List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7010268/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Translational coupling at an intercistronic boundary of the Escherichia coli galactose operon. Cell, 1982, 30, 865-871.	13.5	238
2	Regulation of histone mRNA in the unperturbed cell cycle: evidence suggesting control at two posttranscriptional steps Molecular and Cellular Biology, 1991, 11, 2416-2424.	1.1	228
3	Unique Sm core structure of U7 snRNPs: assembly by a specialized SMN complex and the role of a new component, Lsm11, in histone RNA processing. Genes and Development, 2003, 17, 2321-2333.	2.7	188
4	Regulation of Histone mRNA in the Unperturbed Cell Cycle: Evidence Suggesting Control at Two Posttranscriptional Steps. Molecular and Cellular Biology, 1991, 11, 2416-2424.	1.1	156
5	3' editing of mRNAs: sequence requirements and involvement of a 60-nucleotide RNA in maturation of histone mRNA precursors Proceedings of the National Academy of Sciences of the United States of America, 1984, 81, 1057-1061.	3.3	153
6	The gene for histone RNA hairpin binding protein is located on human chromosome 4and encodes a novel type of RNA binding protein. EMBO Journal, 1997, 16, 769-778.	3.5	142
7	Purified U7 snRNPs lack the Sm proteins D1 and D2 but contain Lsm10, a new 14 kDa Sm D1-like protein. EMBO Journal, 2001, 20, 5470-5479.	3.5	142
8	Multilevel regulation of replication-dependent histone genes. Trends in Genetics, 1988, 4, 187-191.	2.9	132
9	The special Sm core structure of the U7 snRNP: far-reaching significance of a small nuclear ribonucleoprotein. Cellular and Molecular Life Sciences, 2004, 61, 2560-2570.	2.4	120
10	RNA 3′ processing regulates histone mRNA levels in a mammalian cell cycle mutant. A processing factor becomes limiting in G1-arrested cells EMBO Journal, 1987, 6, 1721-1726.	3.5	105
11	Affecting gene expression by altering the length and sequence of the 5' leader Proceedings of the National Academy of Sciences of the United States of America, 1984, 81, 7698-7702.	3.3	101
12	Stable alteration of pre-mRNA splicing patterns by modified U7 small nuclear RNAs. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 4929-4934.	3.3	100
13	Rescue of a severe mouse model for spinal muscular atrophy by U7 snRNA-mediated splicing modulation. Human Molecular Genetics, 2009, 18, 546-555.	1.4	91
14	Polydnavirus of the parasitic wasp Chelonus inanitus (Braconidae): characterization, genome organization and time point of replication. Journal of General Virology, 1994, 75, 3353-3363.	1.3	89
15	The low abundance of U7 snRNA is partly determined by its Sm binding site EMBO Journal, 1993, 12, 1229-1238.	3.5	85
16	Structural and functional characterization of mouse U7 small nuclear RNA active in 3' processing of histone pre-mRNA Molecular and Cellular Biology, 1988, 8, 1518-1524.	1.1	84
17	The expression in yeast of the Escherichia coli galK gene on CYCI :: galK fusion plasmids. Gene, 1983, 25, 249-262.	1.0	81
18	Structure of the galactokinase gene ofEscherichia coli, the last (?) gene of thegaloperon. Nucleic Acids Research, 1985, 13, 1841-1853.	6.5	79

#	Article	IF	CITATIONS
19	RNA 3' processing regulates histone mRNA levels in a mammalian cell cycle mutant. A processing factor becomes limiting in G1-arrested cells. EMBO Journal, 1987, 6, 1721-6.	3.5	78
20	Spinal Muscular Atrophy: SMN2 Pre-mRNA Splicing Corrected by a U7 snRNA Derivative Carrying a Splicing Enhancer Sequence. Molecular Therapy, 2007, 15, 1479-1486.	3.7	76
21	Antisense properties of tricyclo-DNA. Nucleic Acids Research, 2002, 30, 2751-2757.	6.5	72
22	3' processing of pre-mRNA plays a major role in proliferation-dependent regulation of histone gene expression. Nucleic Acids Research, 1988, 16, 9399-9414.	6.5	71
23	Variable effects of the conserved RNA hairpin element upon 3′ end processing of histone pre-mRNAin vitro. Nucleic Acids Research, 1993, 21, 1569-1575.	6.5	65
24	Assemble, nuclear import and function of U7 snRNPs studied by microinjection of synthetic U7 RNA intoXenopusoocytes. Nucleic Acids Research, 1995, 23, 3141-3151.	6.5	65
25	U7 snRNAs induce correction of mutated dystrophin pre-mRNA by exon skipping. Cellular and Molecular Life Sciences, 2003, 60, 557-566.	2.4	64
26	Efficient expression of Escherichia coli galactokinase gene in mammalian cells Proceedings of the National Academy of Sciences of the United States of America, 1982, 79, 257-261.	3.3	59
27	The stem-loop binding protein stimulates histone translation at an early step in the initiation pathway. Rna, 2005, 11, 1030-1042.	1.6	59
28	The U7 snRNP and the hairpin binding protein: Key players in histone mRNA metabolism. Seminars in Cell and Developmental Biology, 1997, 8, 567-576.	2.3	54
29	The C-terminal domain of coilin interacts with Sm proteins and U snRNPs. Chromosoma, 2005, 114, 155-166.	1.0	54
30	Structural and functional characterization of mouse U7 small nuclear RNA active in 3' processing of histone pre-mRNA. Molecular and Cellular Biology, 1988, 8, 1518-1524.	1.1	54
31	Double-Target Antisense U7 snRNAs Promote Efficient Skipping of an Aberrant Exon in Three Human Â-Thalassemic Mutations. Human Molecular Genetics, 1999, 8, 2415-2423.	1.4	53
32	Interactions of CstF-64, CstF-77, and symplekin: Implications on localisation and function. Molecular Biology of the Cell, 2011, 22, 91-104.	0.9	51
33	Mammalian pre-mRNA 3′ End Processing Factor CF I <sub>m</sub> 68 Functions in mRNA Export. Molecular Biology of the Cell, 2009, 20, 5211-5223.	0.9	50
34	Inhibition of HIV-1 multiplication by antisense U7 snRNAs and siRNAs targeting cyclophilin A. Nucleic Acids Research, 2004, 32, 3752-3759.	6.5	49
35	The low abundance of U7 snRNA is partly determined by its Sm binding site. EMBO Journal, 1993, 12, 1229-38.	3.5	49
36	Ultrastructural changes in diaphragm neuromuscular junctions in a severe mouse model for Spinal Muscular Atrophy and their prevention by bifunctional U7 snRNA correcting SMN2 splicing. Neuromuscular Disorders, 2010, 20, 744-752.	0.3	48

#	Article	IF	CITATIONS
37	Structure of the histone mRNA hairpin required for cell cycle regulation of histone gene expression. Rna, 2002, 8, 29-46.	1.6	45
38	Cycling in the nucleus: regulation of RNA 3′ processing and nuclear organization of replication-dependent histone genes. Current Opinion in Cell Biology, 2016, 40, 23-31.	2.6	43
39	Biochemical demonstration of complex formation of histone pre-mRNA with U7 small nuclear ribonucleoprotein and hairpin binding factors. EMBO Journal, 1992, 11, 691-7.	3.5	43
40	Differential activation of the mouse beta-globin promoter by enhancers Molecular and Cellular Biology, 1983, 3, 1246-1254.	1.1	42
41	3′ End processing of mouse histone pre-mRNA: evidence for additional base-pairing between U7 snRNA and pre-mRNA. Nucleic Acids Research, 1994, 22, 4023-4030.	6.5	42
42	The Caenorhabditis elegans histone hairpin-binding protein is required for core histone gene expression and is essential for embryonic and postembryonic cell division. Journal of Cell Science, 2002, 115, 857-66.	1.2	41
43	CstF64: Cell Cycle Regulation and Functional Role in 3′ End Processing of Replication-Dependent Histone mRNAs. Molecular and Cellular Biology, 2014, 34, 4272-4284.	1.1	39
44	Toward an Assembly Line for U7 snRNPs. Journal of Biological Chemistry, 2005, 280, 34435-34440.	1.6	38
45	Synthesis and cellular activity of stereochemically-pure 2′-O-(2-methoxyethyl)-phosphorothioate oligonucleotides. Chemical Communications, 2017, 53, 541-544.	2.2	37
46	Nucleotide sequence of two mouse histone H4 genes. Nucleic Acids Research, 1989, 17, 795-795.	6.5	36
47	Sensitivity of splice sites to antisense oligonucleotides in vivo. Rna, 1999, 5, 369-377.	1.6	33
48	FUS/TLS contributes to replication-dependent histone gene expression by interaction with U7 snRNPs and histone-specific transcription factors. Nucleic Acids Research, 2015, 43, gkv794.	6.5	32
49	A 5′-3′ exonuclease activity involved in forming the 3′ products of histone pre-mRNA processing in vitro. Rna, 1998, 4, 1034-1046.	1.6	31
50	Differential activation of the mouse beta-globin promoter by enhancers. Molecular and Cellular Biology, 1983, 3, 1246-1254.	1.1	30
51	Positive and negative mutant selection in the human histone hairpin-binding protein using the yeast three-hybrid system. Nucleic Acids Research, 2000, 28, 1594-1603.	6.5	29
52	Repair of pre-mRNA splicing. RNA Biology, 2010, 7, 430-440.	1.5	29
53	Splicing changes in SMA mouse motoneurons and SMN-depleted neuroblastoma cells: Evidence for involvement of splicing regulatory proteins. RNA Biology, 2014, 11, 1430-1446.	1.5	29
54	Isolation of an active gene and of two pseudogenes for mouse U7 small nuclear RNA. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1991, 1088, 151-154.	2.4	28

#	Article	IF	CITATIONS
55	Inhibition of HIV-1 multiplication by a modified U7 snRNA inducing Tat and Rev exon skipping. Journal of Gene Medicine, 2007, 9, 323-334.	1.4	27
56	U7 snRNP-specific Lsm11 protein: dual binding contacts with the 100 kDa zinc finger processing factor (ZFP100) and a ZFP100-independent function in histone RNA 3' end processing. Nucleic Acids Research, 2005, 33, 2106-2117.	6.5	25
57	Evolutionary conservation of the U7 small nuclear ribonucleoprotein in Drosophila melanogaster. Rna, 2003, 9, 1532-1541.	1.6	23
58	Functional importance of conserved nucleotides at the histone RNA 3' processing site. Rna, 1998, 4, 246-56.	1.6	21
59	Specificities of Caenorhabditis elegans and human hairpin binding proteins for the first nucleotide in the histone mRNA hairpin loop. Rna, 2000, 6, 1539-1550.	1.6	20
60	The 68 kDa subunit of mammalian cleavage factor I interacts with the U7 small nuclear ribonucleoprotein and participates in 3′-end processing of animal histone mRNAs. Nucleic Acids Research, 2010, 38, 7637-7650.	6.5	20
61	Somatic Therapy of a Mouse SMA Model with a U7 snRNA Gene Correcting SMN2 Splicing. Molecular Therapy, 2016, 24, 1797-1805.	3.7	18
62	Doxycycline-controlled splicing modulation by regulated antisense U7 snRNA expression cassettes. Gene Therapy, 2009, 16, 70-77.	2.3	17
63	Development and characterization of a triple combination gene therapy vector inhibiting HIVâ€1 multiplication. Journal of Gene Medicine, 2008, 10, 1059-1070.	1.4	16
64	Central and peripheral defects in motor units of the diaphragm of spinal muscular atrophy mice. Molecular and Cellular Neurosciences, 2016, 70, 30-41.	1.0	16
65	Delivery of oligonucleotides to bone marrow to modulate ferrochelatase splicing in a mouse model of erythropoietic protoporphyria. Nucleic Acids Research, 2020, 48, 4658-4671.	6.5	16
66	mRNA 3 <sup>′</sup> end processing and more—multiple functions of mammalian cleavage factor lâ€68. Wiley Interdisciplinary Reviews RNA, 2011, 2, 79-91.	3.2	15
67	Spinal Muscular Atrophy: Position and Functional Importance of the Branch Site Preceding SMN Exon 7. RNA Biology, 2007, 4, 34-37.	1.5	13
68	A synthetic histone pre-mRNA-U7 small nuclear RNA chimera undergoingciscleavage in the cytoplasm ofXenopusoocytes. Nucleic Acids Research, 1995, 23, 3152-3160.	6.5	12
69	RNAs and ribonucleoproteins in recognition and catalysis. , 1994, 219, 25-41.		12
70	Antisense derivatives of U7 and other small nuclear RNAs as tools to modify pre-mRNA splicing patterns. Gene Therapy and Regulation, 2004, 2, 321-349.	0.3	10
71	Chapter 5 Isolation of Neuronal Nuclei from Rat Brain Cortex, Rat Cerebellum, and Pigeon Forebrain. Methods in Cell Biology, 1977, 15, 89-96.	0.5	9
72	Modelling the ferrochelatase c.315-48C modifier mutation for erythropoietic protoporphyria (EPP) in mice. DMM Disease Models and Mechanisms, 2017, 10, 225-233.	1.2	9

#	Article	IF	CITATIONS
73	Histone H4 mRNA from the nematode Ascaris lumbricoides is cis-spliced and polyadenylated. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1997, 1350, 259-261.	2.4	8
74	The craniosacral progression of muscle development influences the emergence of neuromuscular junction alterations in a severe murine model for spinal muscular atrophy. Neuropathology and Applied Neurobiology, 2014, 40, 416-434.	1.8	7
75	Repurposing of glycine transport inhibitors for the treatment of erythropoietic protoporphyria. Cell Chemical Biology, 2021, 28, 1221-1234.e6.	2.5	7
76	Antisense Genes to Induce Exon Inclusion. Methods in Molecular Biology, 2012, 867, 325-347.	0.4	4
77	Positive cofactor 4 (PC4) contributes to the regulation of replication-dependent canonical histone gene expression. BMC Molecular Biology, 2018, 19, 9.	3.0	3
78	T.O.5 Spinal muscular atrophy SMA: SMNs spatial requirement and therapies. Neuromuscular Disorders, 2012, 22, 907-908.	0.3	0
79	O.8 Intrathecal delivery of AAV9 vectors to model and rescue a large animal model of SMA. Neuromuscular Disorders, 2013, 23, 797.	0.3	0
80	Rudolf Weber (1922–2015): a driving force in the transition of developmental biology into a molecular and cellular science. Development Genes and Evolution, 2016, 226, 65-67.	0.4	0
81	Transcriptional and Post-Transcriptional Control of Histone Gene Expression. , 1985, , 171-176.		0