Andreas R Gruber

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Discovery of physiological and cancer-related regulators of 3′ UTR processing with KAPAC. Genome Biology, 2018, 19, 44.	8.8	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. Genome Research, 2016, 26, 1145-1159.	5.5	196
3	Roquin recognizes a non-canonical hexaloop structure in the 3′-UTR of Ox40. Nature Communications, 2016, 7, 11032.	12.8	38
4	An updated human snoRNAome. Nucleic Acids Research, 2016, 44, 5068-5082.	14.5	216
5	Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. Genome Biology, 2015, 16, 150.	9.6	126
6	The ViennaRNA Web Services. Methods in Molecular Biology, 2015, 1269, 307-326.	0.9	135
7	Means to an end: mechanisms of alternative polyadenylation of messenger <scp>RNA</scp> precursors. Wiley Interdisciplinary Reviews RNA, 2014, 5, 183-196.	6.4	68
8	Reconstitution of CPSF active in polyadenylation: recognition of the polyadenylation signal by WDR33. Genes and Development, 2014, 28, 2381-2393.	5.9	201
9	Clobal 3′ UTR shortening has a limited effect on protein abundance in proliferating T cells. Nature Communications, 2014, 5, 5465.	12.8	164
10	RNA Polymerase III promoter screen uncovers a novel noncoding RNA family conserved in Caenorhabditis and other clade V nematodes. Gene, 2014, 544, 236-240.	2.2	2
11	Translation-dependent displacement of UPF1 from coding sequences causes its enrichment in 3′ UTRs. Nature Structural and Molecular Biology, 2013, 20, 936-943.	8.2	155
12	Insights into snoRNA biogenesis and processing from PAR-CLIP of snoRNA core proteins and small RNA sequencing. Genome Biology, 2013, 14, R45.	9.6	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. Cell Reports, 2012, 1, 753-763.	6.4	341
14	Cleavage factor I _m is a key regulator of 3′ UTR length. RNA Biology, 2012, 9, 1405-1412.	3.1	125
15	AREsite: a database for the comprehensive investigation of AU-rich elements. Nucleic Acids Research, 2011, 39, D66-D69.	14.5	140
16	Tristetraprolinâ€driven regulatory circuit controls quality and timing of mRNA decay in inflammation. Molecular Systems Biology, 2011, 7, 560.	7.2	110
17	Animal snoRNAs and scaRNAs with exceptional structures. RNA Biology, 2011, 8, 938-946.	3.1	30
18	Nematode sbRNAs: Homologs of Vertebrate Y RNAs. Journal of Molecular Evolution, 2010, 70, 346-358.	1.8	32

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19	Invertebrate 7SK snRNAs. Journal of Molecular Evolution, 2008, 66, 107-115.	1.8	37
20	Strategies for measuring evolutionary conservation of RNA secondary structures. BMC Bioinformatics, 2008, 9, 122.	2.6	63
21	RNAalifold: improved consensus structure prediction for RNA alignments. BMC Bioinformatics, 2008, 9, 474.	2.6	505
22	Arthropod 7SK RNA. Molecular Biology and Evolution, 2008, 25, 1923-1930.	8.9	45
23	The Vienna RNA Websuite. Nucleic Acids Research, 2008, 36, W70-W74.	14.5	2,012
24	The RNAz web server: prediction of thermodynamically stable and evolutionarily conserved RNA structures. Nucleic Acids Research, 2007, 35, W335-W338.	14.5	84
25	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	5.5	150
26	Mapping Protein-RNA Interactions by CLIP. Materials and Methods, 0, 1, .	0.0	0