Andreas R Gruber

List of Publications by Year
in descending order

26 papers	5,158 citations	257101 24 h-index	580395 25 g-index
27 all docs	27 docs citations	27 times ranked	8709 citing authors

#	Article	IF	Citations
1	The Vienna RNA Websuite. Nucleic Acids Research, 2008, 36, W70-W74.	6.5	2,012
2	RNAalifold: improved consensus structure prediction for RNA alignments. BMC Bioinformatics, 2008, 9, 474.	1.2	505
3	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.	2.9	341
4	An updated human snoRNAome. Nucleic Acids Research, 2016, 44, 5068-5082.	6.5	216
5	Reconstitution of CPSF active in polyadenylation: recognition of the polyadenylation signal by WDR33. Genes and Development, 2014, 28, 2381-2393.	2.7	201
6	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.	2.4	196
7	Global 3′ UTR shortening has a limited effect on protein abundance in proliferating T cells. Nature Communications, 2014, 5, 5465.	5.8	164
8	Translation-dependent displacement of UPF1 from coding sequences causes its enrichment in 3′ UTRs. Nature Structural and Molecular Biology, 2013, 20, 936-943.	3.6	155
9	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	2.4	150
10	AREsite: a database for the comprehensive investigation of AU-rich elements. Nucleic Acids Research, 2011, 39, D66-D69.	6.5	140
11	The ViennaRNA Web Services. Methods in Molecular Biology, 2015, 1269, 307-326.	0.4	135
12	Insights into snoRNA biogenesis and processing from PAR-CLIP of snoRNA core proteins and small RNA sequencing. Genome Biology, 2013, 14, R45.	13.9	129
13	Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. Genome Biology, 2015, 16, 150.	13.9	126
14	Cleavage factor I$_m$ is a key regulator of 3′ UTR length. RNA Biology, 2012, 9, 1405-1412.	1.5	125
15	Tristetraprolin‑driven regulatory circuit controls quality and timing of mRNA decay in inflammation. Molecular Systems Biology, 2011, 7, 560.	3.2	110
16	The RNAz web server: prediction of thermodynamically stable and evolutionarily conserved RNA structures. Nucleic Acids Research, 2007, 35, W335-W338.	6.5	84
17	Means to an end: mechanisms of alternative polyadenylation of messenger RNA precursors. Wiley Interdisciplinary Reviews RNA, 2014, 5, 183-196.	3.2	68
18	Strategies for measuring evolutionary conservation of RNA secondary structures. BMC Bioinformatics, 2008, 9, 122.	1.2	63

#	Article	IF	Citations
19	Discovery of physiological and cancer-related regulators of 3â€² UTR processing with KAPAC. Genome Biology, 2018, 19, 44.	3.8	54
20	Arthropod 7SK RNA. Molecular Biology and Evolution, 2008, 25, 1923-1930.	3.5	45
21	Roquin recognizes a non-canonical hexaloop structure in the 3â€²-UTR of Ox40. Nature Communications, 2016, 7, 11032.	5.8	38
22	Invertebrate 7SK snRNAs. Journal of Molecular Evolution, 2008, 66, 107-115.	0.8	37
23	Nematode sbRNAs: Homologs of Vertebrate Y RNAs. Journal of Molecular Evolution, 2010, 70, 346-358.	0.8	32
24	Animal snoRNAs and scaRNAs with exceptional structures. RNA Biology, 2011, 8, 938-946.	1.5	30
25	RNA Polymerase III promoter screen uncovers a novel noncoding RNA family conserved in Caenorhabditis and other clade V nematodes. Gene, 2014, 544, 236-240.	1.0	2
26	Mapping Protein-RNA Interactions by CLIP. Materials and Methods, 0, 1, .	0.0	0