <i>Genome Biology</i> , 2013, 14, R45.	13.9	129
13	Genome-wide Analysis of Pre-mRNA 3' End Processing Reveals a Decisive Role of Human Cleavage Factor I in the Regulation of 3' UTR Length. <i>Cell Reports</i> , 2012, 1, 753-763.	2.9	341
14	Cleavage factor I _m is a key regulator of 3' UTR length. <i>RNA Biology</i> , 2012, 9, 1405-1412.	1.5	125
15	AREsite: a database for the comprehensive investigation of AU-rich elements. <i>Nucleic Acids Research</i> , 2011, 39, D66-D69.	6.5	140
16	Tristetraprolin-driven regulatory circuit controls quality and timing of mRNA decay in inflammation. <i>Molecular Systems Biology</i> , 2011, 7, 560.	3.2	110
17	Animal snoRNAs and scaRNAs with exceptional structures. <i>RNA Biology</i> , 2011, 8, 938-946.	1.5	30
18	Nematode sbRNAs: Homologs of Vertebrate Y RNAs. <i>Journal of Molecular Evolution</i> , 2010, 70, 346-358.	0.8	32

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19	Invertebrate 7SK snRNAs. <i>Journal of Molecular Evolution</i> , 2008, 66, 107-115.	0.8	37
20	Strategies for measuring evolutionary conservation of RNA secondary structures. <i>BMC Bioinformatics</i> , 2008, 9, 122.	1.2	63
21	RNAalifold: improved consensus structure prediction for RNA alignments. <i>BMC Bioinformatics</i> , 2008, 9, 474.	1.2	505
22	Arthropod 7SK RNA. <i>Molecular Biology and Evolution</i> , 2008, 25, 1923-1930.	3.5	45
23	The Vienna RNA Websuite. <i>Nucleic Acids Research</i> , 2008, 36, W70-W74.	6.5	2,012
24	The RNAz web server: prediction of thermodynamically stable and evolutionarily conserved RNA structures. <i>Nucleic Acids Research</i> , 2007, 35, W335-W338.	6.5	84
25	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	2.4	150
26	Mapping Protein-RNA Interactions by CLIP. <i>Materials and Methods</i> , 0, 1, .	0.0	0