Didier Auboeuf

List of Publications by Year in descending order

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DIDIED AUROFUE

#	Article	IF	CITATIONS
1	Coordinate Regulation of Transcription and Splicing by Steroid Receptor Coregulators. Science, 2002, 298, 416-419.	12.6	342
2	The multiple functions of RNA helicases as drivers and regulators of gene expression. Nature Reviews Molecular Cell Biology, 2016, 17, 426-438.	37.0	212
3	RNA Helicases DDX5 and DDX17 Dynamically Orchestrate Transcription, miRNA, and Splicing Programs in Cell Differentiation. Cell Reports, 2014, 7, 1900-1913.	6.4	176
4	Steroid Hormone Receptor Coactivation and Alternative RNA Splicing by U2AF65-Related Proteins CAPERα and CAPERβ. Molecular Cell, 2005, 17, 429-439.	9.7	173
5	Splicing misregulation of SCN5A contributes to cardiac-conduction delay and heart arrhythmia in myotonic dystrophy. Nature Communications, 2016, 7, 11067.	12.8	155
6	CoAA, a Nuclear Receptor Coactivator Protein at the Interface of Transcriptional Coactivation and RNA Splicing. Molecular and Cellular Biology, 2004, 24, 442-453.	2.3	149
7	Cotranscriptional exon skipping in the genotoxic stress response. Nature Structural and Molecular Biology, 2010, 17, 1358-1366.	8.2	143
8	The Use of the Reverse Transcription-Competitive Polymerase Chain Reaction to Investigate thein VivoRegulation of Gene Expression in Small Tissue Samples. Analytical Biochemistry, 1997, 245, 141-148.	2.4	123
9	Splicing switch of an epigenetic regulator by RNA helicases promotes tumor-cell invasiveness. Nature Structural and Molecular Biology, 2012, 19, 1139-1146.	8.2	117
10	Splicing factor and exon profiling across human tissues. Nucleic Acids Research, 2010, 38, 2825-2838.	14.5	114
11	Regulation of Alternative Splicing by the ATP-Dependent DEAD-Box RNA Helicase p72. Molecular and Cellular Biology, 2002, 22, 5698-5707.	2.3	113
12	Candidate gene prioritization with Endeavour. Nucleic Acids Research, 2016, 44, W117-W121.	14.5	111
13	Differential recruitment of nuclear receptor coactivators may determine alternative RNA splice site choice in target genes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2270-2274.	7.1	110
14	The emerging role of pre-messenger RNA splicing in stress responses: Sending alternative messages and silent messengers. RNA Biology, 2011, 8, 740-747.	3.1	91
15	A Subset of Nuclear Receptor Coregulators Act as Coupling Proteins during Synthesis and Maturation of RNA Transcripts. Molecular and Cellular Biology, 2005, 25, 5307-5316.	2.3	90
16	Alteration of cyclin D1 transcript elongation by a mutated transcription factor up-regulates the oncogenic D1b splice isoform in cancer. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6004-6009.	7.1	85
17	FAST DB: a website resource for the study of the expression regulation of human gene products. Nucleic Acids Research, 2005, 33, 4276-4284.	14.5	77
18	A new advance in alternative splicing databases: from catalogue to detailed analysis of regulation of expression and function of human alternative splicing variants. BMC Bioinformatics, 2007, 8, 180.	2.6	64

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19	In Vitro and In Vivo Modulation of Alternative Splicing by the Biguanide Metformin. Molecular Therapy - Nucleic Acids, 2015, 4, e262.	5.1	63
20	Coregulators: transducing signal from transcription to alternative splicing. Trends in Endocrinology and Metabolism, 2007, 18, 122-129.	7.1	61
21	Endothelial, epithelial, and fibroblast cells exhibit specific splicing programs independently of their tissue of origin. Genome Research, 2014, 24, 511-521.	5.5	61
22	Exon-Based Clustering of Murine Breast Tumor Transcriptomes Reveals Alternative Exons Whose Expression Is Associated with Metastasis. Cancer Research, 2010, 70, 896-905.	0.9	59
23	Nucleosome eviction in mitosis assists condensin loading and chromosome condensation. EMBO Journal, 2016, 35, 1565-1581.	7.8	53
24	Identification of protein features encoded by alternative exons using Exon Ontology. Genome Research, 2017, 27, 1087-1097.	5.5	45
25	The Ddx5 and Ddx17 RNA helicases are cornerstones in the complex regulatory array of steroid hormone-signaling pathways. Nucleic Acids Research, 2014, 42, 2197-2207.	14.5	44
26	Splicing Programs and Cancer. Journal of Nucleic Acids, 2012, 2012, 1-9.	1.2	43
27	The RNA helicase DDX17 controls the transcriptional activity of REST and the expression of proneural microRNAs in neuronal differentiation. Nucleic Acids Research, 2018, 46, 7686-7700.	14.5	43
28	A recently evolved class of alternative 3′-terminal exons involved in cell cycle regulation by topoisomerase inhibitors. Nature Communications, 2014, 5, 3395.	12.8	39
29	Alternative splicing and breast cancer. RNA Biology, 2010, 7, 403-411.	3.1	35
30	Coupled alteration of transcription and splicing by a single oncogene: Boosting the effect on cyclin D1 activity. Cell Cycle, 2008, 7, 2299-2305.	2.6	32
31	Complementarity of assembly-first and mapping-first approaches for alternative splicing annotation and differential analysis from RNAseq data. Scientific Reports, 2018, 8, 4307.	3.3	31
32	The RNA helicase DDX5/p68 is a key factor promoting c-fos expression at different levels from transcription to mRNA export. Nucleic Acids Research, 2013, 41, 554-564.	14.5	30
33	ZRANB2 and SYF2-mediated splicing programs converging on ECT2 are involved in breast cancer cell resistance to doxorubicin. Nucleic Acids Research, 2020, 48, 2676-2693.	14.5	30
34	Cotranscriptional Splicing Potentiates the mRNA Production from a Subset of Estradiol-Stimulated Genes. Molecular and Cellular Biology, 2008, 28, 5811-5824.	2.3	24
35	Intragenic recruitment of NF-κB drives splicing modifications upon activation by the oncogene Tax of HTLV-1. Nature Communications, 2020, 11, 3045.	12.8	24
36	Oncogene- and drug resistance-associated alternative exon usage in acute myeloid leukemia (AML). Oncotarget, 2016, 7, 2889-2909.	1.8	19

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37	Characterizing the interplay between gene nucleotide composition bias and splicing. Genome Biology, 2019, 20, 259.	8.8	18
38	HTLV-1-infected CD4+ T-cells display alternative exon usages that culminate in adult T-cell leukemia. Retrovirology, 2014, 11, 119.	2.0	16
39	Interplay between coding and exonic splicing regulatory sequences. Genome Research, 2019, 29, 711-722.	5.5	14
40	Physicochemical Foundations of Life that Direct Evolution: Chance and Natural Selection are not Evolutionary Driving Forces. Life, 2020, 10, 7.	2.4	14
41	Alternative mRNA processing sites decrease genetic variability while increasing functional diversity. Transcription, 2018, 9, 75-87.	3.1	11
42	Integrative Cell Type-Specific Multi-Omics Approaches Reveal Impaired Programs of Glial Cell Differentiation in Mouse Culture Models of DM1. Frontiers in Cellular Neuroscience, 2021, 15, 662035.	3.7	11
43	Modulation of alternative splicing during early infection of human primary B lymphocytes with Epstein-Barr virus (EBV): a novel function for the viral EBNA-LP protein. Nucleic Acids Research, 2021, 49, 10657-10676.	14.5	11
44	Alternative Splicing and Cancer. Journal of Nucleic Acids, 2012, 2012, 1-2.	1.2	6
45	Myotonic dystrophy RNA toxicity alters morphology, adhesion and migration of mouse and human astrocytes. Nature Communications, 2022, 13, .	12.8	6
46	Putative RNA-directed adaptive mutations in cancer evolution. Transcription, 2016, 7, 164-187.	3.1	5
47	Genome evolution is driven by gene expressionâ€generated biophysical constraints through RNAâ€directed genetic variation: A hypothesis. BioEssays, 2017, 39, 1700069.	2.5	4
48	The RNA helicase DDX5 is a reprogramming roadblock. Stem Cell Investigation, 2017, 4, 79-79.	3.0	3
49	The proto-oncogenic protein TAL1 controls TGF-β1 signaling through interaction with SMAD3. Biochimie Open, 2016, 2, 69-78.	3.2	2
50	The Physics–Biology continuum challenges darwinism: Evolution is directed by the homeostasis-dependent bidirectional relation between genome and phenotype. Progress in Biophysics and Molecular Biology, 2021, 167, 121-139.	2.9	2
51	Altered splicing of <scp>ATG16‣1</scp> mediates acquired resistance to tyrosine kinase inhibitors of <scp>EGFR</scp> by blocking autophagy in nonâ€small cell lung cancer. Molecular Oncology, 2022, 16, 3490-3508.	4.6	2