Daniel SchÃ¼mperli

List of Publications by Year
in descending order

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81
papers

4,362
citations

76196
40
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110170
64
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83
all docs

83
docs citations

83
times ranked

2447
citing authors

#	Article	IF	Citations
1	Repurposing of glycine transport inhibitors for the treatment of erythropoietic protoporphyria. Cell Chemical Biology, 2021, 28, 1221-1234.e6.	2.5	7
2	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
3	Positive cofactor 4 (PC4) contributes to the regulation of replication-dependent canonical histone gene expression. BMC Molecular Biology, 2018, 19, 9.	3.0	3
4	Synthesis and cellular activity of stereochemically-pure 2â€²-O-(2-methoxyethyl)-phosphorothioate oligonucleotides. Chemical Communications, 2017, 53, 541-544.	2.2	37
5	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
6	Somatic Therapy of a Mouse SMA Model with a U7 snRNA Gene Correcting SMN2 Splicing. Molecular Therapy, 2016, 24, 1797-1805.	3.7	18
7	Rudolf Weber (1922â€“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
8	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
9	Cycling in the nucleus: regulation of RNA 3â€² processing and nuclear organization of replication-dependent histone genes. Current Opinion in Cell Biology, 2016, 40, 23-31.	2.6	43
10	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
11	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
12	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
13	CstF64: Cell Cycle Regulation and Functional Role in 3â€² End Processing of Replication-Dependent Histone mRNAs. Molecular and Cellular Biology, 2014, 34, 4272-4284.	1.1	39
14	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
15	T.O.5 Spinal muscular atrophy SMA: SMNs spatial requirement and therapies. Neuromuscular Disorders, 2012, 22, 907-908.	0.3	0
16	Antisense Genes to Induce Exon Inclusion. Methods in Molecular Biology, 2012, 867, 325-347.	0.4	4
17	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
18	mRNA 3^{â€²} end processing and moreâ€”multiple functions of mammalian cleavage factor Iâ€68. Wiley Interdisciplinary Reviews RNA, 2011, 2, 79-91.	3.2	15

#	Article	IF	Citations
19	The 68â€‰kDa subunit of mammalian cleavage factor I interacts with the U7 small nuclear ribonucleoprotein and participates in 3â€²-end processing of animal histone mRNAs. Nucleic Acids Research, 2010, 38, 7637-7650.	6.5	20
20	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
21	Repair of pre-mRNA splicing. RNA Biology, 2010, 7, 430-440.	1.5	29
22	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
23	Mammalian pre-mRNA 3â€² End Processing Factor CF I_m68 Functions in mRNA Export. Molecular Biology of the Cell, 2009, 20, 5211-5223.	0.9	50
24	Doxycycline-controlled splicing modulation by regulated antisense U7 snRNA expression cassettes. Gene Therapy, 2009, 16, 70-77.	2.3	17
25	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
26	Spinal Muscular Atrophy: Position and Functional Importance of the Branch Site Preceding SMN Exon 7. RNA Biology, 2007, 4, 34-37.	1.5	13
27	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
28	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
29	The C-terminal domain of coilin interacts with Sm proteins and U snRNPs. Chromosoma, 2005, 114, 155-166.	1.0	54
30	Toward an Assembly Line for U7 snRNPs. Journal of Biological Chemistry, 2005, 280, 34435-34440.	1.6	38
31	The stem-loop binding protein stimulates histone translation at an early step in the initiation pathway. Rna, 2005, 11, 1030-1042.	1.6	59
32	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
33	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
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 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
36	U7 snRNAs induce correction of mutated dystrophin pre-mRNA by exon skipping. Cellular and Molecular Life Sciences, 2003, 60, 557-566.	2.4	64

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37	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
38	Evolutionary conservation of the U7 small nuclear ribonucleoprotein in Drosophila melanogaster. Rna, 2003, 9, 1532-1541.	1.6	23
39	Antisense properties of tricyclo-DNA. Nucleic Acids Research, 2002, 30, 2751-2757.	6.5	72
40	Structure of the histone mRNA hairpin required for cell cycle regulation of histone gene expression. Rna, 2002, 8, 29-46.	1.6	45
41	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
42	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
43	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
44	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
45	Sensitivity of splice sites to antisense oligonucleotides in vivo. Rna, 1999, 5, 369-377.	1.6	33
46	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
47	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
48	A 5â€²-3â€² exonuclease activity involved in forming the 3â€² products of histone pre-mRNA processing in vitro. Rna, 1998, 4, 1034-1046.	1.6	31
49	Functional importance of conserved nucleotides at the histone RNA 3' processing site. Rna, 1998, 4, 246-56.	1.6	21
50	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
51	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
52	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
53	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
54	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

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55	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
56	3â€² 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
57	RNAs and ribonucleoproteins in recognition and catalysis. , 1994, 219, 25-41.		12
58	Variable effects of the conserved RNA hairpin element upon 3â€² end processing of histone pre-mRNAin vitro. Nucleic Acids Research, 1993, 21, 1569-1575.	6.5	65
59	The low abundance of U7 snRNA is partly determined by its Sm binding site.. EMBO Journal, 1993, 12, 1229-1238.	3.5	85
60	The low abundance of U7 snRNA is partly determined by its Sm binding site. EMBO Journal, 1993, 12, 1229-38.	3.5	49
61	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
62	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
63	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
64	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
65	Nucleotide sequence of two mouse histone H4 genes. Nucleic Acids Research, 1989, 17, 795-795.	6.5	36
66	Multilevel regulation of replication-dependent histone genes. Trends in Genetics, 1988, 4, 187-191.	2.9	132
67	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
68	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
69	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
70	RNA 3â€² 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
71	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
72	Structure of the galactokinase gene ofEscherichia coli, the last (?) gene of thegaloperon. Nucleic Acids Research, 1985, 13, 1841-1853.	6.5	79

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73	Transcriptional and Post-Transcriptional Control of Histone Gene Expression. , 1985, , 171-176.		0
74	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
75	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
76	The expression in yeast of the Escherichia coli galK gene on CYCI :: galK fusion plasmids. Gene, 1983, 25, 249-262.	1.0	81
77	Differential activation of the mouse beta-globin promoter by enhancers.. Molecular and Cellular Biology, 1983, 3, 1246-1254.	1.1	42
78	Differential activation of the mouse beta-globin promoter by enhancers. Molecular and Cellular Biology, 1983, 3, 1246-1254.	1.1	30
79	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
80	Translational coupling at an intercistronic boundary of the Escherichia coli galactose operon. Cell, 1982, 30, 865-871.	13.5	238
81	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