

# CITATION REPORT

List of articles citing

Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions

DOI: 10.1002/msb.135068

Molecular Systems Biology, 2014, 10, 719.

**Source:** <https://exaly.com/paper-pdf/58337076/citation-report.pdf>

**Version:** 2024-04-26

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
80	Global analyses of determinants of RNA decay. <i>Nature Reviews Genetics</i> , <b>2014</b> , 15, 217-217	30.1	1
79	Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 719	12.2	64
78	Systems cell biology. <i>Journal of Cell Biology</i> , <b>2014</b> , 206, 695-706	7.3	29
77	Global 3' UTR shortening has a limited effect on protein abundance in proliferating T cells. <i>Nature Communications</i> , <b>2014</b> , 5, 5465	17.4	129
76	Alternative polyadenylation regulates CELF1/CUGBP1 target transcripts following T cell activation. <i>Gene</i> , <b>2014</b> , 550, 93-100	3.8	19
75	Alternative polyadenylation: less than meets the eye?. <i>Biochemical Society Transactions</i> , <b>2014</b> , 42, 1190-5.1	5.1	13
74	Genome-wide identification of transcript start and end sites by transcript isoform sequencing. <i>Nature Protocols</i> , <b>2014</b> , 9, 1740-59	18.8	46
73	Transcriptional profiling of macrophages derived from monocytes and iPS cells identifies a conserved response to LPS and novel alternative transcription. <i>Scientific Reports</i> , <b>2015</b> , 5, 12524	4.9	61
72	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 812	12.2	40
71	Feedforward regulation of mRNA stability by prolonged extracellular signal-regulated kinase activity. <i>FEBS Journal</i> , <b>2015</b> , 282, 613-29	5.7	9
70	Alternative mRNA transcription, processing, and translation: insights from RNA sequencing. <i>Trends in Genetics</i> , <b>2015</b> , 31, 128-39	8.5	190
69	Computational challenges, tools, and resources for analyzing co- and post-transcriptional events in high throughput. <i>Wiley Interdisciplinary Reviews RNA</i> , <b>2015</b> , 6, 291-310	9.3	13
68	Nuclear Tau and Its Potential Role in Alzheimer's Disease. <i>Biomolecules</i> , <b>2016</b> , 6, 9	5.9	70
67	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> , <b>2016</b> , 26, 1145-59	9.7	122
66	Complex Selection on Human Polyadenylation Signals Revealed by Polymorphism and Divergence Data. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 1971-9	3.9	4
65	Dynamics of Translation of Single mRNA Molecules In Vivo. <i>Cell</i> , <b>2016</b> , 165, 976-89	56.2	275
64	The differential expression of alternatively polyadenylated transcripts is a common stress-induced response mechanism that modulates mammalian mRNA expression in a quantitative and qualitative fashion. <i>Rna</i> , <b>2016</b> , 22, 1441-53	5.8	26

63	RNA polymerase II depletion promotes transcription of alternative mRNA species. <i>BMC Molecular Biology</i> , <b>2016</b> , 17, 20	4.5	5
62	Alternative Polyadenylation in Triple-Negative Breast Tumors Allows NRAS and c-JUN to Bypass PUMILIO Posttranscriptional Regulation. <i>Cancer Research</i> , <b>2016</b> , 76, 7231-7241	10.1	32
61	Translational Capacity of a Cell Is Determined during Transcription Elongation via the Ccr4-Not Complex. <i>Cell Reports</i> , <b>2016</b> , 15, 1782-94	10.6	28
60	The cellular growth rate controls overall mRNA turnover, and modulates either transcription or degradation rates of particular gene regulons. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 3643-58	20.1	31
59	Subcellular RNA profiling links splicing and nuclear DICER1 to alternative cleavage and polyadenylation. <i>Genome Research</i> , <b>2016</b> , 26, 24-35	9.7	51
58	Evolution and Biological Roles of Alternative 3'UTRs. <i>Trends in Cell Biology</i> , <b>2016</b> , 26, 227-237	18.3	174
57	Alternative Polyadenylation Directs Tissue-Specific miRNA Targeting in Somatic Tissues. <i>Genetics</i> , <b>2017</b> , 206, 757-774	4	38
56	Cleavage and polyadenylation: Ending the message expands gene regulation. <i>RNA Biology</i> , <b>2017</b> , 14, 865-890	4.8	62
55	-regulatory elements explain most of the mRNA stability variation across genes in yeast. <i>Rna</i> , <b>2017</b> , 23, 1648-1659	5.8	38
54	Yeast Terminator Function Can Be Modulated and Designed on the Basis of Predictions of Nucleosome Occupancy. <i>ACS Synthetic Biology</i> , <b>2017</b> , 6, 2086-2095	5.7	24
53	Emerging Themes in Regulation of Global mRNA Turnover in cis. <i>Trends in Biochemical Sciences</i> , <b>2017</b> , 42, 16-27	10.3	28
52	Upregulation of SPS100 gene expression by an antisense RNA via a switch of mRNA isoforms with different stabilities. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 11144-11158	20.1	4
51	Dysregulation of Alternative Poly-adenylation as a Potential Player in Autism Spectrum Disorder. <i>Frontiers in Molecular Neuroscience</i> , <b>2017</b> , 10, 279	6.1	6
50	Determining Genome-wide Transcript Decay Rates in Proliferating and Quiescent Human Fibroblasts. <i>Journal of Visualized Experiments</i> , <b>2018</b> ,	1.6	2
49	APATrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Bioinformatics</i> , <b>2018</b> , 34, 1841-1849	7.2	46
48	Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 582-592	20.1	113
47	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. <i>Cell</i> , <b>2018</b> , 172, 106-120.e21	56.2	55
46	Identification and Characterization of Transcripts Regulated by Circadian Alternative Polyadenylation in Mouse Liver. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 3539-3548	3.2	8

45	Extensive Structural Differences of Closely Related 3' mRNA Isoforms: Links to Pab1 Binding and mRNA Stability. <i>Molecular Cell</i> , <b>2018</b> , 72, 849-861.e6	17.6	16
44	Alternative polyadenylation factors link cell cycle to migration. <i>Genome Biology</i> , <b>2018</b> , 19, 176	18.3	10
43	Intron retention and nuclear loss of SFPQ are molecular hallmarks of ALS. <i>Nature Communications</i> , <b>2018</b> , 9, 2010	17.4	73
42	Differential 3' Processing of Specific Transcripts Expands Regulatory and Protein Diversity Across Neuronal Cell Types. <i>ELife</i> , <b>2018</b> , 7,	8.9	14
41	AOX1-Subfamily Gene Members in <i>Olea europaea</i> cv. "Galega Vulgar"-Gene Characterization and Expression of Transcripts during IBA-Induced in Vitro Adventitious Rooting. <i>International Journal of Molecular Sciences</i> , <b>2018</b> , 19,	6.3	13
40	Developmental dynamics of gene expression and alternative polyadenylation in the <i>Caenorhabditis elegans</i> germline. <i>Genome Biology</i> , <b>2018</b> , 19, 8	18.3	17
39	Genome-wide transcriptome profiling of the medicinal plant <i>Zanthoxylum planispinum</i> using a single-molecule direct RNA sequencing approach. <i>Genomics</i> , <b>2019</b> , 111, 973-979	4.3	20
38	Novel insights into global translational regulation through Pumilio family RNA-binding protein Puf3p revealed by ribosomal profiling. <i>Current Genetics</i> , <b>2019</b> , 65, 201-212	2.9	8
37	Probing In Vivo Structure of Individual mRNA 3' Isoforms Using Dimethyl Sulfate. <i>Current Protocols in Molecular Biology</i> , <b>2019</b> , 128, e99	2.9	
36	Proximity labeling to detect RNA-protein interactions in live cells. <i>FEBS Open Bio</i> , <b>2019</b> , 9, 1860-1868	2.7	9
35	Chromatin-sensitive cryptic promoters putatively drive expression of alternative protein isoforms in yeast. <i>Genome Research</i> , <b>2019</b> , 29, 1974-1984	9.7	6
34	Comparative Evaluation of the Nutritive, Mineral, and Antinutritive Composition of L. (Banana) and L. (Plantain) Fruit Compartments. <i>Plants</i> , <b>2019</b> , 8,	4.5	24
33	What Are 3' UTRs Doing?. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2019</b> , 11,	10.2	106
32	RNA polymerase II ChIP-seq-a powerful and highly affordable method for studying fungal genomics and physiology. <i>Biophysical Reviews</i> , <b>2019</b> , 11, 79-82	3.7	10
31	A survey on identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1261-1276	13.4	12
30	Rpb4 and Puf3 imprint and post-transcriptionally control the stability of a common set of mRNAs in yeast. <i>RNA Biology</i> , <b>2021</b> , 18, 1206-1220	4.8	1
29	Mitochondrial Biogenesis Is Positively Regulated by Casein Kinase I Hrr25 Through Phosphorylation of Puf3 in. <i>Genetics</i> , <b>2020</b> , 215, 463-482	4	0
28	Alternative polyadenylation of mRNA and its role in cancer. <i>Genes and Diseases</i> , <b>2021</b> , 8, 61-72	6.6	15

27	Long-read RNA sequencing reveals widespread sex-specific alternative splicing in threespine stickleback fish. <i>Genome Research</i> , <b>2021</b> , 31, 1486-1497	9.7	2
26	Landscape of the Dark Transcriptome Revealed Through Re-mining Massive RNA-Seq Data. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 722981	4.5	0
25	Alternative polyadenylation dysregulation contributes to the differentiation block of acute myeloid leukemia. <i>Blood</i> , <b>2021</b> ,	2.2	1
24	Alternative polyadenylation: An enigma of transcript length variation in health and disease. <i>Wiley Interdisciplinary Reviews RNA</i> , <b>2021</b> , e1692	9.3	2
23	From transcriptional complexity to cellular phenotypes: Lessons from yeast. <i>Yeast</i> , <b>2017</b> , 34, 475-482	3.4	1
22	Genome-Wide Identification of Alternative Polyadenylation Events Using 3'T-Fill. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1358, 295-302	1.4	1
21	PAT-Seq: A Method for Simultaneous Quantitation of Gene Expression, Poly(A)-Site Selection and Poly(A)-Length Distribution in Yeast Transcriptomes. <i>Methods in Molecular Biology</i> , <b>2019</b> , 2049, 141-164	1.4	1
20	Cleavage factor 25 deregulation contributes to pulmonary fibrosis through alternative polyadenylation. <i>Journal of Clinical Investigation</i> , <b>2019</b> , 129, 1984-1999	15.9	32
19	The transcriptional elongation rate regulates alternative polyadenylation in yeast. <i>ELife</i> , <b>2020</b> , 9,	8.9	6
18	Longitudinal network theory approaches identify crucial factors affecting sporulation efficiency in yeast.		1
17	Cis-regulatory elements explain most of the mRNA stability variation across genes in yeast.		0
16	Post-transcriptional remodelling is temporally deregulated during motor neurogenesis in human ALS models.		
15	Differential 3D Processing of Specific Transcripts Expands Regulatory and Protein Diversity Across Neuronal Cell Types.		1
14	Chromatin-sensitive cryptic promoters encode alternative protein isoforms in yeast.		
13	Rpb4 and Puf3 imprint and post-transcriptionally control the stability of a common set of mRNAs in yeast.		
12	Long-read RNA sequencing reveals widespread sex-specific alternative splicing in threespine stickleback fish.		0
11	Alternative polyadenylation can regulate post-translational membrane localization. <i>Trends in Cell &amp; Molecular Biology</i> , <b>2015</b> , 10, 37-47		6
10	A compensatory link between cleavage/polyadenylation and mRNA turnover regulates steady-state mRNA levels in yeast.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119,	11.5	0

9	Proteinopathies as Hallmarks of Impaired Gene Expression, Proteostasis and Mitochondrial Function in Amyotrophic Lateral Sclerosis.. <i>Frontiers in Neuroscience</i> , <b>2021</b> , 15, 783624	5.1	1
8	Puf3p facilitates fermentative mitochondrial functions via monosome-enriched nuclear-encoded mitochondrial mRNAs in budding yeast.		
7	A Survey on Methods for Predicting Polyadenylation Sites from DNA Sequences, Bulk RNA-seq, and Single-cell RNA-seq.		
6	stAPAminer: Mining Spatial Patterns of Alternative Polyadenylation for Spatially Resolved Transcriptomic Studies.		
5	3' Untranslated Regions Are Modular Entities That Determine Polyadenylation Profiles.		1
4	A Survey on Methods for Predicting Polyadenylation Sites from DNA Sequences, Bulk RNA-seq, and Single-cell RNA-seq. <b>2022</b> ,		0
3	A comparative analysis of the proximate and mineral composition of whole Citrus limon and Citrus clementina as a prospective alternative feed resource for livestock farming in South Africa. 6,		0
2	stAPAminer: Mining Spatial Patterns of Alternative Polyadenylation for Spatially Resolved Transcriptomic Studies. <b>2023</b> ,		0
1	The association of the RSC remodeler complex with chromatin depends on prefoldin-like Bud27 and determines nucleosome positioning and polyadenylation sites usage in <i>Saccharomyces cerevisiae</i> .		0