

Alternative isoform regulation in human tissue transcri

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Citation Report

#	ARTICLE	IF	CITATIONS
2	HITS-CLIP yields genome-wide insights into brain alternative RNA processing. <i>Nature</i> , 2008, 456, 464-469.	13.7	1,245
4	A compatible exon-exon junction database for the identification of exon skipping events using tandem mass spectrum data. <i>BMC Bioinformatics</i> , 2008, 9, 537.	1.2	24
5	Genomic Convergence Analysis of Schizophrenia: mRNA Sequencing Reveals Altered Synaptic Vesicular Transport in Post-Mortem Cerebellum. <i>PLoS ONE</i> , 2008, 3, e3625.	1.1	106
6	The Pivotal Roles of TIA Proteins in 5' Splice-Site Selection of Alu Exons and Across Evolution. <i>PLoS Genetics</i> , 2009, 5, e1000717.	1.5	33
7	A Global View of Cancer-Specific Transcript Variants by Subtractive Transcriptome-Wide Analysis. <i>PLoS ONE</i> , 2009, 4, e4732.	1.1	72
8	High-Throughput Proteomics Detection of Novel Splice Isoforms in Human Platelets. <i>PLoS ONE</i> , 2009, 4, e5001.	1.1	38
9	Evolution of Alternative Splicing Regulation: Changes in Predicted Exonic Splicing Regulators Are Not Associated with Changes in Alternative Splicing Levels in Primates. <i>PLoS ONE</i> , 2009, 4, e5800.	1.1	16
10	Probe-Level Analysis of Expression Microarrays Characterizes Isoform-Specific Degradation during Mouse Oocyte Maturation. <i>PLoS ONE</i> , 2009, 4, e7479.	1.1	27
11	A Unique, Consistent Identifier for Alternatively Spliced Transcript Variants. <i>PLoS ONE</i> , 2009, 4, e7631.	1.1	8
12	Alternative Splicing and Transcriptome Profiling of Experimental Autoimmune Encephalomyelitis Using Genome-Wide Exon Arrays. <i>PLoS ONE</i> , 2009, 4, e7773.	1.1	20
13	Reprogramming of 3' Untranslated Regions of mRNAs by Alternative Polyadenylation in Generation of Pluripotent Stem Cells from Different Cell Types. <i>PLoS ONE</i> , 2009, 4, e8419.	1.1	245
14	Inverse relationship between genetic diversity and epigenetic complexity. <i>Nature Precedings</i> , 0, , .	0.1	20
15	Towards Reliable Isoform Quantification Using RNA-Seq Data. , 2009, , .		2
16	hnRNP A2 Regulates Alternative mRNA Splicing of TP53INP2 to Control Invasive Cell Migration. <i>Cancer Research</i> , 2009, 69, 9219-9227.	0.4	71
17	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3264-3269.	3.3	201
18	Nature's Genetic Gradients and the Clinical Phenotype. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 537-539.	5.1	37
19	<i>DISC1</i> splice variants are upregulated in schizophrenia and associated with risk polymorphisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15873-15878.	3.3	162
20	Functional Pre-mRNA trans-Splicing of Coactivator CoAA and Corepressor RBM4 during Stem/Progenitor Cell Differentiation. <i>Journal of Biological Chemistry</i> , 2009, 284, 18033-18046.	1.6	38

#	ARTICLE	IF	CITATIONS
21	Limited complementarity between U1 snRNA and a retroviral 5' splice site permits its attenuation via RNA secondary structure. <i>Nucleic Acids Research</i> , 2009, 37, 7429-7440.	6.5	22
22	Genotypic analysis of gene expression in the dissection of the aetiology of complex neurological and psychiatric diseases. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 194-198.	3.8	4
23	Affy exon tissues: exon levels in normal tissues in human, mouse and rat. <i>Bioinformatics</i> , 2009, 25, 2442-2443.	1.8	11
24	Accurate prediction of NAGNAG alternative splicing. <i>Nucleic Acids Research</i> , 2009, 37, 3569-3579.	6.5	25
25	Heterogeneous Nuclear Ribonucleoprotein K Represses the Production of Pro-apoptotic Bcl-xS Splice Isoform. <i>Journal of Biological Chemistry</i> , 2009, 284, 21458-21467.	1.6	69
26	Co-transcriptional splicing of constitutive and alternative exons. <i>Rna</i> , 2009, 15, 1896-1908.	1.6	250
27	CUGBP2 directly interacts with U2 17S snRNP components and promotes U2 snRNA binding to cardiac troponin T pre-mRNA. <i>Nucleic Acids Research</i> , 2009, 37, 4275-4286.	6.5	23
28	Alternative Splicing in Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2009, 4, 674-678.	0.5	52
29	The epithelial splicing factors ESRP1 and ESRP2 positively and negatively regulate diverse types of alternative splicing events. <i>RNA Biology</i> , 2009, 6, 546-562.	1.5	201
30	Role and mechanism of U1-independent pre-mRNA splicing in the regulation of alternative splicing. <i>RNA Biology</i> , 2009, 6, 395-398.	1.5	9
31	Chapter 6 Posttranscriptional Gene Regulation in Kaposi's Sarcoma-Associated Herpesvirus. <i>Advances in Applied Microbiology</i> , 2009, 68, 241-261.	1.3	19
32	Spliceosomes walk the line: Splicing errors and their impact on cellular function. <i>RNA Biology</i> , 2009, 6, 526-530.	1.5	26
33	Getting Started in Gene Expression Microarray Analysis. <i>PLoS Computational Biology</i> , 2009, 5, e1000543.	1.5	127
34	Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. <i>PLoS Computational Biology</i> , 2009, 5, e1000566.	1.5	143
35	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000598.	1.5	777
36	Predicting Functional Alternative Splicing by Measuring RNA Selection Pressure from Multigenome Alignments. <i>PLoS Computational Biology</i> , 2009, 5, e1000608.	1.5	22
37	Conserved Alternative Splicing and Expression Patterns of Arthropod N-Cadherin. <i>PLoS Genetics</i> , 2009, 5, e1000441.	1.5	14
38	Identification and Functional Analyses of 11 769 Full-length Human cDNAs Focused on Alternative Splicing. <i>DNA Research</i> , 2009, 16, 371-383.	1.5	13

#	ARTICLE	IF	CITATIONS
39	Fine-Scale Variation and Genetic Determinants of Alternative Splicing across Individuals. <i>PLoS Genetics</i> , 2009, 5, e1000766.	1.5	81
40	Whole genome transcriptome analysis. <i>RNA Biology</i> , 2009, 6, 107-112.	1.5	44
41	MicroRNA-Biogenesis and Pre-mRNA Splicing Crosstalk. <i>Journal of Biomedicine and Biotechnology</i> , 2009, 2009, 1-6.	3.0	76
42	A hierarchical Bayesian model for comparing transcriptomes at the individual transcript isoform level. <i>Nucleic Acids Research</i> , 2009, 37, e75-e75.	6.5	49
43	Evidence for large diversity in the human transcriptome created by Alu RNA editing. <i>Nucleic Acids Research</i> , 2009, 37, 6905-6915.	6.5	58
44	Control of Alternative Splicing by Signal-dependent Degradation of Splicing-regulatory Proteins. <i>Journal of Biological Chemistry</i> , 2009, 284, 10737-10746.	1.6	31
45	Establishing legitimacy and function in the new transcriptome. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 424-436.	3.8	62
46	<i>De novo</i> transcriptome assembly with ABySS. <i>Bioinformatics</i> , 2009, 25, 2872-2877.	1.8	371
47	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 3056-3059.	1.8	54
48	To localize or not to localize: mRNA fate is in 3'UTR ends. <i>Trends in Cell Biology</i> , 2009, 19, 465-474.	3.6	313
49	The Role of HMGR Alternative Splicing in Statin Efficacy. <i>Trends in Cardiovascular Medicine</i> , 2009, 19, 173-177.	2.3	45
50	Focus on the splicing of Secretin GPCRs transmembrane-domain 7. <i>Trends in Biochemical Sciences</i> , 2009, 34, 443-452.	3.7	40
51	Differential splicing using whole-transcript microarrays. <i>BMC Bioinformatics</i> , 2009, 10, 156.	1.2	16
52	Rodent-specific alternative exons are more frequent in rapidly evolving genes and in paralogs. <i>BMC Evolutionary Biology</i> , 2009, 9, 142.	3.2	7
53	Evolution of alternative and constitutive regions of mammalian 5'UTRs. <i>BMC Genomics</i> , 2009, 10, 162.	1.2	62
54	Transcriptome sequencing of the Microarray Quality Control (MAQC) RNA reference samples using next generation sequencing. <i>BMC Genomics</i> , 2009, 10, 264.	1.2	67
55	Characterization of the <i>Zoarces viviparus</i> liver transcriptome using massively parallel pyrosequencing. <i>BMC Genomics</i> , 2009, 10, 345.	1.2	65
56	Computational prediction of splicing regulatory elements shared by Tetrapoda organisms. <i>BMC Genomics</i> , 2009, 10, 508.	1.2	5

#	ARTICLE	IF	CITATIONS
57	Discovery of novel human transcript variants by analysis of intronic single-block EST with polyadenylation site. <i>BMC Genomics</i> , 2009, 10, 518.	1.2	12
58	Comparison of Affymetrix Gene Array with the Exon Array shows potential application for detection of transcript isoform variation. <i>BMC Genomics</i> , 2009, 10, 519.	1.2	17
59	Genome-wide analysis of chimpanzee genes with premature termination codons. <i>BMC Genomics</i> , 2009, 10, 56.	1.2	12
60	A practical comparison of methods for detecting transcription factor binding sites in ChIP-seq experiments. <i>BMC Genomics</i> , 2009, 10, 618.	1.2	105
61	Conserved sequences in the final intron of MDM2 are essential for the regulation of alternative splicing of MDM2 in response to stress. <i>Experimental Cell Research</i> , 2009, 315, 3419-3432.	1.2	20
62	Translational up-regulation of AuroraA in EGFR-overexpressed cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2010, 14, 1520-1531.	1.6	24
63	The influence of calcium signaling on the regulation of alternative splicing. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2009, 1793, 979-984.	1.9	16
64	Translational control from head to tail. <i>Current Opinion in Cell Biology</i> , 2009, 21, 444-451.	2.6	50
65	Decrypting the genome's alternative messages. <i>Current Opinion in Cell Biology</i> , 2009, 21, 377-386.	2.6	55
66	Quantitative proteomics: a tool to assess cell differentiation. <i>Current Opinion in Cell Biology</i> , 2009, 21, 761-766.	2.6	23
67	ssSNPTarget: genome-wide splice-site single nucleotide polymorphism database. <i>Human Mutation</i> , 2009, 30, E1010-E1020.	1.1	21
68	Muscleblind-like 1 is a negative regulator of TGF β -dependent epithelial-mesenchymal transition of atrioventricular canal endocardial cells. <i>Developmental Dynamics</i> , 2009, 238, 3266-3272.	0.8	18
69	RNA editing: a driving force for adaptive evolution?. <i>BioEssays</i> , 2009, 31, 1137-1145.	1.2	116
70	Regulation of mammalian pre-mRNA splicing. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 253-260.	1.3	18
71	Alternative splicing of G protein-coupled receptors: physiology and pathophysiology. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 3337-3352.	2.4	88
72	Fox-1 family of RNA-binding proteins. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 3895-3907.	2.4	167
73	High resolution analysis of the human transcriptome: detection of extensive alternative splicing independent of transcriptional activity. <i>BMC Genetics</i> , 2009, 10, 63.	2.7	14
74	Arabidopsis RNA immunoprecipitation. <i>Plant Journal</i> , 2009, 59, 163-168.	2.8	75

#	ARTICLE	IF	CITATIONS
75	Complement receptor 2 polymorphisms associated with systemic lupus erythematosus modulate alternative splicing. <i>Genes and Immunity</i> , 2009, 10, 457-469.	2.2	40
76	Argonaute HITS-CLIP decodes microRNA-mRNA interaction maps. <i>Nature</i> , 2009, 460, 479-486.	13.7	1,651
77	How to map billions of short reads onto genomes. <i>Nature Biotechnology</i> , 2009, 27, 455-457.	9.4	257
78	mRNA-Seq whole-transcriptome analysis of a single cell. <i>Nature Methods</i> , 2009, 6, 377-382.	9.0	2,736
79	Digital transcriptome profiling using selective hexamer priming for cDNA synthesis. <i>Nature Methods</i> , 2009, 6, 647-649.	9.0	160
80	Computation for ChIP-seq and RNA-seq studies. <i>Nature Methods</i> , 2009, 6, S22-S32.	9.0	489
81	Engineering splicing factors with designed specificities. <i>Nature Methods</i> , 2009, 6, 825-830.	9.0	136
82	New insights into the aetiology of colorectal cancer from genome-wide association studies. <i>Nature Reviews Genetics</i> , 2009, 10, 353-358.	7.7	355
83	Mechanisms of alternative splicing regulation: insights from molecular and genomics approaches. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 741-754.	16.1	1,037
84	Spinal muscular atrophy: why do low levels of survival motor neuron protein make motor neurons sick?. <i>Nature Reviews Neuroscience</i> , 2009, 10, 597-609.	4.9	632
85	Cancer-associated regulation of alternative splicing. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 670-676.	3.6	327
86	Nucleosome positioning as a determinant of exon recognition. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 996-1001.	3.6	406
87	Splice site strength-dependent activity and genetic buffering by poly-G runs. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1094-1100.	3.6	112
88	Alternative splicing: regulation without regulators. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 13-15.	3.6	20
89	Differential stabilities of alternative exon-skipped rod motifs of dystrophin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 921-928.	1.1	25
90	TopHat: discovering splice junctions with RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1105-1111.	1.8	11,265
91	A Strand-Specific RNA-Seq Analysis of the Transcriptome of the Typhoid Bacillus <i>Salmonella Typhi</i> . <i>PLoS Genetics</i> , 2009, 5, e1000569.	1.5	202
92	Silent (Synonymous) SNPs: Should We Care About Them?. <i>Methods in Molecular Biology</i> , 2009, 578, 23-39.	0.4	214

#	ARTICLE	IF	CITATIONS
93	Transcriptome of embryonic and neonatal mouse cortex by high-throughput RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12741-12746.	3.3	72
94	The Centrality of RNA. <i>Cell</i> , 2009, 136, 577-580.	13.5	397
95	RNA and Disease. <i>Cell</i> , 2009, 136, 777-793.	13.5	991
96	Regulation of Vertebrate Nervous System Alternative Splicing and Development by an SR-Related Protein. <i>Cell</i> , 2009, 138, 898-910.	13.5	195
97	Widespread Shortening of 3'UTRs by Alternative Cleavage and Polyadenylation Activates Oncogenes in Cancer Cells. <i>Cell</i> , 2009, 138, 673-684.	13.5	1,427
98	Shotgun Proteomics in Neuroscience. <i>Neuron</i> , 2009, 63, 12-26.	3.8	48
99	Regiospecific Phosphorylation Control of the SR Protein ASF/SF2 by SRPK1. <i>Journal of Molecular Biology</i> , 2009, 390, 618-634.	2.0	31
100	Genome-wide Analysis of Alternative Pre-mRNA Splicing and RNA-Binding Specificities of the Drosophila hnRNP A/B Family Members. <i>Molecular Cell</i> , 2009, 33, 438-449.	4.5	79
101	Biased Chromatin Signatures around Polyadenylation Sites and Exons. <i>Molecular Cell</i> , 2009, 36, 245-254.	4.5	347
102	Genome-wide Analysis of PTB-RNA Interactions Reveals a Strategy Used by the General Splicing Repressor to Modulate Exon Inclusion or Skipping. <i>Molecular Cell</i> , 2009, 36, 996-1006.	4.5	429
103	Deep sequencing of the zebrafish transcriptome response to mycobacterium infection. <i>Molecular Immunology</i> , 2009, 46, 2918-2930.	1.0	203
104	Protein-binding microarrays: probing disease markers at the interface of proteomics and genomics. <i>Trends in Molecular Medicine</i> , 2009, 15, 352-358.	3.5	14
105	High-throughput sequencing methods to study neuronal RNA-protein interactions. <i>Biochemical Society Transactions</i> , 2009, 37, 1278-1280.	1.6	8
107	Transcript length bias in RNA-seq data confounds systems biology. <i>Biology Direct</i> , 2009, 4, 14.	1.9	422
108	Next-Generation Sequencing: From Basic Research to Diagnostics. <i>Clinical Chemistry</i> , 2009, 55, 641-658.	1.5	668
109	Single Nucleotide Polymorphisms. <i>Methods in Molecular Biology</i> , 2009, , .	0.4	44
110	Statistical inferences for isoform expression in RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1026-1032.	1.8	405
111	A global view of protein expression in human cells, tissues, and organs. <i>Molecular Systems Biology</i> , 2009, 5, 337.	3.2	175

#	ARTICLE	IF	CITATIONS
112	Neuroproteomics. <i>Methods in Molecular Biology</i> , 2009, , .	0.4	1
113	Probe-level estimation improves the detection of differential splicing in Affymetrix exon array studies. <i>Genome Biology</i> , 2009, 10, R77.	13.9	23
114	Evaluation of next generation sequencing platforms for population targeted sequencing studies. <i>Genome Biology</i> , 2009, 10, R32.	13.9	510
115	Characterization of taxonomically restricted genes in a phylum-restricted cell type. <i>Genome Biology</i> , 2009, 10, R8.	13.9	59
116	Global analysis of alternative splicing regulation by insulin and wingless signaling in <i>Drosophila</i> cells. <i>Genome Biology</i> , 2009, 10, R11.	13.9	42
117	Studying chromosome-wide transcriptional networks: new insights into disease?. <i>Genome Medicine</i> , 2009, 1, 50.	3.6	6
118	Current-generation high-throughput sequencing: deepening insights into mammalian transcriptomes. <i>Genes and Development</i> , 2009, 23, 1379-1386.	2.7	140
119	Global Changes in Processing of mRNA 3' Untranslated Regions Characterize Clinically Distinct Cancer Subtypes. <i>Cancer Research</i> , 2009, 69, 9422-9430.	0.4	136
120	Measuring cis-acting regulatory variants genome-wide: new insights into expression genetics and disease susceptibility. <i>Genome Medicine</i> , 2009, 1, 116.	3.6	15
121	Getting under the Skin of Alternative Splicing: Identification of Epithelial-Specific Splicing Factors. <i>Molecular Cell</i> , 2009, 33, 674-676.	4.5	6
122	Splicing in the eukaryotic ancestor: form, function and dysfunction. <i>Trends in Ecology and Evolution</i> , 2009, 24, 447-455.	4.2	47
123	The Methodology of Neuroproteomics. <i>Methods in Molecular Biology</i> , 2009, 566, 1-21.	0.4	3
124	Applications of Genomics in Melanoma Oncogene Discovery. <i>Hematology/Oncology Clinics of North America</i> , 2009, 23, 397-414.	0.9	26
125	Alternative polyadenylation. <i>Plant Signaling and Behavior</i> , 2009, 4, 440-442.	1.2	7
126	Connections between Alternative Transcription and Alternative Splicing in Mammals. <i>Genome Biology and Evolution</i> , 2010, 2, 791-799.	1.1	31
127	Identification of New Pancreatic Beta Cell Targets for In Vivo Imaging by a Systems Biology Approach. <i>Current Pharmaceutical Design</i> , 2010, 16, 1609-1618.	0.9	11
128	DNA sequence variants and the practice of medicine. <i>Current Opinion in Cardiology</i> , 2010, 25, 182-185.	0.8	2
129	Association pattern mining of intron retention events in human based on hybrid learning machine. <i>Genes and Genetic Systems</i> , 2010, 85, 383-394.	0.2	2

#	ARTICLE	IF	CITATIONS
130	Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. <i>Nature Precedings</i> , 2010, , .	0.1	13
131	Heritability in the Efficiency of Nonsense-Mediated mRNA Decay in Humans. <i>PLoS ONE</i> , 2010, 5, e11657.	1.1	17
132	Relationship between genome size and organismal complexity in the lineage leading from prokaryotes to mammals. <i>Paleontological Journal</i> , 2010, 44, 363-373.	0.2	26
133	The Nuclear-Retained Noncoding RNA MALAT1 Regulates Alternative Splicing by Modulating SR Splicing Factor Phosphorylation. <i>Molecular Cell</i> , 2010, 39, 925-938.	4.5	1,906
134	Tissue-specific mechanisms of alternative polyadenylation: testis, brain, and beyond. <i>Wiley Interdisciplinary Reviews RNA</i> , 2010, 1, 494-501.	3.2	53
135	HITS-CLIP: panoramic views of protein-RNA regulation in living cells. <i>Wiley Interdisciplinary Reviews RNA</i> , 2010, 1, 266-286.	3.2	358
136	In junk we trust: repetitive DNA, epigenetics and facioscapulohumeral muscular dystrophy. <i>Epigenomics</i> , 2010, 2, 271-287.	1.0	26
137	Turning on a Fuel Switch of Cancer: hnRNP Proteins Regulate Alternative Splicing of Pyruvate Kinase mRNA. <i>Cancer Research</i> , 2010, 70, 8977-8980.	0.4	189
139	RNA-seq: from technology to biology. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 569-579.	2.4	423
140	MEPE evolution in mammals reveals regions and residues of prime functional importance. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 305-320.	2.4	23
141	Transposable elements in disease-associated cryptic exons. <i>Human Genetics</i> , 2010, 127, 135-154.	1.8	95
142	The Genome-Wide Association Study—A New Era for Common Polygenic Disorders. <i>Journal of Cardiovascular Translational Research</i> , 2010, 3, 173-182.	1.1	26
143	Genome-Wide Association Studies—Data Generation, Storage, Interpretation, and Bioinformatics. <i>Journal of Cardiovascular Translational Research</i> , 2010, 3, 183-188.	1.1	14
144	Molecular Function of TCF7L2: Consequences of TCF7L2 Splicing for Molecular Function and Risk for Type 2 Diabetes. <i>Current Diabetes Reports</i> , 2010, 10, 444-451.	1.7	56
145	Structural annotation of equine protein-coding genes determined by mRNA sequencing. <i>Animal Genetics</i> , 2010, 41, 121-130.	0.6	46
146	The carboxy terminal domain of RNA polymerase II and alternative splicing. <i>Trends in Biochemical Sciences</i> , 2010, 35, 497-504.	3.7	132
147	SplicerAV: a tool for mining microarray expression data for changes in RNA processing. <i>BMC Bioinformatics</i> , 2010, 11, 108.	1.2	12
148	TassDB2 - A comprehensive database of subtle alternative splicing events. <i>BMC Bioinformatics</i> , 2010, 11, 216.	1.2	20

#	ARTICLE	IF	CITATIONS
149	A method of predicting changes in human gene splicing induced by genetic variants in context of cis-acting elements. <i>BMC Bioinformatics</i> , 2010, 11, 22.	1.2	15
150	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. <i>BMC Bioinformatics</i> , 2010, 11, 94.	1.2	1,421
151	The utility of mass spectrometry-based proteomic data for validation of novel alternative splice forms reconstructed from RNA-Seq data: a preliminary assessment. <i>BMC Bioinformatics</i> , 2010, 11, S14.	1.2	52
152	A comprehensive survey of human polymorphisms at conserved splice dinucleotides and its evolutionary relationship with alternative splicing. <i>BMC Evolutionary Biology</i> , 2010, 10, 122.	3.2	9
153	Human functional genetic studies are biased against the medically most relevant primate-specific genes. <i>BMC Evolutionary Biology</i> , 2010, 10, 316.	3.2	16
154	Genomic analysis of expressed sequence tags in American black bear <i>Ursus americanus</i> . <i>BMC Genomics</i> , 2010, 11, 201.	1.2	16
155	Development of a novel splice array platform and its application in the identification of alternative splice variants in lung cancer. <i>BMC Genomics</i> , 2010, 11, 352.	1.2	25
156	Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. <i>BMC Genomics</i> , 2010, 11, 383.	1.2	97
157	Heart transcriptome of the bank vole (<i>Myodes glareolus</i>): towards understanding the evolutionary variation in metabolic rate. <i>BMC Genomics</i> , 2010, 11, 390.	1.2	22
158	Alternative splicing is frequent during early embryonic development in mouse. <i>BMC Genomics</i> , 2010, 11, 399.	1.2	92
159	Normal colon epithelium: a dataset for the analysis of gene expression and alternative splicing events in colon disease. <i>BMC Genomics</i> , 2010, 11, 5.	1.2	38
160	Assessment of orthologous splicing isoforms in human and mouse orthologous genes. <i>BMC Genomics</i> , 2010, 11, 534.	1.2	37
161	Analysis of transcript and protein overlap in a human osteosarcoma cell line. <i>BMC Genomics</i> , 2010, 11, 684.	1.2	13
162	Comparison of transcriptomic landscapes of bovine embryos using RNA-Seq. <i>BMC Genomics</i> , 2010, 11, 711.	1.2	75
163	A molecular inversion probe assay for detecting alternative splicing. <i>BMC Genomics</i> , 2010, 11, 712.	1.2	6
164	Refining orthologue groups at the transcript level. <i>BMC Genomics</i> , 2010, 11, S11.	1.2	5
165	Alternative splicing enriched cDNA libraries identify breast cancer-associated transcripts. <i>BMC Genomics</i> , 2010, 11, S4.	1.2	10
166	Complementary genetic and genomic approaches help characterize the linkage group I seed protein QTL in soybean. <i>BMC Plant Biology</i> , 2010, 10, 41.	1.6	96

#	ARTICLE	IF	CITATIONS
167	Identification and characterization of NAGNAG alternative splicing in the moss <i>Physcomitrella patens</i> . <i>BMC Plant Biology</i> , 2010, 10, 76.	1.6	13
168	Deep sequencing of coding and non-coding RNA in the CNS. <i>Brain Research</i> , 2010, 1338, 146-154.	1.1	10
169	Differential expression and alternative splicing of genes in lumbar spinal cord of an amyotrophic lateral sclerosis mouse model. <i>Brain Research</i> , 2010, 1340, 52-69.	1.1	22
170	Analysis of the Wnt/B-catenin/TCF4 pathway using SAGE, genome-wide microarray and promoter analysis: Identification of BRI3 and HSF2 as novel targets. <i>Cellular Signalling</i> , 2010, 22, 1523-1535.	1.7	17
171	Alternative splicing of genes during neuronal differentiation of NT2 pluripotential human embryonal carcinoma cells. <i>FEBS Letters</i> , 2010, 584, 4041-4047.	1.3	3
172	Regulation of splicing enhancer activities by RNA secondary structures. <i>FEBS Letters</i> , 2010, 584, 4401-4407.	1.3	21
173	Manganese Superoxide Dismutase (SOD2) 3'-Untranslated Region: a Novel Molecular Sensor for Environmental Stress. <i>Free Radical Biology and Medicine</i> , 2010, 49, S127.	1.3	0
174	Recent advances in DNA sequencing methods – general principles of sample preparation. <i>Experimental Cell Research</i> , 2010, 316, 1339-1343.	1.2	66
175	Heterogeneity in mammalian RNA 3' end formation. <i>Experimental Cell Research</i> , 2010, 316, 1357-1364.	1.2	35
176	Subtle discrepancies of SF2/ASF ESE sequence motif among human tissues: A computational approach. <i>Computational Biology and Chemistry</i> , 2010, 34, 203-209.	1.1	1
177	Towards reliable isoform quantification using RNA-SEQ data. <i>BMC Bioinformatics</i> , 2010, 11, S6.	1.2	32
178	A copy number variation in human NCF1 and its pseudogenes. <i>BMC Genetics</i> , 2010, 11, 13.	2.7	23
179	Genetic variations regulate alternative splicing in the 5' untranslated regions of the mouse glioma-associated oncogene 1, Gli1. <i>BMC Molecular Biology</i> , 2010, 11, 32.	3.0	19
180	Systematic analysis of short internal indels and their impact on protein folding. <i>BMC Structural Biology</i> , 2010, 10, 24.	2.3	44
181	Differential splicing of the apoptosis-associated speck like protein containing a caspase recruitment domain (ASC) regulates inflammasomes. <i>Journal of Inflammation</i> , 2010, 7, 23.	1.5	99
182	A comparative approach for the investigation of biological information processing: An examination of the structure and function of computer hard drives and DNA. <i>Theoretical Biology and Medical Modelling</i> , 2010, 7, 3.	2.1	14
183	Systematic analysis of posttranscriptional gene expression. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 162-180.	6.6	98
184	Systems analysis of alternative splicing and its regulation. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 550-565.	6.6	14

#	ARTICLE	IF	CITATIONS
185	The pathobiology of splicing. <i>Journal of Pathology</i> , 2010, 220, 152-163.	2.1	335
186	Alternative splicing: global insights. <i>FEBS Journal</i> , 2010, 277, 856-866.	2.2	128
187	Polypyrimidine tract-binding protein homologues from Arabidopsis underlie regulatory circuits based on alternative splicing and downstream control. <i>Plant Journal</i> , 2010, 64, 243-255.	2.8	64
188	AphidBase: a centralized bioinformatic resource for annotation of the pea aphid genome. <i>Insect Molecular Biology</i> , 2010, 19, 5-12.	1.0	108
189	SF2/ASF autoregulation involves multiple layers of post-transcriptional and translational control. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 306-312.	3.6	165
190	Structural basis of G-tract recognition and encaging by hnRNP F quasi-RRMs. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 853-861.	3.6	132
191	Position-dependent alternative splicing activity revealed by global profiling of alternative splicing events regulated by PTB. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1114-1123.	3.6	218
192	The intronic splicing code: multiple factors involved in ATM pseudoexon definition. <i>EMBO Journal</i> , 2010, 29, 749-760.	3.5	34
193	Stoichiometry of a regulatory splicing complex revealed by single-molecule analyses. <i>EMBO Journal</i> , 2010, 29, 2161-2172.	3.5	47
194	An ESRP-regulated splicing programme is abrogated during the epithelialâ€mesenchymal transition. <i>EMBO Journal</i> , 2010, 29, 3286-3300.	3.5	346
195	A functional human Poly(A) site requires only a potent DSE and an A-rich upstream sequence. <i>EMBO Journal</i> , 2010, 29, 1523-1536.	3.5	78
196	Understanding mechanisms underlying human gene expression variation with RNA sequencing. <i>Nature</i> , 2010, 464, 768-772.	13.7	1,200
197	Transcriptome genetics using second generation sequencing in a Caucasian population. <i>Nature</i> , 2010, 464, 773-777.	13.7	782
198	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. <i>Nature</i> , 2010, 464, 1351-1356.	13.7	463
199	Deciphering the splicing code. <i>Nature</i> , 2010, 465, 53-59.	13.7	781
200	Ab initio reconstruction of cell typeâ€specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. <i>Nature Biotechnology</i> , 2010, 28, 503-510.	9.4	1,251
201	Advancing RNA-Seq analysis. <i>Nature Biotechnology</i> , 2010, 28, 421-423.	9.4	192
202	Haploidy with histones. <i>Nature Biotechnology</i> , 2010, 28, 423-424.	9.4	10

#	ARTICLE	IF	CITATIONS
203	RNA sequencing shows no dosage compensation of the active X-chromosome. <i>Nature Genetics</i> , 2010, 42, 1043-1047.	9.4	199
204	Characterization of missing human genome sequences and copy-number polymorphic insertions. <i>Nature Methods</i> , 2010, 7, 365-371.	9.0	138
205	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010, 7, 709-715.	9.0	662
206	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , 2010, 7, 843-847.	9.0	283
207	Analysis and design of RNA sequencing experiments for identifying isoform regulation. <i>Nature Methods</i> , 2010, 7, 1009-1015.	9.0	1,224
208	RNA-Seq analysis to capture the transcriptome landscape of a single cell. <i>Nature Protocols</i> , 2010, 5, 516-535.	5.5	450
209	Visualization and genetic analysis of alternative splicing regulation in vivo using fluorescence reporters in transgenic <i>Caenorhabditis elegans</i> . <i>Nature Protocols</i> , 2010, 5, 1495-1517.	5.5	69
210	RNA processing and its regulation: global insights into biological networks. <i>Nature Reviews Genetics</i> , 2010, 11, 75-87.	7.7	639
211	Alternative splicing and evolution: diversification, exon definition and function. <i>Nature Reviews Genetics</i> , 2010, 11, 345-355.	7.7	921
213	The neuronal splicing factor Nova co-localizes with target RNAs in the dendrite. <i>Frontiers in Neural Circuits</i> , 2010, 4, 5.	1.4	57
214	A Statistical Method for the Detection of Alternative Splicing Using RNA-Seq. <i>PLoS ONE</i> , 2010, 5, e8529.	1.1	36
215	Tumor Transcriptome Sequencing Reveals Allelic Expression Imbalances Associated with Copy Number Alterations. <i>PLoS ONE</i> , 2010, 5, e9317.	1.1	134
216	Splicing Reporter Mice Revealed the Evolutionally Conserved Switching Mechanism of Tissue-Specific Alternative Exon Selection. <i>PLoS ONE</i> , 2010, 5, e10946.	1.1	29
217	Splice Isoforms of the Polyglutamine Disease Protein Ataxin-3 Exhibit Similar Enzymatic yet Different Aggregation Properties. <i>PLoS ONE</i> , 2010, 5, e13695.	1.1	57
218	HMMSplicer: A Tool for Efficient and Sensitive Discovery of Known and Novel Splice Junctions in RNA-Seq Data. <i>PLoS ONE</i> , 2010, 5, e13875.	1.1	50
219	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. <i>PLoS ONE</i> , 2010, 5, e14040.	1.1	215
220	Aspectos evolutivos do splicing alternativo.. <i>Revista Da Biologia</i> , 2010, 4, 44-49.	0.2	0
221	The Human Transcriptome. , 2010, , 89-103.		2

#	ARTICLE	IF	CITATIONS
222	H-DBAS: human-transcriptome database for alternative splicing: update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D86-D90.	6.5	38
223	Global regulation of alternative splicing during myogenic differentiation. <i>Nucleic Acids Research</i> , 2010, 38, 7651-7664.	6.5	135
224	The adaptive significance of unproductive alternative splicing in primates. <i>Rna</i> , 2010, 16, 2014-2022.	1.6	18
225	Ontogenomic study of the relationship between number of gene splice variants and GO categorization. <i>Bioinformatics</i> , 2010, 26, 1945-1949.	1.8	2
226	Evolutionary history of regulatory variation in human populations. <i>Human Molecular Genetics</i> , 2010, 19, R197-R203.	1.4	10
227	A global comparison between nuclear and cytosolic transcriptomes reveals differential compartmentalization of alternative transcript isoforms. <i>Nucleic Acids Research</i> , 2010, 38, 1086-1097.	6.5	25
228	Heart Failure-associated Changes in RNA Splicing of Sarcomere Genes. <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 138-146.	5.1	137
229	Intron retention facilitates splice variant diversity in calcium-activated big potassium channel populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21152-21157.	3.3	60
230	Computational identification of tissue-specific alternative splicing elements in mouse genes from RNA-Seq. <i>Nucleic Acids Research</i> , 2010, 38, 7895-7907.	6.5	15
231	Nuclear pre-mRNA 3'-end processing regulates synapse and axon development in <i>C. elegans</i> . <i>Development (Cambridge)</i> , 2010, 137, 2237-2250.	1.2	19
232	RNA looping by PTB: Evidence using FRET and NMR spectroscopy for a role in splicing repression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4105-4110.	3.3	96
233	Alternate processing of Flt1 transcripts is directed by conserved cis-elements within an intronic region of FLT1 that reciprocally regulates splicing and polyadenylation. <i>Nucleic Acids Research</i> , 2010, 38, 5130-5140.	6.5	25
234	hnRNP A1 and hnRNP H can collaborate to modulate 5' splice site selection. <i>Rna</i> , 2010, 16, 228-238.	1.6	55
235	SRp40 and SRp55 Promote the Translation of Unspliced Human Immunodeficiency Virus Type 1 RNA. <i>Journal of Virology</i> , 2010, 84, 6748-6759.	1.5	60
236	Modulation of the Human Glucuronosyltransferase UGT1A Pathway by Splice Isoform Polypeptides Is Mediated through Protein-Protein Interactions. <i>Journal of Biological Chemistry</i> , 2010, 285, 3600-3607.	1.6	38
237	MBNL1 binds GC motifs embedded in pyrimidines to regulate alternative splicing. <i>Nucleic Acids Research</i> , 2010, 38, 2467-2484.	6.5	127
238	An unexpected ending: Noncanonical 3' end processing mechanisms. <i>Rna</i> , 2010, 16, 259-266.	1.6	54
239	Molecular mechanisms of eukaryotic pre-mRNA 3' end processing regulation. <i>Nucleic Acids Research</i> , 2010, 38, 2757-2774.	6.5	322

#	ARTICLE	IF	CITATIONS
240	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. <i>Nucleic Acids Research</i> , 2010, 38, e17-e17.	6.5	200
241	Characterization of Alternatively Spliced Transcript Variants of CLEC2D Gene. <i>Journal of Biological Chemistry</i> , 2010, 285, 36207-36215.	1.6	50
242	A network of conserved co-occurring motifs for the regulation of alternative splicing. <i>Nucleic Acids Research</i> , 2010, 38, 7916-7926.	6.5	12
243	Human RBMY regulates germline-specific splicing events by modulating the function of the serine/arginine-rich proteins 9G8 and Tra2- β . <i>Journal of Cell Science</i> , 2010, 123, 40-50.	1.2	44
244	Into the unknown: expression profiling without genome sequence information in CHO by next generation sequencing. <i>Nucleic Acids Research</i> , 2010, 38, 3999-4010.	6.5	97
245	Alternative splicing of CD200 is regulated by an exonic splicing enhancer and SF2/ASF. <i>Nucleic Acids Research</i> , 2010, 38, 6684-6696.	6.5	16
246	Unconstrained mining of transcript data reveals increased alternative splicing complexity in the human transcriptome. <i>Nucleic Acids Research</i> , 2010, 38, 4740-4754.	6.5	55
247	Heterogeneous ribonucleoprotein C displays a repressor activity mediated by T-cell intracellular antigen-1-related/like protein to modulate Fas exon 6 splicing through a mechanism involving Hu antigen R. <i>Nucleic Acids Research</i> , 2010, 38, 8001-8014.	6.5	46
248	Cytokines Interleukin-1 β and Tumor Necrosis Factor- α Regulate Different Transcriptional and Alternative Splicing Networks in Primary β -Cells. <i>Diabetes</i> , 2010, 59, 358-374.	0.3	134
249	Deep mRNA Sequencing for In Vivo Functional Analysis of Cardiac Transcriptional Regulators. <i>Circulation Research</i> , 2010, 106, 1459-1467.	2.0	76
250	Circulation Research and Human Genetic Studies. <i>Circulation Research</i> , 2010, 107, 6-8.	2.0	5
251	Competing Upstream 5' Splice Sites Enhance the Rate of Proximal Splicing. <i>Molecular and Cellular Biology</i> , 2010, 30, 1878-1886.	1.1	35
252	Noncanonical transcript forms in yeast and their regulation during environmental stress. <i>Rna</i> , 2010, 16, 1256-1267.	1.6	72
253	Defining the transcriptome and proteome in three functionally different human cell lines. <i>Molecular Systems Biology</i> , 2010, 6, 450.	3.2	324
254	MicroRNAs coordinate an alternative splicing network during mouse postnatal heart development. <i>Genes and Development</i> , 2010, 24, 653-658.	2.7	114
255	Genome-wide evidence for selection acting on single amino acid repeats. <i>Genome Research</i> , 2010, 20, 755-760.	2.4	35
256	Digital Gene Expression Signatures for Maize Development. <i>Plant Physiology</i> , 2010, 154, 1024-1039.	2.3	82
257	Splicing factor and exon profiling across human tissues. <i>Nucleic Acids Research</i> , 2010, 38, 2825-2838.	6.5	114

#	ARTICLE	IF	CITATIONS
258	The neurofibromatosis type I pre-mRNA is a novel target of CELF protein-mediated splicing regulation. <i>Nucleic Acids Research</i> , 2010, 38, 253-264.	6.5	33
259	Evolution of alternative splicing in primate brain transcriptomes. <i>Human Molecular Genetics</i> , 2010, 19, 2958-2973.	1.4	47
260	Sam68 regulates EMT through alternative splicing and activated nonsense-mediated mRNA decay of the SF2/ASF proto-oncogene. <i>Journal of Cell Biology</i> , 2010, 191, 87-99.	2.3	146
261	Single molecule analysis of combinatorial splicing. <i>Nucleic Acids Research</i> , 2010, 38, e163-e163.	6.5	13
262	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 961-974.	1.5	121
263	Anti-tumor activity of splice-switching oligonucleotides. <i>Nucleic Acids Research</i> , 2010, 38, 8348-8356.	6.5	121
264	A model in vitro system for co-transcriptional splicing. <i>Nucleic Acids Research</i> , 2010, 38, 7570-7578.	6.5	13
265	Prediction of alternative isoforms from exon expression levels in RNA-Seq experiments. <i>Nucleic Acids Research</i> , 2010, 38, e112-e112.	6.5	134
266	Splice Variant Identification and Expression Analysis of the Fat Mass and Obesity-Associated <i>FTO</i> Gene in Intact and Castrated Male Pigs. <i>DNA and Cell Biology</i> , 2010, 29, 729-733.	0.9	8
267	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. <i>Nucleic Acids Research</i> , 2010, 38, e178-e178.	6.5	946
268	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. <i>Nucleic Acids Research</i> , 2010, 38, 4570-4578.	6.5	300
269	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010, 20, 646-654.	2.4	435
270	Understanding neuronal connectivity through the post-transcriptional toolkit. <i>Genes and Development</i> , 2010, 24, 625-635.	2.7	51
271	Quantitative and Qualitative RNA-Seq-Based Evaluation of Epstein-Barr Virus Transcription in Type I Latency Burkitt's Lymphoma Cells. <i>Journal of Virology</i> , 2010, 84, 13053-13058.	1.5	43
272	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , 2010, 20, 1639-1650.	2.4	76
273	Alternative splicing produces high levels of noncoding isoforms of bHLH transcription factors during development. <i>Genes and Development</i> , 2010, 24, 229-234.	2.7	8
274	ISOFORM ABUNDANCE INFERENCE PROVIDES A MORE ACCURATE ESTIMATION OF GENE EXPRESSION LEVELS IN RNA-SEQ. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 177-192.	0.3	33
275	A two-parameter generalized Poisson model to improve the analysis of RNA-seq data. <i>Nucleic Acids Research</i> , 2010, 38, e170-e170.	6.5	131

#	ARTICLE	IF	CITATIONS
276	Coupling genetics and post-genomic approaches to decipher the cellular splicing code at a systems-wide level. <i>Biochemical Society Transactions</i> , 2010, 38, 237-241.	1.6	6
277	Model-based detection of alternative splicing signals. <i>Bioinformatics</i> , 2010, 26, i325-i333.	1.8	22
278	Alternative pre-mRNA splicing regulation in cancer: pathways and programs unhinged. <i>Genes and Development</i> , 2010, 24, 2343-2364.	2.7	697
279	Functional selection and systematic analysis of intronic splicing elements identify active sequence motifs and associated splicing factors. <i>Nucleic Acids Research</i> , 2010, 38, 5152-5165.	6.5	25
280	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5254-5259.	3.3	168
281	Massive expansions of <i>Dscam</i> splicing diversity via staggered homologous recombination during arthropod evolution. <i>Rna</i> , 2010, 16, 91-105.	1.6	36
282	The neuronal splicing factor Nova controls alternative splicing in N-type and P-type Ca _v 2 calcium channels. <i>Channels</i> , 2010, 4, 483-489.	1.5	43
283	PLANdbAffy: probe-level annotation database for Affymetrix expression microarrays. <i>Nucleic Acids Research</i> , 2010, 38, D726-D730.	6.5	25
284	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	2.4	239
285	Usage of cancer associated autoantibodies in the detection of disease. <i>Cancer Biomarkers</i> , 2010, 6, 257-270.	0.8	30
286	Analysis of the expression of human tumor antigens in ovarian cancer tissues. <i>Cancer Biomarkers</i> , 2010, 6, 33-48.	0.8	21
287	Microdissection of the gene expression codes driving nephrogenesis. <i>Organogenesis</i> , 2010, 6, 263-269.	0.4	4
288	Noisy Splicing Drives mRNA Isoform Diversity in Human Cells. <i>PLoS Genetics</i> , 2010, 6, e1001236.	1.5	254
289	Uncovering the Complexity of Transcriptomes with RNA-Seq. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-19.	3.0	315
290	AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. <i>Nucleic Acids Research</i> , 2010, 38, W755-W762.	6.5	310
291	Alternative-splicing forms of the major phase II conjugating UGT1A gene negatively regulate glucuronidation in human carcinoma cell lines. <i>Pharmacogenomics Journal</i> , 2010, 10, 431-441.	0.9	27
292	mRNA-seq with agnostic splice site discovery for nervous system transcriptomics tested in chronic pain. <i>Genome Research</i> , 2010, 20, 847-860.	2.4	71
293	Promotion of exon 6 inclusion in HuD pre-mRNA by Hu protein family members. <i>Nucleic Acids Research</i> , 2010, 38, 3760-3770.	6.5	44

#	ARTICLE	IF	CITATIONS
294	An exonic splicing enhancer within a bidirectional coding sequence regulates alternative splicing of an antisense mRNA. <i>RNA Biology</i> , 2010, 7, 179-190.	1.5	8
295	An emerging role for nuclear RNA-mediated responses to genotoxic stress. <i>RNA Biology</i> , 2010, 7, 390-396.	1.5	13
296	Conserved developmental alternative splicing of muscleblind-like (MBNL) transcripts regulates MBNL localization and activity. <i>RNA Biology</i> , 2010, 7, 43-55.	1.5	51
297	Alternative splicing and muscular dystrophy. <i>RNA Biology</i> , 2010, 7, 441-452.	1.5	55
298	Editorial on alternative splicing and disease. <i>RNA Biology</i> , 2010, 7, 388-389.	1.5	7
299	Alternative splicing in multiple sclerosis and other autoimmune diseases. <i>RNA Biology</i> , 2010, 7, 462-473.	1.5	66
300	High-throughput quantification of splicing isoforms. <i>Rna</i> , 2010, 16, 442-449.	1.6	77
301	MamPhEA: a web tool for mammalian phenotype enrichment analysis. <i>Bioinformatics</i> , 2010, 26, 2212-2213.	1.8	26
302	Analysis of SRp86-regulated alternative splicing. <i>RNA Biology</i> , 2010, 7, 486-494.	1.5	4
303	HnRNP L-mediated regulation of mammalian alternative splicing by interference with splice site recognition. <i>RNA Biology</i> , 2010, 7, 56-64.	1.5	43
304	Novel roles of U1 snRNP in alternative splicing regulation. <i>RNA Biology</i> , 2010, 7, 412-419.	1.5	36
305	Pro-metastatic splicing of Ron proto-oncogene mRNA can be reversed: Therapeutic potential of bifunctional oligonucleotides and indole derivatives. <i>RNA Biology</i> , 2010, 7, 495-503.	1.5	65
306	ARH: predicting splice variants from genome-wide data with modified entropy. <i>Bioinformatics</i> , 2010, 26, 84-90.	1.8	18
307	Rapid-Response Splicing Reporter Screens Identify Differential Regulators of Constitutive and Alternative Splicing. <i>Molecular and Cellular Biology</i> , 2010, 30, 1718-1728.	1.1	110
308	Embracing the complexity of pre-mRNA splicing. <i>Cell Research</i> , 2010, 20, 866-868.	5.7	7
309	Alternative splicing and breast cancer. <i>RNA Biology</i> , 2010, 7, 403-411.	1.5	35
310	The function of spliceosome components in open mitosis. <i>Nucleus</i> , 2010, 1, 447-459.	0.6	42
311	Experimental Approaches to the Human Renal Transcriptome. <i>Seminars in Nephrology</i> , 2010, 30, 455-467.	0.6	8

#	ARTICLE	IF	CITATIONS
312	A scaling normalization method for differential expression analysis of RNA-seq data. <i>Genome Biology</i> , 2010, 11, R25.	13.9	6,234
313	Standardizing the Next Generation of Bioinformatics Software Development with BioHDF (HDF5). <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 693-700.	0.8	18
314	A Novel Method for Splice Sites Recognition Using Comprehensive Information. , 2010, , .		0
316	Genome-Wide Approaches to Monitor Pre-mRNA Splicing. <i>Methods in Enzymology</i> , 2010, 470, 51-75.	0.4	12
317	FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. <i>Genome Biology</i> , 2010, 11, R104.	3.8	137
318	Integrative analysis of the melanoma transcriptome. <i>Genome Research</i> , 2010, 20, 413-427.	2.4	248
319	Algorithms in Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2010, , .	1.0	0
320	Exploring plant transcriptomes using ultra high-throughput sequencing. <i>Briefings in Functional Genomics</i> , 2010, 9, 118-128.	1.3	108
321	When ribosomes go bad: diseases of ribosome biogenesis. <i>Molecular BioSystems</i> , 2010, 6, 481.	2.9	149
322	The snoRNA MBII-52 (SNORD 115) is processed into smaller RNAs and regulates alternative splicing. <i>Human Molecular Genetics</i> , 2010, 19, 1153-1164.	1.4	259
323	Context-Dependent Regulatory Mechanism of the Splicing Factor hnRNP L. <i>Molecular Cell</i> , 2010, 37, 223-234.	4.5	84
324	An Ancient Mechanism for Splicing Control: U11 snRNP as an Activator of Alternative Splicing. <i>Molecular Cell</i> , 2010, 37, 821-833.	4.5	37
325	A Splicing-Independent Function of SF2/ASF in MicroRNA Processing. <i>Molecular Cell</i> , 2010, 38, 67-77.	4.5	175
326	A2BP1 as a novel susceptible gene for primary biliary cirrhosis in Japanese patients. <i>Human Immunology</i> , 2010, 71, 520-524.	1.2	18
327	Context-Dependent Remodeling of Structure in Two Large Protein Fragments. <i>Journal of Molecular Biology</i> , 2010, 402, 720-730.	2.0	8
328	Long Noncoding RNAs with Enhancer-like Function in Human Cells. <i>Cell</i> , 2010, 143, 46-58.	13.5	1,664
329	Upf1 Senses 3'UTR Length to Potentiate mRNA Decay. <i>Cell</i> , 2010, 143, 379-389.	13.5	316
330	Nova2 Regulates Neuronal Migration through an RNA Switch in Disabled-1 Signaling. <i>Neuron</i> , 2010, 66, 848-858.	3.8	150

#	ARTICLE	IF	CITATIONS
331	The plasticity of the mammalian transcriptome. <i>Genomics</i> , 2010, 95, 1-6.	1.3	64
332	A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. <i>Genomics</i> , 2010, 96, 259-265.	1.3	184
333	Repair of pre-mRNA splicing. <i>RNA Biology</i> , 2010, 7, 430-440.	1.5	29
334	RNA Targeting Therapeutics: Molecular Mechanisms of Antisense Oligonucleotides as a Therapeutic Platform. <i>Annual Review of Pharmacology and Toxicology</i> , 2010, 50, 259-293.	4.2	1,136
335	Distinct Patterns of Expression and Evolution of Intronless and Intron-Containing Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2010, 27, 1745-1749.	3.5	116
336	Expansion of the eukaryotic proteome by alternative splicing. <i>Nature</i> , 2010, 463, 457-463.	13.7	1,787
337	Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. <i>Nature Biotechnology</i> , 2010, 28, 511-515.	9.4	13,805
338	Desperately seeking microRNA targets. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1169-1174.	3.6	456
339	Vascular smooth muscle cell differentiation 2010. <i>Journal of Biomedical Research</i> , 2010, 24, 169-180.	0.7	18
340	Fast and SNP-tolerant detection of complex variants and splicing in short reads. <i>Bioinformatics</i> , 2010, 26, 873-881.	1.8	1,774
341	Genome-wide mapping of alternative splicing in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2010, 20, 45-58.	2.4	825
342	Genome-wide analysis of allelic expression imbalance in human primary cells by high-throughput transcriptome resequencing. <i>Human Molecular Genetics</i> , 2010, 19, 122-134.	1.4	197
343	Survey of the transcriptome of <i>Aspergillus oryzae</i> via massively parallel mRNA sequencing. <i>Nucleic Acids Research</i> , 2010, 38, 5075-5087.	6.5	189
344	Integrative Modeling Defines the Nova Splicing-Regulatory Network and Its Combinatorial Controls. <i>Science</i> , 2010, 329, 439-443.	6.0	261
345	Advances in Computational Biology. <i>Advances in Experimental Medicine and Biology</i> , 2010, , .	0.8	2
346	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 181-197.	3.2	141
348	Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , 2010, 38, e131-e131.	6.5	573
349	Advanced Intelligent Computing Theories and Applications. <i>Communications in Computer and Information Science</i> , 2010, , .	0.4	2

#	ARTICLE	IF	CITATIONS
350	Annotating conserved and novel features of primate transcriptomes using sequencing. <i>Genome Biology</i> , 2010, 11, 125.	13.9	1
351	Identification of novel exons and transcribed regions by chimpanzee transcriptome sequencing. <i>Genome Biology</i> , 2010, 11, R78.	13.9	26
352	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	13.9	391
353	Modeling non-uniformity in short-read rates in RNA-Seq data. <i>Genome Biology</i> , 2010, 11, R50.	13.9	165
354	Genome-wide functional analysis of human 5' untranslated region introns. <i>Genome Biology</i> , 2010, 11, R29.	13.9	68
355	Global and unbiased detection of splice junctions from RNA-seq data. <i>Genome Biology</i> , 2010, 11, R34.	13.9	75
356	Gene ontology analysis for RNA-seq: accounting for selection bias. <i>Genome Biology</i> , 2010, 11, R14.	13.9	5,824
357	The Cell Biology of Stem Cells. <i>Advances in Experimental Medicine and Biology</i> , 2010, , .	0.8	3
358	Data mining of mRNA-Seq and small RNA-Seq data to find microRNA targets. , 2010, , .		0
359	UGT genomic diversity: beyond gene duplication. <i>Drug Metabolism Reviews</i> , 2010, 42, 24-44.	1.5	124
360	Estimating the Expression of Transcript Isoforms from mRNA-Seq via Nonnegative Least Squares. , 2010, , .		3
361	RNA Processing and Export. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a000752-a000752.	2.3	142
362	Function annotation of the rice transcriptome at single-nucleotide resolution by RNA-seq. <i>Genome Research</i> , 2010, 20, 1238-1249.	2.4	307
363	The real cost of sequencing: higher than you think!. <i>Genome Biology</i> , 2011, 12, 125.	13.9	299
364	Characterization of intronic structures and alternative splicing in <i>Phytophthora sojae</i> by comparative analysis of expressed sequence tags and genomic sequences. <i>Canadian Journal of Microbiology</i> , 2011, 57, 84-90.	0.8	19
365	Improved RNA-Seq Partitions in Linear Models for Isoform Quantification. , 2011, , .		0
366	Differential genome-wide profiling of tandem 3' UTRs among human breast cancer and normal cells by high-throughput sequencing. <i>Genome Research</i> , 2011, 21, 741-747.	2.4	252
367	Posterior Probability of Discovery and Expected Rate of Discovery for Multiple Hypothesis Testing and High Throughput Assays. <i>Journal of the American Statistical Association</i> , 2011, 106, 984-996.	1.8	3

#	ARTICLE	IF	CITATIONS
368	A comparison of RNA-Seq and high-density exon array for detecting differential gene expression between closely related species. <i>Nucleic Acids Research</i> , 2011, 39, 578-588.	6.5	123
369	RNA-sequence analysis of human B-cells. <i>Genome Research</i> , 2011, 21, 991-998.	2.4	126
370	Tissue-Specific Proteins and Functional Implications. <i>Journal of Proteome Research</i> , 2011, 10, 1893-1903.	1.8	31
371	Ending the message: poly(A) signals then and now. <i>Genes and Development</i> , 2011, 25, 1770-1782.	2.7	490
372	Alternative transcription exceeds alternative splicing in generating the transcriptome diversity of cerebellar development. <i>Genome Research</i> , 2011, 21, 1260-1272.	2.4	192
373	Genetic Neuropathology of Schizophrenia: New Approaches to an Old Question and New Uses for Postmortem Human Brains. <i>Biological Psychiatry</i> , 2011, 69, 140-145.	0.7	83
374	Pharmacogenomics and adverse drug reactions: the case of statins. <i>Expert Opinion on Pharmacotherapy</i> , 2011, 12, 1499-1509.	0.9	22
375	Adopting orphans: comprehensive genetic testing of Mendelian diseases of childhood by next-generation sequencing. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 855-868.	1.5	45
376	Sequencing technology does not eliminate biological variability. <i>Nature Biotechnology</i> , 2011, 29, 572-573.	9.4	193
377	Evidence That "Brain-Specific" Fox-1, Fox-2, and nPTB Alternatively Spliced Isoforms Are Produced in the Lens. <i>Current Eye Research</i> , 2011, 36, 321-327.	0.7	14
378	Transcriptional activity regulates alternative cleavage and polyadenylation. <i>Molecular Systems Biology</i> , 2011, 7, 534.	3.2	111
379	Reconstitution of CF IA from Overexpressed Subunits Reveals Stoichiometry and Provides Insights into Molecular Topology. <i>Biochemistry</i> , 2011, 50, 10203-10214.	1.2	30
380	Insights into Global Mechanisms and Disease by Gene Expression Profiling. <i>Methods in Molecular Biology</i> , 2011, 719, 269-298.	0.4	2
381	Otosclerosis. <i>Advances in Oto-Rhino-Laryngology</i> , 2011, 70, 122-129.	1.6	38
382	Yeast Systems Biology. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	7
383	RNA. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	5
384	Functional Implications of Structural Predictions for Alternative Splice Proteins Expressed in Her2/neu-Induced Breast Cancers. <i>Journal of Proteome Research</i> , 2011, 10, 5503-5511.	1.8	40
385	The relationship between proteome size, structural disorder and organism complexity. <i>Genome Biology</i> , 2011, 12, R120.	13.9	161

#	ARTICLE	IF	CITATIONS
386	Genomewide characterization of non-polyadenylated RNAs. <i>Genome Biology</i> , 2011, 12, R16.	13.9	365
387	Coding potential of the products of alternative splicing in human. <i>Genome Biology</i> , 2011, 12, R9.	3.8	38
388	Transcriptome instability in colorectal cancer identified by exon microarray analyses: Associations with splicing factor expression levels and patient survival. <i>Genome Medicine</i> , 2011, 3, 32.	3.6	73
389	Epigenetics in Alternative Pre-mRNA Splicing. <i>Cell</i> , 2011, 144, 16-26.	13.5	697
390	FMRP Stalls Ribosomal Translocation on mRNAs Linked to Synaptic Function and Autism. <i>Cell</i> , 2011, 146, 247-261.	13.5	1,864
391	Conserved Function of lincRNAs in Vertebrate Embryonic Development despite Rapid Sequence Evolution. <i>Cell</i> , 2011, 147, 1537-1550.	13.5	1,072
392	Expression of the Splicing Factor Gene SFRS10 Is Reduced in Human Obesity and Contributes to Enhanced Lipogenesis. <i>Cell Metabolism</i> , 2011, 14, 208-218.	7.2	130
393	More than a splicing code: integrating the role of RNA, chromatin and non-coding RNA in alternative splicing regulation. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 366-372.	1.5	108
394	Decoding muscle alternative splicing. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 380-387.	1.5	49
395	RNA structure and the mechanisms of alternative splicing. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 373-379.	1.5	222
396	Observations on novel splice junctions from RNA sequencing data. <i>Biochemical and Biophysical Research Communications</i> , 2011, 409, 299-303.	1.0	16
397	Alternative splicing of T-box transcription factor genes. <i>Biochemical and Biophysical Research Communications</i> , 2011, 412, 513-517.	1.0	17
398	Alternative splicing variants of human arsenic (+3 oxidation state) methyltransferase. <i>Biochemical and Biophysical Research Communications</i> , 2011, 415, 48-53.	1.0	12
399	CTCF-promoted RNA polymerase II pausing links DNA methylation to splicing. <i>Nature</i> , 2011, 479, 74-79.	13.7	853
400	Pervasive haplotypic variation in the spliceo-transcriptome of the human major histocompatibility complex. <i>Genome Research</i> , 2011, 21, 1042-1054.	2.4	63
401	The Post-transcriptional Operon. <i>Methods in Molecular Biology</i> , 2011, 703, 237-245.	0.4	12
402	CD44 splice isoform switching in human and mouse epithelium is essential for epithelial-mesenchymal transition and breast cancer progression. <i>Journal of Clinical Investigation</i> , 2011, 121, 1064-1074.	3.9	543
403	Synthetic spike-in standards for RNA-seq experiments. <i>Genome Research</i> , 2011, 21, 1543-1551.	2.4	588

#	ARTICLE	IF	CITATIONS
404	Cell-specific expression of TLR9 isoforms in inflammation. <i>Journal of Autoimmunity</i> , 2011, 36, 76-86.	3.0	26
405	p38 MAPK Controls Prothrombin Expression by Regulated RNA 3' End Processing. <i>Molecular Cell</i> , 2011, 41, 298-310.	4.5	70
406	Cross-Regulation between an Alternative Splicing Activator and a Transcription Repressor Controls Neurogenesis. <i>Molecular Cell</i> , 2011, 43, 843-850.	4.5	124
407	Mechanisms and Consequences of Alternative Polyadenylation. <i>Molecular Cell</i> , 2011, 43, 853-866.	4.5	626
408	From genome-wide association studies to etiology: probing autoimmunity genes by RNAi. <i>Trends in Molecular Medicine</i> , 2011, 17, 634-640.	3.5	5
409	RNA Induces Conformational Changes in the SF1/U2AF65 Splicing Factor Complex. <i>Journal of Molecular Biology</i> , 2011, 405, 1128-1138.	2.0	12
410	Evolutionary Connections between Coding and Splicing Regulatory Regions in the Fibronectin EDA Exon. <i>Journal of Molecular Biology</i> , 2011, 411, 1-15.	2.0	1
411	Mapping in vivo protein-RNA interactions at single-nucleotide resolution from HITS-CLIP data. <i>Nature Biotechnology</i> , 2011, 29, 607-614.	9.4	384
412	Transcriptome profiling and digital gene expression by deep-sequencing in normal/regenerative tissues of planarian <i>Dugesia japonica</i> . <i>Genomics</i> , 2011, 97, 364-371.	1.3	56
413	RNA splicing in regulation of nitric oxide receptor soluble guanylyl cyclase. <i>Nitric Oxide - Biology and Chemistry</i> , 2011, 25, 265-274.	1.2	17
414	Introduction and Historical Overview of DNA Sequencing. <i>Current Protocols in Molecular Biology</i> , 2011, 96, 7.0.1.	2.9	1
416	Construction of Normalized RNA-seq Libraries for Next-Generation Sequencing Using the Crab Duplex-specific Nuclease. <i>Current Protocols in Molecular Biology</i> , 2011, 94, Unit4.12.	2.9	72
417	SNP discovery in black cottonwood (<i>Populus trichocarpa</i>) by population transcriptome resequencing. <i>Molecular Ecology Resources</i> , 2011, 11, 81-92.	2.2	104
418	Improving RNA-Seq expression estimates by correcting for fragment bias. <i>Genome Biology</i> , 2011, 12, R22.	13.9	1,164
419	Artemis splice defects cause atypical SCID and can be restored in vitro by an antisense oligonucleotide. <i>Genes and Immunity</i> , 2011, 12, 434-444.	2.2	27
420	Targeted enrichment beyond the consensus coding DNA sequence exome reveals exons with higher variant densities. <i>Genome Biology</i> , 2011, 12, R68.	13.9	192
421	ExpressionPlot: a web-based framework for analysis of RNA-Seq and microarray gene expression data. <i>Genome Biology</i> , 2011, 12, R69.	3.8	32
422	Differential expression of heat shock protein genes and their splice variants in bovine preimplantation embryos. <i>Journal of Dairy Science</i> , 2011, 94, 4174-4182.	1.4	31

#	ARTICLE	IF	CITATIONS
423	Short communication: Expression and alternative splicing of POU1F1 pathway genes in preimplantation bovine embryos. <i>Journal of Dairy Science</i> , 2011, 94, 4220-4223.	1.4	11
424	Autoantibodies as biomarkers for ovarian cancer. <i>Cancer Biomarkers</i> , 2011, 8, 187-201.	0.8	18
425	Desmosomal Cadherins in Basal Cell Carcinomas. , 0, , .		0
427	Cell-to-cell variability of alternative RNA splicing. <i>Molecular Systems Biology</i> , 2011, 7, 506.	3.2	87
428	Myb proteins: angels and demons in normal and transformed cells. <i>Frontiers in Bioscience - Landmark</i> , 2011, 16, 1109.	3.0	70
430	The Genetic Background Effect on Domesticated Species: A Mouse Evolutionary Perspective. <i>Scientific World Journal, The</i> , 2011, 11, 429-436.	0.8	7
431	SOAPSplICE: Genome-Wide ab initio Detection of Splice Junctions from RNA-Seq Data. <i>Frontiers in Genetics</i> , 2011, 2, 46.	1.1	89
432	Molecular Evolution of the Non-Coding Eosinophil Granule Ontogeny Transcript. <i>Frontiers in Genetics</i> , 2011, 2, 69.	1.1	12
433	Trans-splicing in Higher Eukaryotes: Implications for Cancer Development?. <i>Frontiers in Genetics</i> , 2011, 2, 92.	1.1	30
434	Computational Detection of Alternative Exon Usage. <i>Frontiers in Neuroscience</i> , 2011, 5, 69.	1.4	8
435	Depolarization-Mediated Regulation of Alternative Splicing. <i>Frontiers in Neuroscience</i> , 2011, 5, 141.	1.4	17
436	Comprehensive Analysis of Alternative Splicing and Functionality in Neuronal Differentiation of P19 Cells. <i>PLoS ONE</i> , 2011, 6, e16880.	1.1	19
437	Evaluating Gene Expression in C57BL/6J and DBA/2J Mouse Striatum Using RNA-Seq and Microarrays. <i>PLoS ONE</i> , 2011, 6, e17820.	1.1	215
438	Functional Diversity of Human Basic Helix-Loop-Helix Transcription Factor TCF4 Isoforms Generated by Alternative 5' Exon Usage and Splicing. <i>PLoS ONE</i> , 2011, 6, e22138.	1.1	106
439	Comparative Analysis of mRNA Isoform Expression in Cardiac Hypertrophy and Development Reveals Multiple Post-Transcriptional Regulatory Modules. <i>PLoS ONE</i> , 2011, 6, e22391.	1.1	65
440	Alternative Transcript Initiation and Splicing as a Response to DNA Damage. <i>PLoS ONE</i> , 2011, 6, e25758.	1.1	45
441	Incorporating Evolutionary Information and Functional Domains for Identifying RNA Splicing Factors in Humans. <i>PLoS ONE</i> , 2011, 6, e27567.	1.1	16
442	Identification of Novel Androgen-Regulated Pathways and mRNA Isoforms through Genome-Wide Exon-Specific Profiling of the LNCaP Transcriptome. <i>PLoS ONE</i> , 2011, 6, e29088.	1.1	39

#	ARTICLE	IF	CITATIONS
443	Statistical Modeling of RNA-Seq Data. <i>Statistical Science</i> , 2011, 26, .	1.6	64
444	Advances in Whole Genome Sequencing Technology. <i>Current Pharmaceutical Biotechnology</i> , 2011, 12, 293-305.	0.9	62
445	Transcriptional diversity at the UGT2B7 locus is dictated by extensive pre-mRNA splicing mechanisms that give rise to multiple mRNA splice variants. <i>Pharmacogenetics and Genomics</i> , 2011, 21, 631-641.	0.7	26
447	Characterization of Alternative Spliceforms and the RNA Splicing Machinery in Pancreatic Cancer. <i>Pancreas</i> , 2011, 40, 281-288.	0.5	13
448	Understanding the pathogenesis of Alzheimer's disease: will RNA-seq realize the promise of transcriptomics?. <i>Journal of Neurochemistry</i> , 2011, 116, 937-946.	2.1	65
449	Deep RNA sequencing improved the structural annotation of the <i>Tuber melanosporum</i> transcriptome. <i>New Phytologist</i> , 2011, 189, 883-891.	3.5	54
450	A structured RNA in hepatitis B virus post-transcriptional regulatory element represses alternative splicing in a sequence-independent and position-dependent manner. <i>FEBS Journal</i> , 2011, 278, 1533-1546.	2.2	16
451	Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477.	9.0	919
452	Long pre-mRNA depletion and RNA missplicing contribute to neuronal vulnerability from loss of TDP-43. <i>Nature Neuroscience</i> , 2011, 14, 459-468.	7.1	1,050
453	RNA sequencing: advances, challenges and opportunities. <i>Nature Reviews Genetics</i> , 2011, 12, 87-98.	7.7	1,770
454	Functional consequences of developmentally regulated alternative splicing. <i>Nature Reviews Genetics</i> , 2011, 12, 715-729.	7.7	624
455	Evolution of microRNA diversity and regulation in animals. <i>Nature Reviews Genetics</i> , 2011, 12, 846-860.	7.7	645
456	Histone H3 lysine 9 trimethylation and HP1 ³ favor inclusion of alternative exons. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 337-344.	3.6	228
457	Alternative splicing of SYK regulates mitosis and cell survival. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 673-679.	3.6	99
458	SGCE isoform characterization and expression in human brain: implications for myoclonus/dystonia pathogenesis?. <i>European Journal of Human Genetics</i> , 2011, 19, 438-444.	1.4	63
459	Acetylation and phosphorylation of SRSF2 control cell fate decision in response to cisplatin. <i>EMBO Journal</i> , 2011, 30, 510-523.	3.5	115
460	Formation, regulation and evolution of <i>Caenorhabditis elegans</i> 3'UTRs. <i>Nature</i> , 2011, 469, 97-101.	13.7	432
461	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 473-479.	13.7	1,379

#	ARTICLE	IF	CITATIONS
462	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	9.4	17,264
463	Pre-mRNA splicing: where and when in the nucleus. <i>Trends in Cell Biology</i> , 2011, 21, 336-343.	3.6	118
464	DEGRADE, MOVE, REGROUP: signaling control of splicing proteins. <i>Trends in Biochemical Sciences</i> , 2011, 36, 397-404.	3.7	72
465	The study of eQTL variations by RNA-seq: from SNPs to phenotypes. <i>Trends in Genetics</i> , 2011, 27, 72-79.	2.9	216
466	Understanding splicing regulation through RNA splicing maps. <i>Trends in Genetics</i> , 2011, 27, 89-97.	2.9	228
467	RNA in pieces. <i>Trends in Genetics</i> , 2011, 27, 422-432.	2.9	124
468	17A, a novel non-coding RNA, regulates GABA B alternative splicing and signaling in response to inflammatory stimuli and in Alzheimer disease. <i>Neurobiology of Disease</i> , 2011, 41, 308-317.	2.1	199
469	Rbfox-regulated alternative splicing is critical for zebrafish cardiac and skeletal muscle functions. <i>Developmental Biology</i> , 2011, 359, 251-261.	0.9	84
470	CELF and PTB proteins modulate the inclusion of the β -tropomyosin exon 6B during myogenic differentiation. <i>Experimental Cell Research</i> , 2011, 317, 94-106.	1.2	16
471	Measuring and analyzing tissue specificity of human genes and protein complexes. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2011, 2011, 5.	1.4	16
472	Deep RNA sequencing analysis of readthrough gene fusions in human prostate adenocarcinoma and reference samples. <i>BMC Medical Genomics</i> , 2011, 4, 11.	0.7	140
473	Alterations of pre-mRNA splicing in human inflammatory bowel disease. <i>European Journal of Cell Biology</i> , 2011, 90, 603-611.	1.6	41
474	Anti-apoptosis and cell survival: A review. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011, 1813, 238-259.	1.9	527
475	The evolution of gene expression levels in mammalian organs. <i>Nature</i> , 2011, 478, 343-348.	13.7	1,080
476	A Disease-associated Polymorphism Alters Splicing of the Human CD45 Phosphatase Gene by Disrupting Combinatorial Repression by Heterogeneous Nuclear Ribonucleoproteins (hnRNPs). <i>Journal of Biological Chemistry</i> , 2011, 286, 20043-20053.	1.6	28
477	RNA-Seq unleashed. <i>Nature Biotechnology</i> , 2011, 29, 599-600.	9.4	23
478	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
479	Pre-mRNA splicing during transcription in the mammalian system. <i>Wiley Interdisciplinary Reviews RNA</i> , 2011, 2, 700-717.	3.2	26

#	ARTICLE	IF	CITATIONS
480	Plant serine/arginine-rich proteins: roles in precursor messenger RNA splicing, plant development, and stress responses. <i>Wiley Interdisciplinary Reviews RNA</i> , 2011, 2, 875-889.	3.2	111
481	Identification of an alternative splicing isoform of chicken Lmbr1. <i>Molecular Biology Reports</i> , 2011, 38, 4397-4403.	1.0	2
482	Ca ²⁺ -Signaling, Alternative Splicing and Endoplasmic Reticulum Stress Responses. <i>Neurochemical Research</i> , 2011, 36, 1198-1211.	1.6	30
483	Periostin expression and epithelial-mesenchymal transition in cancer: a review and an update. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2011, 459, 465-475.	1.4	213
484	Integrative computational biology for cancer research. <i>Human Genetics</i> , 2011, 130, 465-481.	1.8	28
485	A Model of Genetic Search for Beneficial Mutations: Estimating the Constructive Capacities of Mutagenesis. <i>Journal of Molecular Evolution</i> , 2011, 73, 337-354.	0.8	0
486	New isoforms of human mitochondrial transcription factor A detected in normal and tumoral cells. <i>Mitochondrion</i> , 2011, 11, 287-295.	1.6	4
487	Observations on potential novel transcripts from RNA-Seq data. <i>Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities</i> , 2011, 6, 275-282.	0.6	1
488	The four Zn fingers of MBNL1 provide a flexible platform for recognition of its RNA binding elements. <i>BMC Molecular Biology</i> , 2011, 12, 20.	3.0	35
489	SWI/SNF regulates the alternative processing of a specific subset of pre-mRNAs in <i>Drosophila melanogaster</i> . <i>BMC Molecular Biology</i> , 2011, 12, 46.	3.0	21
490	Assessing the contribution of alternative splicing to proteome diversity in <i>Arabidopsis thaliana</i> using proteomics data. <i>BMC Plant Biology</i> , 2011, 11, 82.	1.6	37
491	The asthma candidate gene NPSR1 mediates isoform specific downstream signalling. <i>BMC Pulmonary Medicine</i> , 2011, 11, 39.	0.8	20
492	Long noncoding intronic RNAs are differentially expressed in primary and metastatic pancreatic cancer. <i>Molecular Cancer</i> , 2011, 10, 141.	7.9	153
493	Genomic sequencing in clinical trials. <i>Journal of Translational Medicine</i> , 2011, 9, 222.	1.8	28
494	Estimation of alternative splicing isoform frequencies from RNA-Seq data. <i>Algorithms for Molecular Biology</i> , 2011, 6, 9.	0.3	155
495	Prioritizing single-nucleotide variations that potentially regulate alternative splicing. <i>BMC Proceedings</i> , 2011, 5, S40.	1.8	5
496	Exon array analysis reveals neuroblastoma tumors have distinct alternative splicing patterns according to stage and MYCN amplification status. <i>BMC Medical Genomics</i> , 2011, 4, 35.	0.7	40
497	Purification, crystallization and preliminary X-ray crystallographic analysis of a central domain of human splicing factor 1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 486-490.	0.7	4

#	ARTICLE	IF	CITATIONS
498	Shape-based peak identification for ChIP-Seq. <i>BMC Bioinformatics</i> , 2011, 12, 15.	1.2	52
499	Predicting mutually exclusive spliced exons based on exon length, splice site and reading frame conservation, and exon sequence homology. <i>BMC Bioinformatics</i> , 2011, 12, 270.	1.2	23
500	miRTar: an integrated system for identifying miRNA-target interactions in human. <i>BMC Bioinformatics</i> , 2011, 12, 300.	1.2	128
501	IsoformEx: isoform level gene expression estimation using weighted non-negative least squares from mRNA-Seq data. <i>BMC Bioinformatics</i> , 2011, 12, 305.	1.2	24
502	RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. <i>BMC Bioinformatics</i> , 2011, 12, 323.	1.2	16,042
503	ReCount: A multi-experiment resource of analysis-ready RNA-seq gene count datasets. <i>BMC Bioinformatics</i> , 2011, 12, 449.	1.2	144
504	Support vector machines-based identification of alternative splicing in <i>Arabidopsis thaliana</i> from whole-genome tiling arrays. <i>BMC Bioinformatics</i> , 2011, 12, 55.	1.2	21
505	A global view of porcine transcriptome in three tissues from a full-sib pair with extreme phenotypes in growth and fat deposition by paired-end RNA sequencing. <i>BMC Genomics</i> , 2011, 12, 448.	1.2	103
506	The classification of mRNA expression levels by the phosphorylation state of RNAPII CTD based on a combined genome-wide approach. <i>BMC Genomics</i> , 2011, 12, 516.	1.2	36
507	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. <i>BMC Genomics</i> , 2011, 12, 552.	1.2	127
508	Interrogation of alternative splicing events in duplicated genes during evolution. <i>BMC Genomics</i> , 2011, 12, S16.	1.2	13
509	Lights and shadows of proteomic technologies for the study of protein species including isoforms, splicing variants and protein post-translational modifications. <i>Proteomics</i> , 2011, 11, 590-603.	1.3	19
510	Functional genomics of the brain: uncovering networks in the CNS using a systems approach. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 628-648.	6.6	11
511	Numerous isoforms of Fgf8 reflect its multiple roles in the developing brain. <i>Journal of Cellular Physiology</i> , 2011, 226, 1722-1726.	2.0	17
512	A novel exon 15-deleted, splicing variant of Slit2 shows potential for growth inhibition in addition to invasion inhibition in lung cancer. <i>Cancer</i> , 2011, 117, 3404-3415.	2.0	8
513	Comprehensive identification and quantification of microbial transcriptomes by genome-wide unbiased methods. <i>Current Opinion in Biotechnology</i> , 2011, 22, 32-41.	3.3	60
514	The Tpr protein regulates export of mRNAs with retained introns that traffic through the Nxf1 pathway. <i>Rna</i> , 2011, 17, 1344-1356.	1.6	79
515	Where splicing joins chromatin. <i>Nucleus</i> , 2011, 2, 182-188.	0.6	54

#	ARTICLE	IF	CITATIONS
516	Age-dependent gain of alternative splice forms and biased duplication explain the relation between splicing and duplication. <i>Genome Research</i> , 2011, 21, 357-363.	2.4	50
517	Complex and dynamic landscape of RNA polyadenylation revealed by PAS-Seq. <i>Rna</i> , 2011, 17, 761-772.	1.6	388
518	Conservation of an RNA regulatory map between <i>Drosophila</i> and mammals. <i>Genome Research</i> , 2011, 21, 193-202.	2.4	208
519	MPromDb update 2010: an integrated resource for annotation and visualization of mammalian gene promoters and ChIP-seq experimental data. <i>Nucleic Acids Research</i> , 2011, 39, D92-D97.	6.5	33
520	The <i>Drosophila melanogaster</i> transcriptome by paired-end RNA sequencing. <i>Genome Research</i> , 2011, 21, 315-324.	2.4	123
521	Distinct regulatory programs establish widespread sex-specific alternative splicing in <i>Drosophila melanogaster</i> . <i>Rna</i> , 2011, 17, 453-468.	1.6	32
522	A comparison of analog and Next-Generation transcriptomic tools for mammalian studies. <i>Briefings in Functional Genomics</i> , 2011, 10, 135-150.	1.3	59
523	Huge Splicing Frequency in Human Y Chromosomal <i>UTY</i> Gene. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 141-154.	1.0	11
524	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Molecular Systems Biology</i> , 2011, 7, 497.	3.2	265
525	Systematic reconstruction of splicing regulatory modules by integrating many RNA-seq datasets. , 2011, , .		0
526	Networking in a global world: Establishing functional connections between neural splicing regulators and their target transcripts. <i>Rna</i> , 2011, 17, 775-791.	1.6	65
527	Identification of Alternative Splicing Events Regulated by an Arabidopsis Serine/Arginine-Like Protein, atSR45a, in Response to High-Light Stress using a Tiling Array. <i>Plant and Cell Physiology</i> , 2011, 52, 1786-1805.	1.5	29
528	SpliceTrap: a method to quantify alternative splicing under single cellular conditions. <i>Bioinformatics</i> , 2011, 27, 3010-3016.	1.8	86
529	Global Profiling and Molecular Characterization of Alternative Splicing Events Misregulated in Lung Cancer. <i>Molecular and Cellular Biology</i> , 2011, 31, 138-150.	1.1	149
530	Genome-wide analysis of alternative splicing in <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2011, 21, 342-348.	2.4	137
531	Design principles for bifunctional targeted oligonucleotide enhancers of splicing. <i>Nucleic Acids Research</i> , 2011, 39, 7194-7208.	6.5	40
532	c-Myc Regulates RNA Splicing of the A-Raf Kinase and Its Activation of the ERK Pathway. <i>Cancer Research</i> , 2011, 71, 4664-4674.	0.4	61
533	GETPrime: a gene- or transcript-specific primer database for quantitative real-time PCR. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar040.	1.4	43

#	ARTICLE	IF	CITATIONS
534	Deep-transcriptome and ribonome sequencing redefines the molecular networks of pluripotency and the extracellular space in human embryonic stem cells. <i>Genome Research</i> , 2011, 21, 2014-2025.	2.4	23
535	Verification of alternative splicing variants based on domain integrity, truncation length and intrinsic protein disorder. <i>Nucleic Acids Research</i> , 2011, 39, 1208-1219.	6.5	46
536	FDM: a graph-based statistical method to detect differential transcription using RNA-seq data. <i>Bioinformatics</i> , 2011, 27, 2633-2640.	1.8	50
537	Context-dependent robustness to 5' splice site polymorphisms in human populations. <i>Human Molecular Genetics</i> , 2011, 20, 1084-1096.	1.4	18
538	Pyicos: a versatile toolkit for the analysis of high-throughput sequencing data. <i>Bioinformatics</i> , 2011, 27, 3333-3340.	1.8	86
539	Autoregulated Splicing of muscleblind-like 1 (MBNL1) Pre-mRNA. <i>Journal of Biological Chemistry</i> , 2011, 286, 34224-34233.	1.6	62
540	Dynamic usage of alternative splicing exons during mouse retina development. <i>Nucleic Acids Research</i> , 2011, 39, 7920-7930.	6.5	33
541	The Comprehensive Phytopathogen Genomics Resource: a web-based resource for data-mining plant pathogen genomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar053-bar053.	1.4	26
542	Extensive relationship between antisense transcription and alternative splicing in the human genome. <i>Genome Research</i> , 2011, 21, 1203-1212.	2.4	68
543	Efficient internal exon recognition depends on near equal contributions from the 3' and 5' splice sites. <i>Nucleic Acids Research</i> , 2011, 39, 8928-8937.	6.5	36
544	Genome-wide mapping of RNA Pol-II promoter usage in mouse tissues by ChIP-seq. <i>Nucleic Acids Research</i> , 2011, 39, 190-201.	6.5	81
545	Functional analysis of BBS3 A89V that results in non-syndromic retinal degeneration. <i>Human Molecular Genetics</i> , 2011, 20, 1625-1632.	1.4	38
546	Intron cleavage affects processing of alternatively spliced transcripts. <i>Rna</i> , 2011, 17, 1604-1613.	1.6	5
547	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3707-3712.	3.3	122
548	Inhibition of Nonsense-Mediated RNA Decay by the Tumor Microenvironment Promotes Tumorigenesis. <i>Molecular and Cellular Biology</i> , 2011, 31, 3670-3680.	1.1	131
549	Developments in RNA Splicing and Disease. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a000778-a000778.	2.3	79
550	Zebrafish mRNA sequencing deciphers novelties in transcriptome dynamics during maternal to zygotic transition. <i>Genome Research</i> , 2011, 21, 1328-1338.	2.4	247
551	The Origins, Evolution, and Functional Potential of Alternative Splicing in Vertebrates. <i>Molecular Biology and Evolution</i> , 2011, 28, 2949-2959.	3.5	74

#	ARTICLE	IF	CITATIONS
552	Function of <i>ERBB4</i> is determined by alternative splicing. <i>Cell Cycle</i> , 2011, 10, 2647-2657.	1.3	95
553	Competing RNA secondary structures are required for mutually exclusive splicing of the <i>Dscam</i> exon 6 cluster. <i>Rna</i> , 2011, 17, 222-229.	1.6	54
554	ELAV-Mediated 3' End Processing of <i>ewg</i> Transcripts Is Evolutionarily Conserved Despite Sequence Degeneration of the ELAV-Binding Site. <i>Genetics</i> , 2011, 189, 97-107.	1.2	22
555	Real-time imaging of cotranscriptional splicing reveals a kinetic model that reduces noise: implications for alternative splicing regulation. <i>Journal of Cell Biology</i> , 2011, 193, 819-829.	2.3	104
556	Inference of Isoforms from Short Sequence Reads. <i>Journal of Computational Biology</i> , 2011, 18, 305-321.	0.8	54
557	Accurate quantification of transcriptome from RNA-Seq data by effective length normalization. <i>Nucleic Acids Research</i> , 2011, 39, e9-e9.	6.5	101
558	Ultraconserved cDNA segments in the human transcriptome exhibit resistance to folding and implicate function in translation and alternative splicing. <i>Nucleic Acids Research</i> , 2011, 39, 1967-1979.	6.5	21
559	Synthesis and Characterization of Pseudocantharidins, Novel Phosphatase Modulators That Promote the Inclusion of Exon 7 into the SMN (Survival of Motoneuron) pre-mRNA*. <i>Journal of Biological Chemistry</i> , 2011, 286, 10126-10136.	1.6	26
560	A pipeline for RNA-seq data processing and quality assessment. <i>Bioinformatics</i> , 2011, 27, 867-869.	1.8	52
561	Kaviar: an accessible system for testing SNV novelty. <i>Bioinformatics</i> , 2011, 27, 3216-3217.	1.8	187
562	The Soluble CTLA-4 Splice Variant Protects From Type 1 Diabetes and Potentiates Regulatory T-Cell Function. <i>Diabetes</i> , 2011, 60, 1955-1963.	0.3	79
563	Using non-uniform read distribution models to improve isoform expression inference in RNA-Seq. <i>Bioinformatics</i> , 2011, 27, 502-508.	1.8	91
564	RNA Polymerase II Elongation at the Crossroads of Transcription and Alternative Splicing. <i>Genetics Research International</i> , 2011, 2011, 1-9.	2.0	25
565	Whole Transcriptome Sequencing Reveals Gene Expression and Splicing Differences in Brain Regions Affected by Alzheimer's Disease. <i>PLoS ONE</i> , 2011, 6, e16266.	1.1	266
566	SR Proteins Induce Alternative Exon Skipping through Their Activities on the Flanking Constitutive Exons. <i>Molecular and Cellular Biology</i> , 2011, 31, 793-802.	1.1	72
567	Identification of MBNL1 and MBNL3 domains required for splicing activation and repression. <i>Nucleic Acids Research</i> , 2011, 39, 2769-2780.	6.5	44
568	<i>Bcar3</i> Is Expressed in Sertoli Cells and Germ Cells of the Developing Testis in Mice. <i>Sexual Development</i> , 2011, 5, 197-204.	1.1	2
569	Context-dependent splicing regulation. <i>RNA Biology</i> , 2011, 8, 384-388.	1.5	29

#	ARTICLE	IF	CITATIONS
570	Protein Kinase A-Dependent Phosphorylation of Serine 119 in the Proto-Oncogenic Serine/Arginine-Rich Splicing Factor 1 Modulates Its Activity as a Splicing Enhancer Protein. <i>Genes and Cancer</i> , 2011, 2, 841-851.	0.6	9
571	Efficiently identifying genome-wide changes with next-generation sequencing data. <i>Nucleic Acids Research</i> , 2011, 39, e130-e130.	6.5	29
572	A role for SR proteins in plant stress responses. <i>Plant Signaling and Behavior</i> , 2011, 6, 49-54.	1.2	131
573	Modulation of RNA splicing as a potential treatment for cancer. <i>Bioengineered Bugs</i> , 2011, 2, 125-128.	2.0	25
574	Constant Splice-Isoform Ratios in Human Lymphoblastoid Cells Support the Concept of a Splico-Stat. <i>Genetics</i> , 2011, 187, 761-770.	1.2	10
575	RNA sequencing reveals the role of splicing polymorphisms in regulating human gene expression. <i>Genome Research</i> , 2011, 21, 545-554.	2.4	107
576	Alternatively spliced domains interact to regulate BK potassium channel gating. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20784-20789.	3.3	37
577	Alternative splicing and genetic diversity: silencers are more frequently modified by SNVs associated with alternative exon/intron borders. <i>Nucleic Acids Research</i> , 2011, 39, 4942-4948.	6.5	11
578	Widespread establishment and regulatory impact of Alu exons in human genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2837-2842.	3.3	119
579	Hu proteins regulate alternative splicing by inducing localized histone hyperacetylation in an RNA-dependent manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E627-35.	3.3	123
580	Bayesian prediction of tissue-regulated splicing using RNA sequence and cellular context. <i>Bioinformatics</i> , 2011, 27, 2554-2562.	1.8	77
581	Molecular design of a splicing switch responsive to the RNA binding protein Tra2. <i>Nucleic Acids Research</i> , 2011, 39, 8092-8104.	6.5	22
582	Evidence for dosage compensation between the X chromosome and autosomes in mammals. <i>Nature Genetics</i> , 2011, 43, 1167-1169.	9.4	81
583	Relative overexpression of X-linked genes in mouse embryonic stem cells is consistent with Ohno's hypothesis. <i>Nature Genetics</i> , 2011, 43, 1169-1170.	9.4	71
584	Signal- and Development-Dependent Alternative Splicing of LEF1 in T Cells Is Controlled by CELF2. <i>Molecular and Cellular Biology</i> , 2011, 31, 2184-2195.	1.1	48
585	Characterization of the single-cell transcriptional landscape by highly multiplex RNA-seq. <i>Genome Research</i> , 2011, 21, 1160-1167.	2.4	828
586	Alternative Splicing of SLC39A14 in Colorectal Cancer is Regulated by the Wnt Pathway. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.002998.	2.5	73
587	Regulation of alternative splicing by the core spliceosomal machinery. <i>Genes and Development</i> , 2011, 25, 373-384.	2.7	181

#	ARTICLE	IF	CITATIONS
588	PRPF mutations are associated with generalized defects in spliceosome formation and pre-mRNA splicing in patients with retinitis pigmentosa. <i>Human Molecular Genetics</i> , 2011, 20, 2116-2130.	1.4	120
589	Next-generation insights into regulatory T cells: expression profiling and FoxP3 occupancy in Human. <i>Nucleic Acids Research</i> , 2011, 39, 7946-7960.	6.5	81
590	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. <i>Nucleic Acids Research</i> , 2011, 39, D80-D85.	6.5	38
591	A Detailed History of Intron-rich Eukaryotic Ancestors Inferred from a Global Survey of 100 Complete Genomes. <i>PLoS Computational Biology</i> , 2011, 7, e1002150.	1.5	160
592	Innovative technology for cancer risk analysis. <i>Annals of Oncology</i> , 2011, 22, i37-i43.	0.6	2
593	mRNA isoform diversity can obscure detection of miRNA-mediated control of translation. <i>Rna</i> , 2011, 17, 1025-1031.	1.6	23
594	Misfolded human tRNA isodecoder binds and neutralizes a 3' UTR-embedded Alu element. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E794-802.	3.3	34
595	De Novo Origin of Human Protein-Coding Genes. <i>PLoS Genetics</i> , 2011, 7, e1002379.	1.5	153
596	An EMT-Driven Alternative Splicing Program Occurs in Human Breast Cancer and Modulates Cellular Phenotype. <i>PLoS Genetics</i> , 2011, 7, e1002218.	1.5	399
597	Genomes, Proteomes, and the Central Dogma. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 576-576.	5.1	24
598	In vivo effects on intron retention and exon skipping by the U2AF large subunit and SF1/BBP in the nematode <i>Caenorhabditis elegans</i> . <i>Rna</i> , 2011, 17, 2201-2211.	1.6	16
599	Shotgun proteomics aids discovery of novel protein-coding genes, alternative splicing, and resurrected pseudogenes in the mouse genome. <i>Genome Research</i> , 2011, 21, 756-767.	2.4	113
600	Computational discovery of human coding and non-coding transcripts with conserved splice sites. <i>Bioinformatics</i> , 2011, 27, 1894-1900.	1.8	24
601	RNA splicing control. <i>RNA Biology</i> , 2011, 8, 968-977.	1.5	52
602	Increased levels of noisy splicing in cancers, but not for oncogene-derived transcripts. <i>Human Molecular Genetics</i> , 2011, 20, 4422-4429.	1.4	32
603	Global impact of RNA polymerase II elongation inhibition on alternative splicing regulation. <i>Genome Research</i> , 2011, 21, 390-401.	2.4	203
604	Chromatin Organization in Sperm May Be the Major Functional Consequence of Base Composition Variation in the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002036.	1.5	90
605	mRNA degradation controls differentiation state-dependent differences in transcript and splice variant abundance. <i>Nucleic Acids Research</i> , 2011, 39, 556-566.	6.5	95

#	ARTICLE	IF	CITATIONS
606	The strength of intron donor splice sites in human genes displays a bell-shaped pattern. <i>Bioinformatics</i> , 2011, 27, 3079-3084.	1.8	0
607	SRPK1 inhibition <i>in vivo</i> : modulation of VEGF splicing and potential treatment for multiple diseases. <i>Biochemical Society Transactions</i> , 2012, 40, 831-835.	1.6	45
608	Multiple insert size paired-end sequencing for deconvolution of complex transcriptomes. <i>RNA Biology</i> , 2012, 9, 596-609.	1.5	2
609	p53 Family: Role of Protein Isoforms in Human Cancer. <i>Journal of Nucleic Acids</i> , 2012, 2012, 1-19.	0.8	78
610	Co-transcriptional degradation of aberrant pre-mRNA by Xrn2. <i>EMBO Journal</i> , 2012, 31, 2566-2578.	3.5	81
611	Cotranscriptional splicing efficiency differs dramatically between <i>Drosophila</i> and mouse. <i>Rna</i> , 2012, 18, 2174-2186.	1.6	92
612	A Limited Role for Gene Duplications in the Evolution of Platypus Venom. <i>Molecular Biology and Evolution</i> , 2012, 29, 167-177.	3.5	33
613	The transition in spliceosome assembly from complex E to complex A purges surplus U1 snRNPs from alternative splice sites. <i>Nucleic Acids Research</i> , 2012, 40, 6850-6862.	6.5	23
614	Eine kurze Geschichte der Genetik. , 2012, , .		23
615	Alternative splicing of the neurofibromatosis type1 pre-mRNA. <i>Bioscience Reports</i> , 2012, 32, 131-138.	1.1	41
616	AS-EAST: a functional annotation tool for putative proteins encoded by alternatively spliced transcripts. <i>Bioinformatics</i> , 2012, 28, 2076-2077.	1.8	3
617	Hominoid-Specific De Novo Protein-Coding Genes Originating from Long Non-Coding RNAs. <i>PLoS Genetics</i> , 2012, 8, e1002942.	1.5	130
618	Muscle-Specific Splicing Factors ASD-2 and SUP-12 Cooperatively Switch Alternative Pre-mRNA Processing Patterns of the ADF/Cofilin Gene in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2012, 8, e1002991.	1.5	39
619	Role of splice variants in the metastatic progression of prostate cancer. <i>Biochemical Society Transactions</i> , 2012, 40, 870-874.	1.6	27
620	Variants Affecting Exon Skipping Contribute to Complex Traits. <i>PLoS Genetics</i> , 2012, 8, e1002998.	1.5	53
621	Transcription initiation arising from E-cadherin/CDH1 intron2: a novel protein isoform that increases gastric cancer cell invasion and angiogenesis. <i>Human Molecular Genetics</i> , 2012, 21, 4253-4269.	1.4	16
622	PASSion: a pattern growth algorithm-based pipeline for splice junction detection in paired-end RNA-Seq data. <i>Bioinformatics</i> , 2012, 28, 479-486.	1.8	26
623	Current and emerging approaches to define intestinal epithelium-specific transcriptional networks. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 302, G277-G286.	1.6	15

#	ARTICLE	IF	CITATIONS
624	Ten Years of Pathway Analysis: Current Approaches and Outstanding Challenges. <i>PLoS Computational Biology</i> , 2012, 8, e1002375.	1.5	1,267
625	Identification and Functional Characterization of a Novel UDP-Glucuronosyltransferase 2A1 Splice Variant: Potential Importance in Tobacco-Related Cancer Susceptibility. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2012, 343, 712-724.	1.3	25
626	Identification of Gene Mutations in Autosomal Dominant Polycystic Kidney Disease through Targeted Resequencing. <i>Journal of the American Society of Nephrology: JASN</i> , 2012, 23, 915-933.	3.0	149
627	Age-related changes of gene expression in the neocortex: Preliminary data on RNA-Seq of the transcriptome in three functionally distinct cortical areas. <i>Development and Psychopathology</i> , 2012, 24, 1427-1442.	1.4	22
628	An Indel Polymorphism in the Hybrid Incompatibility Gene Lethal Hybrid Rescue of <i>Drosophila</i> Is Functionally Relevant. <i>Genetics</i> , 2012, 192, 683-691.	1.2	5
629	Alternative polyadenylation: New insights from global analyses. <i>Rna</i> , 2012, 18, 2105-2117.	1.6	189
630	The regulation of glial-specific splicing of <i>Neurexin IV</i> requires HOW and Cdk12 activity. <i>Development (Cambridge)</i> , 2012, 139, 1765-1776.	1.2	38
631	Alternative Cleavage and Polyadenylation during Colorectal Cancer Development. <i>Clinical Cancer Research</i> , 2012, 18, 5256-5266.	3.2	108
632	HEXEvent: a database of Human EXon splicing Events. <i>Nucleic Acids Research</i> , 2012, 41, D118-D124.	6.5	64
633	SpliceDisease database: linking RNA splicing and disease. <i>Nucleic Acids Research</i> , 2012, 40, D1055-D1059.	6.5	52
634	Regulated functional alternative splicing in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2012, 40, 1-10.	6.5	656
635	Gene Array Analyzer: alternative usage of gene arrays to study alternative splicing events. <i>Nucleic Acids Research</i> , 2012, 40, 2414-2425.	6.5	15
636	A novel source for miR-21 expression through the alternative polyadenylation of VMP1 gene transcripts. <i>Nucleic Acids Research</i> , 2012, 40, 6821-6833.	6.5	79
637	Quantitative biology of single neurons. <i>Journal of the Royal Society Interface</i> , 2012, 9, 3165-3183.	1.5	18
638	Comparative Proteomics Reveals a Significant Bias Toward Alternative Protein Isoforms with Conserved Structure and Function. <i>Molecular Biology and Evolution</i> , 2012, 29, 2265-2283.	3.5	71
639	An in-depth map of polyadenylation sites in cancer. <i>Nucleic Acids Research</i> , 2012, 40, 8460-8471.	6.5	126
640	Genome-wide alternative polyadenylation in animals: insights from high-throughput technologies. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 352-361.	1.5	41
641	RNA-Seq Mapping and Detection of Gene Fusions with a Suffix Array Algorithm. <i>PLoS Computational Biology</i> , 2012, 8, e1002464.	1.5	45

#	ARTICLE	IF	CITATIONS
642	YB-1 binds to CAUC motifs and stimulates exon inclusion by enhancing the recruitment of U2AF to weak polypyrimidine tracts. <i>Nucleic Acids Research</i> , 2012, 40, 8622-8636.	6.5	88
643	ELAV mediates 3' UTR extension in the <i>Drosophila</i> nervous system. <i>Genes and Development</i> , 2012, 26, 2259-2264.	2.7	97
644	Extensive alternative polyadenylation during zebrafish development. <i>Genome Research</i> , 2012, 22, 2054-2066.	2.4	305
645	MATS: a Bayesian framework for flexible detection of differential alternative splicing from RNA-Seq data. <i>Nucleic Acids Research</i> , 2012, 40, e61-e61.	6.5	330
646	Specific PABP effect on translation of YB-1 mRNA is neutralized by polyadenylation through a mini-loop at 3' UTR. <i>RNA Biology</i> , 2012, 9, 1473-1487.	1.5	10
647	Four parameters increase the sensitivity and specificity of the exon array analysis and disclose 25 novel aberrantly spliced exons in myotonic dystrophy. <i>Journal of Human Genetics</i> , 2012, 57, 368-374.	1.1	15
648	An integer programming approach to novel transcript reconstruction from paired-end RNA-Seq reads. , 2012, , .		15
649	Databases and software to make your research life easier. , 2012, , 7-47.		0
650	Estimation of alternative splicing variability in human populations. <i>Genome Research</i> , 2012, 22, 528-538.	2.4	59
651	Proteins Associated with the Exon Junction Complex Also Control the Alternative Splicing of Apoptotic Regulators. <i>Molecular and Cellular Biology</i> , 2012, 32, 954-967.	1.1	113
652	Evolutionarily conserved A-to-I editing increases protein stability of the alternative splicing factor Nova1. <i>RNA Biology</i> , 2012, 9, 12-21.	1.5	40
653	An Emerging Role of RNA-Binding Proteins as Multifunctional Regulators of Lymphocyte Development and Function. <i>Advances in Immunology</i> , 2012, 115, 161-185.	1.1	15
654	A quantitative atlas of polyadenylation in five mammals. <i>Genome Research</i> , 2012, 22, 1173-1183.	2.4	557
655	Analysis of <i>C. elegans</i> intestinal gene expression and polyadenylation by fluorescence-activated nuclei sorting and 3'-end-seq. <i>Nucleic Acids Research</i> , 2012, 40, 6304-6318.	6.5	69
656	Splicing of internal large exons is defined by novel cis-acting sequence elements. <i>Nucleic Acids Research</i> , 2012, 40, 9244-9254.	6.5	25
657	Do human transposable element small RNAs serve primarily as genome defenders or genome regulators?. <i>Mobile Genetic Elements</i> , 2012, 2, 19-25.	1.8	6
658	SPLOOCE. <i>RNA Biology</i> , 2012, 9, 1339-1343.	1.5	7
659	Revealing stable processing products from ribosome-associated small RNAs by deep-sequencing data analysis. <i>Nucleic Acids Research</i> , 2012, 40, 4013-4024.	6.5	53

#	ARTICLE	IF	CITATIONS
660	Human gene copy number spectra analysis in congenital heart malformations. <i>Physiological Genomics</i> , 2012, 44, 518-541.	1.0	93
661	R2KS: A Novel Measure for Comparing Gene Expression Based on Ranked Gene Lists. <i>Journal of Computational Biology</i> , 2012, 19, 766-775.	0.8	6
662	Inhibition of mRNA maturation in trypanosomes causes the formation of novel foci at the nuclear periphery containing cytoplasmic regulators of mRNA fate. <i>Journal of Cell Science</i> , 2012, 125, 2896-909.	1.2	34
663	Subcellular and Subnuclear Distribution of High-Light Responsive Serine/Arginine-Rich Proteins, atSR45a and atSR30, in <i>Arabidopsis thaliana</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 2075-2081.	0.6	9
664	Transposase mediated construction of RNA-seq libraries. <i>Genome Research</i> , 2012, 22, 134-141.	2.4	85
665	Workshop: Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. , 2012, , .		0
666	Chromatin and epigenetic regulation of pre-mRNA processing. <i>Human Molecular Genetics</i> , 2012, 21, R90-R96.	1.4	80
667	Incorporating RNA-seq data into the zebrafish Ensembl genebuild. <i>Genome Research</i> , 2012, 22, 2067-2078.	2.4	96
668	Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. <i>Bioinformatics</i> , 2012, 28, 2914-2921.	1.8	87
669	Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , 2012, 22, 2008-2017.	2.4	1,341
670	Mapping the regulatory sequences controlling 93 breast cancer-associated miRNA genes leads to the identification of two functional promoters of the Hsa-mir-200b cluster, methylation of which is associated with metastasis or hormone receptor status in advanced breast cancer. <i>Oncogene</i> , 2012, 31, 4182-4195.	2.6	75
671	The Cellular Processing Capacity Limits the Amounts of Chimeric U7 snRNA Available for Antisense Delivery. <i>Molecular Therapy - Nucleic Acids</i> , 2012, 1, e31.	2.3	10
672	Mutations affecting the cytoplasmic functions of the co-chaperone DNAJB6 cause limb-girdle muscular dystrophy. <i>Nature Genetics</i> , 2012, 44, 450-455.	9.4	226
673	TGF- β 2 drives epithelial-mesenchymal transition through β 1-mediated downregulation of ESRP. <i>Oncogene</i> , 2012, 31, 3190-3201.	2.6	199
674	Regulation of CUG-binding Protein 1 (CUGBP1) Binding to Target Transcripts upon T Cell Activation. <i>Journal of Biological Chemistry</i> , 2012, 287, 950-960.	1.6	49
675	The Role of CYP3A4 mRNA Transcript with Shortened 3' Untranslated Region in Hepatocyte Differentiation, Liver Development, and Response to Drug Induction. <i>Molecular Pharmacology</i> , 2012, 81, 86-96.	1.0	10
676	Transcript-Specific Associations of SLC12A5 (KCC2) in Human Prefrontal Cortex with Development, Schizophrenia, and Affective Disorders. <i>Journal of Neuroscience</i> , 2012, 32, 5216-5222.	1.7	84
677	What are the determinants of gene expression levels and breadths in the human genome?. <i>Human Molecular Genetics</i> , 2012, 21, 46-56.	1.4	38

#	ARTICLE	IF	CITATIONS
678	Discovery in Context: Leveraging Multidimensional Glioblastoma Datasets to Identify Targetable Regulatory Networks: Figure 1.. <i>Cancer Discovery</i> , 2012, 2, 676-678.	7.7	3
679	SplicerEX: A tool for the automated detection and classification of mRNA changes from conventional and splice-sensitive microarray expression data. <i>Rna</i> , 2012, 18, 1435-1445.	1.6	2
680	Alternative Splicing Mediates Responses of the <i>Arabidopsis</i> Circadian Clock to Temperature Changes. <i>Plant Cell</i> , 2012, 24, 961-981.	3.1	325
681	Pyruvate kinase M2-specific siRNA induces apoptosis and tumor regression. <i>Journal of Experimental Medicine</i> , 2012, 209, 217-224.	4.2	204
682	Activity-Dependent Alternative Splicing Increases Persistent Sodium Current and Promotes Seizure. <i>Journal of Neuroscience</i> , 2012, 32, 7267-7277.	1.7	57
683	Intronic hammerhead ribozymes in mRNA biogenesis. <i>Biological Chemistry</i> , 2012, 393, 1317-1326.	1.2	17
684	mRNA Transcript Diversity Creates New Opportunities for Pharmacological Intervention. <i>Molecular Pharmacology</i> , 2012, 81, 620-630.	1.0	42
685	Alternative splicing and <i>trans</i> -splicing events revealed by analysis of the <i>Bombyx mori</i> transcriptome. <i>Rna</i> , 2012, 18, 1395-1407.	1.6	38
686	Genome-Wide Determination of a Broad ESRP-Regulated Posttranscriptional Network by High-Throughput Sequencing. <i>Molecular and Cellular Biology</i> , 2012, 32, 1468-1482.	1.1	127
687	Quantification of Hepatic UDP Glucuronosyltransferase 1A Splice Variant Expression and Correlation of UDP Glucuronosyltransferase 1A1 Variant Expression with Glucuronidation Activity. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2012, 342, 720-729.	1.3	22
688	Control of alternative splicing by forskolin through hnRNP K during neuronal differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 8059-8071.	6.5	49
689	Alternative Splicing: A Potential Source of Functional Innovation in the Eukaryotic Genome. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-10.	1.0	66
690	A Quantitative High-Throughput <i>In Vitro</i> Splicing Assay Identifies Inhibitors of Spliceosome Catalysis. <i>Molecular and Cellular Biology</i> , 2012, 32, 1271-1283.	1.1	36
691	The importance of identifying alternative splicing in vertebrate genome annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas014.	1.4	28
692	AutismKB: an evidence-based knowledgebase of autism genetics. <i>Nucleic Acids Research</i> , 2012, 40, D1016-D1022.	6.5	157
693	RNASEQ—a streamlined and accurate RNA-seq sequence analysis program. <i>Nucleic Acids Research</i> , 2012, 40, e42-e42.	6.5	33
694	HnRNP L and L-like cooperate in multiple-exon regulation of CD45 alternative splicing. <i>Nucleic Acids Research</i> , 2012, 40, 5666-5678.	6.5	45
695	Linear motifs confer functional diversity onto splice variants. <i>Nucleic Acids Research</i> , 2012, 40, 7123-7131.	6.5	65

#	ARTICLE	IF	CITATIONS
696	Targeting a pre-mRNA structure with bipartite antisense molecules modulates tau alternative splicing. <i>Nucleic Acids Research</i> , 2012, 40, 9836-9849.	6.5	43
697	Dynamic regulation of HIV-1 mRNA populations analyzed by single-molecule enrichment and long-read sequencing. <i>Nucleic Acids Research</i> , 2012, 40, 10345-10355.	6.5	114
698	Exon Arrays Reveal Alternative Splicing Aberrations in Parkinson's Disease Leukocytes. <i>Neurodegenerative Diseases</i> , 2012, 10, 203-206.	0.8	29
699	The distribution of phosphorylated SR proteins and alternative splicing are regulated by RANBP2. <i>Molecular Biology of the Cell</i> , 2012, 23, 1115-1128.	0.9	37
700	GenomicTools: an open source platform for developing high-throughput analytics in genomics. , 2012, , 189-220.		0
701	Alternative splicing of apoptosis-related genes in imatinib-treated K562 cells identified by exon array analysis. <i>International Journal of Molecular Medicine</i> , 2012, 29, 690-698.	1.8	18
702	Knowledge Enrichment Analysis for Human Tissue- Specific Genes Uncover New Biological Insights. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 28-39.	1.0	0
703	Enhanced Steroid Response of a Human Glucocorticoid Receptor Splice Variant. <i>Shock</i> , 2012, 38, 11-17.	1.0	17
704	Evaluating the Evidence for Transmission Distortion in Human Pedigrees. <i>Genetics</i> , 2012, 191, 215-232.	1.2	43
705	Biomedical Impact of Splicing Mutations Revealed through Exome Sequencing. <i>Molecular Medicine</i> , 2012, 18, 314-319.	1.9	13
706	A Method for Isoform Prediction from RNA-Seq Data by Iterative Mapping. <i>IPSI Transactions on Bioinformatics</i> , 2012, 5, 27-33.	0.2	0
707	How to program like a bioinformatician?. , 2012, , 49-74.		0
708	- Characterization of Cancer Cells Using Electrical Impedance Spectroscopy. , 2012, , 584-597.		0
709	RNA Sequencing Reveals Dynamic Changes of mRNA Abundance of Cytochromes P450 and Their Alternative Transcripts during Mouse Liver Development. <i>Drug Metabolism and Disposition</i> , 2012, 40, 1198-1209.	1.7	52
710	Research Resource: Transcriptional Response to Glucocorticoids in Childhood Acute Lymphoblastic Leukemia. <i>Molecular Endocrinology</i> , 2012, 26, 178-193.	3.7	22
711	Genome-wide Transcription Factor Gene Prediction and their Expressional Tissue-specificities in Maize. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 616-630.	4.1	82
712	Concentration-dependent control of pyruvate kinase M mutually exclusive splicing by hnRNP proteins. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 346-354.	3.6	93
713	Transcriptional and Post-transcriptional Regulation in TGF- β -mediated epithelial-mesenchymal transition. <i>Journal of Biochemistry</i> , 2012, 151, 563-571.	0.9	49

#	ARTICLE	IF	CITATIONS
714	Splice isoforms as therapeutic targets for colorectal cancer. <i>Carcinogenesis</i> , 2012, 33, 2311-2319.	1.3	47
715	Mechanisms of <i>Drosophila Dscam</i> mutually exclusive splicing regulation. <i>Biochemical Society Transactions</i> , 2012, 40, 804-809.	1.6	19
716	The expanding scope of DNA sequencing. <i>Nature Biotechnology</i> , 2012, 30, 1084-1094.	9.4	280
717	Cardiovascular Genomics: A Biomarker Identification Pipeline. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2012, 16, 809-822.	3.6	13
718	Comprehensive structural annotation of <i>Pichia pastoris</i> transcriptome and the response to various carbon sources using deep paired-end RNA sequencing. <i>BMC Genomics</i> , 2012, 13, 738.	1.2	59
719	Intronic splicing enhancers, cognate splicing factors and context-dependent regulation rules. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1044-1052.	3.6	142
720	Novel transcripts and alternatively spliced genes are associated with early development in bovine embryos. <i>Animal</i> , 2012, 6, 1199-1205.	1.3	5
721	FMRP targets distinct mRNA sequence elements to regulate protein expression. <i>Nature</i> , 2012, 492, 382-386.	13.7	656
722	Integrated miRNA, mRNA and protein expression analysis reveals the role of post-transcriptional regulation in controlling CHO cell growth rate. <i>BMC Genomics</i> , 2012, 13, 656.	1.2	70
723	Evolutionary Dynamics of Gene and Isoform Regulation in Mammalian Tissues. <i>Science</i> , 2012, 338, 1593-1599.	6.0	853
725	How to Analyze Gene Expression Using RNA-Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 802, 259-274.	0.4	23
726	Distinct Contributions of Replication and Transcription to Mutation Rate Variation of Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 4-10.	3.0	31
727	The Transcript-centric Mutations in Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 11-22.	3.0	21
728	Identification of novel human receptor activator of nuclear factor- κ B isoforms generated through alternative splicing: implications in breast cancer cell survival and migration. <i>Breast Cancer Research</i> , 2012, 14, R112.	2.2	35
729	SpliceGrapher: detecting patterns of alternative splicing from RNA-Seq data in the context of gene models and EST data. <i>Genome Biology</i> , 2012, 13, R4.	13.9	140
730	Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. <i>Genome Biology</i> , 2012, 13, R84.	13.9	140
731	Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. <i>Genome Biology</i> , 2012, 13, R35.	13.9	113
732	Regulation of alternative splicing by the circadian clock and food related cues. <i>Genome Biology</i> , 2012, 13, R54.	13.9	89

#	ARTICLE	IF	CITATIONS
733	Alternative transcription start site selection leads to large differences in translation activity in yeast. <i>Rna</i> , 2012, 18, 2299-2305.	1.6	111
734	Introns in UTRs: Why we should stop ignoring them. <i>BioEssays</i> , 2012, 34, 1025-1034.	1.2	119
735	Issues in Omics Data Integration for Gene Set Analysis and Aberrant Pathway Identification. <i>Drug Development Research</i> , 2012, 73, 528-534.	1.4	0
736	The exon 29 c.3535A>T in the alpha-2-macroglobulin gene causing aberrant splice variants is associated with mastitis in dairy cattle. <i>Immunogenetics</i> , 2012, 64, 807-816.	1.2	18
737	Mutation of a U2 snRNA Gene Causes Global Disruption of Alternative Splicing and Neurodegeneration. <i>Cell</i> , 2012, 148, 296-308.	13.5	123
738	Transcriptome-wide Regulation of Pre-mRNA Splicing and mRNA Localization by Muscleblind Proteins. <i>Cell</i> , 2012, 150, 710-724.	13.5	425
739	The Cellular EJC Interactome Reveals Higher-Order mRNP Structure and an EJC-SR Protein Nexus. <i>Cell</i> , 2012, 151, 750-764.	13.5	287
740	Discovery and characterization of new transcripts from RNA-seq data in mouse CD4+ T cells. <i>Genomics</i> , 2012, 100, 303-313.	1.3	12
741	Genetic variation in the alternative splicing regulator RBM20 is associated with dilated cardiomyopathy. <i>Heart Rhythm</i> , 2012, 9, 390-396.	0.3	136
742	The splicing factor SRSF1 regulates apoptosis and proliferation to promote mammary epithelial cell transformation. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 220-228.	3.6	342
743	Cloning and Characterization of BuffaloNANOG Gene: Alternative Transcription Start Sites, Splicing, and Polyadenylation in Embryonic Stem Cell-Like Cells. <i>DNA and Cell Biology</i> , 2012, 31, 721-731.	0.9	7
744	Pharmacogene regulatory elements: from discovery to applications. <i>Genome Medicine</i> , 2012, 4, 45.	3.6	18
745	Searching for Alternative Splicing With a Joint Model on Probe Measurability and Expression Intensities. <i>Journal of the American Statistical Association</i> , 2012, 107, 935-945.	1.8	1
746	Rewiring the dynamic interactome. <i>Molecular BioSystems</i> , 2012, 8, 2054.	2.9	26
747	TCERG1 Regulates Alternative Splicing of the <i>Bcl-x</i> Gene by Modulating the Rate of RNA Polymerase II Transcription. <i>Molecular and Cellular Biology</i> , 2012, 32, 751-762.	1.1	47
748	Alternative splicing networks regulated by signaling in human T cells. <i>Rna</i> , 2012, 18, 1029-1040.	1.6	90
749	A greatly extended PPARGC1A genomic locus encodes several new brain-specific isoforms and influences Huntington disease age of onset. <i>Human Molecular Genetics</i> , 2012, 21, 3461-3473.	1.4	85
750	An exon-centric perspective Canadian Society of Molecular Biosciences (CSMB) Senior Investigator Award. <i>Biochemistry and Cell Biology</i> , 2012, 90, 603-612.	0.9	13

#	ARTICLE	IF	CITATIONS
751	Next-generation sequencing technologies for gene expression profiling in plants. <i>Briefings in Functional Genomics</i> , 2012, 11, 63-70.	1.3	135
752	Identification of Splice Variants, Targeted MicroRNAs and Functional Single Nucleotide Polymorphisms of the <i>BOLA-DQA2</i> Gene in Dairy Cattle. <i>DNA and Cell Biology</i> , 2012, 31, 739-744.	0.9	37
753	RBFOX1 regulates both splicing and transcriptional networks in human neuronal development. <i>Human Molecular Genetics</i> , 2012, 21, 4171-4186.	1.4	192
754	Alternative splicing and nonsense-mediated decay modulate expression of important regulatory genes in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2012, 40, 2454-2469.	6.5	439
755	<i>Oases</i> : robust <i>de novo</i> RNA-seq assembly across the dynamic range of expression levels. <i>Bioinformatics</i> , 2012, 28, 1086-1092.	1.8	1,351
756	A Broad Range of Conformations Contribute to the Solution Ensemble of the Essential Splicing Factor U2AF ⁶⁵ . <i>Biochemistry</i> , 2012, 51, 5223-5225.	1.2	17
757	Histone H2A variants in nucleosomes and chromatin: more or less stable?. <i>Nucleic Acids Research</i> , 2012, 40, 10719-10741.	6.5	248
758	Transcriptome-wide analysis of protein-RNA interactions using high-throughput sequencing. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 206-212.	2.3	58
759	Identification and characterization of novel splice variants of the human EPM2A gene mutated in Lafora progressive myoclonus epilepsy. <i>Genomics</i> , 2012, 99, 36-43.	1.3	14
760	Detection, annotation and visualization of alternative splicing from RNA-Seq data with SplicingViewer. <i>Genomics</i> , 2012, 99, 178-182.	1.3	43
761	Identification of long non-protein coding RNAs in chicken skeletal muscle using next generation sequencing. <i>Genomics</i> , 2012, 99, 292-298.	1.3	173
762	Regulation of eukaryotic gene expression by the untranslated gene regions and other non-coding elements. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 3613-3634.	2.4	481
763	Coordinated regulation of neuronal mRNA steady-state levels through developmentally controlled intron retention. <i>Genes and Development</i> , 2012, 26, 1209-1223.	2.7	247
764	Dual RNA-seq of pathogen and host. <i>Nature Reviews Microbiology</i> , 2012, 10, 618-630.	13.6	660
765	OSA: a fast and accurate alignment tool for RNA-Seq. <i>Bioinformatics</i> , 2012, 28, 1933-1934.	1.8	119
766	Assessing Determinants of Exonic Evolutionary Rates in Mammals. <i>Molecular Biology and Evolution</i> , 2012, 29, 3121-3129.	3.5	13
767	SpliceSeq: a resource for analysis and visualization of RNA-Seq data on alternative splicing and its functional impacts. <i>Bioinformatics</i> , 2012, 28, 2385-2387.	1.8	231
768	hnRNP A1 Proofreads 3' Splice Site Recognition by U2AF. <i>Molecular Cell</i> , 2012, 45, 314-329.	4.5	87

#	ARTICLE	IF	CITATIONS
769	Tissue-Specific Alternative Splicing Remodels Protein-Protein Interaction Networks. <i>Molecular Cell</i> , 2012, 46, 884-892.	4.5	366
770	Tissue-Specific Splicing of Disordered Segments that Embed Binding Motifs Rewires Protein Interaction Networks. <i>Molecular Cell</i> , 2012, 46, 871-883.	4.5	344
771	High throughput gene expression analysis of the inner ear. <i>Hearing Research</i> , 2012, 288, 77-88.	0.9	33
772	Association of the RAVER2 gene with increased susceptibility for ulcerative colitis. <i>Human Immunology</i> , 2012, 73, 732-735.	1.2	6
773	Detecting outlier peptides in quantitative high-throughput mass spectrometry data. <i>Journal of Proteomics</i> , 2012, 75, 3230-3239.	1.2	5
774	Targeted proteome investigation via selected reaction monitoring mass spectrometry. <i>Journal of Proteomics</i> , 2012, 75, 3495-3513.	1.2	59
775	Co-transcriptional regulation of alternative pre-mRNA splicing. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 673-683.	0.9	79
776	Gene expression and behaviour in mouse models of HD. <i>Brain Research Bulletin</i> , 2012, 88, 276-284.	1.4	28
777	The age of the "ome" Genome, transcriptome and proteome data set collection and analysis. <i>Brain Research Bulletin</i> , 2012, 88, 294-301.	1.4	13
778	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307.	13.5	1,134
779	U1 snRNP Determines mRNA Length and Regulates Isoform Expression. <i>Cell</i> , 2012, 150, 53-64.	13.5	392
780	Integrative Genome-wide Analysis Reveals Cooperative Regulation of Alternative Splicing by hnRNP Proteins. <i>Cell Reports</i> , 2012, 1, 167-178.	2.9	420
781	Differential GC Content between Exons and Introns Establishes Distinct Strategies of Splice-Site Recognition. <i>Cell Reports</i> , 2012, 1, 543-556.	2.9	249
782	Transcriptional regulation of the human Raver2 ribonucleoprotein gene. <i>Gene</i> , 2012, 493, 243-252.	1.0	6
783	Functional coupling of transcription and splicing. <i>Gene</i> , 2012, 501, 104-117.	1.0	54
784	Molecular cloning of novel alternatively spliced variants of BCL2L12, a new member of the BCL2 gene family, and their expression analysis in cancer cells. <i>Gene</i> , 2012, 505, 153-166.	1.0	30
785	Revisit on the evolutionary relationship between alternative splicing and gene duplication. <i>Gene</i> , 2012, 504, 102-106.	1.0	20
786	Genome-wide impact of endogenous antisense transcripts in eukaryotes. <i>Frontiers in Bioscience - Landmark</i> , 2012, 17, 300.	3.0	13

#	ARTICLE	IF	CITATIONS
787	Neuronal Elav-like (Hu) Proteins Regulate RNA Splicing and Abundance to Control Glutamate Levels and Neuronal Excitability. <i>Neuron</i> , 2012, 75, 1067-1080.	3.8	190
788	Identification of an intronic splicing regulatory element involved in auto-regulation of alternative splicing of <i>SCL33</i> pre-mRNA. <i>Plant Journal</i> , 2012, 72, 935-946.	2.8	71
789	dsPIG: a tool to predict imprinted genes from the deep sequencing of whole transcriptomes. <i>BMC Bioinformatics</i> , 2012, 13, 271.	1.2	12
790	BEAT: Bioinformatics Exon Array Tool to store, analyze and visualize Affymetrix GeneChip Human Exon Array data from disease experiments. <i>BMC Bioinformatics</i> , 2012, 13, S21.	1.2	5
791	Transcriptome landscape of the human placenta. <i>BMC Genomics</i> , 2012, 13, 115.	1.2	83
792	RNA-Seq analysis uncovers transcriptomic variations between morphologically similar in vivo- and in vitro-derived bovine blastocysts. <i>BMC Genomics</i> , 2012, 13, 118.	1.2	97
793	Whole genome SNP discovery and analysis of genetic diversity in Turkey (<i>Meleagris gallopavo</i>). <i>BMC Genomics</i> , 2012, 13, 391.	1.2	63
794	Plant polyadenylation factors: conservation and variety in the polyadenylation complex in plants. <i>BMC Genomics</i> , 2012, 13, 641.	1.2	62
795	De novo reconstruction of the <i>Toxoplasma gondii</i> transcriptome improves on the current genome annotation and reveals alternatively spliced transcripts and putative long non-coding RNAs. <i>BMC Genomics</i> , 2012, 13, 696.	1.2	38
796	Alternative splicing of the neurofibromatosis type 1 pre-mRNA is regulated by the muscleblind-like proteins and the CUG-BP and ELAV-like factors. <i>BMC Molecular Biology</i> , 2012, 13, 35.	3.0	13
797	Genome-wide analysis of the MYB transcription factor superfamily in soybean. <i>BMC Plant Biology</i> , 2012, 12, 106.	1.6	339
798	Immunohistochemical analysis of medullary breast carcinoma autoantigens in different histological types of breast carcinomas. <i>Diagnostic Pathology</i> , 2012, 7, 161.	0.9	14
799	Next Generation Microarray Bioinformatics. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	8
800	HLA typing from RNA-Seq sequence reads. <i>Genome Medicine</i> , 2012, 4, 102.	3.6	204
801	Global impact of RNA splicing on transcriptome remodeling in the heart. <i>Journal of Zhejiang University: Science B</i> , 2012, 13, 603-608.	1.3	1
802	Deciphering the Plant Splicing Code: Experimental and Computational Approaches for Predicting Alternative Splicing and Splicing Regulatory Elements. <i>Frontiers in Plant Science</i> , 2012, 3, 18.	1.7	78
807	Regulation and Function of Adiponectin Receptors in Skeletal Muscle. <i>Vitamins and Hormones</i> , 2012, 90, 95-123.	0.7	12
808	The Human Salivary RNA Transcriptome Revealed by Massively Parallel Sequencing. <i>Clinical Chemistry</i> , 2012, 58, 1314-1321.	1.5	57

#	ARTICLE	IF	CITATIONS
809	Complex changes in alternative pre-mRNA splicing play a central role in the epithelial-to-mesenchymal transition (EMT). <i>Seminars in Cancer Biology</i> , 2012, 22, 417-427.	4.3	127
810	The Long Non-Coding RNAs: A New (P)layer in the "Dark Matter". <i>Frontiers in Genetics</i> , 2011, 2, 107.	1.1	113
811	Identification of novel splice variants and exons of human endothelial cell-specific chemotactic regulator (ECSCR) by bioinformatics analysis. <i>Computational Biology and Chemistry</i> , 2012, 41, 41-50.	1.1	5
812	A global view of gene activity at the flowering transition phase in precocious trifoliolate orange and its wild-type [<i>Poncirus trifoliata</i> (L.) Raf.] by transcriptome and proteome analysis. <i>Gene</i> , 2012, 510, 47-58.	1.0	12
813	Molecular analysis of SLC25A13 gene in human peripheral blood lymphocytes: Marked transcript diversity, and the feasibility of cDNA cloning as a diagnostic tool for citrin deficiency. <i>Gene</i> , 2012, 511, 227-234.	1.0	21
814	Linear motifs: lost in (pre)translation. <i>Trends in Biochemical Sciences</i> , 2012, 37, 333-341.	3.7	61
815	Novel MDM2 splice variants identified from oral squamous cell carcinoma. <i>Oral Oncology</i> , 2012, 48, 1128-1135.	0.8	9
816	Alternative transcription and alternative splicing in cancer. , 2012, 136, 283-294.		107
817	Genotoxic stress modulates CDC25C phosphatase alternative splicing in human breast cancer cell lines. <i>Molecular Oncology</i> , 2012, 6, 542-552.	2.1	20
819	Gene Prediction. <i>Methods in Molecular Biology</i> , 2012, 855, 175-201.	0.4	14
820	DNA Diagnostics and Exon Skipping. <i>Methods in Molecular Biology</i> , 2012, 867, 3-16.	0.4	1
821	Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells. <i>Nature Biotechnology</i> , 2012, 30, 777-782.	9.4	1,347
822	Characterization of ABL exon 7 deletion by molecular genetic and bioinformatic methods reveals no association with imatinib resistance in chronic myeloid leukemia. <i>Medical Oncology</i> , 2012, 29, 2136-2142.	1.2	8
823	Post-transcriptional regulation in cancer progression. <i>Journal of Cell Communication and Signaling</i> , 2012, 6, 233-248.	1.8	32
824	Muscleblind-like 2-Mediated Alternative Splicing in the Developing Brain and Dysregulation in Myotonic Dystrophy. <i>Neuron</i> , 2012, 75, 437-450.	3.8	296
825	Modeling RNA degradation for RNA-Seq with applications. <i>Biostatistics</i> , 2012, 13, 734-747.	0.9	25
826	Exon Skipping. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	1
828	Argonaute proteins couple chromatin silencing to alternative splicing. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 998-1004.	3.6	245

#	ARTICLE	IF	CITATIONS
829	Neurofibromatosis Type 1. , 2012, , .		23
830	Aberrant Expression of Splicing Factors in Newly Diagnosed Acute Myeloid Leukemia. <i>Onkologie</i> , 2012, 35, 335-340.	1.1	39
831	Human ESC/iPSC-based "omics"™ and bioinformatics for translational research. <i>Drug Discovery Today: Disease Models</i> , 2012, 9, e161-e170.	1.2	8
837	Human NRDRB1, an Alternatively Spliced Isoform of NADP(H)-Dependent Retinol Dehydrogenase/Reductase Enhanced Enzymatic Activity of Benzil. <i>Cellular Physiology and Biochemistry</i> , 2012, 30, 1371-1382.	1.1	2
838	Transcriptome profiling of UPF3B/NMD-deficient lymphoblastoid cells from patients with various forms of intellectual disability. <i>Molecular Psychiatry</i> , 2012, 17, 1103-1115.	4.1	97
839	Long Noncoding RNAs with snoRNA Ends. <i>Molecular Cell</i> , 2012, 48, 219-230.	4.5	389
840	Accuracy of RNA-Seq and its dependence on sequencing depth. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	25
841	Alt Event Finder: a tool for extracting alternative splicing events from RNA-seq data. <i>BMC Genomics</i> , 2012, 13, S10.	1.2	23
842	BM-Map: an efficient software package for accurately allocating multireads of RNA-sequencing data. <i>BMC Genomics</i> , 2012, 13, S9.	1.2	6
843	RNA-Seq analysis implicates dysregulation of the immune system in schizophrenia. <i>BMC Genomics</i> , 2012, 13, S2.	1.2	63
844	Identification of 3â€² gene ends using transcriptional and genomic conservation across vertebrates. <i>BMC Genomics</i> , 2012, 13, 708.	1.2	5
845	Genome-wide Profiling of RNA splicing in prostate tumor from RNA-seq data using virtual microarrays. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 21.	1.2	2
846	Combinations of Histone Modifications Mark Exon Inclusion Levels. <i>PLoS ONE</i> , 2012, 7, e29911.	1.1	38
847	Characterization and Comparison of the Leukocyte Transcriptomes of Three Cattle Breeds. <i>PLoS ONE</i> , 2012, 7, e30244.	1.1	33
848	Expression Profiling of <i>Cucumis sativus</i> in Response to Infection by <i>Pseudoperonospora cubensis</i> . <i>PLoS ONE</i> , 2012, 7, e34954.	1.1	54
849	Gene Transcription and Splicing of T-Type Channels Are Evolutionarily-Conserved Strategies for Regulating Channel Expression and Gating. <i>PLoS ONE</i> , 2012, 7, e37409.	1.1	28
850	FOX-2 Dependent Splicing of Ataxin-2 Transcript Is Affected by Ataxin-1 Overexpression. <i>PLoS ONE</i> , 2012, 7, e37985.	1.1	10
851	Transcriptome Sequencing and Comparative Analysis of <i>Saccharina japonica</i> (Laminariales.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	1.1	93

#	ARTICLE	IF	CITATIONS
852	Global Transcriptome Analysis of the Scorpion <i>Centruroides noxius</i> : New Toxin Families and Evolutionary Insights from an Ancestral Scorpion Species. <i>PLoS ONE</i> , 2012, 7, e43331.	1.1	69
853	Biosignatures for Parkinson's Disease and Atypical Parkinsonian Disorders Patients. <i>PLoS ONE</i> , 2012, 7, e43595.	1.1	52
854	Abnormal Expression of the Pre-mRNA Splicing Regulators SRSF1, SRSF2, SRPK1 and SRPK2 in Non Small Cell Lung Carcinoma. <i>PLoS ONE</i> , 2012, 7, e46539.	1.1	119
855	Comparative Transcriptome Profiling of the Early Response to <i>Magnaporthe oryzae</i> in Durable Resistant vs Susceptible Rice (<i>Oryza sativa</i> L.) Genotypes. <i>PLoS ONE</i> , 2012, 7, e51609.	1.1	149
856	Splicing Programs and Cancer. <i>Journal of Nucleic Acids</i> , 2012, 2012, 1-9.	0.8	43
857	Alternative Splicing Regulated by Butyrate in Bovine Epithelial Cells. <i>PLoS ONE</i> , 2012, 7, e39182.	1.1	13
858	The Human Transcriptome: An Unfinished Story. <i>Genes</i> , 2012, 3, 344-360.	1.0	121
859	Applications for next-generation sequencing in fish ecotoxicogenomics. <i>Frontiers in Genetics</i> , 2012, 3, 62.	1.1	55
860	Global Approaches to the Role of miRNAs in Drug-Induced Changes in Gene Expression. <i>Frontiers in Genetics</i> , 2012, 3, 109.	1.1	21
861	Genetic variations and alternative splicing: the Glioma associated oncogene 1, <i>GLI1</i> . <i>Frontiers in Genetics</i> , 2012, 3, 119.	1.1	7
862	Estimation of Gene Expression at Isoform Level from mRNA-Seq Data by Bayesian Hierarchical Modeling. <i>Frontiers in Genetics</i> , 2012, 3, 239.	1.1	0
863	Emerging Roles of Alternative Pre-mRNA Splicing Regulation in Neuronal Development and Function. <i>Frontiers in Neuroscience</i> , 2012, 6, 122.	1.4	82
864	Genome-Wide Approaches to Dissect the Roles of RNA Binding Proteins in Translational Control: Implications for Neurological Diseases. <i>Frontiers in Neuroscience</i> , 2012, 6, 144.	1.4	47
865	Tumor-specific histone signature and DNA methylation in multiple myeloma and leukemia cells. <i>Neoplasia</i> , 2012, 59, 450-462.	0.7	11
866	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 0, , .	0.1	21
867	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 0, , .	0.1	17
868	Beyond the Gene List: Exploring Transcriptomics Data in Search for Gene Function, Trait Mechanisms and Genetic Architecture. , 2012, , .		2
869	CELF1, a Multifunctional Regulator of Posttranscriptional Networks. , 2012, , .		5

#	ARTICLE	IF	CITATIONS
870	Translational Biology Approach to Identify Causative Factors for Rare Toxicities in Humans and Animals. <i>Current Drug Discovery Technologies</i> , 2012, 9, 77-80.	0.6	1
872	Identification of gene-oriented exon orthology between human and mouse. <i>BMC Genomics</i> , 2012, 13, S10.	1.2	12
873	Quantification of protein isoforms in mesenchymal stem cells by reductive dimethylation of lysines in intact proteins. <i>Proteomics</i> , 2012, 12, 369-379.	1.3	25
874	Evolution of SR protein and hnRNP splicing regulatory factors. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 1-12.	3.2	301
875	Unscrambling genetic information at the RNA level. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 213-228.	3.2	25
876	Signals for pre-mRNA cleavage and polyadenylation. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 385-396.	3.2	192
877	Genetic variation of pre-mRNA alternative splicing in human populations. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 581-592.	3.2	42
878	Evolution of Human-Specific Neural SRGAP2 Genes by Incomplete Segmental Duplication. <i>Cell</i> , 2012, 149, 912-922.	13.5	341
879	Dynamic Fluorescent and Luminescent Reporters for Cell-Based Splicing Screens. <i>Methods in Molecular Biology</i> , 2012, 867, 273-287.	0.4	7
880	Ultrashort and progressive 4sU-tagging reveals key characteristics of RNA processing at nucleotide resolution. <i>Genome Research</i> , 2012, 22, 2031-2042.	2.4	132
881	Dark matter RNA: an intelligent scaffold for the dynamic regulation of the nuclear information landscape. <i>Frontiers in Genetics</i> , 2012, 3, 57.	1.1	23
882	JETTA: junction and exon toolkits for transcriptome analysis. <i>Bioinformatics</i> , 2012, 28, 1274-1275.	1.8	20
883	Mouse endogenous retroviruses can trigger premature transcriptional termination at a distance. <i>Genome Research</i> , 2012, 22, 870-884.	2.4	43
884	A beginner's guide to eukaryotic genome annotation. <i>Nature Reviews Genetics</i> , 2012, 13, 329-342.	7.7	553
885	King of hearts: a splicing factor rules cardiac proteins. <i>Nature Medicine</i> , 2012, 18, 660-661.	15.2	16
886	Ptbp2 represses adult-specific splicing to regulate the generation of neuronal precursors in the embryonic brain. <i>Genes and Development</i> , 2012, 26, 1626-1642.	2.7	171
887	Genetics and Epigenetics of the Skin Meet Deep Sequence. <i>Journal of Investigative Dermatology</i> , 2012, 132, 923-932.	0.3	15
888	Cell-autonomous regulation of fast troponin T pre-mRNA alternative splicing in response to mechanical stretch. <i>American Journal of Physiology - Cell Physiology</i> , 2012, 303, C298-C307.	2.1	10

#	ARTICLE	IF	CITATIONS
889	VERSE: A Varying Effect Regression for Splicing Elements Discovery. <i>Journal of Computational Biology</i> , 2012, 19, 855-865.	0.8	5
890	PTBP1-dependent regulation of USP5 alternative RNA splicing plays a role in glioblastoma tumorigenesis. <i>Molecular Carcinogenesis</i> , 2012, 51, 895-906.	1.3	75
891	Translational control by changes in poly(A) tail length: recycling mRNAs. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 577-585.	3.6	298
892	Utilizing RNA-Seq data for <i>de novo</i> coexpression network inference. <i>Bioinformatics</i> , 2012, 28, 1592-1597.	1.8	112
893	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design. , 2012, , 169-190.		4
894	Designing a transcriptome next-generation sequencing project for a nonmodel plant species ¹ . <i>American Journal of Botany</i> , 2012, 99, 257-266.	0.8	192
895	Tailoring of Membrane Proteins by Alternative Splicing of Pre-mRNA. <i>Biochemistry</i> , 2012, 51, 5541-5556.	1.2	28
896	CEDER: Accurate Detection of Differentially Expressed Genes by Combining Significance of Exons Using RNA-Seq. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1281-1292.	1.9	17
897	Making alternative splicing decisions during epithelial-to-mesenchymal transition (EMT). <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 2515-2526.	2.4	56
899	Deeply Dissecting Stemness: Making Sense to Non-Coding RNAs in Stem Cells. <i>Stem Cell Reviews and Reports</i> , 2012, 8, 78-86.	5.6	17
900	Subgroup-specific alternative splicing in medulloblastoma. <i>Acta Neuropathologica</i> , 2012, 123, 485-499.	3.9	28
901	Brain-derived neurotrophic factor expression is repressed during myogenic differentiation by miR-206. <i>Journal of Neurochemistry</i> , 2012, 120, 230-238.	2.1	78
902	A GC-rich element forms a G-quadruplex and regulates BACE1 mRNA alternative splicing. <i>Journal of Neurochemistry</i> , 2012, 121, 763-773.	2.1	84
903	Regulation of chemoresistance via alternative messenger RNA splicing. <i>Biochemical Pharmacology</i> , 2012, 83, 1063-1072.	2.0	22
904	Using human pluripotent stem cells to study post-transcriptional mechanisms of neurodegenerative diseases. <i>Brain Research</i> , 2012, 1462, 129-138.	1.1	4
905	The Hypothalamic-Neurohypophyseal System: From Genome to Physiology. <i>Journal of Neuroendocrinology</i> , 2012, 24, 539-553.	1.2	41
906	Androgen receptor (AR) aberrations in castration-resistant prostate cancer. <i>Molecular and Cellular Endocrinology</i> , 2012, 360, 38-43.	1.6	156
907	Developmental regulation of gene expression in the absence of transcriptional control: The case of kinetoplastids. <i>Molecular and Biochemical Parasitology</i> , 2012, 181, 61-72.	0.5	132

#	ARTICLE	IF	CITATIONS
908	Quantitative analysis of 5HT2C receptor RNA editing patterns in psychiatric disorders. <i>Neurobiology of Disease</i> , 2012, 45, 8-13.	2.1	33
909	Design principles of interconnections between chromatin and pre-mRNA splicing. <i>Trends in Biochemical Sciences</i> , 2012, 37, 248-253.	3.7	49
910	New connections between splicing and human disease. <i>Trends in Genetics</i> , 2012, 28, 147-154.	2.9	160
911	Alternative splicing interference by xenobiotics. <i>Toxicology</i> , 2012, 296, 1-12.	2.0	44
912	Splicing in oncogenesis and tumor suppression. <i>Cancer Science</i> , 2012, 103, 1611-1616.	1.7	57
913	Defects in spliceosomal machinery: a new pathway of leukaemogenesis. <i>British Journal of Haematology</i> , 2012, 158, 165-173.	1.2	66
914	Advances in plant genome sequencing. <i>Plant Journal</i> , 2012, 70, 177-190.	2.8	156
915	Isoform diversity and its importance for axon regeneration. <i>Neuropathology</i> , 2012, 32, 420-431.	0.7	4
916	Glucocorticoid receptor isoforms generated by alternative splicing and alternative translation initiation. <i>Russian Journal of Genetics: Applied Research</i> , 2012, 2, 205-213.	0.4	3
917	KIS SPLICE: de-novo calling alternative splicing events from RNA-seq data. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	85
918	A context-based approach to identify the most likely mapping for RNA-seq experiments. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	14
919	Identification of conserved splicing motifs in mutually exclusive exons of 15 insect species. <i>BMC Genomics</i> , 2012, 13, S1.	1.2	3
920	Integrating many co-splicing networks to reconstruct splicing regulatory modules. <i>BMC Systems Biology</i> , 2012, 6, S17.	3.0	14
921	Menzerath's law at the gene-exon level in the human genome. <i>Complexity</i> , 2012, 17, 49-53.	0.9	41
922	SpliceAid 2: A database of human splicing factors expression data and RNA target motifs. <i>Human Mutation</i> , 2012, 33, 81-85.	1.1	234
923	The complex world of post-transcriptional mechanisms: is their deregulation a common link for diseases? Focus on ELAV-like RNA-binding proteins. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 501-517.	2.4	75
924	Annotation of the domestic dog genome sequence: finding the missing genes. <i>Mammalian Genome</i> , 2012, 23, 124-131.	1.0	13
925	Alternative splicing and mRNA expression analysis of bovine SLAMF7 gene in healthy and mastitis mammary tissues. <i>Molecular Biology Reports</i> , 2012, 39, 4155-4161.	1.0	10

#	ARTICLE	IF	CITATIONS
926	Tissue-Specific Expression of Splice Variants of Human IL-4 and IL-6 Gene mRNA. <i>Bulletin of Experimental Biology and Medicine</i> , 2012, 152, 329-332.	0.3	2
927	eQTL Mapping Using RNA-seq Data. <i>Statistics in Biosciences</i> , 2013, 5, 198-219.	0.6	73
928	SOAPfuse: an algorithm for identifying fusion transcripts from paired-end RNA-Seq data. <i>Genome Biology</i> , 2013, 14, R12.	13.9	197
929	Inferring the kinetics of stochastic gene expression from single-cell RNA-sequencing data. <i>Genome Biology</i> , 2013, 14, R7.	13.9	180
930	Isoform level expression profiles provide better cancer signatures than gene level expression profiles. <i>Genome Medicine</i> , 2013, 5, 33.	3.6	44
931	Emerging mechanisms and consequences of calcium regulation of alternative splicing in neurons and endocrine cells. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 4527-4536.	2.4	28
932	ZRANB2 localizes to supraspliceosomes and influences the alternative splicing of multiple genes in the transcriptome. <i>Molecular Biology Reports</i> , 2013, 40, 5381-5395.	1.0	33
933	Testing for Natural Selection in Human Exonic Splicing Regulators Associated with Evolutionary Rate Shifts. <i>Journal of Molecular Evolution</i> , 2013, 76, 228-239.	0.8	3
934	In situ sequencing for RNA analysis in preserved tissue and cells. <i>Nature Methods</i> , 2013, 10, 857-860.	9.0	650
935	Control of alternative splicing in immune responses: many regulators, many predictions, much still to learn. <i>Immunological Reviews</i> , 2013, 253, 216-236.	2.8	158
936	Independent specialization of the human and mouse X chromosomes for the male germ line. <i>Nature Genetics</i> , 2013, 45, 1083-1087.	9.4	164
937	GDNF family ligand dependent STAT3 activation is mediated by specific alternatively spliced isoforms of GFR α 2 and RET. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 2789-2802.	1.9	9
938	Ultra-deep profiling of alternatively spliced Drosophila Dscam isoforms by circularization-assisted multi-segment sequencing. <i>EMBO Journal</i> , 2013, 32, 2029-2038.	3.5	61
939	Deep Sequencing Data Analysis. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	5
940	Competition between Pre-mRNAs for the Splicing Machinery Drives Global Regulation of Splicing. <i>Molecular Cell</i> , 2013, 51, 338-348.	4.5	99
941	Pairwise comparisons of ten porcine tissues identify differential transcriptional regulation at the gene, isoform, promoter and transcription start site level. <i>Biochemical and Biophysical Research Communications</i> , 2013, 438, 346-352.	1.0	29
943	Whole transcriptome sequencing of the aging rat brain reveals dynamic RNA changes in the dark matter of the genome. <i>Age</i> , 2013, 35, 763-776.	3.0	94
944	Impact of gene gains, losses and duplication modes on the origin and diversification of vertebrates. <i>Seminars in Cell and Developmental Biology</i> , 2013, 24, 83-94.	2.3	87

#	ARTICLE	IF	CITATIONS
945	Mutation screen and RNA analysis disclose the changed splicing of the E-cadherin transcription in gastric cancer. <i>Familial Cancer</i> , 2013, 12, 547-554.	0.9	3
946	Alternative <scp>RNA</scp> splicing and cancer. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 547-566.	3.2	80
947	A Hierarchical Bayesian Model for Estimating and Inferring Differential Isoform Expression for Multi-sample RNA-Seq Data. <i>Statistics in Biosciences</i> , 2013, 5, 119-137.	0.6	8
948	Statistical and Computational Methods for High-Throughput Sequencing Data Analysis of Alternative Splicing. <i>Statistics in Biosciences</i> , 2013, 5, 138-155.	0.6	11
949	CLASS: constrained transcript assembly of RNA-seq reads. <i>BMC Bioinformatics</i> , 2013, 14, S14.	1.2	30
950	Gene set enrichment analysis of RNA-Seq data: integrating differential expression and splicing. <i>BMC Bioinformatics</i> , 2013, 14, S16.	1.2	43
951	Estimation of data-specific constitutive exons with RNA-Seq data. <i>BMC Bioinformatics</i> , 2013, 14, 31.	1.2	6
952	Fine-tuning of microRNA-mediated repression of mRNA by splicing-regulated and highly repressive microRNA recognition element. <i>BMC Genomics</i> , 2013, 14, 438.	1.2	19
953	The developing xylem transcriptome and genome-wide analysis of alternative splicing in <i>Populus trichocarpa</i> (black cottonwood) populations. <i>BMC Genomics</i> , 2013, 14, 359.	1.2	76
954	Differential transcript isoform usage pre- and post-zygotic genome activation in zebrafish. <i>BMC Genomics</i> , 2013, 14, 331.	1.2	33
955	Intron retention and transcript chimerism conserved across mammals: Ly6g5b and Csnk2b-Ly6g5b as examples. <i>BMC Genomics</i> , 2013, 14, 199.	1.2	10
956	Transcriptional analysis of the three Nlrp1 paralogs in mice. <i>BMC Genomics</i> , 2013, 14, 188.	1.2	62
957	Determination of dosage compensation of the mammalian X chromosome by RNA-seq is dependent on analytical approach. <i>BMC Genomics</i> , 2013, 14, 150.	1.2	35
958	RNA-Seq analysis reveals new gene models and alternative splicing in the fungal pathogen <i>Fusarium graminearum</i> . <i>BMC Genomics</i> , 2013, 14, 21.	1.2	79
959	E-cadherin gene re-expression in chronic lymphocytic leukemia cells by HDAC inhibitors. <i>BMC Cancer</i> , 2013, 13, 88.	1.1	28
960	Interplay between estrogen receptor and AKT in Estradiol-induced alternative splicing. <i>BMC Medical Genomics</i> , 2013, 6, 21.	0.7	25
961	Alternative pre-mRNA splicing in neurons: growing up and extending its reach. <i>Trends in Genetics</i> , 2013, 29, 442-448.	2.9	98
962	RNA and Cancer. <i>Cancer Treatment and Research</i> , 2013, , .	0.2	3

#	ARTICLE	IF	CITATIONS
963	Intragenic epigenetic changes modulate NCAM alternative splicing in neuronal differentiation. <i>EMBO Journal</i> , 2013, 32, 2264-2274.	3.5	81
964	Single-cell sequencing-based technologies will revolutionize whole-organism science. <i>Nature Reviews Genetics</i> , 2013, 14, 618-630.	7.7	1,012
965	Chromatin's thread to alternative splicing regulation. <i>Chromosoma</i> , 2013, 122, 465-474.	1.0	40
966	Ets1 and heat shock factor 1 regulate transcription of the Transformer 2 ¹² gene in human colon cancer cells. <i>Journal of Gastroenterology</i> , 2013, 48, 1222-1233.	2.3	22
967	The Alternative Heart: Impact of Alternative Splicing in Heart Disease. <i>Journal of Cardiovascular Translational Research</i> , 2013, 6, 945-955.	1.1	76
968	Integrative analysis revealed the molecular mechanism underlying $\text{RBM}10$ -mediated splicing regulation. <i>EMBO Molecular Medicine</i> , 2013, 5, 1431-1442.	3.3	106
969	Identification and characterization of novel alternative splice variants of human SAMD11. <i>Gene</i> , 2013, 530, 215-221.	1.0	9
970	Coupling Between Transcription and Alternative Splicing. <i>Cancer Treatment and Research</i> , 2013, 158, 1-24.	0.2	51
971	Human mucin MUC1 RNA undergoes different types of alternative splicing resulting in multiple isoforms. <i>Cancer Immunology, Immunotherapy</i> , 2013, 62, 423-435.	2.0	43
972	Genome-wide identification of cancer-related polyadenylated and non-polyadenylated RNAs in human breast and lung cell lines. <i>Science China Life Sciences</i> , 2013, 56, 503-512.	2.3	3
973	CUG-BP, Elav-like family (CELF)-mediated alternative splicing regulation in the brain during health and disease. <i>Molecular and Cellular Neurosciences</i> , 2013, 56, 456-464.	1.0	55
974	Aberrant splicing in neurological diseases. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 631-649.	3.2	47
975	Identification of a splice variant of mouse TRPA1 that regulates TRPA1 activity. <i>Nature Communications</i> , 2013, 4, 2399.	5.8	64
976	RNA binding proteins in the regulation of heart development. <i>International Journal of Biochemistry and Cell Biology</i> , 2013, 45, 2467-2478.	1.2	52
977	RNA-Seq analysis of the parietal cortex in Alzheimer's disease reveals alternatively spliced isoforms related to lipid metabolism. <i>Neuroscience Letters</i> , 2013, 536, 90-95.	1.0	77
978	Global Splicing Pattern Reversion during Somatic Cell Reprogramming. <i>Cell Reports</i> , 2013, 5, 357-366.	2.9	53
979	Cellular Source and Mechanisms of High Transcriptome Complexity in the Mammalian Testis. <i>Cell Reports</i> , 2013, 3, 2179-2190.	2.9	497
980	Next-Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine. , 2013, , 39-61.		4

#	ARTICLE	IF	CITATIONS
981	BRANCH: boosting RNA-Seq assemblies with partial or related genomic sequences. <i>Bioinformatics</i> , 2013, 29, 1250-1259.	1.8	28
982	Benchmarking RNA-Seq quantification tools. , 2013, 2013, 647-50.		33
983	All's well that ends well: alternative polyadenylation and its implications for stem cell biology. <i>Current Opinion in Cell Biology</i> , 2013, 25, 222-232.	2.6	30
984	Integrative Mechanisms of Oriented Neuronal Migration in the Developing Brain. <i>Annual Review of Cell and Developmental Biology</i> , 2013, 29, 299-353.	4.0	134
985	hnRNP A1: The Swiss Army Knife of Gene Expression. <i>International Journal of Molecular Sciences</i> , 2013, 14, 18999-19024.	1.8	232
986	Misregulation of Pre-mRNA Alternative Splicing in Cancer. <i>Cancer Discovery</i> , 2013, 3, 1228-1237.	7.7	265
987	Analysis of the canine brain transcriptome with an emphasis on the hypothalamus and cerebral cortex. <i>Mammalian Genome</i> , 2013, 24, 484-499.	1.0	26
989	New Insights into Functional Roles of the Polypyrimidine Tract-Binding Protein. <i>International Journal of Molecular Sciences</i> , 2013, 14, 22906-22932.	1.8	100
990	Alternative splicing of mutually exclusive exonsâ€”A review. <i>BioSystems</i> , 2013, 114, 31-38.	0.9	62
991	RNA sequencing of cancer reveals novel splicing alterations. <i>Scientific Reports</i> , 2013, 3, 1689.	1.6	162
992	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2013, 14, 671-683.	3.2	1,064
993	RNA-seq analyses of gene expression in the microsclerotia of <i>Verticillium dahliae</i> . <i>BMC Genomics</i> , 2013, 14, 607.	1.2	75
994	Analysis of the transcriptome in molecular epidemiology studies. <i>Environmental and Molecular Mutagenesis</i> , 2013, 54, 500-517.	0.9	38
995	Gene- and exon-expression profiling reveals an extensive LPS-induced response in immune cells in patients with cirrhosis. <i>Journal of Hepatology</i> , 2013, 58, 936-948.	1.8	66
996	A single-molecule long-read survey of the human transcriptome. <i>Nature Biotechnology</i> , 2013, 31, 1009-1014.	9.4	600
997	Effect of Alternative Splicing on the Degree Centrality of Nodes in Proteinâ€”Protein Interaction Networks of <i>Homo sapiens</i> . <i>Journal of Proteome Research</i> , 2013, 12, 1980-1988.	1.8	12
998	FUS regulates genes coding for RNA-binding proteins in neurons by binding to their highly conserved introns. <i>Rna</i> , 2013, 19, 498-509.	1.6	112
999	Predicting gene regulatory networks of soybean nodulation from RNA-Seq transcriptome data. <i>BMC Bioinformatics</i> , 2013, 14, 278.	1.2	22

#	ARTICLE	IF	CITATIONS
1000	Comprehensive analysis of RNA-seq data reveals the complexity of the transcriptome in <i>Brassica rapa</i> . <i>BMC Genomics</i> , 2013, 14, 689.	1.2	172
1001	Transcriptome analysis of human tissues and cell lines reveals one dominant transcript per gene. <i>Genome Biology</i> , 2013, 14, R70.	13.9	219
1002	GLiMMPS: Robust statistical model for regulatory variation of alternative splicing using RNA-seq data. <i>Genome Biology</i> , 2013, 14, R74.	13.9	76
1003	Distinct polyadenylation landscapes of diverse human tissues revealed by a modified PA-seq strategy. <i>BMC Genomics</i> , 2013, 14, 615.	1.2	43
1004	Inferring the expression variability of human transposable element-derived exons by linear model analysis of deep RNA sequencing data. <i>BMC Genomics</i> , 2013, 14, 584.	1.2	6
1005	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. <i>Epigenetics and Chromatin</i> , 2013, 6, 26.	1.8	192
1006	CRAC: an integrated approach to the analysis of RNA-seq reads. <i>Genome Biology</i> , 2013, 14, R30.	13.9	73
1007	Spliceosomal introns in the 5' untranslated region of plant BTL RING-H2 ubiquitin ligases are evolutionary conserved and required for gene expression. <i>BMC Plant Biology</i> , 2013, 13, 179.	1.6	13
1008	DNA from dead cancer cells induces TLR9-mediated invasion and inflammation in living cancer cells. <i>Breast Cancer Research and Treatment</i> , 2013, 142, 477-487.	1.1	31
1009	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. <i>Molecular Cancer</i> , 2013, 12, 140.	7.9	59
1010	Design of RNA splicing analysis null models for post hoc filtering of <i>Drosophila</i> head RNA-Seq data with the splicing analysis kit (Spanki). <i>BMC Bioinformatics</i> , 2013, 14, 320.	1.2	40
1011	Assessing the impact of human genome annotation choice on RNA-seq expression estimates. <i>BMC Bioinformatics</i> , 2013, 14, S8.	1.2	49
1012	MBNL1 and RBFOX2 cooperate to establish a splicing programme involved in pluripotent stem cell differentiation. <i>Nature Communications</i> , 2013, 4, 2480.	5.8	120
1013	Global versus Local Hubs in Human Protein-Protein Interaction Network. <i>Journal of Proteome Research</i> , 2013, 12, 5436-5446.	1.8	24
1014	Reliable Identification of Genomic Variants from RNA-Seq Data. <i>American Journal of Human Genetics</i> , 2013, 93, 641-651.	2.6	319
1015	Intron retention: a human <i>DKC1</i> gene common splicing event. <i>Biochemistry and Cell Biology</i> , 2013, 91, 506-512.	0.9	13
1016	During Embryogenesis, <i>Esrp1</i> Expression Is Restricted to a Subset of Epithelial Cells and Is Associated With Splicing of a Number of Developmentally Important Genes. <i>Developmental Dynamics</i> , 2013, 242, 281-290.	0.8	27
1017	Genetic architecture of retinal and macular degenerative diseases: the promise and challenges of next-generation sequencing. <i>Genome Medicine</i> , 2013, 5, 84.	3.6	33

#	ARTICLE	IF	CITATIONS
1018	Expansion of the mutually exclusive spliced exome in <i>Drosophila</i> . <i>Nature Communications</i> , 2013, 4, 2460.	5.8	21
1019	Complexity of the Alternative Splicing Landscape in Plants. <i>Plant Cell</i> , 2013, 25, 3657-3683.	3.1	731
1020	Drift and conservation of differential exon usage across tissues in primate species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15377-15382.	3.3	103
1021	Shrimp Dscam and its cytoplasmic tail splicing activator serine/arginine (SR)-rich protein B52 were both induced after white spot syndrome virus challenge. <i>Fish and Shellfish Immunology</i> , 2013, 34, 209-219.	1.6	51
1022	Genomic analysis reveals novel connections between alternative splicing and circadian regulatory networks. <i>Briefings in Functional Genomics</i> , 2013, 12, 13-24.	1.3	19
1023	Differential analysis of gene regulation at transcript resolution with RNA-seq. <i>Nature Biotechnology</i> , 2013, 31, 46-53.	9.4	3,256
1024	Bias Correction in RNA-Seq Short-Read Counts Using Penalized Regression. <i>Statistics in Biosciences</i> , 2013, 5, 88-99.	0.6	1
1025	Analysis of alternative cleavage and polyadenylation by 3' region extraction and deep sequencing. <i>Nature Methods</i> , 2013, 10, 133-139.	9.0	386
1026	Downregulation of splicing factor SRSF3 induces p53 ^Δ , an alternatively spliced isoform of p53 that promotes cellular senescence. <i>Oncogene</i> , 2013, 32, 2792-2798.	2.6	127
1027	Transcriptomics in the RNA-seq era. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 4-11.	2.8	273
1028	Gene Expression in the Human Brain: The Current State of the Study of Specificity and Spatiotemporal Dynamics. <i>Child Development</i> , 2013, 84, 76-88.	1.7	59
1029	Omics and Drug Response. <i>Annual Review of Pharmacology and Toxicology</i> , 2013, 53, 475-502.	4.2	130
1030	Two methods for full-length RNA sequencing for low quantities of cells and single cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 594-599.	3.3	103
1031	Toward a Genome-Wide Landscape of Translational Control. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012302-a012302.	2.3	50
1032	Detection of Viral RNA Splicing in Diagnostic Virology. , 2013, , 693-748.		4
1033	Challenges and strategies in transcriptome assembly and differential gene expression quantification. A comprehensive <i>in silico</i> assessment of RNA-seq experiments. <i>Molecular Ecology</i> , 2013, 22, 620-634.	2.0	210
1034	RNA sequencing reveals a diverse and dynamic repertoire of the <i>Xenopus tropicalis</i> transcriptome over development. <i>Genome Research</i> , 2013, 23, 201-216.	2.4	128
1035	Achieving high throughput sequencing of a cDNA library utilizing an alternative protocol for the bench top next-generation sequencing system. <i>Journal of Microbiological Methods</i> , 2013, 92, 122-126.	0.7	2

#	ARTICLE	IF	CITATIONS
1036	A High-Throughput Assay to Identify Small-Molecule Modulators of Alternative Pre-mRNA Splicing. <i>Journal of Biomolecular Screening</i> , 2013, 18, 180-190.	2.6	17
1037	Nonsense-mediated mRNA decay: from mechanistic insights to impacts on human health. <i>Briefings in Functional Genomics</i> , 2013, 12, 25-36.	1.3	40
1038	Connections between chromatin signatures and splicing. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 77-91.	3.2	46
1039	Untangling regulatory networks to spot drivers and modulators of cardiac disease. <i>Journal of Molecular and Cellular Cardiology</i> , 2013, 63, 1-3.	0.9	0
1040	Molecular characterization, alternative splicing and expression analysis of bovine DBC1. <i>Gene</i> , 2013, 527, 689-693.	1.0	12
1041	SRp20: An overview of its role in human diseases. <i>Biochemical and Biophysical Research Communications</i> , 2013, 436, 1-5.	1.0	60
1042	Alternative splicing generates a truncated isoform of human TNFRSF11A (RANK) with an altered capacity to activate NF- κ B. <i>Gene</i> , 2013, 525, 124-129.	1.0	10
1043	Alternative splicing of iodothyronine deiodinases in pituitary adenomas. Regulation by oncoprotein SF2/ASF. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2013, 1832, 763-772.	1.8	4
1044	Alterations of Alternative Splicing Patterns of Ser/Arg-Rich (SR) Genes in Response to Hormones and Stresses Treatments in Different Ecotypes of Rice (<i>Oryza sativa</i>). <i>Journal of Integrative Agriculture</i> , 2013, 12, 737-748.	1.7	25
1045	Expression profile analyses of human HCT-116 colon cancer cell line before and after serum induction. <i>Gene</i> , 2013, 517, 236-239.	1.0	0
1046	The splicing factor hnRNP C regulates expression of co-stimulatory molecules CD80 and CD40 in dendritic cells. <i>Immunology Letters</i> , 2013, 153, 27-32.	1.1	8
1047	Global detection and identification of developmental stage specific transcripts in mouse brain using subtractive cross-screening algorithm. <i>Genomics</i> , 2013, 102, 229-236.	1.3	5
1048	Alternative splicing and protein interaction data sets. <i>Nature Biotechnology</i> , 2013, 31, 292-293.	9.4	10
1049	Simultaneous Surface Display and Secretion of Proteins from Mammalian Cells Facilitate Efficient In Vitro Selection and Maturation of Antibodies. <i>Journal of Biological Chemistry</i> , 2013, 288, 19861-19869.	1.6	28
1050	Discovery and Mass Spectrometric Analysis of Novel Splice-junction Peptides Using RNA-Seq. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2341-2353.	2.5	115
1051	Exposing the subunit diversity within protein complexes: A mass spectrometry approach. <i>Methods</i> , 2013, 59, 270-277.	1.9	31
1052	Distinct tissue expression profiles of chicken Lpin1- Δ 12 isoforms and the effect of the variation on muscle fiber traits. <i>Gene</i> , 2013, 515, 281-290.	1.0	8
1053	Pleiotropic and isoform-specific functions for Pitx2 in superior colliculus and hypothalamic neuronal development. <i>Molecular and Cellular Neurosciences</i> , 2013, 52, 128-139.	1.0	11

#	ARTICLE	IF	CITATIONS
1054	The expression analysis of Sfrs10 and Celf4 during mouse retinal development. <i>Gene Expression Patterns</i> , 2013, 13, 425-436.	0.3	8
1055	Polyadenylation site-specific differences in the activity of the neuronal \hat{I}^2 CstF-64 protein in PC-12 cells. <i>Gene</i> , 2013, 529, 220-227.	1.0	9
1056	Alternative splicing switching in stem cell lineages. <i>Frontiers in Biology</i> , 2013, 8, 50-59.	0.7	22
1057	Divergent transcription of long noncoding RNA/mRNA gene pairs in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2876-2881.	3.3	409
1058	Computational analysis of associations between alternative splicing and histone modifications. <i>FEBS Letters</i> , 2013, 587, 516-521.	1.3	29
1059	Molecular Pathophysiology of Myelodysplastic Syndromes. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2013, 8, 21-47.	9.6	78
1060	The Coding and the Non-coding Transcriptome. , 2013, , 27-41.		3
1061	Identifying differentially spliced genes from two groups of RNA-seq samples. <i>Gene</i> , 2013, 518, 164-170.	1.0	48
1062	On the physiological significance of alternative splicing events in higher plants. <i>Protoplasma</i> , 2013, 250, 639-650.	1.0	83
1063	Untangling the transcriptome from fungus-infected plant tissues. <i>Gene</i> , 2013, 519, 238-244.	1.0	6
1064	Dynamic Integration of Splicing within Gene Regulatory Pathways. <i>Cell</i> , 2013, 152, 1252-1269.	13.5	371
1065	CPEB1 coordinates alternative 3' UTR formation with translational regulation. <i>Nature</i> , 2013, 495, 121-125.	13.7	156
1066	Regulation of gene expression in mammalian nervous system through alternative pre-mRNA splicing coupled with RNA quality control mechanisms. <i>Molecular and Cellular Neurosciences</i> , 2013, 56, 420-428.	1.0	64
1067	Next-Generation Sequencing: From Understanding Biology to Personalized Medicine. <i>Biology</i> , 2013, 2, 378-398.	1.3	35
1068	Opportunities and methods for studying alternative splicing in cancer with RNA-Seq. <i>Cancer Letters</i> , 2013, 340, 179-191.	3.2	107
1069	Genomics-Guided Discovery of Thailanstatins A, B, and C As Pre-mRNA Splicing Inhibitors and Antiproliferative Agents from <i>Burkholderia thailandensis</i> MSMB43. <i>Journal of Natural Products</i> , 2013, 76, 685-693.	1.5	118
1070	Chromatin remodeling and alternative splicing: Pre- and post-transcriptional regulation of the Arabidopsis circadian clock. <i>Seminars in Cell and Developmental Biology</i> , 2013, 24, 399-406.	2.3	36
1071	A Robust Method for Transcript Quantification with RNA-Seq Data. <i>Journal of Computational Biology</i> , 2013, 20, 167-187.	0.8	13

#	ARTICLE	IF	CITATIONS
1072	Regulation of splicing by SR proteins and SR protein-specific kinases. <i>Chromosoma</i> , 2013, 122, 191-207.	1.0	358
1073	The novel tumor suppressor NOL7 post-transcriptionally regulates thrombospondin-1 expression. <i>Oncogene</i> , 2013, 32, 4377-4386.	2.6	9
1074	Live or let die: posttranscriptional gene regulation in cell stress and cell death. <i>Immunological Reviews</i> , 2013, 253, 237-252.	2.8	31
1075	Rapid screening of yeast mutants with reporters identifies new splicing phenotypes. <i>FEBS Journal</i> , 2013, 280, 2712-2726.	2.2	6
1076	The relevance of the TGF- β Paradox to EMT-MET programs. <i>Cancer Letters</i> , 2013, 341, 30-40.	3.2	174
1077	The RUNX family in breast cancer: relationships with estrogen signaling. <i>Oncogene</i> , 2013, 32, 2121-2130.	2.6	105
1078	Systematic study of human long intergenic non-coding RNAs and their impact on cancer. <i>Science China Life Sciences</i> , 2013, 56, 324-334.	2.3	36
1079	Exploring the sampling universe of RNA-seq. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 175-88.	0.2	5
1080	A simple model to explain evolutionary trends of eukaryotic gene architecture and expression. <i>BioEssays</i> , 2013, 35, 561-570.	1.2	13
1081	Long Noncoding RNA MALAT1 Controls Cell Cycle Progression by Regulating the Expression of Oncogenic Transcription Factor B-MYB. <i>PLoS Genetics</i> , 2013, 9, e1003368.	1.5	655
1082	Molecular Mechanisms of Toxicity of Silver Nanoparticles in Zebrafish Embryos. <i>Environmental Science & Technology</i> , 2013, 47, 8005-8014.	4.6	198
1083	Alternative cleavage and polyadenylation: extent, regulation and function. <i>Nature Reviews Genetics</i> , 2013, 14, 496-506.	7.7	712
1084	The dark matter rises: the expanding world of regulatory RNAs. <i>Essays in Biochemistry</i> , 2013, 54, 1-16.	2.1	73
1085	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. <i>Nature</i> , 2013, 498, 236-240.	13.7	1,103
1086	Alternative splicing: Functional diversity among voltage-gated calcium channels and behavioral consequences. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 1522-1529.	1.4	101
1087	Antisense Oligonucleotides: Treating Neurodegeneration at the Level of RNA. <i>Neurotherapeutics</i> , 2013, 10, 486-497.	2.1	133
1088	Alternative cleavage and polyadenylation: the long and short of it. <i>Trends in Biochemical Sciences</i> , 2013, 38, 312-320.	3.7	297
1089	New Insights from Existing Sequence Data: Generating Breakthroughs without a Pipette. <i>Molecular Cell</i> , 2013, 49, 605-617.	4.5	12

#	ARTICLE	IF	CITATIONS
1090	Alternative splicing of intrinsically disordered regions and rewiring of protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 443-450.	2.6	166
1091	RNA Protein Interaction in Neurons. <i>Annual Review of Neuroscience</i> , 2013, 36, 243-270.	5.0	155
1092	The mechanism of alternative splicing of the X-linked NDUFB11 gene of the respiratory chain complex I, impact of rotenone treatment in neuroblastoma cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 211-218.	0.9	9
1093	The emerging roles of 3' UTR untranslated regions in cancer. <i>Cancer Letters</i> , 2013, 337, 22-25.	3.2	26
1094	RNA-binding proteins in Mendelian disease. <i>Trends in Genetics</i> , 2013, 29, 318-327.	2.9	211
1095	DNase I hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859.	9.4	112
1096	Alternative splicing in ascomycetes. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4235-4241.	1.7	33
1097	Untranslated Gene Regions and Other Non-coding Elements. <i>SpringerBriefs in Biochemistry and Molecular Biology</i> , 2013, , 1-56.	0.3	4
1099	Transcriptomics in the Age of Ultra High-Throughput Sequencing. , 2013, , 145-154.		0
1100	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. <i>Nature</i> , 2013, 498, 241-245.	13.7	326
1101	Transcriptional elongation and alternative splicing. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 134-140.	0.9	78
1102	IGF-I 3' UTR Untranslated Region: Strain-Specific Polymorphisms and Motifs Regulating IGF-I in Osteoblasts. <i>Endocrinology</i> , 2013, 154, 253-262.	1.4	21
1103	AVISPA: a web tool for the prediction and analysis of alternative splicing. <i>Genome Biology</i> , 2013, 14, R114.	13.9	37
1104	Development and Characterization of cDNA Resources for the Common Marmoset: One of the Experimental Primate Models. <i>DNA Research</i> , 2013, 20, 255-262.	1.5	12
1105	Identification of Wilms' Tumor 1-associating Protein Complex and Its Role in Alternative Splicing and the Cell Cycle. <i>Journal of Biological Chemistry</i> , 2013, 288, 33292-33302.	1.6	262
1106	Genome-Guided Transcriptome Assembly in the Age of Next-Generation Sequencing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1234-1240.	1.9	16
1107	Simultaneous Isoform Discovery and Quantification from RNA-Seq. <i>Statistics in Biosciences</i> , 2013, 5, 100-118.	0.6	18
1108	Transcriptome analyses of the human retina identify unprecedented transcript diversity and 3.5 Mb of novel transcribed sequence via significant alternative splicing and novel genes. <i>BMC Genomics</i> , 2013, 14, 486.	1.2	151

#	ARTICLE	IF	CITATIONS
1109	Myomegalin is necessary for the formation of centrosomal and Golgi-derived microtubules. <i>Biology Open</i> , 2013, 2, 238-250.	0.6	70
1110	Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs. <i>Bioinformatics</i> , 2013, 29, 2300-2310.	1.8	23
1111	Multiplatform single-sample estimates of transcriptional activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17778-17783.	3.3	86
1112	Tissue-specific splicing of a ubiquitously expressed transcription factor is essential for muscle differentiation. <i>Genes and Development</i> , 2013, 27, 1247-1259.	2.7	94
1113	Fluorescence-based alternative splicing reporters for the study of epithelial plasticity in vivo. <i>Rna</i> , 2013, 19, 116-127.	1.6	25
1114	Quantification of stochastic noise of splicing and polyadenylation in <i>Entamoeba histolytica</i> . <i>Nucleic Acids Research</i> , 2013, 41, 1936-1952.	6.5	71
1115	Functional transcriptomics in the post-ENCODE era. <i>Genome Research</i> , 2013, 23, 1961-1973.	2.4	58
1116	p53 is activated in response to disruption of the pre-mRNA splicing machinery. <i>Oncogene</i> , 2013, 32, 1-14.	2.6	93
1117	DBATE: database of alternative transcripts expression. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat050.	1.4	11
1118	The splicing landscape is globally reprogrammed during male meiosis. <i>Nucleic Acids Research</i> , 2013, 41, 10170-10184.	6.5	71
1119	Alternative mRNA Splicing of G Protein-Coupled Receptors. <i>Methods in Enzymology</i> , 2013, 520, 323-335.	0.4	6
1120	Host Cell Transcriptome Profile during Wild-Type and Attenuated Dengue Virus Infection. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2107.	1.3	68
1121	Computational Assessment of the Cooperativity between RNA Binding Proteins and MicroRNAs in Transcript Decay. <i>PLoS Computational Biology</i> , 2013, 9, e1003075.	1.5	30
1122	Alterations in Polyadenylation and Its Implications for Endocrine Disease. <i>Frontiers in Endocrinology</i> , 2013, 4, 53.	1.5	36
1123	APPRIS: annotation of principal and alternative splice isoforms. <i>Nucleic Acids Research</i> , 2013, 41, D110-D117.	6.5	205
1124	The Conserved Intronic Cleavage and Polyadenylation Site of CstF-77 Gene Imparts Control of 3' End Processing Activity through Feedback Autoregulation and by U1 snRNP. <i>PLoS Genetics</i> , 2013, 9, e1003613.	1.5	44
1125	Cancer metabolism meets systems biology: Pyruvate kinase isoform PKM2 is a metabolic master regulator. <i>Journal of Carcinogenesis</i> , 2013, 12, 14.	2.5	52
1126	Genome-wide identification and predictive modeling of tissue-specific alternative polyadenylation. <i>Bioinformatics</i> , 2013, 29, i108-i116.	1.8	27

#	ARTICLE	IF	CITATIONS
1127	Roles for transcript leaders in translation and mRNA decay revealed by transcript leader sequencing. <i>Genome Research</i> , 2013, 23, 977-987.	2.4	152
1128	Oncogenic Alternative Splicing Switches: Role in Cancer Progression and Prospects for Therapy. <i>International Journal of Cell Biology</i> , 2013, 2013, 1-17.	1.0	89
1129	CELF Family RNA-Binding Protein UNC-75 Regulates Two Sets of Mutually Exclusive Exons of the <i>unc-32</i> Gene in Neuron-Specific Manners in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2013, 9, e1003337.	1.5	37
1130	A Novel Intra-U1 snRNP Cross-Regulation Mechanism: Alternative Splicing Switch Links U1C and U1-70K Expression. <i>PLoS Genetics</i> , 2013, 9, e1003856.	1.5	25
1131	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. <i>International Journal of Molecular Sciences</i> , 2013, 14, 15423-15458.	1.8	22
1132	Structural Disorder Provides Increased Adaptability for Vesicle Trafficking Pathways. <i>PLoS Computational Biology</i> , 2013, 9, e1003144.	1.5	46
1133	Distinct Types of Disorder in the Human Proteome: Functional Implications for Alternative Splicing. <i>PLoS Computational Biology</i> , 2013, 9, e1003030.	1.5	62
1134	Posttranscriptional Regulation of Insulin Family Ligands and Receptors. <i>International Journal of Molecular Sciences</i> , 2013, 14, 19202-19229.	1.8	20
1135	Crystal structure and functional characterization of the human RBM25 PWI domain and its flanking basic region. <i>Biochemical Journal</i> , 2013, 450, 85-94.	1.7	8
1136	Grape RNA-Seq analysis pipeline environment. <i>Bioinformatics</i> , 2013, 29, 614-621.	1.8	30
1137	An Emerging Role for Long Non-Coding RNA Dysregulation in Neurological Disorders. <i>International Journal of Molecular Sciences</i> , 2013, 14, 20427-20442.	1.8	62
1138	Isolated pseudo-RNA-recognition motifs of SR proteins can regulate splicing using a noncanonical mode of RNA recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2802-11.	3.3	109
1139	TIGAR: transcript isoform abundance estimation method with gapped alignment of RNA-Seq data by variational Bayesian inference. <i>Bioinformatics</i> , 2013, 29, 2292-2299.	1.8	36
1140	Alternative splicing in the regulation of cholesterol homeostasis. <i>Current Opinion in Lipidology</i> , 2013, 24, 147-152.	1.2	24
1141	Accurate detection of differential RNA processing. <i>Nucleic Acids Research</i> , 2013, 41, 5189-5198.	6.5	39
1142	OLego: fast and sensitive mapping of spliced mRNA-Seq reads using small seeds. <i>Nucleic Acids Research</i> , 2013, 41, 5149-5163.	6.5	116
1143	MBNL1 and PTB cooperate to repress splicing of <i>Tpm1</i> exon 3. <i>Nucleic Acids Research</i> , 2013, 41, 4765-4782.	6.5	39
1144	Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 387-397.	0.8	59

#	ARTICLE	IF	CITATIONS
1145	Differential splicing across immune system lineages. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14324-14329.	3.3	64
1146	UV damage regulates alternative polyadenylation of the RPB2 gene in yeast. Nucleic Acids Research, 2013, 41, 3104-3114.	6.5	17
1147	Genetic Variants Contribute to Gene Expression Variability in Humans. Genetics, 2013, 193, 95-108.	1.2	98
1148	An intronic structure enabled by a long-distance interaction serves as a novel target for splicing correction in spinal muscular atrophy. Nucleic Acids Research, 2013, 41, 8144-8165.	6.5	74
1149	The Differential Transcription Network between Embryo and Endosperm in the Early Developing Maize Seed. Plant Physiology, 2013, 162, 440-455.	2.3	76
1150	Position-dependent and neuron-specific splicing regulation by the CELF family RNA-binding protein UNC-75 in <i>Caenorhabditis elegans</i> . Nucleic Acids Research, 2013, 41, 4015-4025.	6.5	42
1151	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. Nucleic Acids Research, 2013, 41, D125-D131.	6.5	148
1152	HnRNP A1 controls a splicing regulatory circuit promoting mesenchymal-to-epithelial transition. Nucleic Acids Research, 2013, 41, 8665-8679.	6.5	77
1153	U2AF65 adapts to diverse pre-mRNA splice sites through conformational selection of specific and promiscuous RNA recognition motifs. Nucleic Acids Research, 2013, 41, 3859-3873.	6.5	43
1154	Overlapping and distinct functions of CstF64 and CstF64 ^Δ in mammalian mRNA 3' processing. Rna, 2013, 19, 1781-1790.	1.6	59
1155	RhesusBase: a knowledgebase for the monkey research community. Nucleic Acids Research, 2013, 41, D892-D905.	6.5	27
1156	Widespread and extensive lengthening of 3' UTRs in the mammalian brain. Genome Research, 2013, 23, 812-825.	2.4	308
1157	IQdb: an intelligence quotient score-associated gene resource for human intelligence. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat063.	1.4	15
1158	Tissue-specific and SRSF1-dependent splicing of fibronectin, a matrix protein that controls host cell invasion. Molecular Biology of the Cell, 2013, 24, 3164-3176.	0.9	15
1159	A Novel EGFR Isoform Confers Increased Invasiveness to Cancer Cells. Cancer Research, 2013, 73, 7056-7067.	0.4	23
1160	Reactivation of Fetal Splicing Programs in Diabetic Hearts Is Mediated by Protein Kinase C Signaling. Journal of Biological Chemistry, 2013, 288, 35372-35386.	1.6	54
1161	Epstein-Barr Virus Induces Global Changes in Cellular mRNA Isoform Usage That Are Important for the Maintenance of Latency. Journal of Virology, 2013, 87, 12291-12301.	1.5	12
1162	Recent advances of studies on alternative intron retention. Trends in Evolutionary Biology, 2013, 5, 1.	0.4	3

#	ARTICLE	IF	CITATIONS
1163	A Statistical Method without Training Step for the Classification of Coding Frame in Transcriptome Sequences. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S10053.	1.0	8
1164	Detecting various types of differential splicing events using RNA-Seq data. , 2013, , .		2
1165	A New Exon Derived from a Mammalian Apparent LTR Retrotransposon of theSUPT16HGene. <i>International Journal of Genomics</i> , 2013, 2013, 1-9.	0.8	4
1166	Computational prediction and characterisation of ubiquitously expressed new splice variant of Prkaca gene in mouse. <i>Cell Biology International</i> , 2013, 37, 687-693.	1.4	3
1167	Widespread splicing changes in human brain development and aging. <i>Molecular Systems Biology</i> , 2013, 9, 633.	3.2	183
1168	Orchestration of Neurodevelopmental Programs by RBFOX1. <i>International Review of Neurobiology</i> , 2013, 113, 251-267.	0.9	64
1169	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. , 2013, , .		0
1170	Stability, delivery and functions of human sperm RNAs at fertilization. <i>Nucleic Acids Research</i> , 2013, 41, 4104-4117.	6.5	288
1171	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. <i>Nucleic Acids Research</i> , 2013, 41, e39-e39.	6.5	138
1172	Tissue-dependent regulation of RNAP II dynamics. <i>Transcription</i> , 2013, 4, 172-176.	1.7	3
1173	EBSeq: an empirical Bayes hierarchical model for inference in RNA-seq experiments. <i>Bioinformatics</i> , 2013, 29, 1035-1043.	1.8	1,111
1174	Half Pint/Puf68 is required for negative regulation of splicing by the SR factor Transformer2. <i>RNA Biology</i> , 2013, 10, 1396-1406.	1.5	7
1175	Recurrent reciprocal RNA chimera involving YPEL5 and PPP1CB in chronic lymphocytic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3035-3040.	3.3	44
1176	Frac-seq reveals isoform-specific recruitment to polyribosomes. <i>Genome Research</i> , 2013, 23, 1615-1623.	2.4	93
1177	Functional characterization of motif sequences under purifying selection. <i>Nucleic Acids Research</i> , 2013, 41, 2105-2120.	6.5	2
1178	PQBP1, a factor linked to intellectual disability, affects alternative splicing associated with neurite outgrowth. <i>Genes and Development</i> , 2013, 27, 615-626.	2.7	65
1179	HnRNPH1/H2, U1 snRNP, and U11 snRNP cooperate to regulate the stability of the <i>U11-48K</i> pre-mRNA. <i>Rna</i> , 2013, 19, 380-389.	1.6	24
1180	Tips for Preparing mRNA-Seq Libraries from Poly(A) ⁺ mRNA for Illumina Transcriptome High-Throughput Sequencing. <i>Cold Spring Harbor Protocols</i> , 2013, 2013, pdb.ip073908.	0.2	1

#	ARTICLE	IF	CITATIONS
1181	Regulation of alternative splicing in obesity and weight loss. <i>Adipocyte</i> , 2013, 2, 143-147.	1.3	13
1182	A dynamic interplay between alternative polyadenylation and microRNA regulation: Implications for cancer. <i>International Journal of Oncology</i> , 2013, 43, 995-1001.	1.4	23
1183	Not Junk After All: Non-Protein-Coding DNA Carries Extensive Biological Information. , 2013, , .		1
1186	Aberrant Alternative Splicing Events in Parkinson's Disease. <i>Cell Transplantation</i> , 2013, 22, 653-661.	1.2	39
1187	Transcriptomic Analysis of PNN- and ESRP1-Regulated Alternative Pre-mRNA Splicing in Human Corneal Epithelial Cells. , 2013, 54, 697.		17
1189	In situ mutation detection and visualization of intratumor heterogeneity for cancer research and diagnostics. <i>Oncotarget</i> , 2013, 4, 2407-2418.	0.8	42
1191	Clk/STY (cdc2-Like Kinase 1) and Akt Regulate Alternative Splicing and Adipogenesis in 3T3-L1 Pre-Adipocytes. <i>PLoS ONE</i> , 2013, 8, e53268.	1.1	26
1192	Efficient and Comprehensive Representation of Uniqueness for Next-Generation Sequencing by Minimum Unique Length Analyses. <i>PLoS ONE</i> , 2013, 8, e53822.	1.1	29
1193	Identification of Human HK Genes and Gene Expression Regulation Study in Cancer from Transcriptomics Data Analysis. <i>PLoS ONE</i> , 2013, 8, e54082.	1.1	22
1194	A Biophysical Model for Identifying Splicing Regulatory Elements and Their Interactions. <i>PLoS ONE</i> , 2013, 8, e54885.	1.1	5
1195	Expression Profile of Ectopic Olfactory Receptors Determined by Deep Sequencing. <i>PLoS ONE</i> , 2013, 8, e55368.	1.1	240
1196	The Drosophila Splicing Factor PSI Is Phosphorylated by Casein Kinase II and Tousled-Like Kinase. <i>PLoS ONE</i> , 2013, 8, e56401.	1.1	3
1197	Gene Expression Analyses Implicate an Alternative Splicing Program in Regulating Contractile Gene Expression and Serum Response Factor Activity in Mice. <i>PLoS ONE</i> , 2013, 8, e56590.	1.1	11
1198	Differential MicroRNA Regulation Correlates with Alternative Polyadenylation Pattern between Breast Cancer and Normal Cells. <i>PLoS ONE</i> , 2013, 8, e56958.	1.1	29
1199	The Baboon Kidney Transcriptome: Analysis of Transcript Sequence, Splice Variants, and Abundance. <i>PLoS ONE</i> , 2013, 8, e57563.	1.1	21
1200	Splicing-Related Features of Introns Serve to Propel Evolution. <i>PLoS ONE</i> , 2013, 8, e58547.	1.1	4
1201	RNA-Seq Analysis of <i>Cocos nucifera</i> : Transcriptome Sequencing and De Novo Assembly for Subsequent Functional Genomics Approaches. <i>PLoS ONE</i> , 2013, 8, e59997.	1.1	71
1202	Recent Adaptive Events in Human Brain Revealed by Meta-Analysis of Positively Selected Genes. <i>PLoS ONE</i> , 2013, 8, e61280.	1.1	12

#	ARTICLE	IF	CITATIONS
1203	A Novel Approach for Characterizing Microsatellite Instability in Cancer Cells. PLoS ONE, 2013, 8, e63056.	1.1	47
1204	FFPred 2.0: Improved Homology-Independent Prediction of Gene Ontology Terms for Eukaryotic Protein Sequences. PLoS ONE, 2013, 8, e63754.	1.1	40
1205	Evaluating the Impact of Sequencing Depth on Transcriptome Profiling in Human Adipose. PLoS ONE, 2013, 8, e66883.	1.1	60
1206	Detecting Splicing Variants in Idiopathic Pulmonary Fibrosis from Non-Differentially Expressed Genes. PLoS ONE, 2013, 8, e68352.	1.1	26
1207	Characterization and Comparative Analyses of Muscle Transcriptomes in Dorper and Small-Tailed Han Sheep Using RNA-Seq Technique. PLoS ONE, 2013, 8, e72686.	1.1	53
1208	A Polymorphic 3'UTR Element in ATP1B1 Regulates Alternative Polyadenylation and Is Associated with Blood Pressure. PLoS ONE, 2013, 8, e76290.	1.1	17
1209	Optimal Scaling of Digital Transcriptomes. PLoS ONE, 2013, 8, e77885.	1.1	44
1210	rSeqDiff: Detecting Differential Isoform Expression from RNA-Seq Data Using Hierarchical Likelihood Ratio Test. PLoS ONE, 2013, 8, e79448.	1.1	29
1211	Epidermal Growth-Factor Induced Transcript Isoform Variation Drives Mammary Cell Migration. PLoS ONE, 2013, 8, e80566.	1.1	15
1212	Alternative Splicing Events Is Not a Key Event for Gene Expression Regulation in Uremia. PLoS ONE, 2013, 8, e82702.	1.1	0
1213	Genome-Wide Survey of Cold Stress Regulated Alternative Splicing in Arabidopsis thaliana with Tiling Microarray. PLoS ONE, 2013, 8, e66511.	1.1	64
1214	Blockage of Notch Signaling Inhibits the Migration and Proliferation of Retinal Pigment Epithelial Cells. Scientific World Journal, The, 2013, 2013, 1-6.	0.8	20
1215	Cytoplasmic Inheritance Redux. Advances in Child Development and Behavior, 2013, 44, 225-255.	0.7	2
1216	The Merit of Alternative Messenger RNA Splicing as a New Mine for the Next Generation Ovarian Cancer Biomarkers. , 2013, , .		0
1217	Statistical Analysis of Mapped Reads from mRNA-Seq Data. , 0, , 77-104.		0
1218	Model-Based Methods for Transcript Expression-Level Quantification in RNA-Seq. , 2013, , 105-125.		1
1219	V.3. Comparative Genomics. , 2013, , 380-386.		1
1220	Comprehensive Analysis of Alternative Splicing in Digitalis purpurea by Strand-Specific RNA-Seq. PLoS ONE, 2014, 9, e106001.	1.1	12

#	ARTICLE	IF	CITATIONS
1221	A Comparative Study of Techniques for Differential Expression Analysis on RNA-Seq Data. PLoS ONE, 2014, 9, e103207.	1.1	195
1222	SnapShot-Seq: A Method for Extracting Genome-Wide, In Vivo mRNA Dynamics from a Single Total RNA Sample. PLoS ONE, 2014, 9, e89673.	1.1	53
1223	Expression Microarray Analysis Reveals Alternative Splicing of LAMA3 and DST Genes in Head and Neck Squamous Cell Carcinoma. PLoS ONE, 2014, 9, e91263.	1.1	35
1224	Genome Wide Identification of Aberrant Alternative Splicing Events in Myotonic Dystrophy Type 2. PLoS ONE, 2014, 9, e93983.	1.1	27
1225	Analysis of Prostate-Specific Antigen Transcripts in Chimpanzees, Cynomolgus Monkeys, Baboons, and African Green Monkeys. PLoS ONE, 2014, 9, e94522.	1.1	5
1226	The Impacts of Read Length and Transcriptome Complexity for De Novo Assembly: A Simulation Study. PLoS ONE, 2014, 9, e94825.	1.1	32
1227	Identification of a Novel Function of CX-4945 as a Splicing Regulator. PLoS ONE, 2014, 9, e94978.	1.1	76
1228	A Subtle Alternative Splicing Event Gives Rise to a Widely Expressed Human RNase k Isoform. PLoS ONE, 2014, 9, e96557.	1.1	4
1229	Characterization of Transcriptional Complexity during Adipose Tissue Development in Bovines of Different Ages and Sexes. PLoS ONE, 2014, 9, e101261.	1.1	32
1230	Alternative Splicing of TAF6: Downstream Transcriptome Impacts and Upstream RNA Splice Control Elements. PLoS ONE, 2014, 9, e102399.	1.1	5
1231	Integrated Exon Level Expression Analysis of Driver Genes Explain Their Role in Colorectal Cancer. PLoS ONE, 2014, 9, e110134.	1.1	23
1232	Detection Theory in Identification of RNA-DNA Sequence Differences Using RNA-Sequencing. PLoS ONE, 2014, 9, e112040.	1.1	7
1233	The landscape of alternative splicing in cervical squamous cell carcinoma. OncoTargets and Therapy, 2015, 8, 73.	1.0	15
1234	Illuminating the Transcriptome through the Genome. Genes, 2014, 5, 235-253.	1.0	7
1235	Alternative splicing during Arabidopsis flower development results in constitutive and stage-regulated isoforms. Frontiers in Genetics, 2014, 5, 25.	1.1	45
1236	The analytical landscape of static and temporal dynamics in transcriptome data. Frontiers in Genetics, 2014, 5, 35.	1.1	27
1237	Brain-expressed 3'UTR extensions strengthen miRNA cross-talk between ion channel/transporter encoding mRNAs. Frontiers in Genetics, 2014, 5, 41.	1.1	16
1238	Dephosphorylation of NSSR1 regulates alternative splicing of the GluR-B minigene. Genetics and Molecular Research, 2014, 13, 1753-1763.	0.3	2

#	ARTICLE	IF	CITATIONS
1239	Mapping Splicing Quantitative Trait Loci in RNA-Seq. <i>Cancer Informatics</i> , 2014, 13s4, CIN.S13971.	0.9	6
1240	Transcriptomics: Better Resolutions. <i>Gene Technology</i> , 2014, 04, .	0.5	0
1241	Expression of a novel splice variant of FRMD7 in developing human fetal brains that is upregulated upon the differentiation of NT2 cells. <i>Experimental and Therapeutic Medicine</i> , 2014, 8, 1131-1136.	0.8	3
1242	The role of mRNA splicing in prostate cancer. <i>Asian Journal of Andrology</i> , 2014, 16, 515.	0.8	21
1245	Identification and characterization of yak (<i>Bos grunniens</i>) b-Boule gene and its alternative splice variants. <i>Gene</i> , 2014, 550, 193-199.	1.0	8
1246	Transcriptional profiling of the responses to infection by the false smut fungus <i>Ustilagoidea virens</i> in resistant and susceptible rice varieties. <i>Canadian Journal of Plant Pathology</i> , 2014, 36, 377-388.	0.8	12
1247	Comparative analysis of RNA-seq data from polyA RNAs selection and ribosomal RNAs deletion protocol by strand-specific RNA sequencing technology. , 2014, , .		0
1248	Temporal and spatial variations in the relationship between urbanization and water quality. <i>Environmental Science and Pollution Research</i> , 2014, 21, 13646-13655.	2.7	67
1249	A comprehensive survey of non-canonical splice sites in the human transcriptome. <i>Nucleic Acids Research</i> , 2014, 42, 10564-10578.	6.5	109
1250	ESclassifier: A random forest classifier for detection of exon skipping events from RNA-Seq data. , 2014, , .		1
1251	PMD patient mutations reveal a long-distance intronic interaction that regulates PLP1/DM20 alternative splicing. <i>Human Molecular Genetics</i> , 2014, 23, 5464-5478.	1.4	32
1252	Differential evolution of signal-responsive RNA elements and upstream factors that control alternative splicing. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 4347-4360.	2.4	21
1253	Phenotypic noise: effects of post-transcriptional regulatory processes affecting mRNA. <i>Wiley Interdisciplinary Reviews RNA</i> , 2014, 5, 197-207.	3.2	9
1254	SpliceVista, a Tool for Splice Variant Identification and Visualization in Shotgun Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1552-1562.	2.5	28
1255	Comprehensive analysis of small RNA-seq data reveals that combination of miRNA with its isomiRs increase the accuracy of target prediction in <i>Arabidopsis thaliana</i> . <i>RNA Biology</i> , 2014, 11, 1414-1429.	1.5	46
1256	Interplay of chromatin modifications and non-coding RNAs in the heart. <i>Epigenetics</i> , 2014, 9, 101-112.	1.3	36
1257	RNA Helicase A Is a Downstream Mediator of KIF1B ^{Δ2} Tumor-Suppressor Function in Neuroblastoma. <i>Cancer Discovery</i> , 2014, 4, 434-451.	7.7	48
1258	An integrated transcriptome and expressed variant analysis of sepsis survival and death. <i>Genome Medicine</i> , 2014, 6, 111.	3.6	70

#	ARTICLE	IF	CITATIONS
1259	A robust estimation of exon expression to identify alternative spliced genes applied to human tissues and cancer samples. <i>BMC Genomics</i> , 2014, 15, 879.	1.2	12
1260	microRNA regulation of mammalian target of rapamycin expression and activity controls estrogen receptor function and RAD001 sensitivity. <i>Molecular Cancer</i> , 2014, 13, 229.	7.9	26
1261	Physiological state co-regulates thousands of mammalian mRNA splicing events at tandem splice sites and alternative exons. <i>Nucleic Acids Research</i> , 2014, 42, 8895-8904.	6.5	14
1262	Alternative splicing at GYNNGY 5â€² splice sites: more noise, less regulation. <i>Nucleic Acids Research</i> , 2014, 42, 13969-13980.	6.5	22
1263	Redirecting splicing with bifunctional oligonucleotides. <i>Nucleic Acids Research</i> , 2014, 42, e40-e40.	6.5	41
1264	FineSplice, enhanced splice junction detection and quantification: a novel pipeline based on the assessment of diverse RNA-Seq alignment solutions. <i>Nucleic Acids Research</i> , 2014, 42, e71-e71.	6.5	30
1265	Tissue-Specific RNA-Seq in Human Evoked Inflammation Identifies Blood and Adipose LincRNA Signatures of Cardiometabolic Diseases. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 902-912.	1.1	75
1266	The transcriptional co-activator SND1 is a novel regulator of alternative splicing in prostate cancer cells. <i>Oncogene</i> , 2014, 33, 3794-3802.	2.6	75
1267	THEISTIC EVOLUTION IN THE POSTGENOMIC ERA. <i>Zygon</i> , 2014, 49, 829-854.	0.2	0
1268	Methods to Study Splicing from High-Throughput RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2014, 1126, 357-397.	0.4	68
1269	The splicing activator DAZAP1 integrates splicing control into MEK/Erk-regulated cell proliferation and migration. <i>Nature Communications</i> , 2014, 5, 3078.	5.8	55
1270	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014, 5, 3650.	5.8	131
1271	Defining a personal, allele-specific, and single-molecule long-read transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9869-9874.	3.3	259
1272	ProteoAnnotator â€œ Open source proteogenomics annotation software supporting PSI standards. <i>Proteomics</i> , 2014, 14, 2731-2741.	1.3	38
1273	CRE promoter sites modulate alternative splicing via p300-mediated histone acetylation. <i>RNA Biology</i> , 2014, 11, 865-874.	1.5	18
1274	Evolution of Gene Structural Complexity: An Alternative-Splicing-Based Model Accounts for Intron-Containing Retrogenes. <i>Plant Physiology</i> , 2014, 165, 412-423.	2.3	19
1275	The genetic basis for individual differences in mRNA splicing and APOBEC1 editing activity in murine macrophages. <i>Genome Research</i> , 2014, 24, 377-389.	2.4	13
1276	Correcting for Differential Transcript Coverage Reveals a Strong Relationship between Alternative Splicing and Organism Complexity. <i>Molecular Biology and Evolution</i> , 2014, 31, 1402-1413.	3.5	124

#	ARTICLE	IF	CITATIONS
1277	Comparative Analysis of Human Tissue Interactomes Reveals Factors Leading to Tissue-Specific Manifestation of Hereditary Diseases. <i>PLoS Computational Biology</i> , 2014, 10, e1003632.	1.5	70
1278	Effects of RNAi-Mediated Knockdown of Histone Methyltransferases on the Sex-Specific mRNA Expression of Imp in the Silkworm <i>Bombyx mori</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 6772-6796.	1.8	7
1279	Regulation of mRNA Abundance by Polypyrimidine Tract-Binding Protein-Controlled Alternate 5â€² Splice Site Choice. <i>PLoS Genetics</i> , 2014, 10, e1004771.	1.5	22
1280	Bioinformatic Approaches to Increase Proteome Coverage. <i>Comprehensive Analytical Chemistry</i> , 2014, , 385-419.	0.7	1
1281	RNA-dependent dynamic histone acetylation regulates MCL1 alternative splicing. <i>Nucleic Acids Research</i> , 2014, 42, 1656-1670.	6.5	46
1282	De Novo Prediction of PTBP1 Binding and Splicing Targets Reveals Unexpected Features of Its RNA Recognition and Function. <i>PLoS Computational Biology</i> , 2014, 10, e1003442.	1.5	56
1283	Gene self-control: when pre-mRNA splicing variants become competing endogenous RNAs. <i>Frontiers in Genetics</i> , 2014, 5, 405.	1.1	1
1284	Abscisic Acid (ABA) Regulation of Arabidopsis SR Protein Gene Expression. <i>International Journal of Molecular Sciences</i> , 2014, 15, 17541-17564.	1.8	57
1285	Multifunctional RNA Processing Protein SRm160 Induces Apoptosis and Regulates Eye and Genital Development in <i>Drosophila</i> . <i>Genetics</i> , 2014, 197, 1251-1265.	1.2	11
1286	Evolution of Chloroplast Transcript Processing in Plasmodium and Its Chromerid Algal Relatives. <i>PLoS Genetics</i> , 2014, 10, e1004008.	1.5	18
1287	Evolutionary Interrogation of Human Biology in Well-Annotated Genomic Framework of Rhesus Macaque. <i>Molecular Biology and Evolution</i> , 2014, 31, 1309-1324.	3.5	35
1288	Alternative Splicing in Plant Immunity. <i>International Journal of Molecular Sciences</i> , 2014, 15, 10424-10445.	1.8	106
1289	Current Challenges Towards the Development of a Blood Test for Parkinsonâ€™s Disease. <i>Diagnostics</i> , 2014, 4, 153-164.	1.3	10
1290	A Targeted Oligonucleotide Enhancer of SMN2 Exon 7 Splicing Forms Competing Quadruplex and Protein Complexes in Functional Conditions. <i>Cell Reports</i> , 2014, 9, 193-205.	2.9	12
1291	The Supraspliceosome â€” A Multi-Task Machine for Regulated Pre-mRNA Processing in the Cell Nucleus. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 113-122.	1.9	28
1292	Identification of genetic variants associated with alternative splicing using sQTLseeker. <i>Nature Communications</i> , 2014, 5, 4698.	5.8	121
1293	Disrupted auto-regulation of the spliceosomal gene SNRPB causes cerebroâ€”costoâ€”mandibular syndrome. <i>Nature Communications</i> , 2014, 5, 4483.	5.8	57
1294	High-Resolution Sequencing and Modeling Identifies Distinct Dynamic RNA Regulatory Strategies. <i>Cell</i> , 2014, 159, 1698-1710.	13.5	196

#	ARTICLE	IF	CITATIONS
1295	Differential Expression Analysis on RNA-Seq Count Data Based on Penalized Matrix Decomposition. IEEE Transactions on Nanobioscience, 2014, 13, 12-18.	2.2	12
1296	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. Cell, 2014, 159, 1511-1523.	13.5	546
1297	Normal and aberrant splicing of LMNA. Journal of Medical Genetics, 2014, 51, 215-223.	1.5	30
1298	Intragenic Controls Utilizing Radiation-Induced Alternative Transcript Regions Improves Gene Expression Biodosimetry. Radiation Research, 2014, 181, 314.	0.7	10
1299	Nuclear ARVCF Protein Binds Splicing Factors and Contributes to the Regulation of Alternative Splicing. Journal of Biological Chemistry, 2014, 289, 12421-12434.	1.6	9
1300	LaSSO, a strategy for genome-wide mapping of intronic lariats and branch points using RNA-seq. Genome Research, 2014, 24, 1169-1179.	2.4	64
1301	Eukaryotic Flagella: Variations in Form, Function, and Composition during Evolution. BioScience, 2014, 64, 1103-1114.	2.2	28
1302	3' UTRs take a long shot in the brain. BioEssays, 2014, 36, 39-45.	1.2	29
1303	Pre-mRNA splicing is facilitated by an optimal RNA polymerase II elongation rate. Genes and Development, 2014, 28, 2663-2676.	2.7	250
1304	Global Dissection of Alternative Splicing in Paleopolyploid Soybean. Plant Cell, 2014, 26, 996-1008.	3.1	273
1305	Brain-specific noncoding RNAs are likely to originate in repeats and may play a role in up-regulating genes in cis. International Journal of Biochemistry and Cell Biology, 2014, 54, 331-337.	1.2	20
1306	Modulation of alternative splicing by expression of small nuclear ribonucleoprotein polypeptide N. FEBS Journal, 2014, 281, 5194-5207.	2.2	17
1307	Should pharmacologists care about alternative splicing? IUPHAR Review 4. British Journal of Pharmacology, 2014, 171, 1231-1240.	2.7	7
1308	A bioinformatic and computational study of myosin phosphatase subunit diversity. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2014, 307, R256-R270.	0.9	21
1309	rMATS: Robust and flexible detection of differential alternative splicing from replicate RNA-Seq data. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5593-601.	3.3	1,774
1310	Alternative-splicing-mediated gene expression. Physical Review E, 2014, 89, 012713.	0.8	29
1311	SpliceProt: A protein sequence repository of predicted human splice variants. Proteomics, 2014, 14, 181-185.	1.3	16
1312	Cytoplasmic intron retention, function, splicing, and the sentinel <i>scp</i> RNA hypothesis. Wiley Interdisciplinary Reviews RNA, 2014, 5, 223-230.	3.2	50

#	ARTICLE	IF	CITATIONS
1313	Identification of distinct miRNA target regulation between breast cancer molecular subtypes using AGO2-PAR-CLIP and patient datasets. <i>Genome Biology</i> , 2014, 15, R9.	13.9	63
1314	A Comprehensive Transcriptomic Analysis of Infant and Adult Mouse Ovary. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 239-248.	3.0	20
1315	The SERRATE protein is involved in alternative splicing in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2014, 42, 1224-1244.	6.5	94
1316	Differential Transcriptional and Posttranslational Transcription Factor 7-Like 2 Regulation Among Nondiabetic Individuals and Type 2 Diabetic Patients. <i>Molecular Endocrinology</i> , 2014, 28, 1558-1570.	3.7	9
1317	Transcriptome de novo assembly and differentially expressed genes related to cytoplasmic male sterility in kenaf (<i>Hibiscus cannabinus</i> L.). <i>Molecular Breeding</i> , 2014, 34, 1879-1891.	1.0	33
1318	Exon expression QTL (eeQTL) analysis highlights distant genomic variations associated with splicing regulation. <i>Quantitative Biology</i> , 2014, 2, 71-79.	0.3	6
1319	Genes with a large intronic burden show greater evolutionary conservation on the protein level. <i>BMC Evolutionary Biology</i> , 2014, 14, 50.	3.2	63
1320	Genome-wide analysis of alternative splicing in <i>Volvox carteri</i> . <i>BMC Genomics</i> , 2014, 15, 1117.	1.2	37
1321	Evolutionarily emerged G tracts between the polypyrimidine tract and 3' AG are splicing silencers enriched in genes involved in cancer. <i>BMC Genomics</i> , 2014, 15, 1143.	1.2	25
1322	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. <i>BMC Genomics</i> , 2014, 15, 1148.	1.2	13
1323	IUTA: a tool for effectively detecting differential isoform usage from RNA-Seq data. <i>BMC Genomics</i> , 2014, 15, 862.	1.2	21
1324	Next generation sequencing and de novo transcriptomics to study gene evolution. <i>Plant Methods</i> , 2014, 10, 34.	1.9	23
1325	Computational extraction of a neural molecular network through alternative splicing. <i>BMC Research Notes</i> , 2014, 7, 934.	0.6	5
1326	Proteomic Analysis Reveals CACN-1 Is a Component of the Spliceosome in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1555-1564.	0.8	12
1327	High-resolution functional annotation of human transcriptome: predicting isoform functions by a novel multiple instance-based label propagation method. <i>Nucleic Acids Research</i> , 2014, 42, e39-e39.	6.5	45
1328	PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. <i>Nucleic Acids Research</i> , 2014, 42, e20-e20.	6.5	33
1329	Complexities in Quantitative Systems Analysis of Signaling Networks. , 2014, , 65-88.		2
1330	ARH-seq: identification of differential splicing in RNA-seq data. <i>Nucleic Acids Research</i> , 2014, 42, e110-e110.	6.5	10

#	ARTICLE	IF	CITATIONS
1331	Mammalian COPII Coat Component SEC24C Is Required for Embryonic Development in Mice. <i>Journal of Biological Chemistry</i> , 2014, 289, 20858-20870.	1.6	28
1332	Reproducible probe-level analysis of the Affymetrix Exon 1.0 ST array with R/Bioconductor. <i>Briefings in Bioinformatics</i> , 2014, 15, 519-533.	3.2	10
1333	Detection of Alternative Splicing During Epithelial-Mesenchymal Transition. <i>Journal of Visualized Experiments</i> , 2014, , e51845.	0.2	2
1334	Identification by high-throughput imaging of the histone methyltransferase EHMT2 as an epigenetic regulator of VEGFA alternative splicing. <i>Nucleic Acids Research</i> , 2014, 42, 13662-13673.	6.5	44
1335	MBNL proteins and their target RNAs, interaction and splicing regulation. <i>Nucleic Acids Research</i> , 2014, 42, 10873-10887.	6.5	168
1336	Elucidating the Genotype-Phenotype Relationships and Network Perturbations of Human Shared and Specific Disease Genes from an Evolutionary Perspective. <i>Genome Biology and Evolution</i> , 2014, 6, 2741-2753.	1.1	6
1337	An efficient algorithm for accurate computation of the Dirichlet-multinomial log-likelihood function. <i>Bioinformatics</i> , 2014, 30, 1547-1554.	1.8	22
1338	A novel human aquaporin-4 splice variant exhibits a dominant-negative activity: a new mechanism to regulate water permeability. <i>Molecular Biology of the Cell</i> , 2014, 25, 470-480.	0.9	36
1339	RNA-Binding Proteins in Heart Development. <i>Advances in Experimental Medicine and Biology</i> , 2014, 825, 389-429.	0.8	17
1340	Evolutionary Conservation and Expression of Human RNA-Binding Proteins and Their Role in Human Genetic Disease. <i>Advances in Experimental Medicine and Biology</i> , 2014, 825, 1-55.	0.8	119
1341	Computational analysis reveals a correlation of exon-skipping events with splicing, transcription and epigenetic factors. <i>Nucleic Acids Research</i> , 2014, 42, 2856-2869.	6.5	26
1342	Bioinformatics Tools for Next-Generation RNA Sequencing Analysis. , 2014, , 371-391.		2
1343	Evolution at protein ends: major contribution of alternative transcription initiation and termination to the transcriptome and proteome diversity in mammals. <i>Nucleic Acids Research</i> , 2014, 42, 7132-7144.	6.5	40
1344	RNA-Binding Proteins in Regulation of Alternative Cleavage and Polyadenylation. <i>Advances in Experimental Medicine and Biology</i> , 2014, 825, 97-127.	0.8	45
1345	Alternative Splicing Generates Different Parkin Protein Isoforms: Evidences in Human, Rat, and Mouse Brain. <i>BioMed Research International</i> , 2014, 2014, 1-14.	0.9	24
1346	Unraveling RNA-mediated networks: new insights from new technologies. <i>Biological Chemistry</i> , 2014, 395, 51-60.	1.2	1
1347	Muscleblind-like 1 activates insulin receptor exon 11 inclusion by enhancing U2AF65 binding and splicing of the upstream intron. <i>Nucleic Acids Research</i> , 2014, 42, 1893-1903.	6.5	36
1348	Regulation of BCL-X splicing reveals a role for the polypyrimidine tract binding protein (PTBP1/hnRNP I) in alternative 5' splice site selection. <i>Nucleic Acids Research</i> , 2014, 42, 12070-12081.	6.5	65

#	ARTICLE	IF	CITATIONS
1349	Comprehensive annotation of splice junctions supports pervasive alternative splicing at the BRCA1 locus: a report from the ENIGMA consortium. <i>Human Molecular Genetics</i> , 2014, 23, 3666-3680.	1.4	96
1350	Structure and evolution of the spliceosomal peptidyl-prolyl<i>cis</i>-<i>trans</i>-isomerase Cwc27. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3110-3123.	2.5	19
1351	Preferential star strand biogenesis of pre-miR-24 targets PKC α and suppresses cell survival in MCF7 breast cancer cells. <i>Molecular Carcinogenesis</i> , 2014, 53, 38-48.	1.3	45
1352	In silico to in vivo splicing analysis using splicing code models. <i>Methods</i> , 2014, 67, 3-12.	1.9	14
1353	Viral miRNA targeting of bicistronic and polycistronic transcripts. <i>Current Opinion in Virology</i> , 2014, 7, 66-72.	2.6	12
1354	A Comprehensive Analysis of CXCL12 Isoforms in Breast Cancer ^{1,2} . <i>Translational Oncology</i> , 2014, 7, 429-438.	1.7	33
1355	Five novel variants of GPR103 and their expression in different tissues of goose (<i>Anser cygnoides</i>). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2014, 171, 18-25.	0.7	2
1356	Identification of splice variants, expression analysis and single nucleotide polymorphisms of the PRMT2 gene in dairy cattle. <i>Gene</i> , 2014, 539, 37-43.	1.0	5
1357	Phosphoproteomics Screen Reveals Akt Isoform-Specific Signals Linking RNA Processing to Lung Cancer. <i>Molecular Cell</i> , 2014, 53, 577-590.	4.5	119
1358	The Potential of Targeting Splicing for Cancer Therapy. <i>Cancer Drug Discovery and Development</i> , 2014, , 313-336.	0.2	1
1360	Transcriptome sequencing of sea cucumber (<i>Apostichopus japonicus</i>) and the identification of gene-associated markers. <i>Molecular Ecology Resources</i> , 2014, 14, 127-138.	2.2	69
1361	Imaging dynamic interactions between spliceosomal proteins and pre-mRNA in living cells. <i>Methods</i> , 2014, 65, 359-366.	1.9	10
1362	Polyadenylation. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	0
1363	Evolution of splicing regulatory networks in <i>Drosophila</i> . <i>Genome Research</i> , 2014, 24, 786-796.	2.4	34
1364	Differential gene expression identified by RNA-Seq and qPCR in two sizes of pearl oyster (<i>Pinctada</i>) Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	1.0	62
1365	Fabrication of Reduced Graphene Oxide (RGO)/Co ₃ O ₄ Nanohybrid Particles and a RGO/Co ₃ O ₄ /Poly(vinylidene fluoride) Composite with Enhanced Wave-absorption Properties. <i>ChemPlusChem</i> , 2014, 79, 375-381.	1.3	76
1366	HITS-CLIP and Integrative Modeling Define the Rbfox Splicing-Regulatory Network Linked to Brain Development and Autism. <i>Cell Reports</i> , 2014, 6, 1139-1152.	2.9	326
1367	From single-cell to cell-pool transcriptomes: Stochasticity in gene expression and RNA splicing. <i>Genome Research</i> , 2014, 24, 496-510.	2.4	470

#	ARTICLE	IF	CITATIONS
1368	Rbfox2 controls autoregulation in RNA-binding protein networks. <i>Genes and Development</i> , 2014, 28, 637-651.	2.7	114
1369	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. <i>Nature Communications</i> , 2014, 5, 3230.	5.8	316
1370	Combined analysis of exon splicing and genome wide polymorphism data predict schizophrenia risk loci. <i>Journal of Psychiatric Research</i> , 2014, 52, 44-49.	1.5	37
1371	Diversity and dynamics of the <i>Drosophila</i> transcriptome. <i>Nature</i> , 2014, 512, 393-399.	13.7	647
1372	Phosphorylation of SRSF1 by SRPK1 regulates alternative splicing of tumor-related Rac1b in colorectal cells. <i>Rna</i> , 2014, 20, 474-482.	1.6	83
1373	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. <i>Human Molecular Genetics</i> , 2014, 23, 2198-2209.	1.4	36
1374	The RNA-binding protein hnRNPLL induces a T cell alternative splicing program delineated by differential intron retention in polyadenylated RNA. <i>Genome Biology</i> , 2014, 15, R26.	13.9	48
1375	Incorporating significant amino acid pairs and protein domains to predict RNA splicing-related proteins with functional roles. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 49-60.	1.3	2
1376	A survey of software for genome-wide discovery of differential splicing in RNA-Seq data. <i>Human Genomics</i> , 2014, 8, 3.	1.4	66
1377	A dedicated microarray for in-depth analysis of pre-mRNA splicing events: application to the study of genes involved in the response to targeted anticancer therapies. <i>Molecular Cancer</i> , 2014, 13, 9.	7.9	6
1378	Emerging role for RNA binding motif protein 4 in the development of brown adipocytes. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 769-779.	1.9	27
1379	Reciprocal regulatory links between cotranscriptional splicing and chromatin. <i>Seminars in Cell and Developmental Biology</i> , 2014, 32, 2-10.	2.3	27
1380	An expanding universe of the non-coding genome in cancer biology. <i>Carcinogenesis</i> , 2014, 35, 1209-1216.	1.3	37
1381	A change-point model for identifying 3' UTR switching by next-generation RNA sequencing. <i>Bioinformatics</i> , 2014, 30, 2162-2170.	1.8	43
1382	RRP1B is a metastasis modifier that regulates the expression of alternative mRNA isoforms through interactions with SRSF1. <i>Oncogene</i> , 2014, 33, 1818-1827.	2.6	18
1383	Entering the era of single-cell transcriptomics in biology and medicine. <i>Nature Methods</i> , 2014, 11, 22-24.	9.0	221
1385	Quality control of mRNP biogenesis: Networking at the transcription site. <i>Seminars in Cell and Developmental Biology</i> , 2014, 32, 37-46.	2.3	29
1386	Regulation of alternative splicing by local histone modifications: potential roles for RNA-guided mechanisms. <i>Nucleic Acids Research</i> , 2014, 42, 701-713.	6.5	201

#	ARTICLE	IF	CITATIONS
1387	Post-transcriptional regulation of gene expression in innate immunity. <i>Nature Reviews Immunology</i> , 2014, 14, 361-376.	10.6	301
1388	Inhibition of SULT4A1 Expression Induces Up-Regulation of Phototransduction Gene Expression in 72-Hour Postfertilization Zebrafish Larvae. <i>Drug Metabolism and Disposition</i> , 2014, 42, 947-953.	1.7	8
1389	Ribosome-omics of the human ribosome. <i>Rna</i> , 2014, 20, 1004-1013.	1.6	73
1390	Identification of the RNA recognition element of the RBPMS family of RNA-binding proteins and their transcriptome-wide mRNA targets. <i>Rna</i> , 2014, 20, 1090-1102.	1.6	64
1391	Alternative Splicing of MBD2 Supports Self-Renewal in Human Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2014, 15, 92-101.	5.2	93
1392	Loss of nuclear TDP43 in amyotrophic lateral sclerosis (ALS) causes altered expression of splicing machinery and widespread dysregulation of RNA splicing in motor neurones. <i>Neuropathology and Applied Neurobiology</i> , 2014, 40, 670-685.	1.8	98
1393	Exon 9 skipping of apoptotic caspase-2 pre-mRNA is promoted by SRSF3 through interaction with exon 8. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 25-32.	0.9	25
1394	Endothelial, epithelial, and fibroblast cells exhibit specific splicing programs independently of their tissue of origin. <i>Genome Research</i> , 2014, 24, 511-521.	2.4	61
1395	Hallmarks of alternative splicing in cancer. <i>Oncogene</i> , 2014, 33, 5311-5318.	2.6	569
1396	Epithelial splicing regulatory protein 1 is a favorable prognostic factor in pancreatic cancer that attenuates pancreatic metastases. <i>Oncogene</i> , 2014, 33, 4485-4495.	2.6	82
1397	Joint estimation of isoform expression and isoform-specific read distribution using multisample RNA-Seq data. <i>Bioinformatics</i> , 2014, 30, 506-513.	1.8	20
1398	Full-length RNA-seq from single cells using Smart-seq2. <i>Nature Protocols</i> , 2014, 9, 171-181.	5.5	3,308
1399	Sequencing depth and coverage: key considerations in genomic analyses. <i>Nature Reviews Genetics</i> , 2014, 15, 121-132.	7.7	1,116
1400	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. <i>Genome Research</i> , 2014, 24, 14-24.	2.4	547
1401	Calcium-mediated histone modifications regulate alternative splicing in cardiomyocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4920-8.	3.3	51
1402	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	2.4	175
1403	A new multi-level thresholding algorithm for finding peaks in ChIP-Seq data. , 2014, , .		0
1404	Exon skipping event prediction based on histone modifications. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 241-249.	2.2	10

#	ARTICLE	IF	CITATIONS
1405	Methods for Processing High-Throughput RNA Sequencing Data. Cold Spring Harbor Protocols, 2014, 2014, pdb.top083352.	0.2	6
1407	The functional consequences of intron retention: Alternative splicing coupled to <scp>NMD</scp> as a regulator of gene expression. BioEssays, 2014, 36, 236-243.	1.2	190
1408	Splicing factor TRA2B is required for neural progenitor survival. Journal of Comparative Neurology, 2014, 522, 372-392.	0.9	31
1409	Neuronal <scp>RNA</scp>â€binding proteins in health and disease. Wiley Interdisciplinary Reviews RNA, 2014, 5, 565-576.	3.2	32
1410	<scp>mRNA</scp> 3â€end processing: A tale of the tail reaches the clinic. EMBO Molecular Medicine, 2014, 6, 16-26.	3.3	38
1411	Argonaute-1 binds transcriptional enhancers and controls constitutive and alternative splicing in human cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15622-15629.	3.3	86
1412	Building Robust Transcriptomes with Master Splicing Factors. Cell, 2014, 159, 487-498.	13.5	146
1413	A post-transcriptional mechanism regulates calpastatin expression in bovine skeletal muscle1. Journal of Animal Science, 2014, 92, 443-455.	0.2	20
1414	Exon identity crisis: disease-causing mutations that disrupt the splicing code. Genome Biology, 2014, 15, 201.	13.9	105
1415	Methods for comprehensive experimental identification of RNA-protein interactions. Genome Biology, 2014, 15, 203.	13.9	140
1416	Discovering the complexity of the metazoan transcriptome. Genome Biology, 2014, 15, 112.	13.9	7
1417	Alternative splicing in<i>Drosophila</i> neuronal development. Journal of Neurogenetics, 2014, 28, 199-215.	0.6	18
1418	Cell-Specific Alternative Splicing of Drosophila Dscam2 Is Crucial for Proper Neuronal Wiring. Neuron, 2014, 83, 1376-1388.	3.8	36
1420	Rbfox2-Coordinated Alternative Splicing of Mef2d and Rock2 Controls Myoblast Fusion during Myogenesis. Molecular Cell, 2014, 55, 592-603.	4.5	104
1421	Leveraging the complementary nature of RNAâ€Seq and shotgun proteomics data. Proteomics, 2014, 14, 2676-2687.	1.3	67
1422	Coexpression and Cosplicing Network Approaches for the Study of Mammalian Brain Transcriptomes. International Review of Neurobiology, 2014, 116, 73-93.	0.9	12
1424	Discovery of Novel Genes and Gene Isoforms by Integrating Transcriptomic and Proteomic Profiling from Mouse Liver. Journal of Proteome Research, 2014, 13, 2409-2419.	1.8	25
1425	Genome and transcriptome of the porcine whipworm Trichuris suis. Nature Genetics, 2014, 46, 701-706.	9.4	93

#	ARTICLE	IF	CITATIONS
1426	Aberrant transcriptional regulation could explain phenotypic variability in autosomal recessive polycystic kidney disease. <i>Journal of Molecular Medicine</i> , 2014, 92, 1011-1014.	1.7	2
1427	Identification and molecular characterization of a novel splice variant of human 5- lipoxygenase gene. <i>Molecular Biology Reports</i> , 2014, 41, 8255-8260.	1.0	0
1428	Genetic variability in the regulation of gene expression in ten regions of the human brain. <i>Nature Neuroscience</i> , 2014, 17, 1418-1428.	7.1	620
1429	Widespread intron retention in mammals functionally tunes transcriptomes. <i>Genome Research</i> , 2014, 24, 1774-1786.	2.4	554
1430	Nodes occupying central positions in human tissue specific PPI networks are enriched with many splice variants. <i>Proteomics</i> , 2014, 14, 2242-2248.	1.3	9
1431	Human Proteins with Target Sites of Multiple Post-Translational Modification Types Are More Prone to Be Involved in Disease. <i>Journal of Proteome Research</i> , 2014, 13, 2735-2748.	1.8	31
1432	Modulation of p53 ^{Î²} and p53 ^{Î³} expression by regulating the alternative splicing of TP53 gene modifies cellular response. <i>Cell Death and Differentiation</i> , 2014, 21, 1377-1387.	5.0	80
1433	Regulation of gene expression through production of unstable mRNA isoforms. <i>Biochemical Society Transactions</i> , 2014, 42, 1196-1205.	1.6	23
1434	BCLAF1 and its splicing regulator SRSF10 regulate the tumorigenic potential of colon cancer cells. <i>Nature Communications</i> , 2014, 5, 4581.	5.8	133
1435	An RNA-Sequencing Transcriptome and Splicing Database of Glia, Neurons, and Vascular Cells of the Cerebral Cortex. <i>Journal of Neuroscience</i> , 2014, 34, 11929-11947.	1.7	4,119
1436	Incorporating alternative splicing and mRNA editing into the genetic analysis of complex traits. <i>BioEssays</i> , 2014, 36, 1032-1040.	1.2	4
1437	Coordinated regulation of transcription and alternative splicing by the thyroid hormone receptor and its associating coregulators. <i>Biochemical and Biophysical Research Communications</i> , 2014, 451, 24-29.	1.0	5
1438	RNA-Sequencing: A tool to explore new frontiers in animal genetics. <i>Livestock Science</i> , 2014, 166, 206-216.	0.6	53
1439	RBFOX and SUP-12 sandwich a G base to cooperatively regulate tissue-specific splicing. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 778-786.	3.6	27
1440	Evolutionary dynamics of coding and non-coding transcriptomes. <i>Nature Reviews Genetics</i> , 2014, 15, 734-748.	7.7	209
1441	Origin of Spliceosomal Introns and Alternative Splicing. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016071-a016071.	2.3	112
1442	RNA binding proteins: a common denominator of neuronal function and dysfunction. <i>Neuroscience Bulletin</i> , 2014, 30, 610-626.	1.5	36
1443	Deep sequencing reveals a novel class of bidirectional promoters associated with neuronal genes. <i>BMC Genomics</i> , 2014, 15, 457.	1.2	20

#	ARTICLE	IF	CITATIONS
1444	Transcriptome instability as a molecular pan-cancer characteristic of carcinomas. BMC Genomics, 2014, 15, 672.	1.2	15
1445	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. BMC Genomics, 2014, 15, 703.	1.2	74
1446	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. BMC Genomics, 2014, 15, S7.	1.2	15
1447	RNA-seq analyses of multiple meristems of soybean: novel and alternative transcripts, evolutionary and functional implications. BMC Plant Biology, 2014, 14, 169.	1.6	229
1448	Translational selection in human: more pronounced in housekeeping genes. Biology Direct, 2014, 9, 17.	1.9	45
1449	A mutation in a splicing factor that causes retinitis pigmentosa has a transcriptome-wide effect on mRNA splicing. BMC Research Notes, 2014, 7, 401.	0.6	6
1450	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
1451	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. Nature Biotechnology, 2014, 32, 915-925.	9.4	217
1452	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	9.4	883
1453	Characterization of human gene locus CYR1: a complex multi-transcript system. Molecular Biology Reports, 2014, 41, 6025-6038.	1.0	7
1454	Single-cell analysis of the transcriptome and its application in the characterization of stem cells and early embryos. Cellular and Molecular Life Sciences, 2014, 71, 2707-2715.	2.4	31
1455	Transcriptome dynamics of a desert poplar (<i>Populus pruinosa</i>) in response to continuous salinity stress. Plant Cell Reports, 2014, 33, 1565-1579.	2.8	42
1456	Genomics of alternative splicing: evolution, development and pathophysiology. Human Genetics, 2014, 133, 679-687.	1.8	103
1457	RNAmotifs: prediction of multivalent RNA motifs that control alternative splicing. Genome Biology, 2014, 15, R20.	13.9	49
1458	Alternative splicing regulates vesicular trafficking genes in cardiomyocytes during postnatal heart development. Nature Communications, 2014, 5, 3603.	5.8	133
1459	The Pivotal Regulatory Landscape of RNA Modifications. Annual Review of Genomics and Human Genetics, 2014, 15, 127-150.	2.5	284
1460	SeqGSEA: a Bioconductor package for gene set enrichment analysis of RNA-Seq data integrating differential expression and splicing. Bioinformatics, 2014, 30, 1777-1779.	1.8	62
1461	Visualizing cellular machines with colocalization single molecule microscopy. Chemical Society Reviews, 2014, 43, 1189-1200.	18.7	31

#	ARTICLE	IF	CITATIONS
1462	Spliceosomal Pre-mRNA Splicing. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	6
1463	Hypoxia Regulates Alternative Splicing of HIF and non-HIF Target Genes. <i>Molecular Cancer Research</i> , 2014, 12, 1233-1243.	1.5	46
1464	Single Molecule Fluorescence Approaches Shed Light on Intracellular RNAs. <i>Chemical Reviews</i> , 2014, 114, 3224-3265.	23.0	73
1465	Isolation, characterization, and expression analysis of FGF5 isoforms in cashmere goat. <i>Small Ruminant Research</i> , 2014, 116, 111-117.	0.6	8
1466	Developmental transcriptome analysis of human erythropoiesis. <i>Human Molecular Genetics</i> , 2014, 23, 4528-4542.	1.4	45
1467	Molecular characterization, tissue distribution, and expression of two ovarian Dicer isoforms during follicle development in goose (<i>Anser cygnoides</i>). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2014, 170, 33-41.	0.7	15
1468	Statistical Analysis of Next Generation Sequencing Data. , 2014, , .		20
1469	The human skeletal muscle transcriptome: sex differences, alternative splicing, and tissue homogeneity assessed with RNA sequencing. <i>FASEB Journal</i> , 2014, 28, 4571-4581.	0.2	68
1470	Regulation of alternative splicing of tau exon 10. <i>Neuroscience Bulletin</i> , 2014, 30, 367-377.	1.5	80
1471	DAFS: a data-adaptive flag method for RNA-sequencing data to differentiate genes with low and high expression. <i>BMC Bioinformatics</i> , 2014, 15, 92.	1.2	32
1472	Transcriptome analyses and differential gene expression in a non-model fish species with alternative mating tactics. <i>BMC Genomics</i> , 2014, 15, 167.	1.2	76
1473	Severe hypoxia exerts parallel and cell-specific regulation of gene expression and alternative splicing in human mesenchymal stem cells. <i>BMC Genomics</i> , 2014, 15, 303.	1.2	63
1474	A house finch (<i>Haemorhous mexicanus</i>) spleen transcriptome reveals intra- and interspecific patterns of gene expression, alternative splicing and genetic diversity in passerines. <i>BMC Genomics</i> , 2014, 15, 305.	1.2	12
1475	Transcriptome differences between two sister desert poplar species under salt stress. <i>BMC Genomics</i> , 2014, 15, 337.	1.2	50
1476	IRF-1 regulates alternative mRNA splicing of carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1) in breast epithelial cells generating an immunoreceptor tyrosine-based inhibition motif (ITIM) containing isoform. <i>Molecular Cancer</i> , 2014, 13, 64.	7.9	22
1477	The global landscape of intron retentions in lung adenocarcinoma. <i>BMC Medical Genomics</i> , 2014, 7, 15.	0.7	32
1478	Understanding Complex Transcriptome Dynamics in Schizophrenia and Other Neurological Diseases Using RNA Sequencing. <i>International Review of Neurobiology</i> , 2014, 116, 127-152.	0.9	5
1479	Identification of a new non-coding exon and haplotype variability in the cattle DEF103 gene. <i>Gene</i> , 2014, 551, 183-188.	1.0	2

#	ARTICLE	IF	CITATIONS
1480	Splicing in the Human Brain. <i>International Review of Neurobiology</i> , 2014, 116, 95-125.	0.9	20
1481	Digital Inventory of Arabidopsis Transcripts Revealed by 61 RNA Sequencing Samples. <i>Plant Physiology</i> , 2014, 166, 869-878.	2.3	8
1482	Isoforms of Receptors of Fibroblast Growth Factors. <i>Journal of Cellular Physiology</i> , 2014, 229, 1887-1895.	2.0	63
1483	Genomic Profiling of Collaborative Cross Founder Mice Infected with Respiratory Viruses Reveals Novel Transcripts and Infection-Related Strain-Specific Gene and Isoform Expression. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1429-1444.	0.8	25
1484	RNA-Seq Reveals Novel Transcriptional Reorganization in Human Alcoholic Brain. <i>International Review of Neurobiology</i> , 2014, 116, 275-300.	0.9	50
1485	Networking in an Alternative Splicing World. <i>Molecular Cell</i> , 2014, 54, 903-904.	4.5	2
1487	Alternative splicing regulation of APP exon 7 by RBFOX proteins. <i>Neurochemistry International</i> , 2014, 78, 7-17.	1.9	24
1488	Membrane Patterns Carry Ontogenetic Information that is Specified Independently of DNA. <i>Biophysical Journal</i> , 2014, 106, 596a.	0.2	1
1489	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	6.0	436
1490	RNA Bind-n-Seq: Quantitative Assessment of the Sequence and Structural Binding Specificity of RNA Binding Proteins. <i>Molecular Cell</i> , 2014, 54, 887-900.	4.5	346
1491	An integrative framework identifies alternative splicing events in colorectal cancer development. <i>Molecular Oncology</i> , 2014, 8, 129-141.	2.1	43
1492	Post-transcriptional regulation of the creatine transporter gene: Functional relevance of alternative splicing. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 2070-2079.	1.1	7
1493	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 440-451.	1.2	40
1494	The control of lipid metabolism by mRNA splicing in <i>Drosophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 672-676.	1.0	18
1495	U1 small nuclear RNA variants differentially form ribonucleoprotein particles in vitro. <i>Gene</i> , 2014, 540, 11-15.	1.0	7
1496	Proteome variance differences within populations of European whitefish (<i>Coregonus lavaretus</i>) originating from contrasting salinity environments. <i>Journal of Proteomics</i> , 2014, 105, 144-150.	1.2	14
1497	Systematical identification of splicing regulatory cis-elements and cognate trans-factors. <i>Methods</i> , 2014, 65, 350-358.	1.9	29
1498	Identification of a chemical inhibitor for nuclear speckle formation: Implications for the function of nuclear speckles in regulation of alternative pre-mRNA splicing. <i>Biochemical and Biophysical Research Communications</i> , 2014, 446, 119-124.	1.0	19

#	ARTICLE	IF	CITATIONS
1499	No more non-model species: The promise of next generation sequencing for comparative immunology. <i>Developmental and Comparative Immunology</i> , 2014, 45, 56-66.	1.0	56
1500	Genome-Wide Analysis of Heat-Sensitive Alternative Splicing in <i>Physcomitrella patens</i> . <i>Plant Physiology</i> , 2014, 165, 826-840.	2.3	119
1501	The emerging era of genomic data integration for analyzing splice isoform function. <i>Trends in Genetics</i> , 2014, 30, 340-347.	2.9	82
1502	Identification of the involvement of LOXL4 in generation of keratocystic odontogenic tumors by RNA-Seq analysis. <i>International Journal of Oral Science</i> , 2014, 6, 31-38.	3.6	21
1503	Cytokine Bioassays. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	2
1504	Alternative polyadenylation in the nervous system: To what lengths will 3' UTR extensions take us?. <i>BioEssays</i> , 2014, 36, 766-777.	1.2	51
1505	Widespread Inhibition of Posttranscriptional Splicing Shapes the Cellular Transcriptome following Heat Shock. <i>Cell Reports</i> , 2014, 7, 1362-1370.	2.9	169
1506	Refinement of the spectra of exon usage by combined effects of extracellular stimulus and intracellular factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 537-545.	0.9	6
1507	Integrative analysis of many RNA-seq datasets to study alternative splicing. <i>Methods</i> , 2014, 67, 313-324.	1.9	18
1508	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140020.	2.4	21
1509	Profiling Individual Human Embryonic Stem Cells by Quantitative RT-PCR. <i>Journal of Visualized Experiments</i> , 2014, , .	0.2	3
1510	Diversity in TAF Proteomics: Consequences for Cellular Differentiation and Migration. <i>International Journal of Molecular Sciences</i> , 2014, 15, 16680-16697.	1.8	9
1512	An iteration normalization and test method for differential expression analysis of RNA-seq data. <i>BioData Mining</i> , 2014, 7, 15.	2.2	8
1513	Identification of Key Factors Regulating Self-renewal and Differentiation in EML Hematopoietic Precursor Cells by RNA-sequencing Analysis. <i>Journal of Visualized Experiments</i> , 2014, , e52104.	0.2	1
1514	Depletion of Sf3b1 impairs proliferative capacity of hematopoietic stem cells but is not sufficient to induce myelodysplasia. <i>Blood</i> , 2014, 123, 3336-3343.	0.6	36
1515	Muscleblind-like 1 (Mbnl1) regulates pre-mRNA alternative splicing during terminal erythropoiesis. <i>Blood</i> , 2014, 124, 598-610.	0.6	46
1516	A tour through the transcriptional landscape of platelets. <i>Blood</i> , 2014, 124, 493-502.	0.6	103
1518	On the complexity of Minimum Path Cover with Subpath Constraints for multi-assembly. <i>BMC Bioinformatics</i> , 2014, 15, S5.	1.2	23

#	ARTICLE	IF	CITATIONS
1519	Alternative Splicing. , 2015, , 545-556.		1
1520	Identification of alternative splicing events by RNA sequencing in early growth tomato fruits. BMC Genomics, 2015, 16, 948.	1.2	53
1521	SRSF10 Plays a Role in Myoblast Differentiation and Glucose Production via Regulation of Alternative Splicing. Cell Reports, 2015, 13, 1647-1657.	2.9	35
1522	Tracks through the genome to physiological events. Experimental Physiology, 2015, 100, 1429-1440.	0.9	2
1523	Identification and Characterization of Aberrant <i>GAA</i> Pre-mRNA Splicing in Pompe Disease Using a Generic Approach. Human Mutation, 2015, 36, 57-68.	1.1	28
1524	Neuronal cell-type-specific alternative splicing: A mechanism for specifying connections in the brain?. Neurogenesis (Austin, Tex), 2015, 2, e1122699.	1.5	4
1525	Identification of long noncoding <i>scn</i> RNAs dysregulated in the midbrain of human cocaine abusers. Journal of Neurochemistry, 2015, 135, 50-59.	2.1	38
1526	Profiling of alternative polyadenylation sites in luminal B breast cancer using the SAPAS method. International Journal of Molecular Medicine, 2015, 35, 39-50.	1.8	6
1527	Alternatively spliced products lacking exon 12 dominate the expression of fragile X mental retardation 1 gene in human tissues. Molecular Medicine Reports, 2015, 12, 1957-1962.	1.1	8
1528	Chromatin and genomic determinants of alternative splicing. , 2015, 2015, 345-354.		3
1529	CUG-BP1 regulates RyR1 ASI alternative splicing in skeletal muscle atrophy. Scientific Reports, 2015, 5, 16083.	1.6	15
1530	Splicing noncoding <i>scn</i> RNAs from the inside out. Wiley Interdisciplinary Reviews RNA, 2015, 6, 651-660.	3.2	45
1531	The alternative splicing factor Nova2 regulates vascular development and lumen formation. Nature Communications, 2015, 6, 8479.	5.8	50
1532	Wavelet-based genetic association analysis of functional phenotypes arising from high-throughput sequencing assays. Annals of Applied Statistics, 2015, 9, 655-686.	0.5	22
1533	Differential reduction in cardiac and liver monolysocardiolipin acyltransferase-1 and reduction in cardiac and liver tetralinoleoyl-cardiolipin in the β -subunit of trifunctional protein heterozygous knockout mice. Biochemical Journal, 2015, 471, 123-129.	1.7	14
1534	Predominant contribution of <i>cis</i> regulatory divergence in the evolution of mouse alternative splicing. Molecular Systems Biology, 2015, 11, 816.	3.2	34
1535	Regulation of HPV16 E6 and MCL1 by SF3B1 inhibitor in head and neck cancer cells. Scientific Reports, 2014, 4, 6098.	1.6	37
1536	Transcriptional profiling of macrophages derived from monocytes and iPS cells identifies a conserved response to LPS and novel alternative transcription. Scientific Reports, 2015, 5, 12524.	1.6	94

#	ARTICLE	IF	CITATIONS
1537	Evolutionary Character of Alternative Splicing in Plants. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S33716.	1.0	51
1538	Regulation of alternative splicing at the single-cell level. <i>Molecular Systems Biology</i> , 2015, 11, 845.	3.2	17
1539	Advanced Applications of RNA Sequencing and Challenges. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28991.	1.0	178
1540	Plasma proteomic analysis of active and torpid greater mouse-eared bats (<i>Myotis myotis</i>). <i>Scientific Reports</i> , 2015, 5, 16604.	1.6	11
1541	Analysis of the preferences for splice codes across tissues. <i>Protein and Cell</i> , 2015, 6, 904-907.	4.8	11
1542	Anti-metastatic outcome of isoform-specific prolactin receptor targeting in breast cancer. <i>Cancer Letters</i> , 2015, 366, 84-92.	3.2	36
1543	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	79
1544	Exploration of alternative splicing events in ten different grapevine cultivars. <i>BMC Genomics</i> , 2015, 16, 706.	1.2	21
1545	Transcriptome sequencing and analysis of major genes involved in calcium signaling pathways in pear plants (<i>Pyrus calleryana</i> Decne.). <i>BMC Genomics</i> , 2015, 16, 738.	1.2	19
1546	A polynomial delay algorithm for the enumeration of bubbles with length constraints in directed graphs. <i>Algorithms for Molecular Biology</i> , 2015, 10, 20.	0.3	2
1547	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. <i>Genome Biology</i> , 2015, 16, 236.	3.8	32
1548	Effects of oxaliplatin and oleic acid Gα-protein-derived macrophage-activating factor on murine and human microglia. <i>Journal of Neuroscience Research</i> , 2015, 93, 1364-1377.	1.3	7
1549	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	80
1550	PDEGEM: Modeling non-uniform read distribution in RNA-Seq data. <i>BMC Medical Genomics</i> , 2015, 8, S14.	0.7	1
1551	EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. <i>BMC Bioinformatics</i> , 2015, 16, 278.	1.2	18
1552	Improving RNA-Seq expression estimation by modeling isoform- and exon-specific read sequencing rate. <i>BMC Bioinformatics</i> , 2015, 16, 332.	1.2	14
1553	Alternative transcripts of the SERPINA1 gene in alpha-1 antitrypsin deficiency. <i>Journal of Translational Medicine</i> , 2015, 13, 211.	1.8	23
1554	Differential connectivity of splicing activators and repressors to the human spliceosome. <i>Genome Biology</i> , 2015, 16, 119.	13.9	33

#	ARTICLE	IF	CITATIONS
1555	Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. <i>Genome Biology</i> , 2015, 16, 156.	3.8	108
1556	Effects of SNPs and alternative splicing within HGF gene on its expression patterns in Qinchuan cattle. <i>Journal of Animal Science and Biotechnology</i> , 2015, 6, 55.	2.1	6
1557	MisoMine: a genome-scale high-resolution data portal of expression, function and networks at the splice isoform level in the mouse. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, bav045.	1.4	15
1558	Targeting MicroRNAs in Prevention and Treatment of Neurodegenerative Disorders. <i>Drug Development Research</i> , 2015, 76, 397-418.	1.4	25
1559	Mapping Splicing Quantitative Trait Loci in RNA-Seq. <i>Cancer Informatics</i> , 2015, 14s1, CIN.S24832.	0.9	7
1560	Alternative role of HuD splicing variants in neuronal differentiation. <i>Journal of Neuroscience Research</i> , 2015, 93, 399-409.	1.3	18
1561	Controlling translation via modulation of <scp>tRNA</scp> levels. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 453-470.	3.2	59
1562	Epigenetic Regulation in Heart Failure. <i>Cardiology in Review</i> , 2015, 23, 213-228.	0.6	9
1563	Alternative Splicing Signatures in RNA-seq Data: Percent Spliced in (PSI). <i>Current Protocols in Human Genetics</i> , 2015, 87, 11.16.1-11.16.14.	3.5	104
1564	Global transcriptional profiling of longissimus thoracis muscle tissue in fetal and juvenile domestic goat using <scp>RNA</scp> sequencing. <i>Animal Genetics</i> , 2015, 46, 655-665.	0.6	14
1565	Exposing the subunit diversity and modularity of protein complexes by structural mass spectrometry approaches. <i>Proteomics</i> , 2015, 15, 2777-2791.	1.3	9
1566	COMT gene locus. <i>Pain</i> , 2015, 156, 2072-2083.	2.0	28
1567	Evaluation of Commercially Available RNA Amplification Kits for RNA Sequencing Using Very Low Input Amounts of Total RNA. <i>Journal of Biomolecular Techniques</i> , 2015, 26, 4-18.	0.8	46
1568	Impacts of Alternative Splicing Events on the Differentiation of Adipocytes. <i>International Journal of Molecular Sciences</i> , 2015, 16, 22169-22189.	1.8	21
1569	Clinical Relevance of Serotonin Receptor Splice Variant Distribution in Human Colon. <i>Journal of Neurogastroenterology and Motility</i> , 2015, 21, 303-306.	0.8	1
1570	Abnormalities in Alternative Splicing of Apoptotic Genes and Cardiovascular Diseases. <i>International Journal of Molecular Sciences</i> , 2015, 16, 27171-27190.	1.8	23
1571	The consensus sequence of FAMLF alternative splice variants is overexpressed in undifferentiated hematopoietic cells. <i>Brazilian Journal of Medical and Biological Research</i> , 2015, 48, 603-609.	0.7	2
1572	The RNA Splicing Response to DNA Damage. <i>Biomolecules</i> , 2015, 5, 2935-2977.	1.8	114

#	ARTICLE	IF	CITATIONS
1573	Secretory Gene Recruitments in Vampire Bat Salivary Adaptation and Potential Convergences With Sanguivorous Leeches. <i>Frontiers in Ecology and Evolution</i> , 2015, 3, .	1.1	10
1574	Cosplicing network analysis of mammalian brain RNA-Seq data utilizing WGCNA and Mantel correlations. <i>Frontiers in Genetics</i> , 2015, 6, 174.	1.1	48
1575	Pax2/5/8 and Pax6 alternative splicing events in basal chordates and vertebrates: a focus on paired box domain. <i>Frontiers in Genetics</i> , 2015, 6, 228.	1.1	9
1576	Human Serum Amyloid A3 (SAA3) Protein, Expressed as a Fusion Protein with SAA2, Binds the Oxidized Low Density Lipoprotein Receptor. <i>PLoS ONE</i> , 2015, 10, e0118835.	1.1	21
1577	The Transcriptome of Equine Peripheral Blood Mononuclear Cells. <i>PLoS ONE</i> , 2015, 10, e0122011.	1.1	17
1578	Evaluation of Two Statistical Methods Provides Insights into the Complex Patterns of Alternative Polyadenylation Site Switching. <i>PLoS ONE</i> , 2015, 10, e0124324.	1.1	4
1579	An Iterative Leave-One-Out Approach to Outlier Detection in RNA-Seq Data. <i>PLoS ONE</i> , 2015, 10, e0125224.	1.1	29
1580	Neural Differentiation Modulates the Vertebrate Brain Specific Splicing Program. <i>PLoS ONE</i> , 2015, 10, e0125998.	1.1	10
1581	Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. <i>PLoS Computational Biology</i> , 2015, 11, e1004325.	1.5	80
1582	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. <i>PLoS Computational Biology</i> , 2015, 11, e1004393.	1.5	74
1583	Network-Based Isoform Quantification with RNA-Seq Data for Cancer Transcriptome Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004465.	1.5	17
1584	Identification of Reprogrammed Myeloid Cell Transcriptomes in NSCLC. <i>PLoS ONE</i> , 2015, 10, e0129123.	1.1	17
1585	Exploring Differentially Expressed Genes and Natural Antisense Transcripts in Sheep (<i>Ovis aries</i>) Skin with Different Wool Fiber Diameters by Digital Gene Expression Profiling. <i>PLoS ONE</i> , 2015, 10, e0129249.	1.1	19
1586	Immunological Response to Single Pathogen Challenge with Agents of the Bovine Respiratory Disease Complex: An RNA-Sequence Analysis of the Bronchial Lymph Node Transcriptome. <i>PLoS ONE</i> , 2015, 10, e0131459.	1.1	51
1587	Potential Antileukemia Effect and Structural Analyses of SRPK Inhibition by N-(2-(Piperidin-1-yl)-5-(Trifluoromethyl)Phenyl)Isonicotinamide (SRPIN340). <i>PLoS ONE</i> , 2015, 10, e0134882.	1.1	67
1588	Cwf16p Associating with the Nineteen Complex Ensures Ordered Exon Joining in Constitutive Pre-mRNA Splicing in Fission Yeast. <i>PLoS ONE</i> , 2015, 10, e0136336.	1.1	5
1589	Synaptic Effects of Munc18-1 Alternative Splicing in Excitatory Hippocampal Neurons. <i>PLoS ONE</i> , 2015, 10, e0138950.	1.1	12
1590	Functional Consequences for Apoptosis by Transcription Elongation Regulator 1 (TCERG1)-Mediated Bcl-x and Fas/CD95 Alternative Splicing. <i>PLoS ONE</i> , 2015, 10, e0139812.	1.1	10

#	ARTICLE	IF	CITATIONS
1591	Modeling Exon-Specific Bias Distribution Improves the Analysis of RNA-Seq Data. PLoS ONE, 2015, 10, e0140032.	1.1	1
1592	Role of an SNP in Alternative Splicing of Bovine NCF4 and Mastitis Susceptibility. PLoS ONE, 2015, 10, e0143705.	1.1	21
1593	Calcium Channel Ca _v 1.2 and Ca _v 1.3 Splice Isoforms - Tissue Specificity and Drug Action. Current Molecular Pharmacology, 2015, 8, 22-31.	0.7	36
1594	Global Gene Expression Profiling and Alternative Splicing Events during the Chondrogenic Differentiation of Human Cartilage Endplate-Derived Stem Cells. BioMed Research International, 2015, 2015, 1-11.	0.9	8
1595	Shaping the Arabidopsis Transcriptome through Alternative Splicing. Advances in Botany, 2015, 2015, 1-13.	3.4	11
1596	The splicing regulators Esrp1 and Esrp2 direct an epithelial splicing program essential for mammalian development. ELife, 2015, 4, .	2.8	118
1597	Expression of Caspase-1 Gene Transcript Variant mRNA in Peripheral Blood Mononuclear Cells of Patients with Primary Gout in Different TCM Syndromes. Evidence-based Complementary and Alternative Medicine, 2015, 2015, 1-9.	0.5	7
1598	The Impact of Normalization Methods on RNA-Seq Data Analysis. BioMed Research International, 2015, 2015, 1-10.	0.9	89
1599	Genome-wide profiling of polyadenylation sites reveals a link between selective polyadenylation and cancer metastasis. Human Molecular Genetics, 2015, 24, 3410-3417.	1.4	41
1600	Evolutionary Emergence of a Novel Splice Variant with an Opposite Effect on the Cell Cycle. Molecular and Cellular Biology, 2015, 35, 2203-2214.	1.1	28
1601	Coupling and Coordination in Gene Expression Processes with Pre-mRNA Splicing. International Journal of Molecular Sciences, 2015, 16, 5682-5696.	1.8	6
1602	Genome-wide analysis of alternative transcripts in human breast cancer. Breast Cancer Research and Treatment, 2015, 151, 295-307.	1.1	26
1603	Detecting differential expression from RNA-seq data with expression measurement uncertainty. Frontiers of Computer Science, 2015, 9, 652-663.	1.6	1
1604	SMN2 splice modulators enhance U1 pre-mRNA association and rescue SMA mice. Nature Chemical Biology, 2015, 11, 511-517.	3.9	341
1605	Comparative transcriptomics uncovers alternative splicing changes and signatures of selection from maize improvement. BMC Genomics, 2015, 16, 363.	1.2	33
1606	Regulation of Alternative Splicing Through Coupling with Transcription and Chromatin Structure. Annual Review of Biochemistry, 2015, 84, 165-198.	5.0	377
1607	Aberrant splicing of U12-type introns is the hallmark of ZRSR2 mutant myelodysplastic syndrome. Nature Communications, 2015, 6, 6042.	5.8	192
1608	Exon 4-encoded sequence is a major determinant of cytotoxicity of apolipoprotein L1. American Journal of Physiology - Cell Physiology, 2015, 309, C22-C37.	2.1	49

#	ARTICLE	IF	CITATIONS
1609	RNA-Seq: Improving Our Understanding of Retinal Biology and Disease. Cold Spring Harbor Perspectives in Medicine, 2015, 5, a017152.	2.9	23
1610	A serine-arginine-rich (SR) splicing factor modulates alternative splicing of over a thousand genes in <i>Toxoplasma gondii</i> . Nucleic Acids Research, 2015, 43, 4661-4675.	6.5	45
1611	Transcriptome profile of liver at different physiological stages reveals potential mode for lipid metabolism in laying hens. BMC Genomics, 2015, 16, 763.	1.2	89
1612	SR proteins control a complex network of RNA-processing events. Rna, 2015, 21, 75-92.	1.6	117
1613	Leveraging transcript quantification for fast computation of alternative splicing profiles. Rna, 2015, 21, 1521-1531.	1.6	213
1614	The Ski2-family helicase Obelus regulates Crumbs alternative splicing and cell polarity. Journal of Cell Biology, 2015, 211, 1011-1024.	2.3	7
1615	3D genome organization in health and disease: emerging opportunities in cancer translational medicine. Nucleus, 2015, 6, 382-393.	0.6	45
1616	RAX2: a genome-wide detection method of condition-associated transcription variation. Nucleic Acids Research, 2015, 43, e96-e96.	6.5	3
1617	APPRIS WebServer and WebServices. Nucleic Acids Research, 2015, 43, W455-W459.	6.5	19
1618	RNASeqel: accurate and repeat tolerant realignment of RNA-seq reads. Nucleic Acids Research, 2015, 43, e122-e122.	6.5	7
1619	IsoDOT Detects Differential RNA-Isoform Expression/Usage With Respect to a Categorical or Continuous Covariate With High Sensitivity and Specificity. Journal of the American Statistical Association, 2015, 110, 975-986.	1.8	10
1620	Biochemical identification of new proteins involved in splicing repression at the <i>Drosophila</i> P-element exonic splicing silencer. Genes and Development, 2015, 29, 2298-2311.	2.7	9
1621	Linking Genes to Cardiovascular Diseases: Gene Action and Gene-Environment Interactions. Journal of Cardiovascular Translational Research, 2015, 8, 506-527.	1.1	27
1622	Genome-wide cataloging and analysis of alternatively spliced genes in cereal crops. BMC Genomics, 2015, 16, 721.	1.2	53
1623	Alternative Splicing QTLs in European and African Populations. American Journal of Human Genetics, 2015, 97, 567-575.	2.6	55
1624	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. Cell Reports, 2015, 12, 183-189.	2.9	22
1625	Widespread intron retention diversifies most cancer transcriptomes. Genome Medicine, 2015, 7, 45.	3.6	283
1626	Deciphering targeting rules of splicing modulator compounds: case of TG003. BMC Molecular Biology, 2015, 16, 16.	3.0	22

#	ARTICLE	IF	CITATIONS
1627	Discover hidden splicing variations by mapping personal transcriptomes to personal genomes. <i>Nucleic Acids Research</i> , 2015, 43, 10612-10622.	6.5	13
1628	Transcriptome analysis of distinct <i>Lindera glauca</i> tissues revealed the differences in the unigenes related to terpenoid biosynthesis. <i>Gene</i> , 2015, 559, 22-30.	1.0	49
1629	The Alternative Splicing Regulator Tra2b Is Required for Somitogenesis and Regulates Splicing of an Inhibitory Wnt11b Isoform. <i>Cell Reports</i> , 2015, 10, 527-536.	2.9	26
1630	Vision from next generation sequencing: Multi-dimensional genome-wide analysis for producing gene regulatory networks underlying retinal development, aging and disease. <i>Progress in Retinal and Eye Research</i> , 2015, 46, 1-30.	7.3	50
1631	Expitope: a web server for epitope expression. <i>Bioinformatics</i> , 2015, 31, 1854-1856.	1.8	15
1632	Modulation of Alternative Splicing with Chemical Compounds in New Therapeutics for Human Diseases. <i>ACS Chemical Biology</i> , 2015, 10, 914-924.	1.6	39
1633	Toward defining the anatomical proteomic puzzle of the human brain: An integrative analysis. <i>Proteomics - Clinical Applications</i> , 2015, 9, 796-807.	0.8	13
1634	Comparative genomics reveals tissue-specific regulation of prolactin receptor gene expression. <i>Journal of Molecular Endocrinology</i> , 2015, 54, 1-15.	1.1	23
1635	Developmental insights into the pathology of and therapeutic strategies for DM1: Back to the basics. <i>Developmental Dynamics</i> , 2015, 244, 377-390.	0.8	60
1636	The RNA-binding protein Rbfox1 regulates splicing required for skeletal muscle structure and function. <i>Human Molecular Genetics</i> , 2015, 24, 2360-2374.	1.4	55
1637	Identification of common genetic variants controlling transcript isoform variation in human whole blood. <i>Nature Genetics</i> , 2015, 47, 345-352.	9.4	103
1638	StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. <i>Nature Biotechnology</i> , 2015, 33, 290-295.	9.4	8,385
1639	Post-transcriptional regulation of long noncoding RNAs in cancer. <i>Tumor Biology</i> , 2015, 36, 503-513.	0.8	70
1640	Genome-Wide Analysis of Alternative Splicing Landscapes Modulated during Plant-Virus Interactions in <i>Brachypodium distachyon</i> . <i>Plant Cell</i> , 2015, 27, 71-85.	3.1	145
1641	Functional roles of alternative splicing factors in human disease. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 311-326.	3.2	120
1642	Prp40 pre-mRNA processing factor 40 homolog B (PRPF40B) associates with SF1 and U2AF65 and modulates alternative pre-mRNA splicing in vivo. <i>Rna</i> , 2015, 21, 438-457.	1.6	36
1643	Rbfox proteins regulate tissue-specific alternative splicing of <i>Mef2D</i> required for muscle differentiation. <i>Journal of Cell Science</i> , 2015, 128, 631-7.	1.2	41
1644	Differential Recruitment of Splice Variants from SR Pre-mRNAs to Polysomes During Development and in Response to Stresses. <i>Plant and Cell Physiology</i> , 2015, 56, 421-427.	1.5	24

#	ARTICLE	IF	CITATIONS
1645	Nuclear matrix protein Matrin3 regulates alternative splicing and forms overlapping regulatory networks with <sc>PTB</sc>. EMBO Journal, 2015, 34, 653-668.	3.5	124
1646	Functional characterisation of an intron retaining K⁺ transporter of barley reveals intron-mediated alternate splicing. Plant Biology, 2015, 17, 840-851.	1.8	9
1647	RNA Bioinformatics. Methods in Molecular Biology, 2015, , .	0.4	3
1648	First insights into the giant panda (<i><sc>A</sc>iluropoda melanoleuca</i>) blood transcriptome: a resource for novel gene loci and immunogenetics. Molecular Ecology Resources, 2015, 15, 1001-1013.	2.2	25
1649	Evolutionary conservation of a molecular machinery for export and expression of mRNAs with retained introns. Rna, 2015, 21, 426-437.	1.6	15
1650	PVAAS: identify variants associated with aberrant splicing from RNA-seq. Bioinformatics, 2015, 31, 1668-1670.	1.8	3
1651	<sc>CLUMSY VEIN</sc>, the Arabidopsis <sc>DEAH</sc>-box Prp16 ortholog, is required for auxin-mediated development. Plant Journal, 2015, 81, 183-197.	2.8	24
1652	SRrp35 suppresses cell proliferation and malignancy in hepatocellular carcinoma. Hepatology Research, 2015, 45, 1241-1247.	1.8	1
1653	The role of splicing factors in deregulation of alternative splicing during oncogenesis and tumor progression. Molecular and Cellular Oncology, 2015, 2, e970955.	0.3	31
1654	Methylomic trajectories across human fetal brain development. Genome Research, 2015, 25, 338-352.	2.4	250
1655	A Posttranscriptional Mechanism That Controls Ptbp1 Abundance in the <i>Xenopus</i> Epidermis. Molecular and Cellular Biology, 2015, 35, 758-768.	1.1	7
1656	A survey of computational methods in transcriptome-wide alternative splicing analysis. Biomolecular Concepts, 2015, 6, 59-66.	1.0	18
1657	Conditional Control of Alternative Splicing through Light-Triggered Splice-Switching Oligonucleotides. Journal of the American Chemical Society, 2015, 137, 3656-3662.	6.6	43
1658	Systematic discovery of regulated and conserved alternative exons in the mammalian brain reveals NMD modulating chromatin regulators. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3445-3450.	3.3	131
1659	A Generalized dSpliceType Framework to Detect Differential Splicing and Differential Expression Events Using RNA-Seq. IEEE Transactions on Nanobioscience, 2015, 14, 192-202.	2.2	15
1660	My road to alternative splicing control: from simple paths to loops and interconnections. Biochemistry and Cell Biology, 2015, 93, 171-179.	0.9	2
1661	Transcriptome sequencing and analysis of the entomopathogenic fungus Hirsutella sinensis isolated from Ophiocordyceps sinensis. BMC Genomics, 2015, 16, 106.	1.2	30
1662	Initial Molecular-Level Response to Artificial Selection for Increased Aerobic Metabolism Occurs Primarily through Changes in Gene Expression. Molecular Biology and Evolution, 2015, 32, 1461-1473.	3.5	26

#	ARTICLE	IF	CITATIONS
1663	Deep RNA sequencing reveals a high frequency of alternative splicing events in the fungus <i>Trichoderma longibrachiatum</i> . <i>BMC Genomics</i> , 2015, 16, 54.	1.2	35
1664	Transcriptome analysis of nitrogen-starvation-responsive genes in rice. <i>BMC Plant Biology</i> , 2015, 15, 31.	1.6	107
1665	Insights into alternative splicing of sarcomeric genes in the heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2015, 81, 107-113.	0.9	51
1666	Alternative splicing as a biomarker and potential target for drug discovery. <i>Acta Pharmacologica Sinica</i> , 2015, 36, 1212-1218.	2.8	88
1667	Creating reference gene annotation for the mouse C57BL6/J genome assembly. <i>Mammalian Genome</i> , 2015, 26, 366-378.	1.0	182
1668	Novel CT domain-encoding splice forms of CTGF/CCN2 are expressed in B-lineage acute lymphoblastic leukaemia. <i>Leukemia Research</i> , 2015, 39, 913-920.	0.4	4
1669	Genome-wide peripheral blood transcriptome analysis of Arab female lupus and lupus nephritis. <i>Gene</i> , 2015, 570, 230-238.	1.0	2
1670	Splice variants and regulatory networks associated with host resistance to the intestinal worm <i>Cooperia oncophora</i> in cattle. <i>Veterinary Parasitology</i> , 2015, 211, 241-250.	0.7	6
1671	Target discovery from protein databases: challenges for curation. <i>Drug Discovery Today: Technologies</i> , 2015, 14, 11-16.	4.0	1
1672	Exploiting RNA-sequencing data from the porcine testes to identify the key genes involved in spermatogenesis in Large White pigs. <i>Gene</i> , 2015, 573, 303-309.	1.0	14
1673	Revealing Missing Human Protein Isoforms Based on Ab Initio Prediction, RNA-seq and Proteomics. <i>Scientific Reports</i> , 2015, 5, 10940.	1.6	51
1674	Alternative Splicing of G Protein-Coupled Receptors: Relevance to Pain Management. <i>Mayo Clinic Proceedings</i> , 2015, 90, 1135-1151.	1.4	25
1675	Novel splice isoforms of dairy goat DBC1 and their diverse mRNA expression profiles. <i>Small Ruminant Research</i> , 2015, 130, 15-26.	0.6	5
1676	Systematic Profiling of Poly(A) ⁺ Transcripts Modulated by Core 3 rd End Processing and Splicing Factors Reveals Regulatory Rules of Alternative Cleavage and Polyadenylation. <i>PLoS Genetics</i> , 2015, 11, e1005166.	1.5	217
1677	Alternative Splicing in the Mammalian Nervous System: Recent Insights into Mechanisms and Functional Roles. <i>Neuron</i> , 2015, 87, 14-27.	3.8	391
1678	Regulation of Toll-like Receptor Signaling by the SF3a mRNA Splicing Complex. <i>PLoS Genetics</i> , 2015, 11, e1004932.	1.5	41
1679	Unmasking alternative splicing inside protein-coding exons defines exitrons and their role in proteome plasticity. <i>Genome Research</i> , 2015, 25, 995-1007.	2.4	150
1680	Novel alternative splice variants of NFIX and their diverse mRNA expression patterns in dairy goat. <i>Gene</i> , 2015, 569, 250-258.	1.0	11

#	ARTICLE	IF	CITATIONS
1681	Isoform-Level Gene Expression Profiles of Human Y Chromosome Azoospermia Factor Genes and Their X Chromosome Paralogs in the Testicular Tissue of Non-Obstructive Azoospermia Patients. <i>Journal of Proteome Research</i> , 2015, 14, 3595-3605.	1.8	35
1682	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <i>Scientific Reports</i> , 2015, 5, 11917.	1.6	10
1683	Regulation of Translation Factor EEF1D Gene Function by Alternative Splicing. <i>International Journal of Molecular Sciences</i> , 2015, 16, 3970-3979.	1.8	16
1684	Genomic architecture and functional relationships of intronless, constitutively- and alternatively-spliced genes in <i>Brachypodium distachyon</i> . <i>Plant Signaling and Behavior</i> , 2015, 10, e1042640.	1.2	6
1685	Analysis of intronic and exonic reads in RNA-seq data characterizes transcriptional and post-transcriptional regulation. <i>Nature Biotechnology</i> , 2015, 33, 722-729.	9.4	248
1686	mRNA 3' UTR shortening is a molecular signature of mTORC1 activation. <i>Nature Communications</i> , 2015, 6, 7218.	5.8	55
1687	TRA2 ^{Δ2} controls Mypt1 exon 24 splicing in the developmental maturation of mouse mesenteric artery smooth muscle. <i>American Journal of Physiology - Cell Physiology</i> , 2015, 308, C289-C296.	2.1	15
1688	RNA Structures as Mediators of Neurological Diseases and as Drug Targets. <i>Neuron</i> , 2015, 87, 28-46.	3.8	105
1689	The hitchhiker's guide to PGC-1 ^Δ isoform structure and biological functions. <i>Diabetologia</i> , 2015, 58, 1969-1977.	2.9	159
1690	Novel Transcription Factor Variants through RNA-Sequencing: The Importance of Being "Alternative". <i>International Journal of Molecular Sciences</i> , 2015, 16, 1755-1771.	1.8	8
1691	Lessons from modENCODE. <i>Annual Review of Genomics and Human Genetics</i> , 2015, 16, 31-53.	2.5	46
1692	SplicingTypesAnno: Annotating and quantifying alternative splicing events for RNA-Seq data. <i>Computer Methods and Programs in Biomedicine</i> , 2015, 119, 53-62.	2.6	10
1693	Zebrafish Rnf111 is encoded by multiple transcripts and is required for epiboly progression and prechordal plate development. <i>Differentiation</i> , 2015, 89, 22-30.	1.0	1
1694	Comparative transcriptome analysis of the petal degeneration mutant pdm in Chinese cabbage (<i>Brassica campestris ssp. pekinensis</i>) using RNA-Seq. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1833-1847.	1.0	30
1696	Splice-acceptor site mutation in p53 gene of hu888 zebrafish line. <i>Journal of Applied Genetics</i> , 2015, 56, 115-121.	1.0	3
1697	Current Advances in Noncoding RNA Relevant to Epigenetic Mechanisms. <i>Current Molecular Biology Reports</i> , 2015, 1, 29-38.	0.8	0
1698	Global Promotion of Alternative Internal Exon Usage by mRNA 3' End Formation Factors. <i>Molecular Cell</i> , 2015, 58, 819-831.	4.5	34
1699	Native Elongating Transcript Sequencing Reveals Human Transcriptional Activity at Nucleotide Resolution. <i>Cell</i> , 2015, 161, 541-554.	13.5	342

#	ARTICLE	IF	CITATIONS
1700	Algorithms for differential splicing detection using exon arrays: a comparative assessment. <i>BMC Genomics</i> , 2015, 16, 136.	1.2	3
1701	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	1.2	109
1702	Transcriptome analysis of ageing in uninjured human Achilles tendon. <i>Arthritis Research and Therapy</i> , 2015, 17, 33.	1.6	68
1703	Proteomic Validation of Transcript Isoforms, Including Those Assembled from RNA-Seq Data. <i>Journal of Proteome Research</i> , 2015, 14, 3541-3554.	1.8	13
1705	SplicePie: a novel analytical approach for the detection of alternative, non-sequential and recursive splicing. <i>Nucleic Acids Research</i> , 2015, 43, e80-e80.	6.5	17
1706	RNA Nanotechnology and Therapeutics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	3
1707	Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events. <i>Nature Biotechnology</i> , 2015, 33, 736-742.	9.4	205
1708	Mechanisms and Regulation of Alternative Pre-mRNA Splicing. <i>Annual Review of Biochemistry</i> , 2015, 84, 291-323.	5.0	970
1709	Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. <i>Science Translational Medicine</i> , 2015, 7, 270ra6.	5.8	375
1710	Most Highly Expressed Protein-Coding Genes Have a Single Dominant Isoform. <i>Journal of Proteome Research</i> , 2015, 14, 1880-1887.	1.8	106
1711	RNA-binding proteins in neurodegeneration: Seq and you shall receive. <i>Trends in Neurosciences</i> , 2015, 38, 226-236.	4.2	97
1712	Alternative splicing regulates the expression of G9A and SUV39H2 methyltransferases, and dramatically changes SUV39H2 functions. <i>Nucleic Acids Research</i> , 2015, 43, 1869-1882.	6.5	26
1713	Identification Exon Skipping Events From High-Throughput RNA Sequencing Data. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 562-569.	2.2	2
1714	Lower expression level of two RAGE alternative splicing isoforms in Alzheimer's disease. <i>Neuroscience Letters</i> , 2015, 597, 66-70.	1.0	9
1715	The variation game: Cracking complex genetic disorders with NGS and omics data. <i>Methods</i> , 2015, 79-80, 18-31.	1.9	22
1716	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	6.0	1,127
1717	The alternative role of DNA methylation in splicing regulation. <i>Trends in Genetics</i> , 2015, 31, 274-280.	2.9	458
1718	Splicing predictions reliably classify different types of alternative splicing. <i>Rna</i> , 2015, 21, 813-823.	1.6	22

#	ARTICLE	IF	CITATIONS
1719	<sc>SNP</sc> genotyping and population genomics from expressed sequences â€œ current advances and future possibilities. <i>Molecular Ecology</i> , 2015, 24, 2310-2323.	2.0	99
1720	It's a bit over, is that ok? The subtle surplus from tandem alternative splicing. <i>RNA Biology</i> , 2015, 12, 115-122.	1.5	5
1721	A lncRNA regulates alternative splicing via establishment of a splicing-specific chromatin signature. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 370-376.	3.6	229
1722	Diverse regulation of 3â€² splice site usage. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 4771-4793.	2.4	22
1723	HP1 Is Involved in Regulating the Global Impact of DNA Methylation on Alternative Splicing. <i>Cell Reports</i> , 2015, 10, 1122-1134.	2.9	179
1724	MetaDiff: differential isoform expression analysis using random-effects meta-regression. <i>BMC Bioinformatics</i> , 2015, 16, 208.	1.2	9
1725	Functional genomics of human brain development and implications for autism spectrum disorders. <i>Translational Psychiatry</i> , 2015, 5, e665-e665.	2.4	24
1726	ESRP2 controls an adult splicing programme in hepatocytes to support postnatal liver maturation. <i>Nature Communications</i> , 2015, 6, 8768.	5.8	83
1727	Characterization of the nuclear matrix targeting sequence (NMTS) of the BPV1 E8/E2 protein â€œ the shortest known NMTS. <i>Nucleus</i> , 2015, 6, 289-300.	0.6	5
1728	Non-coding functions of alternative pre-mRNA splicing in development. <i>Seminars in Cell and Developmental Biology</i> , 2015, 47-48, 32-39.	2.3	46
1729	Tinkering signaling pathways by gain and loss of protein isoforms: the case of the EDA pathway regulator EDARADD. <i>BMC Evolutionary Biology</i> , 2015, 15, 129.	3.2	9
1730	Learning the Sequence Determinants of Alternative Splicing from Millions of Random Sequences. <i>Cell</i> , 2015, 163, 698-711.	13.5	223
1731	A comparison of the low temperature transcriptomes of two tomato genotypes that differ in freezing tolerance: <i>Solanum lycopersicum</i> and <i>Solanum habrochaites</i> . <i>BMC Plant Biology</i> , 2015, 15, 132.	1.6	77
1732	HuR antagonizes the effect of an intronic pyrimidine-rich sequence in regulating WT1 +/âˆ™KTS isoforms. <i>RNA Biology</i> , 2015, 12, 1364-1371.	1.5	0
1733	Regulation of alternative gene transcription in the striatum in response to antidepressant drugs. <i>Neuropharmacology</i> , 2015, 99, 328-336.	2.0	8
1734	RNA splicing regulated by RBFOX1 is essential for cardiac function in zebrafish. <i>Journal of Cell Science</i> , 2015, 128, 3030-40.	1.2	16
1735	We can't all be supermodels: the value of comparative transcriptomics to the study of nonâ€œmodel insects. <i>Insect Molecular Biology</i> , 2015, 24, 139-154.	1.0	82
1736	A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples. <i>BMC Bioinformatics</i> , 2015, 16, 262.	1.2	7

#	ARTICLE	IF	CITATIONS
1737	Estrogen receptor beta impacts hormone-induced alternative mRNA splicing in breast cancer cells. <i>BMC Genomics</i> , 2015, 16, 367.	1.2	28
1738	A chromatin code for alternative splicing involving a putative association between CTCF and HP1± proteins. <i>BMC Biology</i> , 2015, 13, 31.	1.7	52
1739	Global analysis of physical and functional RNA targets of hnRNP L reveals distinct sequence and epigenetic features of repressed and enhanced exons. <i>Rna</i> , 2015, 21, 2053-2066.	1.6	28
1740	Expression of an estrogen-regulated variant transcript of the peroxisomal branched chain fatty acid oxidase ACOX2 in breast carcinomas. <i>BMC Cancer</i> , 2015, 15, 524.	1.1	20
1741	Accelerating Discovery and Functional Analysis of Small RNAs with New Technologies. <i>Annual Review of Genetics</i> , 2015, 49, 367-394.	3.2	118
1742	Transcriptomic Approaches to Neural Repair. <i>Journal of Neuroscience</i> , 2015, 35, 13860-13867.	1.7	28
1743	A SteMNESS perspective of survival motor neuron function: splicing factors in stem cell biology and disease. <i>Frontiers in Biology</i> , 2015, 10, 297-309.	0.7	0
1744	Nuclear matrix-associated protein SMAR1 regulates alternative splicing via HDAC6-mediated deacetylation of Sam68. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3374-83.	3.3	43
1745	Regulation of alternative splicing in <i>Drosophila</i> by 56 RNA binding proteins. <i>Genome Research</i> , 2015, 25, 1771-1780.	2.4	77
1746	Human genes with a greater number of transcript variants tend to show biological features of housekeeping and essential genes. <i>Molecular BioSystems</i> , 2015, 11, 2798-2807.	2.9	11
1747	Assessing the consistency of public human tissue RNA-seq data sets. <i>Briefings in Bioinformatics</i> , 2015, 16, 941-949.	3.2	19
1748	Molecular Biology Basics in the "Omics" Era: Genes to Proteins. , 2015, , 3-65.		1
1749	Widespread exon skipping triggers degradation by nuclear RNA surveillance in fission yeast. <i>Genome Research</i> , 2015, 25, 884-896.	2.4	37
1750	Identification of recurrent regulated alternative splicing events across human solid tumors. <i>Nucleic Acids Research</i> , 2015, 43, 5130-5144.	6.5	137
1751	Polymorphisms in alternative splicing associated genes are associated with lung cancer risk in a Chinese population. <i>Lung Cancer</i> , 2015, 89, 238-242.	0.9	9
1752	Unique gene program of rat small resistance mesenteric arteries as revealed by deep RNA sequencing. <i>Physiological Reports</i> , 2015, 3, e12450.	0.7	8
1754	Comparative genomics of grass EST libraries reveals previously uncharacterized splicing events in crop plants. <i>BMC Plant Biology</i> , 2015, 15, 39.	1.6	3
1755	ELAV Links Paused Pol II to Alternative Polyadenylation in the <i>Drosophila</i> Nervous System. <i>Molecular Cell</i> , 2015, 57, 341-348.	4.5	101

#	ARTICLE	IF	CITATIONS
1756	Computational challenges, tools, and resources for analyzing coâ€ and postâ€ transcriptional events in high throughput. Wiley Interdisciplinary Reviews RNA, 2015, 6, 291-310.	3.2	16
1757	Angelman syndrome imprinting center encodes a transcriptional promoter. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6871-6875.	3.3	36
1758	Bioinformatics of cardiovascular miRNA biology. Journal of Molecular and Cellular Cardiology, 2015, 89, 3-10.	0.9	20
1759	Splice factor mutations and alternative splicing as drivers of hematopoietic malignancy. Immunological Reviews, 2015, 263, 257-278.	2.8	43
1760	Intrinsically disordered proteins in cellular signalling and regulation. Nature Reviews Molecular Cell Biology, 2015, 16, 18-29.	16.1	1,849
1761	Human knockout research: new horizons and opportunities. Trends in Genetics, 2015, 31, 108-115.	2.9	42
1762	A highly sensitive and accurate gene expression analysis by sequencing (â€œbead-seqâ€) for a single cell. Analytical Biochemistry, 2015, 471, 9-16.	1.1	18
1763	Regulatory Non-Coding RNAs. Methods in Molecular Biology, 2015, , .	0.4	2
1764	In silico prediction of physical protein interactions and characterization of interactome orphans. Nature Methods, 2015, 12, 79-84.	9.0	148
1765	Transcriptome-wide Landscape of Pre-mRNA Alternative Splicing Associated with Metastatic Colonization. Molecular Cancer Research, 2015, 13, 305-318.	1.5	63
1766	Exploring the function of genetic variants in the non-coding genomic regions: approaches for identifying human regulatory variants affecting gene expression. Briefings in Bioinformatics, 2015, 16, 393-412.	3.2	58
1767	Regulation of membrane excitability: a convergence on voltage-gated sodium conductance. Molecular Neurobiology, 2015, 51, 57-67.	1.9	36
1768	Analysis of the Drought Stress-Responsive Transcriptome of Black Cottonwood (Populus Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Td (1.0	40
1769	The influence of <scp>Argonaute</scp> proteins on alternative <scp>RNA</scp> splicing. Wiley Interdisciplinary Reviews RNA, 2015, 6, 141-156.	3.2	22
1770	Analyses of the Interleukin32 Transcript Variants in Breast Cancer Cell Lines. American Journal of Immunology, 2016, 12, 83-90.	0.1	0
1772	Functional divergence and convergence between the transcript network and gene network in lung adenocarcinoma. OncoTargets and Therapy, 2016, 9, 335.	1.0	2
1773	Altered expression pattern of circular RNAs in primary and metastatic sites of epithelial ovarian carcinoma. Oncotarget, 2016, 7, 36366-36381.	0.8	148
1774	Comparative analysis of the liver tissue transcriptomes of Mongolian and Lanzhou fat-tailed sheep. Genetics and Molecular Research, 2016, 15, .	0.3	11

#	ARTICLE	IF	CITATIONS
1775	Transcriptomic Analysis of Resistant and Susceptible <i>Bombyx mori</i> Strains Following BmNPV Infection Provides Insights into the Antiviral Mechanisms. <i>International Journal of Genomics</i> , 2016, 2016, 1-10.	0.8	26
1776	Splicing repression allows the gradual emergence of new Alu-exons in primate evolution. <i>ELife</i> , 2016, 5, .	2.8	57
1777	General Aspects Related to Nonsense Mutations. , 2016, , 1-76.		1
1778	Transcriptome Profiles Using Next-Generation Sequencing Reveal Liver Changes in the Early Stage of Diabetes in Tree Shrew (<i>Tupaia belangeri chinensis</i>). <i>Journal of Diabetes Research</i> , 2016, 2016, 1-15.	1.0	13
1779	Identification of Alternative Variants and Insertion of the Novel Polymorphic <i>AluY117</i> in <i>TSEN54</i> Gene during Primate Evolution. <i>International Journal of Genomics</i> , 2016, 2016, 1-10.	0.8	4
1780	A new view of transcriptome complexity and regulation through the lens of local splicing variations. <i>ELife</i> , 2016, 5, e11752.	2.8	385
1781	Discovery of clubroot-resistant genes in <i>Brassica napus</i> by transcriptome sequencing. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	7
1782	Does conservation account for splicing patterns?. <i>BMC Genomics</i> , 2016, 17, 787.	1.2	15
1783	Genomic Tools and Animal Health. <i>Veterinary Sciences</i> , 2016, 3, 21.	0.6	4
1784	Structural basis for the recognition of spliceosomal SmN/B/â€™ proteins by the RBM5 OCRE domain in splicing regulation. <i>ELife</i> , 2016, 5, .	2.8	28
1785	Characterization of the Olfactory Receptors Expressed in Human Spermatozoa. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 73.	1.6	74
1786	The Role of Alternative Splicing in the Control of Immune Homeostasis and Cellular Differentiation. <i>International Journal of Molecular Sciences</i> , 2016, 17, 3.	1.8	73
1787	ISOexpresso: a web-based platform for isoform-level expression analysis in human cancer. <i>BMC Genomics</i> , 2016, 17, 631.	1.2	38
1788	Extensive RNA editing and splicing increase immune self-representation diversity in medullary thymic epithelial cells. <i>Genome Biology</i> , 2016, 17, 219.	3.8	67
1789	BinPacker: Packing-Based De Novo Transcriptome Assembly from RNA-seq Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004772.	1.5	116
1790	In Vivo Analysis of Disease-Associated Point Mutations Unveils Profound Differences in mRNA Splicing of Peripherin-2 in Rod and Cone Photoreceptors. <i>PLoS Genetics</i> , 2016, 12, e1005811.	1.5	22
1791	Staufen1 Regulates Multiple Alternative Splicing Events either Positively or Negatively in DM1 Indicating Its Role as a Disease Modifier. <i>PLoS Genetics</i> , 2016, 12, e1005827.	1.5	37
1792	The Impact of Endurance Training on Human Skeletal Muscle Memory, Global Isoform Expression and Novel Transcripts. <i>PLoS Genetics</i> , 2016, 12, e1006294.	1.5	46

#	ARTICLE	IF	CITATIONS
1793	Dose-Dependent Regulation of Alternative Splicing by MBNL Proteins Reveals Biomarkers for Myotonic Dystrophy. <i>PLoS Genetics</i> , 2016, 12, e1006316.	1.5	79
1794	Alternative Splicing within and between <i>Drosophila</i> Species, Sexes, Tissues, and Developmental Stages. <i>PLoS Genetics</i> , 2016, 12, e1006464.	1.5	53
1795	The Transcript Profile of a Traditional Chinese Medicine, <i>Atractylodes lancea</i> , Revealing Its Sesquiterpenoid Biosynthesis of the Major Active Components. <i>PLoS ONE</i> , 2016, 11, e0151975.	1.1	31
1796	Biphasic and Stage-Associated Expression of CPEB4 in Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2016, 11, e0155025.	1.1	8
1797	Identification and Classification of New Transcripts in Dorper and Small-Tailed Han Sheep Skeletal Muscle Transcriptomes. <i>PLoS ONE</i> , 2016, 11, e0159638.	1.1	15
1798	Global Profiling of the Cellular Alternative RNA Splicing Landscape during Virus-Host Interactions. <i>PLoS ONE</i> , 2016, 11, e0161914.	1.1	58
1799	Altered mRNA Splicing in SMN-Depleted Motor Neuron-Like Cells. <i>PLoS ONE</i> , 2016, 11, e0163954.	1.1	15
1800	Comparative Transcriptome Analysis Reveals Substantial Tissue Specificity in Human Aortic Valve. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S37594.	0.6	6
1801	The Mechanisms of Maize Resistance to <i>Fusarium verticillioides</i> by Comprehensive Analysis of RNA-seq Data. <i>Frontiers in Plant Science</i> , 2016, 7, 1654.	1.7	61
1802	Bioinformatics for RNA-seq Data Analysis. , 2016, , .		6
1803	Comprehensive landscape of subtype-specific coding and non-coding RNA transcripts in breast cancer. <i>Oncotarget</i> , 2016, 7, 68851-68863.	0.8	19
1804	Finding SNPs that affect microRNA regulation in disease-associated genomic regions. , 0, , 139-150.		0
1805	Identification of the <i>Mtus1</i> Splice Variant as a Novel Inhibitory Factor Against Cardiac Hypertrophy. <i>Journal of the American Heart Association</i> , 2016, 5, .	1.6	10
1806	The Working Modules of Long Noncoding RNAs in Cancer Cells. <i>Advances in Experimental Medicine and Biology</i> , 2016, 927, 49-67.	0.8	8
1807	Histone methylation, alternative splicing and neuronal differentiation. <i>Neurogenesis (Austin, Tex)</i> , 2016, 3, e1204844.	1.5	17
1808	The role of gene polymorphism in <i>HLA</i> class I splicing. <i>International Journal of Immunogenetics</i> , 2016, 43, 65-78.	0.8	23
1809	MECHANISMS IN ENDOCRINOLOGY: Alternative splicing: the new frontier in diabetes research. <i>European Journal of Endocrinology</i> , 2016, 174, R225-R238.	1.9	50
1810	ACBD2/ECI2-Mediated Peroxisome-Mitochondria Interactions in Leydig Cell Steroid Biosynthesis. <i>Molecular Endocrinology</i> , 2016, 30, 763-782.	3.7	73

#	ARTICLE	IF	CITATIONS
1811	Transcriptome sequencing reveals aberrant alternative splicing in Huntington's disease. <i>Human Molecular Genetics</i> , 2016, 25, 3454-3466.	1.4	102
1812	Global intron retention mediated gene regulation during CD4 ⁺ T cell activation. <i>Nucleic Acids Research</i> , 2016, 44, 6817-6829.	6.5	96
1813	Post-transcriptional regulation of gene expression in neural stem cells. <i>Cell Biochemistry and Function</i> , 2016, 34, 197-208.	1.4	7
1814	A pilot integrative genomics study of GABA and glutamate neurotransmitter systems in suicide, suicidal behavior, and major depressive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 414-426.	1.1	70
1815	Functional genomics analyses of RNA-binding proteins reveal the splicing regulator SNRPB as an oncogenic candidate in glioblastoma. <i>Genome Biology</i> , 2016, 17, 125.	3.8	83
1816	AKAP95 regulates splicing through scaffolding RNAs and RNA processing factors. <i>Nature Communications</i> , 2016, 7, 13347.	5.8	21
1817	Neonatal cardiac dysfunction and transcriptome changes caused by the absence of Celf1. <i>Scientific Reports</i> , 2016, 6, 35550.	1.6	18
1818	Roar: detecting alternative polyadenylation with standard mRNA sequencing libraries. <i>BMC Bioinformatics</i> , 2016, 17, 423.	1.2	64
1819	Transcriptomics resources of human tissues and organs. <i>Molecular Systems Biology</i> , 2016, 12, 862.	3.2	130
1820	DASE: Condition-specific differential alternative splicing variants estimation method without reference genome sequence, and its application to non-model organisms. , 2016, , .		0
1821	Dominant Isoform in Alternative Splicing in HeLa S3 Cell Line Revealed by Single-cell RNA-seq. , 2016, , .		3
1822	Altered microRNA expression and pre-mRNA splicing events reveal new mechanisms associated with early stage <i>Mycobacterium avium</i> subspecies paratuberculosis infection. <i>Scientific Reports</i> , 2016, 6, 24964.	1.6	47
1823	Intronic cleavage and polyadenylation regulates gene expression during DNA damage response through U1 snRNA. <i>Cell Discovery</i> , 2016, 2, 16013.	3.1	36
1824	Landscape and Fruit Developmental Regulation of Alternative Splicing in Tomato by Genome-Wide Analysis. <i>Horticultural Plant Journal</i> , 2016, 2, 338-350.	2.3	11
1825	Pre-mRNA Splicing: Function and Dysfunction. , 2016, , 503-511.		1
1827	JULiP: An efficient model for accurate intron selection from multiple RNA-seq samples. , 2016, , .		0
1828	In silico RNA-seq and experimental analyses reveal the differential expression and splicing of EPDR1 and ZNF518B genes in relation to KRAS mutations in colorectal cancer cells. <i>Oncology Reports</i> , 2016, 36, 3627-3634.	1.2	13
1829	Molecular mechanisms of ROS production and oxidative stress in diabetes. <i>Biochemical Journal</i> , 2016, 473, 4527-4550.	1.7	617

#	ARTICLE	IF	CITATIONS
1830	Transcriptome analysis of root development in bottle gourd (<i>Lagenaria siceraria</i>). <i>Acta Horticulturae</i> , 2016, , 41-48.	0.1	2
1831	Distinct and shared functions of ALS-associated proteins TDP-43, FUS and TAF15 revealed by multisystem analyses. <i>Nature Communications</i> , 2016, 7, 12143.	5.8	137
1832	RBFOX1 and RBFOX2 are dispensable in iPSCs and iPSC-derived neurons and do not contribute to neural-specific paternal UBE3A silencing. <i>Scientific Reports</i> , 2016, 6, 25368.	1.6	19
1833	Targeted Intron Retention and Excision for Rapid Gene Regulation in Response to Neuronal Activity. <i>Neuron</i> , 2016, 92, 1266-1278.	3.8	182
1834	Role of pre-mRNA secondary structures in the regulation of alternative splicing. <i>Molecular Biology</i> , 2016, 50, 823-830.	0.4	10
1835	Comparative transcriptome analysis of peripheral blood mononuclear cells in hepatitis B-related acute-on-chronic liver failure. <i>Scientific Reports</i> , 2016, 6, 20759.	1.6	11
1836	Nuclear poly(A)-binding protein aggregates misplace a pre-mRNA outside of SC35 speckle causing its abnormal splicing. <i>Nucleic Acids Research</i> , 2016, 44, 10929-10945.	6.5	28
1837	PTBP1 and PTBP2 Serve Both Specific and Redundant Functions in Neuronal Pre-mRNA Splicing. <i>Cell Reports</i> , 2016, 17, 2766-2775.	2.9	97
1838	Involvement of PARP1 in the regulation of alternative splicing. <i>Cell Discovery</i> , 2016, 2, 15046.	3.1	63
1839	Sparse singular value decomposition-based feature extraction for identifying differentially expressed genes. , 2016, , .		2
1840	An extended U2AF65â€™RNA-binding domain recognizes the 3â€™ splice site signal. <i>Nature Communications</i> , 2016, 7, 10950.	5.8	58
1841	Undiscovered Physiology of Transcript and Protein Networks. , 2016, 6, 1851-1872.		0
1842	ChIP-Seq Data Analysis to Define Transcriptional Regulatory Networks. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2016, 160, 1-14.	0.6	4
1843	DeepSplice: Deep classification of novel splice junctions revealed by RNA-seq. , 2016, , .		16
1844	Medicinal plant transcriptomes: the new gateways for accelerated understanding of plant secondary metabolism. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 256-269.	0.4	21
1845	Deconvolution of base pair level RNA-Seq read counts for quantification of transcript expression levels. <i>Annals of Applied Statistics</i> , 2016, 10, .	0.5	1
1846	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. <i>Rna</i> , 2016, 22, 839-851.	1.6	622
1847	Soluble Immune Response Suppressor (SIRS): Reassessing the immunosuppressant potential of an elusive peptide. <i>Biochemical Pharmacology</i> , 2016, 117, 1-9.	2.0	1

#	ARTICLE	IF	CITATIONS
1848	Ultraconserved region-containing Transformer 2 ¹²⁴ controls senescence of colon cancer cells. <i>Oncogenesis</i> , 2016, 5, e213-e213.	2.1	18
1849	Proteogenomics: Integrating Next-Generation Sequencing and Mass Spectrometry to Characterize Human Proteomic Variation. <i>Annual Review of Analytical Chemistry</i> , 2016, 9, 521-545.	2.8	91
1850	Macaca specific exon creation event generates a novel ZKSCAN5 transcript. <i>Gene</i> , 2016, 577, 236-243.	1.0	8
1851	Regulatory Implications of Non-Trivial Splicing: Isoform 3 of Rab1A Shows Enhanced Basal Activity and Is Not Controlled by Accessory Proteins. <i>Journal of Molecular Biology</i> , 2016, 428, 1544-1557.	2.0	5
1852	<i>SplAdder</i> : identification, quantification and testing of alternative splicing events from RNA-Seq data. <i>Bioinformatics</i> , 2016, 32, 1840-1847.	1.8	124
1853	CP binding to a cytosine-rich subset of polypyrimidine tracts drives a novel pathway of cassette exon splicing in the mammalian transcriptome. <i>Nucleic Acids Research</i> , 2016, 44, 2283-2297.	6.5	32
1854	Processing and transcriptome expansion at the mRNA 3' end in health and disease: finding the right end. <i>Pflügers Archiv European Journal of Physiology</i> , 2016, 468, 993-1012.	1.3	40
1855	Genome-wide analysis of shoot growth-associated alternative splicing in moso bamboo. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1695-1714.	1.0	33
1856	Exon Skipping in the RET Gene Encodes Novel Isoforms That Differentially Regulate RET Protein Signal Transduction. <i>Journal of Biological Chemistry</i> , 2016, 291, 16249-16262.	1.6	10
1857	<i>De novo</i> assembly of transcriptome from next-generation sequencing data. <i>Quantitative Biology</i> , 2016, 4, 94-105.	0.3	5
1858	Transcript Isoform Variation Associated with Cytosine Modification in Human Lymphoblastoid Cell Lines. <i>Genetics</i> , 2016, 203, 985-995.	1.2	2
1859	Alternative cleavage and polyadenylation in spermatogenesis connects chromatin regulation with post-transcriptional control. <i>BMC Biology</i> , 2016, 14, 6.	1.7	72
1860	Mapping and differential expression analysis from short-read RNA-Seq data in model organisms. <i>Quantitative Biology</i> , 2016, 4, 22-35.	0.3	3
1861	Determination of a Comprehensive Alternative Splicing Regulatory Network and Combinatorial Regulation by Key Factors during the Epithelial-to-Mesenchymal Transition. <i>Molecular and Cellular Biology</i> , 2016, 36, 1704-1719.	1.1	118
1862	Predicting Protein-Protein Interactions from the Molecular to the Proteome Level. <i>Chemical Reviews</i> , 2016, 116, 4884-4909.	23.0	289
1863	Noncanonical registers and base pairs in human 5' splice-site selection. <i>Nucleic Acids Research</i> , 2016, 44, 3908-3921.	6.5	35
1864	Alternative Polyadenylation: Another Foe in Cancer. <i>Molecular Cancer Research</i> , 2016, 14, 507-517.	1.5	51
1865	Molecular characterization of Sp110 gene in pigs. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1431-1442.	1.0	1

#	ARTICLE	IF	CITATIONS
1866	Distinguishing highly similar gene isoforms with a clustering-based bioinformatics analysis of PacBio single-molecule long reads. <i>BioData Mining</i> , 2016, 9, 13.	2.2	20
1867	Structural Basis for the Functional Coupling of the Alternative Splicing Factors Smu1 and RED. <i>Structure</i> , 2016, 24, 762-773.	1.6	25
1868	Towards understanding pre-mRNA splicing mechanisms and the role of SR proteins. <i>Gene</i> , 2016, 587, 107-119.	1.0	46
1869	Coupling of RNA Polymerase II Transcription Elongation with Pre-mRNA Splicing. <i>Journal of Molecular Biology</i> , 2016, 428, 2623-2635.	2.0	245
1870	iGEMS: an integrated model for identification of alternative exon usage events. <i>Nucleic Acids Research</i> , 2016, 44, e109-e109.	6.5	18
1871	The PSI ⁺ U1 snRNP interaction regulates male mating behavior in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5269-5274.	3.3	27
1872	Spliceosomal gene mutations in myelodysplasia: molecular links to clonal abnormalities of hematopoiesis. <i>Genes and Development</i> , 2016, 30, 989-1001.	2.7	95
1873	Transcriptomic dissection of the rice-Fusarium fujikuroi interaction by RNA-Seq. <i>Euphytica</i> , 2016, 211, 123-137.	0.6	12
1874	Cytoplasmic Drosha activity generated by alternative splicing. <i>Nucleic Acids Research</i> , 2016, 44, gkw668.	6.5	37
1875	RNA-Seq Library Construction Methods for Transcriptome Analysis. <i>Current Protocols in Plant Biology</i> , 2016, 1, 197-215.	2.8	8
1876	Therapeutic targeting of splicing in cancer. <i>Nature Medicine</i> , 2016, 22, 976-986.	15.2	484
1877	Functional impact of splice isoform diversity in individual cells. <i>Biochemical Society Transactions</i> , 2016, 44, 1079-1085.	1.6	18
1878	A Transcriptionally Inactive ATF2 Variant Drives Melanomagenesis. <i>Cell Reports</i> , 2016, 15, 1884-1892.	2.9	21
1879	Antisense Oligonucleotides Modulating Activation of a Nonsense-Mediated RNA Decay Switch Exon in the ATM Gene. <i>Nucleic Acid Therapeutics</i> , 2016, 26, 392-400.	2.0	9
1880	Divergent Expression and Metabolic Functions of Human Glucuronosyltransferases through Alternative Splicing. <i>Cell Reports</i> , 2016, 17, 114-124.	2.9	21
1881	New Insights Into the Role of RNA-Binding Proteins in the Regulation of Heart Development. <i>International Review of Cell and Molecular Biology</i> , 2016, 324, 125-185.	1.6	10
1882	Splicing variants of ADAR2 and ADAR2-mediated RNA editing in glioma. <i>Oncology Letters</i> , 2016, 12, 788-792.	0.8	11
1883	An NXF1 mRNA with a retained intron is expressed in hippocampal and neocortical neurons and is translated into a protein that functions as an Nxf1 cofactor. <i>Molecular Biology of the Cell</i> , 2016, 27, 3903-3912.	0.9	29

#	ARTICLE	IF	CITATIONS
1884	Competitive regulation of alternative splicing and alternative polyadenylation by hnRNP H and CstF64 determines acetylcholinesterase isoforms. <i>Nucleic Acids Research</i> , 2016, 45, gkw823.	6.5	53
1885	Distinct splicing signatures affect converged pathways in myelodysplastic syndrome patients carrying mutations in different splicing regulators. <i>Rna</i> , 2016, 22, 1535-1549.	1.6	40
1886	Spliced synthetic genes as internal controls in RNA sequencing experiments. <i>Nature Methods</i> , 2016, 13, 792-798.	9.0	123
1887	Intron retention in mRNA: No longer nonsense. <i>BioEssays</i> , 2016, 38, 41-49.	1.2	163
1888	RNA sequencing provides insights into the toxicogenomic response of ZF4 cells to methyl methanesulfonate. <i>Journal of Applied Toxicology</i> , 2016, 36, 94-104.	1.4	8
1890	Modified Nucleic Acids in Biology and Medicine. <i>RNA Technologies</i> , 2016, , .	0.2	3
1891	Exploiting the CRISPR/Cas9 system to study alternative splicing in vivo: application to titin. <i>Human Molecular Genetics</i> , 2016, 25, ddw280.	1.4	21
1892	The long and the short of TRF2 in neurogenesis. <i>Cell Cycle</i> , 2016, 15, 3026-3032.	1.3	13
1893	TET-catalyzed oxidation of intragenic 5methylcytosine regulates CTCF-dependent alternative splicing. <i>EMBO Journal</i> , 2016, 35, 335-355.	3.5	111
1894	Reflections on MUC1 glycoprotein: the hidden potential of isoforms in carcinogenesis. <i>Apmis</i> , 2016, 124, 913-924.	0.9	17
1895	Distinct recruitment of human eIF4E isoforms to processing bodies and stress granules. <i>BMC Molecular Biology</i> , 2016, 17, 21.	3.0	37
1896	Targeting Splicing in the Treatment of Myelodysplastic Syndromes and Other Myeloid Neoplasms. <i>Current Hematologic Malignancy Reports</i> , 2016, 11, 408-415.	1.2	19
1897	Decoding sORF translation from small proteins to gene regulation. <i>RNA Biology</i> , 2016, 13, 1051-1059.	1.5	54
1898	Cell-Type-Specific Alternative Splicing Governs Cell Fate in the Developing Cerebral Cortex. <i>Cell</i> , 2016, 166, 1147-1162.e15.	13.5	276
1899	Expression dynamics, relationships, and transcriptional regulations of diverse transcripts in mouse spermatogenic cells. <i>RNA Biology</i> , 2016, 13, 1011-1024.	1.5	72
1900	3'ENDS+, a sensitive and accurate method for 3' end sequencing of polyadenylated RNA. <i>Rna</i> , 2016, 22, 1631-1639.	1.6	62
1901	RBM4-Nova1-SRSF6 splicing cascade modulates the development of brown adipocytes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 1368-1379.	0.9	20
1903	An overview of drug delivery vehicles for cancer treatment: Nanocarriers and nanoparticles including photovoltaic nanoparticles. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2016, 164, 151-159.	1.7	28

#	ARTICLE	IF	CITATIONS
1904	Translational plasticity facilitates the accumulation of nonsense genetic variants in the human population. <i>Genome Research</i> , 2016, 26, 1639-1650.	2.4	31
1905	Validation of Alternative Transcript Splicing in Chicken Lines that Differ in Genetic Resistance to Marek's Disease. <i>Animal Biotechnology</i> , 2016, 27, 238-244.	0.7	8
1907	Contextual fear conditioning induces differential alternative splicing. <i>Neurobiology of Learning and Memory</i> , 2016, 134, 221-235.	1.0	28
1908	Alternative splicing of inner-ear-expressed genes. <i>Frontiers of Medicine</i> , 2016, 10, 250-257.	1.5	13
1909	The Interplay of Temperature and Genotype on Patterns of Alternative Splicing in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 204, 315-325.	1.2	50
1910	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , 2016, 7, 13182.	5.8	44
1911	Alternative Splicing of Four Trafficking Genes Regulates Myofiber Structure and Skeletal Muscle Physiology. <i>Cell Reports</i> , 2016, 17, 1923-1933.	2.9	31
1912	LSCplus: a fast solution for improving long read accuracy by short read alignment. <i>BMC Bioinformatics</i> , 2016, 17, 451.	1.2	19
1913	Overexpression of KLHL23 protein from read-through transcription of <i>PHOSPHO2</i> in gastric cancer increases cell proliferation. <i>FEBS Open Bio</i> , 2016, 6, 1155-1164.	1.0	12
1914	Transcriptome profiling of the rat retina after optic nerve transection. <i>Scientific Reports</i> , 2016, 6, 28736.	1.6	35
1915	TransComb: genome-guided transcriptome assembly via combing junctions in splicing graphs. <i>Genome Biology</i> , 2016, 17, 213.	3.8	75
1916	Cajal body function in genome organization and transcriptome diversity. <i>BioEssays</i> , 2016, 38, 1197-1208.	1.2	56
1917	Genome-Wide Analysis of Alternative Splicing Provides Insights into Stress Adaptation of the Pacific Oyster. <i>Marine Biotechnology</i> , 2016, 18, 598-609.	1.1	46
1918	Unusual Processing Generates SPA LncRNAs that Sequester Multiple RNA Binding Proteins. <i>Molecular Cell</i> , 2016, 64, 534-548.	4.5	123
1919	RBM4a-regulated splicing cascade modulates the differentiation and metabolic activities of brown adipocytes. <i>Scientific Reports</i> , 2016, 6, 20665.	1.6	17
1920	Characterization of non-olfactory GPCRs in human sperm with a focus on GPR18. <i>Scientific Reports</i> , 2016, 6, 32255.	1.6	27
1921	The ribosome-engaged landscape of alternative splicing. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1117-1123.	3.6	115
1922	SURVIV for survival analysis of mRNA isoform variation. <i>Nature Communications</i> , 2016, 7, 11548.	5.8	85

#	ARTICLE	IF	CITATIONS
1923	Cellular responses to HSV-1 infection are linked to specific types of alterations in the host transcriptome. <i>Scientific Reports</i> , 2016, 6, 28075.	1.6	61
1924	Genome-wide analysis of alternative splicing during human heart development. <i>Scientific Reports</i> , 2016, 6, 35520.	1.6	29
1926	Complementary Post Transcriptional Regulatory Information is Detected by PUNCH-P and Ribosome Profiling. <i>Scientific Reports</i> , 2016, 6, 21635.	1.6	25
1927	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. <i>Scientific Reports</i> , 2016, 6, 32406.	1.6	28
1928	Comprehensive identification of internal structure and alternative splicing events in circular RNAs. <i>Nature Communications</i> , 2016, 7, 12060.	5.8	249
1929	The contribution of intrinsically disordered regions to protein function, cellular complexity, and human disease. <i>Biochemical Society Transactions</i> , 2016, 44, 1185-1200.	1.6	323
1930	Recognition of the 3' splice site RNA by the U2AF heterodimer involves a dynamic population shift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7169-E7175.	3.3	57
1931	Ablation of the epithelial-specific splicing factor <i>Esrp1</i> results in ureteric branching defects and reduced nephron number. <i>Developmental Dynamics</i> , 2016, 245, 991-1000.	0.8	20
1932	Molecular cloning, characterization and expression of WAG-2 alternative splicing transcripts in developing spikes of <i>Aegilops tauschii</i> . <i>Journal of Genetics</i> , 2016, 95, 581-585.	0.4	4
1933	Transcriptome sequencing of gingival biopsies from chronic periodontitis patients reveals novel gene expression and splicing patterns. <i>Human Genomics</i> , 2016, 10, 28.	1.4	38
1934	A genome wide analysis of alternative splicing events during the osteogenic differentiation of human cartilage endplate-derived stem cells. <i>Molecular Medicine Reports</i> , 2016, 14, 1389-1396.	1.1	4
1935	Experimental and Computational Considerations in the Study of RNA-Binding Protein-RNA Interactions. <i>Advances in Experimental Medicine and Biology</i> , 2016, 907, 1-28.	0.8	15
1936	Different evolutionary patterns of SNPs between domains and unassigned regions in human protein-coding sequences. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1127-1136.	1.0	2
1937	Regulation of Tissue-Specific Alternative Splicing: <i>C. elegans</i> as a Model System. <i>Advances in Experimental Medicine and Biology</i> , 2016, 907, 229-261.	0.8	11
1938	Roles of RNA-binding Proteins and Post-transcriptional Regulation in Driving Male Germ Cell Development in the Mouse. <i>Advances in Experimental Medicine and Biology</i> , 2016, 907, 123-151.	0.8	28
1939	The High-Throughput Sequencing Technologies Triple-W Discussion: Why Use HTS, What Is the Optimal HTS Method to Use, and Which Data Analysis Workflow to Follow. , 2016, , 1-12.		2
1940	Differential mRNA Alternative Splicing. , 2016, , 105-119.		4
1942	RNA splicing factors as oncoproteins and tumour suppressors. <i>Nature Reviews Cancer</i> , 2016, 16, 413-430.	12.8	549

#	ARTICLE	IF	CITATIONS
1943	Statistical modeling of isoform splicing dynamics from RNA-seq time series data. <i>Bioinformatics</i> , 2016, 32, 2965-2972.	1.8	11
1944	RNA Sequencing and Genetic Disease. <i>Current Genetic Medicine Reports</i> , 2016, 4, 49-56.	1.9	0
1945	Prediction of ribosome footprint profile shapes from transcript sequences. <i>Bioinformatics</i> , 2016, 32, i183-i191.	1.8	19
1946	Transcriptome-Wide Analysis Reveals Modulation of Human Macrophage Inflammatory Phenotype Through Alternative Splicing. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2016, 36, 1434-1447.	1.1	35
1947	Polarizing the Neuron through Sustained Co-expression of Alternatively Spliced Isoforms. <i>Cell Reports</i> , 2016, 15, 1316-1328.	2.9	53
1948	Coupling between alternative polyadenylation and alternative splicing is limited to terminal introns. <i>RNA Biology</i> , 2016, 13, 646-655.	1.5	34
1949	RNA Dynamics in the Control of Circadian Rhythm. <i>Advances in Experimental Medicine and Biology</i> , 2016, 907, 107-122.	0.8	17
1950	Cool-temperature-mediated activation of phospholipase C- β 2 in the human hereditary disease PLAID. <i>Cellular Signalling</i> , 2016, 28, 1237-1251.	1.7	24
1951	Alternative Splicing of Neuronal Differentiation Factor TRF2 Regulated by HNRNPH1/H2. <i>Cell Reports</i> , 2016, 15, 926-934.	2.9	55
1952	Genomic structure and expression of the human serotonin 2A receptor gene (HTR2A) locus: identification of novel HTR2A and antisense (HTR2A-AS1) exons. <i>BMC Genetics</i> , 2016, 17, 16.	2.7	26
1953	Identification of mRNA isoform switching in breast cancer. <i>BMC Genomics</i> , 2016, 17, 181.	1.2	27
1954	A reliable method for quantification of splice variants using RT-qPCR. <i>BMC Molecular Biology</i> , 2016, 17, 8.	3.0	32
1955	CIDANE: comprehensive isoform discovery and abundance estimation. <i>Genome Biology</i> , 2016, 17, 16.	3.8	45
1956	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. <i>Progress in Retinal and Eye Research</i> , 2016, 55, 1-31.	7.3	58
1957	The use of proteases complementary to trypsin to probe isoforms and modifications. <i>Proteomics</i> , 2016, 16, 715-728.	1.3	22
1958	Analysis of differential splicing suggests different modes of short-term splicing regulation. <i>Bioinformatics</i> , 2016, 32, i147-i155.	1.8	9
1959	Characterization of the transcriptome and gene expression of four different tissues in the ecologically relevant sea urchin <i>Arbacia lixula</i> using RNA-seq. <i>Molecular Ecology Resources</i> , 2016, 16, 794-808.	2.2	21
1960	Toolbox murders: putting genes in their epigenetic and ecological contexts. <i>Biology and Philosophy</i> , 2016, 31, 125-142.	0.7	6

#	ARTICLE	IF	CITATIONS
1961	Alternative Splicing in CKD. Journal of the American Society of Nephrology: JASN, 2016, 27, 1596-1603.	3.0	15
1962	Sequencing of lariat termini in <i>S. cerevisiae</i> reveals 5' splice sites, branch points, and novel splicing events. Rna, 2016, 22, 237-253.	1.6	33
1963	MYCN controls an alternative RNA splicing program in high-risk metastatic neuroblastoma. Cancer Letters, 2016, 371, 214-224.	3.2	46
1964	Cancer RNA-Seq Nexus: a database of phenotype-specific transcriptome profiling in cancer cells. Nucleic Acids Research, 2016, 44, D944-D951.	6.5	111
1965	Comparative Transcriptome Analysis between the Fungal Plant Pathogens <i>Sclerotinia sclerotiorum</i> and <i>S. trifoliorum</i> Using RNA Sequencing. Journal of Heredity, 2016, 107, 163-172.	1.0	9
1966	A computational method for studying the relation between alternative splicing and DNA methylation. Nucleic Acids Research, 2016, 44, e19-e19.	6.5	12
1967	mRNA expression in different developmental stages of the chicken bursa of Fabricius. Poultry Science, 2016, 95, 1787-1794.	1.5	14
1968	SRPK1 inhibition in prostate cancer: A novel anti-angiogenic treatment through modulation of VEGF alternative splicing. Pharmacological Research, 2016, 107, 276-281.	3.1	23
1969	Evolutionarily conserved autoregulation of alternative pre-mRNA splicing by ribosomal protein L10a. Nucleic Acids Research, 2016, 44, 5585-5596.	6.5	22
1970	Roles for RNA-binding proteins in development and disease. Brain Research, 2016, 1647, 1-8.	1.1	138
1971	Comparative evaluation of isoform-level gene expression estimation algorithms for RNA-seq and exon-array platforms. Briefings in Bioinformatics, 2016, 18, bbw016.	3.2	25
1972	jSplice: a high-performance method for accurate prediction of alternative splicing events and its application to large-scale renal cancer transcriptome data. Bioinformatics, 2016, 32, 2111-2119.	1.8	10
1973	FUS-mediated regulation of alternative RNA processing in neurons: insights from global transcriptome analysis. Wiley Interdisciplinary Reviews RNA, 2016, 7, 330-340.	3.2	34
1974	IntSplice: prediction of the splicing consequences of intronic single-nucleotide variations in the human genome. Journal of Human Genetics, 2016, 61, 633-640.	1.1	29
1975	CLASS2: accurate and efficient splice variant annotation from RNA-seq reads. Nucleic Acids Research, 2016, 44, e98-e98.	6.5	70
1976	An empirical Bayes change-point model for identifying 3' and 5' alternative splicing by next-generation RNA sequencing. Bioinformatics, 2016, 32, 1823-1831.	1.8	13
1977	The CD44s splice isoform is a central mediator for invadopodia activity. Journal of Cell Science, 2016, 129, 1355-65.	1.2	48
1978	Role of antibodies in diagnosis and treatment of ovarian cancer: Basic approach and clinical status. Journal of Controlled Release, 2016, 226, 148-167.	4.8	42

#	ARTICLE	IF	CITATIONS
1979	Effects of high-fat diet-induced obesity and diabetes on Kiss1 and GPR54 expression in the hypothalamicâ€“pituitaryâ€“gonadal (HPG) axis and peripheral organs (fat, pancreas and liver) in male rats. <i>Neuropeptides</i> , 2016, 56, 41-49.	0.9	61
1980	Dysregulation of splicing proteins in head and neck squamous cell carcinoma. <i>Cancer Biology and Therapy</i> , 2016, 17, 219-229.	1.5	25
1981	A network-based analysis of colon cancer splicing changes reveals a tumorigenesis-favoring regulatory pathway emanating from ELK1. <i>Genome Research</i> , 2016, 26, 541-553.	2.4	45
1982	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	13.5	479
1983	RNA Splicing. <i>Circulation Research</i> , 2016, 118, 454-468.	2.0	81
1984	Comparative analysis of housekeeping and tissue-selective genes in human based on network topologies and biological properties. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1227-1241.	1.0	8
1985	IsomiR Bank: a research resource for tracking IsomiRs. <i>Bioinformatics</i> , 2016, 32, 2069-2071.	1.8	52
1986	Isoform prefiltering improves performance of count-based methods for analysis of differential transcript usage. <i>Genome Biology</i> , 2016, 17, 12.	3.8	116
1987	RNA-Protein Complexes and Interactions. <i>Methods in Molecular Biology</i> , 2016, 1421, vii-viii.	0.4	0
1988	Dual function of C/D box small nucleolar RNAs in rRNA modification and alternative pre-mRNA splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1625-34.	3.3	160
1989	Alternative splicing and nonsenseâ€“mediated mRNA decay enforce neural specific gene expression. <i>International Journal of Developmental Neuroscience</i> , 2016, 55, 102-108.	0.7	39
1990	Allelic variation of the COMT gene in a despotic primate society: A haplotype is related to cortisol excretion in <i>Macaca fuscata</i> . <i>Hormones and Behavior</i> , 2016, 78, 220-230.	1.0	14
1991	Dynamic Regulation of Tandem 3â€“ Untranslated Regions in Zebrafish Spleen Cells during Immune Response. <i>Journal of Immunology</i> , 2016, 196, 715-725.	0.4	11
1992	From polyadenylation to splicing: Dual role for mRNA 3' end formation factors. <i>RNA Biology</i> , 2016, 13, 259-264.	1.5	34
1993	Genome defense against exogenous nucleic acids in eukaryotes by non-coding DNA occurs through CRISPR-like mechanisms in the cytosol and the bodyguard protection in the nucleus. <i>Mutation Research - Reviews in Mutation Research</i> , 2016, 767, 31-41.	2.4	5
1994	(Intrinsically disordered) splice variants in the proteome: implications for novel drug discovery. <i>Genes and Genomics</i> , 2016, 38, 577-594.	0.5	10
1995	A genome landscape of SRSF3-regulated splicing events and gene expression in human osteosarcoma U2OS cells. <i>Nucleic Acids Research</i> , 2016, 44, 1854-1870.	6.5	112
1996	Identification of important long non-coding RNAs and highly recurrent aberrant alternative splicing events in hepatocellular carcinoma through integrative analysis of multiple RNA-Seq datasets. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1035-1051.	1.0	31

#	ARTICLE	IF	CITATIONS
1997	Amelogenin Exon4 Forms a Novel miRNA That Directs Ameloblast and Osteoblast Differentiation. <i>Journal of Dental Research</i> , 2016, 95, 423-429.	2.5	15
1998	Transcriptome Survey of the Contribution of Alternative Splicing to Proteome Diversity in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2016, 9, 749-752.	3.9	43
1999	Quantitative evaluation of alternatively spliced mRNA isoforms by label-free real-time plasmonic sensing. <i>Biosensors and Bioelectronics</i> , 2016, 78, 118-125.	5.3	22
2000	TCGASpliceSeq a compendium of alternative mRNA splicing in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D1018-D1022.	6.5	358
2001	RNA mis-splicing in disease. <i>Nature Reviews Genetics</i> , 2016, 17, 19-32.	7.7	935
2002	Pushing the annotation of cellular activities to a higher resolution: Predicting functions at the isoform level. <i>Methods</i> , 2016, 93, 110-118.	1.9	9
2003	Circadian mRNA expression: insights from modeling and transcriptomics. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 497-521.	2.4	27
2004	Transcriptomics and Gene Regulation. <i>Translational Bioinformatics</i> , 2016, , .	0.0	2
2005	Gene set analysis approaches for RNA-seq data: performance evaluation and application guideline. <i>Briefings in Bioinformatics</i> , 2016, 17, 393-407.	3.2	57
2006	Vials: Visualizing Alternative Splicing of Genes. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2016, 22, 399-408.	2.9	15
2007	A Class-Information-Based Sparse Component Analysis Method to Identify Differentially Expressed Genes on RNA-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 392-398.	1.9	19
2008	Regulation of CD44E by DARPP-32-dependent activation of SRp20 splicing factor in gastric tumorigenesis. <i>Oncogene</i> , 2016, 35, 1847-1856.	2.6	25
2009	Aberrant RNA splicing in cancer; expression changes and driver mutations of splicing factor genes. <i>Oncogene</i> , 2016, 35, 2413-2427.	2.6	426
2010	Alternative splicing mechanisms orchestrating post-transcriptional gene expression: intron retention and the intron-rich genome of apicomplexan parasites. <i>Current Genetics</i> , 2016, 62, 31-38.	0.8	17
2011	Connecting the dots: chromatin and alternative splicing in EMT. <i>Biochemistry and Cell Biology</i> , 2016, 94, 12-25.	0.9	28
2012	Cooperation of Genomic and Rapid Nongenomic Actions of Estrogens in Synaptic Plasticity. <i>Molecular Neurobiology</i> , 2017, 54, 4113-4126.	1.9	35
2013	Protein complex analysis: From raw protein lists to protein interaction networks. <i>Mass Spectrometry Reviews</i> , 2017, 36, 600-614.	2.8	22
2014	The Role of Reactive Oxygen and Nitrogen Species in the Expression and Splicing of Nitric Oxide Receptor. <i>Antioxidants and Redox Signaling</i> , 2017, 26, 122-136.	2.5	14

#	ARTICLE	IF	CITATIONS
2015	PBSeq: Modeling base-level bias to estimate gene and isoform expression for RNA-seq data. International Journal of Machine Learning and Cybernetics, 2017, 8, 1247-1258.	2.3	2
2016	<sc>RNA</sc>â€Seq methods for transcriptome analysis. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1364.	3.2	433
2017	A Tissue-Mapped Axolotl De Novo Transcriptome Enables Identification of Limb Regeneration Factors. Cell Reports, 2017, 18, 762-776.	2.9	752
2018	Functional changes in mRNA expression and alternative pre-mRNA splicing associated with the effects of nutrition on apoptosis and spermatogenesis in the adult testis. BMC Genomics, 2017, 18, 64.	1.2	22
2019	A joint-L2,1-norm-constraint-based semi-supervised feature extraction for RNA-Seq data analysis. Neurocomputing, 2017, 228, 263-269.	3.5	27
2020	Splicing imbalances in basal-like breast cancer underpin perturbation of cell surface and oncogenic pathways and are associated with patientsâ€™ survival. Scientific Reports, 2017, 7, 40177.	1.6	12
2021	Emerging roles for RNA-binding proteins as effectors and regulators of cardiovascular disease. European Heart Journal, 2017, 38, ehw567.	1.0	94
2022	Molecular cloning, alternative splicing and mRNA expression analysis of <i>MAG11</i> and its correlation with laying performance in geese. British Poultry Science, 2017, 58, 158-165.	0.8	4
2023	Multilayered Control of Alternative Splicing Regulatory Networks by Transcription Factors. Molecular Cell, 2017, 65, 539-553.e7.	4.5	143
2024	Reproductive modification in forest plantations: impacts on biodiversity and society. New Phytologist, 2017, 213, 1000-1021.	3.5	35
2025	Splicing regulation and dysregulation of cholinergic genes expressed at the neuromuscular junction. Journal of Neurochemistry, 2017, 142, 64-72.	2.1	20
2026	SRSF2 Regulates Alternative Splicing to Drive Hepatocellular Carcinoma Development. Cancer Research, 2017, 77, 1168-1178.	0.4	115
2027	Evaluation of genome-wide susceptibility loci for high myopia in a Han Chinese population. Ophthalmic Genetics, 2017, 38, 330-334.	0.5	3
2028	A Cytoplasmic RNA Virus Alters the Function of the Cell Splicing Protein SRSF2. Journal of Virology, 2017, 91, .	1.5	34
2029	Tissue-specific regulation of alternative polyadenylation represses expression of neuronal ankyrin isoform in <i>C. elegans</i> epidermal development. Development (Cambridge), 2017, 144, 698-707.	1.2	14
2030	Prognostic alternative mRNA splicing signature in non-small cell lung cancer. Cancer Letters, 2017, 393, 40-51.	3.2	214
2031	Microfluidic Device for Studying Controllable Hydrodynamic Flow Induced Cellular Responses. Analytical Chemistry, 2017, 89, 3710-3715.	3.2	17
2032	UV Irradiation Induces a Non-coding RNA that Functionally Opposes the Protein Encoded by the Same Gene. Cell, 2017, 168, 843-855.e13.	13.5	157

#	ARTICLE	IF	CITATIONS
2033	Mutations in the Spliceosome Component CWC27 Cause Retinal Degeneration with or without Additional Developmental Anomalies. <i>American Journal of Human Genetics</i> , 2017, 100, 592-604.	2.6	61
2034	A saga of cancer epigenetics: linking epigenetics to alternative splicing. <i>Biochemical Journal</i> , 2017, 474, 885-896.	1.7	36
2035	Linking Protein and RNA Function within the Same Gene. <i>Cell</i> , 2017, 168, 753-755.	13.5	2
2036	Comprehensive analysis of long non-coding RNAs highlights their spatio-temporal expression patterns and evolutionary conservation in <i>Sus scrofa</i> . <i>Scientific Reports</i> , 2017, 7, 43166.	1.6	75
2037	Single-cell mRNA isoform diversity in the mouse brain. <i>BMC Genomics</i> , 2017, 18, 126.	1.2	70
2038	De novo hybrid assembly of the rubber tree genome reveals evidence of paleotetraploidy in <i>Hevea</i> species. <i>Scientific Reports</i> , 2017, 7, 41457.	1.6	95
2039	Highly sensitive and multiplexed quantification of mRNA splice variants by the direct ligation of DNA probes at the exon junction and universal PCR amplification. <i>Chemical Science</i> , 2017, 8, 3635-3640.	3.7	29
2040	Histone modifications influence skipped exons inclusion. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750003.	0.3	3
2041	Microexons: discovery, regulation, and function. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1418.	3.2	56
2042	Membrane-bound stem cell factor is the major but not only driver of fibroblast-induced murine skin mast cell differentiation. <i>Experimental Dermatology</i> , 2017, 26, 255-262.	1.4	18
2043	Analysis of Ribosome-Associated mRNAs in Rice Reveals the Importance of Transcript Size and GC Content in Translation. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 203-219.	0.8	43
2044	Transcriptome analysis reveals the complexity of alternative splicing regulation in the fungus <i>Verticillium dahliae</i> . <i>BMC Genomics</i> , 2017, 18, 130.	1.2	71
2045	RNA splicing in human disease and in the clinic. <i>Clinical Science</i> , 2017, 131, 355-368.	1.8	78
2046	The role of RNA alternative splicing in regulating cancer metabolism. <i>Human Genetics</i> , 2017, 136, 1113-1127.	1.8	89
2047	Chemotherapy for Leukemia. , 2017, , .		2
2048	Transcriptome profile of the human placenta. <i>Functional and Integrative Genomics</i> , 2017, 17, 551-563.	1.4	29
2049	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	516
2050	The Relationship between Alternative Splicing and Proteomic Complexity. <i>Trends in Biochemical Sciences</i> , 2017, 42, 407-408.	3.7	138

#	ARTICLE	IF	CITATIONS
2051	Alternative splicing as a regulator of development and tissue identity. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 437-451.	16.1	929
2052	WT1-associated protein is a novel prognostic factor in pancreatic ductal adenocarcinoma. <i>Oncology Letters</i> , 2017, 13, 2531-2538.	0.8	38
2053	Drugging Pre-mRNA Splicing. <i>Topics in Medicinal Chemistry</i> , 2017, , 135-176.	0.4	1
2054	Cleavage and polyadenylation: Ending the message expands gene regulation. <i>RNA Biology</i> , 2017, 14, 865-890.	1.5	106
2055	Evidence of nuclei-encoded spliceosome mediating splicing of mitochondrial RNA. <i>Human Molecular Genetics</i> , 2017, 26, 2472-2479.	1.4	21
2056	Normalized long read RNA sequencing in chicken reveals transcriptome complexity similar to human. <i>BMC Genomics</i> , 2017, 18, 323.	1.2	129
2057	Quantitative cardiac phosphoproteomics profiling during ischemia-reperfusion in an immature swine model. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2017, 313, H125-H137.	1.5	9
2058	Association of 5-hydroxymethylation and 5-methylation of DNA cytosine with tissue-specific gene expression. <i>Epigenetics</i> , 2017, 12, 123-138.	1.3	61
2059	Splice variants as novel targets in pancreatic ductal adenocarcinoma. <i>Scientific Reports</i> , 2017, 7, 2980.	1.6	34
2060	Regulated Intron Removal Integrates Motivational State and Experience. <i>Cell</i> , 2017, 169, 836-848.e15.	13.5	35
2061	The Dimensions, Dynamics, and Relevance of the Mammalian Noncoding Transcriptome. <i>Trends in Genetics</i> , 2017, 33, 464-478.	2.9	181
2062	Sex-Specific Transcript Diversity in the Fly Head Is Established during Pupal Stages and Adulthood and Is Largely Independent of the Mating Process and the Germline. <i>Sexual Development</i> , 2017, 11, 94-108.	1.1	0
2063	A tool for integrating genetic and mass spectrometry-based peptide data: Proteogenomics Viewer. <i>BioEssays</i> , 2017, 39, 1700015.	1.2	7
2064	Integrative gene set enrichment analysis utilizing isoform-specific expression. <i>Genetic Epidemiology</i> , 2017, 41, 498-510.	0.6	6
2066	Circulating extracellular DNA levels are acutely elevated in ischaemic stroke and associated with innate immune system activation. <i>Brain Injury</i> , 2017, 31, 1369-1375.	0.6	46
2067	Genome-wide analysis of specific alterations in transcript structure and accumulation caused by nutrient deficiencies in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 91, 741-753.	2.8	46
2068	The Landscape of Isoform Switches in Human Cancers. <i>Molecular Cancer Research</i> , 2017, 15, 1206-1220.	1.5	208
2069	Neuronal activity-regulated alternative mRNA splicing. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 91, 184-193.	1.2	23

#	ARTICLE	IF	CITATIONS
2070	A survey of the complex transcriptome from the highly polyploid sugarcane genome using full-length isoform sequencing and de novo assembly from short read sequencing. <i>BMC Genomics</i> , 2017, 18, 395.	1.2	180
2071	The alternative life of <sc>RNA</sc>â€”sequencing meets single molecule approaches. <i>FEBS Letters</i> , 2017, 591, 1455-1470.	1.3	8
2072	Modulation of aberrant splicing in human RNA diseases by chemical compounds. <i>Human Genetics</i> , 2017, 136, 1237-1245.	1.8	22
2073	On the design and prospects of direct RNA sequencing. <i>Briefings in Functional Genomics</i> , 2017, 16, 326-335.	1.3	18
2074	Highâ€”Throughput Assays to Assess the Functional Impact of Genetic Variants: A Road Towards Genomicâ€”Driven Medicine. <i>Clinical and Translational Science</i> , 2017, 10, 67-77.	1.5	48
2075	Alternative splicing: the pledge, the turn, and the prestige. <i>Human Genetics</i> , 2017, 136, 1015-1042.	1.8	106
2076	Polymorphism and protein expression of MUTYH gene for risk of rheumatoid arthritis. <i>BMC Musculoskeletal Disorders</i> , 2017, 18, 69.	0.8	5
2077	Comprehensive analysis of differentially expressed genes under salt stress in pear (<i>Pyrus betulaefolia</i>) using RNA-Seq. <i>Plant Growth Regulation</i> , 2017, 82, 409-420.	1.8	13
2078	Comparative transcriptome analysis of berry-sizing effects of gibberellin (GA3) on seedless <i>Vitis vinifera</i> L.. <i>Genes and Genomics</i> , 2017, 39, 493-507.	0.5	14
2079	Evolutionary insights into T-type Ca ²⁺ channel structure, function, and ion selectivity from the <i>Trichoplax adhaerens</i> homologue. <i>Journal of General Physiology</i> , 2017, 149, 483-510.	0.9	30
2080	Identified of a novel cis-element regulating the alternative splicing of LcDREB2. <i>Scientific Reports</i> , 2017, 7, 46106.	1.6	35
2081	RNA G-Quadruplexes as Key Motifs of the Transcriptome. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2017, 170, 1-20.	0.6	20
2082	Alternative splicing affects the targeting sequence of peroxisome proteins in Arabidopsis. <i>Plant Cell Reports</i> , 2017, 36, 1027-1036.	2.8	9
2083	How do messenger RNA splicing alterations drive myelodysplasia?. <i>Blood</i> , 2017, 129, 2465-2470.	0.6	28
2084	PTMOracle: A Cytoscape App for Covisualizing and Coanalyzing Post-Translational Modifications in Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2017, 16, 1988-2003.	1.8	17
2085	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. <i>Nature Communications</i> , 2017, 8, 7.	5.8	108
2086	Triple-Stage Mass Spectrometry Unravels the Heterogeneity of an Endogenous Protein Complex. <i>Analytical Chemistry</i> , 2017, 89, 4708-4715.	3.2	52
2087	Identification of a DNA Damageâ€”Induced Alternative Splicing Pathway That Regulates p53 and Cellular Senescence Markers. <i>Cancer Discovery</i> , 2017, 7, 766-781.	7.7	70

#	ARTICLE	IF	CITATIONS
2088	Transcriptome analysis of bronchoalveolar lavage fluid from children with severe Mycoplasma pneumoniae pneumonia reveals novel gene expression and immunodeficiency. Human Genomics, 2017, 11, 4.	1.4	42
2089	Transcriptome analysis reveals critical genes and key pathways involved in early phyllotaxy development in maize. Genes and Genomics, 2017, 39, 15-26.	0.5	1
2090	Pharmacology of Modulators of Alternative Splicing. Pharmacological Reviews, 2017, 69, 63-79.	7.1	72
2091	Dynamic landscape of alternative polyadenylation during retinal development. Cellular and Molecular Life Sciences, 2017, 74, 1721-1739.	2.4	20
2092	Alternative splicing and the evolution of phenotypic novelty. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20150474.	1.8	179
2093	Global identification of alternative splicing via comparative analysis of <sc>SMRT</sc> and Illumina-based <sc>RNA</sc>seq in strawberry. Plant Journal, 2017, 90, 164-176.	2.8	161
2094	Splicing factor gene mutations in hematologic malignancies. Blood, 2017, 129, 1260-1269.	0.6	99
2095	Alternative splicing regulation in tumor necrosis factor-mediated inflammation (Review). Oncology Letters, 2017, 14, 5114-5120.	0.8	10
2096	Deep learning of the splicing (epi)genetic code reveals a novel candidate mechanism linking histone modifications to ESC fate decision. Nucleic Acids Research, 2017, 45, 12100-12112.	6.5	66
2097	The eukaryotic genome is structurally and functionally more like a social insect colony than a book. Epigenomics, 2017, 9, 1469-1483.	1.0	2
2098	ESRP1 Mutations Cause Hearing Loss due to Defects in Alternative Splicing that Disrupt Cochlear Development. Developmental Cell, 2017, 43, 318-331.e5.	3.1	68
2099	Alternative Splicing: Expanding Diversity in Major ABC and SLC Drug Transporters. AAPS Journal, 2017, 19, 1643-1655.	2.2	6
2100	The Potential of Epigenetics Research to Transform Conceptions of Phenotype Development. Human Development, 2017, 60, 69-80.	1.2	43
2101	Analyses of long non-coding RNAs and mRNA profiling through RNA sequencing of MDBK cells at different stages of bovine viral diarrhoea virus infection. Research in Veterinary Science, 2017, 115, 508-516.	0.9	34
2102	Cellular and molecular responses of adult testis to changes in nutrition: novel insights from the sheep model. Reproduction, 2017, 154, R133-R141.	1.1	23
2103	Alternative splicing in aging and age-related diseases. Translational Medicine of Aging, 2017, 1, 32-40.	0.6	28
2104	Biocompatible silver, gold and silver/gold alloy nanoparticles for enhanced cancer therapy: in vitro and in vivo perspectives. Nanoscale, 2017, 9, 16773-16790.	2.8	62
2105	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	2.4	139

#	ARTICLE	IF	CITATIONS
2106	Revealing the Determinants of Widespread Alternative Splicing Perturbation in Cancer. <i>Cell Reports</i> , 2017, 21, 798-812.	2.9	51
2107	Alternative Polyadenylation: Methods, Findings, and Impacts. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 287-300.	3.0	100
2108	Untranslated Parts of Genes Interpreted: Making Heads or Tails of High-Throughput Transcriptomic Data via Computational Methods. <i>BioEssays</i> , 2017, 39, 1700090.	1.2	14
2109	Circular RNAs: Isolation, characterization and their potential role in diseases. <i>RNA Biology</i> , 2017, 14, 1715-1721.	1.5	90
2110	A regulated PNUTS mRNA to lncRNA splice switch mediates EMT and tumour progression. <i>Nature Cell Biology</i> , 2017, 19, 1105-1115.	4.6	262
2111	Comprehensive Analyses of Tissue-Specific Networks with Implications to Psychiatric Diseases. <i>Methods in Molecular Biology</i> , 2017, 1613, 371-402.	0.4	5
2112	SMN regulation in SMA and in response to stress: new paradigms and therapeutic possibilities. <i>Human Genetics</i> , 2017, 136, 1173-1191.	1.8	8
2113	Transcription elongation rate has a tissue-specific impact on alternative cleavage and polyadenylation in <i>Drosophila melanogaster</i> . <i>Rna</i> , 2017, 23, 1807-1816.	1.6	53
2114	Precursor microRNA-122 inhibits synthesis of <i>Insig1</i> isoform mRNA by modulating polyadenylation site usage. <i>Rna</i> , 2017, 23, 1886-1893.	1.6	4
2115	Differential Gene Expression Profiles and Alternative Isoform Regulations in Gill of Nile Tilapia in Response to Acute Hypoxia. <i>Marine Biotechnology</i> , 2017, 19, 551-562.	1.1	42
2116	Loss of NR2E3 represses AHR by LSD1 reprogramming, is associated with poor prognosis in liver cancer. <i>Scientific Reports</i> , 2017, 7, 10662.	1.6	17
2117	PAcluster: Clustering polyadenylation site data using canonical correlation analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750018.	0.3	3
2118	DASE2: differential alternative splicing variants estimation method without reference genome, and comparison with mapping strategy. <i>International Journal of Data Mining and Bioinformatics</i> , 2017, 18, 56.	0.1	0
2119	The developmental transcriptome landscape of receptive endometrium during embryo implantation in dairy goats. <i>Gene</i> , 2017, 633, 82-95.	1.0	16
2120	Differential alternative splicing coupled to nonsense-mediated decay of mRNA ensures dietary restriction-induced longevity. <i>Nature Communications</i> , 2017, 8, 306.	5.8	63
2121	Engineering Artificial Factors to Specifically Manipulate Alternative Splicing in Human Cells. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	0
2122	Shaping and Reshaping Transcriptome Plasticity during Evolution. <i>Trends in Biochemical Sciences</i> , 2017, 42, 682-684.	3.7	4
2123	The emerging role of alternative splicing in senescence and aging. <i>Aging Cell</i> , 2017, 16, 918-933.	3.0	141

#	ARTICLE	IF	CITATIONS
2124	CELF1 preferentially binds to exon-intron boundary and regulates alternative splicing in HeLa cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 911-921.	0.9	111
2125	Nanopore long-read RNAseq reveals widespread transcriptional variation among the surface receptors of individual B cells. <i>Nature Communications</i> , 2017, 8, 16027.	5.8	329
2126	Transcriptomic insights into the alternative splicing-mediated adaptation of the entomopathogenic fungus <i>Beauveria bassiana</i> to host niches: autophagy-related gene 8 as an example. <i>Environmental Microbiology</i> , 2017, 19, 4126-4139.	1.8	20
2127	scRNA sequencing in post-mortem human brains of neuropsychiatric disorders. <i>Psychiatry and Clinical Neurosciences</i> , 2017, 71, 663-672.	1.0	14
2128	An emerging model organism <i>Caenorhabditis elegans</i> for alternative pre-mRNA processing in vivo. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1428.	3.2	10
2129	Evidence of selection on splicing-associated loci in human populations and relevance to disease loci mapping. <i>Scientific Reports</i> , 2017, 7, 5980.	1.6	10
2130	Impact of Alternative Splicing on the Human Proteome. <i>Cell Reports</i> , 2017, 20, 1229-1241.	2.9	145
2131	Isoform Evolution in Primates through Independent Combination of Alternative RNA Processing Events. <i>Molecular Biology and Evolution</i> , 2017, 34, 2453-2468.	3.5	37
2132	Fuzziness enables context dependence of protein interactions. <i>FEBS Letters</i> , 2017, 591, 2682-2695.	1.3	60
2133	Spliceosomal protein <i>eftud2</i> mutation leads to p53-dependent apoptosis in zebrafish neural progenitors. <i>Nucleic Acids Research</i> , 2017, 45, 3422-3436.	6.5	64
2134	Using RNA-Seq to Discover Genetic Polymorphisms That Produce Hidden Splice Variants. <i>Methods in Molecular Biology</i> , 2017, 1648, 129-142.	0.4	2
2135	Single cell transcriptomics of noncoding scRNAs and their cell-specificity. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1433.	3.2	23
2136	Transcriptomic Analysis of Ribosome-Bound mRNA in Cortical Neurites <i>In Vivo</i> . <i>Journal of Neuroscience</i> , 2017, 37, 8688-8705.	1.7	49
2137	Novel landscape of HLA-C isoforms expressed in clear cell renal cell carcinoma patients. <i>Molecular Oncology</i> , 2017, 11, 1561-1578.	2.1	67
2138	Transcriptomic characterization of bovine primary cultured hepatocytes; a cross-comparison with a bovine liver and the Madin-Darby bovine kidney cells. <i>Research in Veterinary Science</i> , 2017, 113, 40-49.	0.9	8
2139	Activity-Dependent Regulation of Alternative Cleavage and Polyadenylation During Hippocampal Long-Term Potentiation. <i>Scientific Reports</i> , 2017, 7, 17377.	1.6	38
2140	Smooth Muscle Phenotypic Diversity. <i>Advances in Pharmacology</i> , 2017, 78, 383-415.	1.2	5
2141	Cell-Type-Specific Splicing of Piezo2 Regulates Mechanotransduction. <i>Cell Reports</i> , 2017, 21, 2760-2771.	2.9	98

#	ARTICLE	IF	CITATIONS
2142	In vitro antimicrobial and in vivo wound healing effect of actinobacterially synthesised nanoparticles of silver, gold and their alloy. <i>RSC Advances</i> , 2017, 7, 51729-51743.	1.7	31
2143	Snail Driving Alternative Splicing of CD44 by ESRP1 Enhances Invasion and Migration in Epithelial Ovarian Cancer. <i>Cellular Physiology and Biochemistry</i> , 2017, 43, 2489-2504.	1.1	49
2144	Selective deletion of the soluble Colony-Stimulating Factor 1 isoform in vivo prevents estrogen-deficiency bone loss in mice. <i>Bone Research</i> , 2017, 5, 17022.	5.4	16
2145	CRISPR/Cas9 Engineering of Adult Mouse Liver Demonstrates That the Dnajb1-Prkaca Gene Fusion Is Sufficient to Induce Tumors Resembling Fibrolamellar Hepatocellular Carcinoma. <i>Gastroenterology</i> , 2017, 153, 1662-1673.e10.	0.6	86
2146	Alternative splicing and start sites: Lessons from the Grainyhead-like family. <i>Developmental Biology</i> , 2017, 429, 12-19.	0.9	16
2147	The determinants of alternative RNA splicing in human cells. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1175-1195.	1.0	68
2148	HuR-Dependent Editing of a New Mineralocorticoid Receptor Splice Variant Reveals an Osmoregulatory Loop for Sodium Homeostasis. <i>Scientific Reports</i> , 2017, 7, 4835.	1.6	8
2149	RNA expression in human retina. <i>Human Molecular Genetics</i> , 2017, 26, R68-R74.	1.4	10
2150	BRIE: transcriptome-wide splicing quantification in single cells. <i>Genome Biology</i> , 2017, 18, 123.	3.8	86
2151	Increasing evidence for the presence of alternative proteins in human tissues and cell lines. <i>Applied Cancer Research</i> , 2017, 37, .	1.0	1
2152	A random effects model for the identification of differential splicing (REIDS) using exon and HTA arrays. <i>BMC Bioinformatics</i> , 2017, 18, 273.	1.2	2
2153	Deciphering alternative splicing and nonsense-mediated decay modulate expression in primary lymphoid tissues of birds infected with avian pathogenic E. coli (APEC). <i>BMC Genetics</i> , 2017, 18, 21.	2.7	8
2154	Single-Cell Alternative Splicing Analysis with Expedition Reveals Splicing Dynamics during Neuron Differentiation. <i>Molecular Cell</i> , 2017, 67, 148-161.e5.	4.5	155
2155	Computational Methods and Correlation of Exon-skipping Events with Splicing, Transcription, and Epigenetic Factors. <i>Methods in Molecular Biology</i> , 2017, 1513, 163-170.	0.4	12
2156	Allele-specific splicing effects on DKKL1 and ZNF419 transcripts in HeLa cells. <i>Gene</i> , 2017, 598, 107-112.	1.0	1
2157	Pre-mRNA mis-splicing of sarcomeric genes in heart failure. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2017, 1863, 2056-2063.	1.8	30
2158	The bromodomain protein BRD4 regulates splicing during heat shock. <i>Nucleic Acids Research</i> , 2017, 45, 382-394.	6.5	54
2159	The roles of RNA processing in translating genotype to phenotype. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 102-114.	16.1	176

#	ARTICLE	IF	CITATIONS
2160	The dynamic landscape of fission yeast meiosis alternative-splice isoforms. <i>Genome Research</i> , 2017, 27, 145-156.	2.4	40
2161	Developmental regulation of <scp>RNA</scp> processing by Rbfox proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1398.	3.2	105
2162	Alternative RNA splicing and gastric cancer. <i>Mutation Research - Reviews in Mutation Research</i> , 2017, 773, 263-273.	2.4	27
2163	Robust identification of Ptbp1-dependent splicing events by a junction-centric approach in <i>Xenopus laevis</i> . <i>Developmental Biology</i> , 2017, 426, 449-459.	0.9	4
2164	Circular RNAs: Unexpected outputs of many protein-coding genes. <i>RNA Biology</i> , 2017, 14, 1007-1017.	1.5	111
2165	Oxidative stress controls the choice of alternative last exons via a Brahmaâ€“BRCA1â€“CstF pathway. <i>Nucleic Acids Research</i> , 2017, 45, 902-914.	6.5	26
2166	Hiding in the Shadows: CPOX Expression and 5-ALA Induced Fluorescence in Human Glioma Cells. <i>Molecular Neurobiology</i> , 2017, 54, 5699-5708.	1.9	35
2167	Transcriptional Elongation Regulator 1 Affects Transcription and Splicing of Genes Associated with Cellular Morphology and Cytoskeleton Dynamics and Is Required for Neurite Outgrowth in Neuroblastoma Cells and Primary Neuronal Cultures. <i>Molecular Neurobiology</i> , 2017, 54, 7808-7823.	1.9	18
2168	Circular RNA Detection from High-throughput Sequencing. , 2017, , .		1
2169	Information transduction capacity reduces the uncertainties in annotation-free isoform discovery and quantification. <i>Nucleic Acids Research</i> , 2017, 45, e143-e143.	6.5	6
2170	RNA G-quadruplex secondary structure promotes alternative splicing via the RNA-binding protein hnRNPF. <i>Genes and Development</i> , 2017, 31, 2296-2309.	2.7	154
2171	The landscape of human mutually exclusive splicing. <i>Molecular Systems Biology</i> , 2017, 13, 959.	3.2	53
2172	Hybrid splicing minigene and antisense oligonucleotides as efficient tools to determine functional protein/RNA interactions. <i>Scientific Reports</i> , 2017, 7, 17587.	1.6	11
2173	Systematic Analyses and Prediction of Human Drug Side Effect Associated Proteins from the Perspective of Protein Evolution. <i>Genome Biology and Evolution</i> , 2017, 9, 337-350.	1.1	8
2174	Rare Intronic Variations in TP73 Gene Found in Patients with Alzheimerâ€™s Disease. <i>International Journal of Human Genetics</i> , 2017, 17, 158-168.	0.1	2
2175	Evaluation and comparison of computational tools for RNA-seq isoform quantification. <i>BMC Genomics</i> , 2017, 18, 583.	1.2	137
2176	Expitope 2.0: a tool to assess immunotherapeutic antigens for their potential cross-reactivity against naturally expressed proteins in human tissues. <i>BMC Cancer</i> , 2017, 17, 892.	1.1	22
2177	Transcriptome Sequencing for Precise and Accurate Measurement of Transcripts and Accessibility of TCGA for Cancer Datasets and Analysis. , 0, , .		0

#	ARTICLE	IF	CITATIONS
2178	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 694.	1.7	109
2179	Transcriptional and Splicing Regulation of Spinal Muscular Atrophy Genes. , 2017, , 75-97.		7
2180	Integrative deep models for alternative splicing. <i>Bioinformatics</i> , 2017, 33, i274-i282.	1.8	50
2181	Genome-wide Analysis of Alternative Splicing in An Inbred Cabbage (<i>Brassica oleracea</i> L.) Line "HO"™ in Response to Heat Stress. <i>Current Genomics</i> , 2017, 19, 12-20.	0.7	10
2182	Sample Size Estimation for Detection of Splicing Events in Transcriptome Sequencing Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1900.	1.8	3
2183	Analysis and Prediction of Exon Skipping Events from RNA-Seq with Sequence Information Using Rotation Forest. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2691.	1.8	3
2184	Rare Splice Variants in Long Non-Coding RNAs. <i>Non-coding RNA</i> , 2017, 3, 23.	1.3	8
2185	Targeting Splicing in the Treatment of Human Disease. <i>Genes</i> , 2017, 8, 87.	1.0	41
2186	Alternative Splicing in Breast Cancer and the Potential Development of Therapeutic Tools. <i>Genes</i> , 2017, 8, 217.	1.0	24
2187	Alternative Pre-mRNA Splicing in Mammals and Teleost Fish: A Effective Strategy for the Regulation of Immune Responses Against Pathogen Infection. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1530.	1.8	51
2188	The Evolutionary Relationship between Alternative Splicing and Gene Duplication. <i>Frontiers in Genetics</i> , 2017, 08, 14.	1.1	49
2189	Jmjd6, a JmjC Dioxygenase with Many Interaction Partners and Pleiotropic Functions. <i>Frontiers in Genetics</i> , 2017, 8, 32.	1.1	49
2190	A Bioinformatics-Based Alternative mRNA Splicing Code that May Explain Some Disease Mutations Is Conserved in Animals. <i>Frontiers in Genetics</i> , 2017, 8, 38.	1.1	14
2191	Characterization of X-Chromosome Gene Expression in Bovine Blastocysts Derived by In vitro Fertilization and Somatic Cell Nuclear Transfer. <i>Frontiers in Genetics</i> , 2017, 8, 42.	1.1	18
2192	New Insights into 5hmC DNA Modification: Generation, Distribution and Function. <i>Frontiers in Genetics</i> , 2017, 8, 100.	1.1	166
2193	Adaptive Evolution of Energy Metabolism-Related Genes in Hypoxia-Tolerant Mammals. <i>Frontiers in Genetics</i> , 2017, 8, 205.	1.1	34
2194	Distinct Transcriptional and Alternative Splicing Signatures of Decidual CD4+ T Cells in Early Human Pregnancy. <i>Frontiers in Immunology</i> , 2017, 8, 682.	2.2	47
2195	Genome-Wide Transcriptome Analysis Reveals Extensive Alternative Splicing Events in the Protoscolecetes of <i>Echinococcus granulosus</i> and <i>Echinococcus multilocularis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 929.	1.5	22

#	ARTICLE	IF	CITATIONS
2196	The Importance of ncRNAs as Epigenetic Mechanisms in Phenotypic Variation and Organic Evolution. <i>Frontiers in Microbiology</i> , 2017, 8, 2483.	1.5	72
2197	Identification of Three Novel Splicing Variants and Expression Analysis of Chicken GPR1 Gene. <i>BioMed Research International</i> , 2017, 2017, 1-10.	0.9	0
2198	The ESRP1-GPR137 axis contributes to intestinal pathogenesis. <i>ELife</i> , 2017, 6, .	2.8	24
2199	LOX-1 and Its Splice Variants: A New Challenge for Atherosclerosis and Cancer-Targeted Therapies. <i>International Journal of Molecular Sciences</i> , 2017, 18, 290.	1.8	29
2200	IsoSel: Protein Isoform Selector for phylogenetic reconstructions. <i>PLoS ONE</i> , 2017, 12, e0174250.	1.1	7
2201	Isolation and characterization of alternatively spliced variants of the mouse sigma1 receptor gene, Sigmar1. <i>PLoS ONE</i> , 2017, 12, e0174694.	1.1	9
2202	A comparison of per sample global scaling and per gene normalization methods for differential expression analysis of RNA-seq data. <i>PLoS ONE</i> , 2017, 12, e0176185.	1.1	60
2203	The identification of switch-like alternative splicing exons among multiple samples with RNA-Seq data. <i>PLoS ONE</i> , 2017, 12, e0178320.	1.1	2
2204	Developmentally regulated internal transcription initiation during meiosis in budding yeast. <i>PLoS ONE</i> , 2017, 12, e0188001.	1.1	16
2205	Functions for fission yeast splicing factors SpSlu7 and SpPrp18 in alternative splice-site choice and stress-specific regulated splicing. <i>PLoS ONE</i> , 2017, 12, e0188159.	1.1	18
2206	Long 3'UTR of Nurr1 mRNAs is targeted by miRNAs in mesencephalic dopamine neurons. <i>PLoS ONE</i> , 2017, 12, e0188177.	1.1	13
2207	Alternate splicing of transcripts shape macrophage response to <i>Mycobacterium tuberculosis</i> infection. <i>PLoS Pathogens</i> , 2017, 13, e1006236.	2.1	79
2208	Stochastic principles governing alternative splicing of RNA. <i>PLoS Computational Biology</i> , 2017, 13, e1005761.	1.5	16
2209	Transcriptome analysis of muskrat scented glands degeneration mechanism. <i>PLoS ONE</i> , 2017, 12, e0176935.	1.1	7
2210	Depletion of Arabidopsis SC35 and SC35-like serine/arginine-rich proteins affects the transcription and splicing of a subset of genes. <i>PLoS Genetics</i> , 2017, 13, e1006663.	1.5	76
2211	Functional classification of DNA variants by hybrid minigenes: Identification of 30 spliceogenic variants of BRCA2 exons 17 and 18. <i>PLoS Genetics</i> , 2017, 13, e1006691.	1.5	53
2212	Alternative exon definition events control the choice between nuclear retention and cytoplasmic export of U11/U12-65K mRNA. <i>PLoS Genetics</i> , 2017, 13, e1006824.	1.5	10
2213	Environmental perturbations lead to extensive directional shifts in RNA processing. <i>PLoS Genetics</i> , 2017, 13, e1006995.	1.5	25

#	ARTICLE	IF	CITATIONS
2214	The combinatorial control of alternative splicing in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2017, 13, e1007033.	1.5	10
2215	ZIKV infection effects changes in gene splicing, isoform composition and lncRNA expression in human neural progenitor cells. <i>Virology Journal</i> , 2017, 14, 217.	1.4	56
2216	A novel mechanism for variable phenotypic expressivity in Mendelian diseases uncovered by an AU-rich element (ARE)-creating mutation. <i>Genome Biology</i> , 2017, 18, 144.	3.8	19
2217	Natural genetic variation of the cardiac transcriptome in non-diseased donors and patients with dilated cardiomyopathy. <i>Genome Biology</i> , 2017, 18, 170.	3.8	70
2218	K-mer clustering algorithm using a MapReduce framework: application to the parallelization of the Inchworm module of Trinity. <i>BMC Bioinformatics</i> , 2017, 18, 467.	1.2	17
2219	Transcriptome analysis reveals the host selection fitness mechanisms of the <i>Rhizoctonia solani</i> AG1A pathogen. <i>Scientific Reports</i> , 2017, 7, 10120.	1.6	43
2220	Molecular cloning of novel transcripts of human kallikrein-related peptidases 5, 6, 7, 8 and 9 (KLK5) Tj ETQq0 0,0rgBT /Overlock 10	1.6	17
2221	DEXseq and Cuffdiff approaches weighing differential spliced genes exons modulation in estrogen receptor (Er) breast cancer cells. <i>African Journal of Biotechnology</i> , 2017, 16, 1404-1427.	0.3	0
2222	IsoPlot: a database for comparison of mRNA isoforms in fruit fly and mosquitoes. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	0
2223	Antisense-Oligonucleotide Modulation of SMN2 Pre-mRNA Splicing. , 2017, , 301-311.		4
2224	A dual transcript-discovery approach to improve the delimitation of gene features from RNA-seq data in the chicken model. <i>Biology Open</i> , 2018, 7, .	0.6	7
2225	Epigenetic Regulation of Neurogenesis by microRNAs. , 2017, , 119-136.		0
2226	Interplay Between Chromatin and Splicing. , 2017, , 191-209.		3
2227	Benchmarking pathway interaction network for colorectal cancer to identify dysregulated pathways. <i>Brazilian Journal of Medical and Biological Research</i> , 2017, 50, e5981.	0.7	1
2228	Optimized Exon-Exon Junction Library and its Application on Rodents' Brain Transcriptome Analysis. <i>Brazilian Archives of Biology and Technology</i> , 2017, 60, .	0.5	0
2229	Proteomic Evidence for In-Frame and Out-of-Frame Alternatively Spliced Isoforms in Human and Mouse. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1284-1289.	1.9	3
2230	PennDiff: detecting differential alternative splicing and transcription by RNA sequencing. <i>Bioinformatics</i> , 2018, 34, 2384-2391.	1.8	14
2231	Epigenetic Research, Computational Methods in. , 2018, , 347-353.		0

#	ARTICLE	IF	CITATIONS
2232	Tracking Alternatively Spliced Isoforms from Long Reads by SpliceHunter. <i>Methods in Molecular Biology</i> , 2018, 1751, 73-88.	0.4	5
2233	Alternative transcription of a shorter, non-anti-angiogenic thrombospondin-2 variant in cancer-associated blood vessels. <i>Oncogene</i> , 2018, 37, 2573-2585.	2.6	22
2234	Behind the scenes of HIV-1 replication: Alternative splicing as the dependency factor on the quiet. <i>Virology</i> , 2018, 516, 176-188.	1.1	44
2235	Integrative omics for health and disease. <i>Nature Reviews Genetics</i> , 2018, 19, 299-310.	7.7	676
2236	Identification of juvenility-associated genes in the mouse hepatocytes and cardiomyocytes. <i>Scientific Reports</i> , 2018, 8, 3132.	1.6	8
2237	Two novel variants of the PHEX gene in patients with X-linked dominant hypophosphatemic rickets and prenatal diagnosis for fetuses in these families. <i>International Journal of Molecular Medicine</i> , 2018, 41, 2012-2020.	1.8	4
2238	Isoform-level gene expression patterns in single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2018, 34, 2392-2400.	1.8	15
2239	RNA-QC-chain: comprehensive and fast quality control for RNA-Seq data. <i>BMC Genomics</i> , 2018, 19, 144.	1.2	46
2240	Developmentally linked human DNA hypermethylation is associated with down-modulation, repression, and upregulation of transcription. <i>Epigenetics</i> , 2018, 13, 275-289.	1.3	31
2241	C3G dynamically associates with nuclear speckles and regulates mRNA splicing. <i>Molecular Biology of the Cell</i> , 2018, 29, 1111-1124.	0.9	7
2242	Transcriptome Data Analysis. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	3
2243	Regulation of Tak1 alternative splicing by splice-switching oligonucleotides. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 1018-1024.	1.0	4
2244	Most human introns are recognized via multiple and tissue-specific branchpoints. <i>Genes and Development</i> , 2018, 32, 577-591.	2.7	95
2245	Transcriptome analysis of alternative splicing in different moso bamboo tissues. <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	7
2246	Network-Based Approaches for Pathway Level Analysis. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 8.25.1-8.25.24.	25.8	33
2247	The comparison of alternative splicing among the multiple tissues in cucumber. <i>BMC Plant Biology</i> , 2018, 18, 5.	1.6	18
2248	PHF5A Epigenetically Inhibits Apoptosis to Promote Breast Cancer Progression. <i>Cancer Research</i> , 2018, 78, 3190-3206.	0.4	62
2249	A 360° view of circular RNAs: From biogenesis to functions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1478.	3.2	356

#	ARTICLE	IF	CITATIONS
2250	Modulation of Abnormal Splicing of RNA Diseases by Small Chemical Compounds. , 2018, , 115-130.		0
2251	RNA Analysis as a Tool to Determine Clinically Relevant Gene Fusions and Splice Variants. Archives of Pathology and Laboratory Medicine, 2018, 142, 474-479.	1.2	16
2252	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
2253	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. Cell Stem Cell, 2018, 22, 575-588.e7.	5.2	40
2254	Impaired Spermatogenesis, Muscle, and Erythrocyte Function in U12 Intron Splicing-Defective Zrsr1 Mutant Mice. Cell Reports, 2018, 23, 143-155.	2.9	33
2256	Inferring the effect of genomic variation in the new era of genomics. Human Mutation, 2018, 39, 756-773.	1.1	24
2257	Applied RNA Bioscience. , 2018, , .		1
2258	Predominant patterns of splicing evolution on human, chimpanzee and macaque evolutionary lineages. Human Molecular Genetics, 2018, 27, 1474-1485.	1.4	18
2259	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. Nature Communications, 2018, 9, 490.	5.8	198
2260	A small, portable RNA device for the control of exon skipping in mammalian cells. Nucleic Acids Research, 2018, 46, e48-e48.	6.5	40
2261	Splicing regulation by long noncoding RNAs. Nucleic Acids Research, 2018, 46, 2169-2184.	6.5	226
2262	3' UTR lengthening as a novel mechanism in regulating cellular senescence. Genome Research, 2018, 28, 285-294.	2.4	90
2263	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	3.9	580
2264	SRSF10-mediated IL1RAP alternative splicing regulates cervical cancer oncogenesis via mIL1RAP-NF- κ B-CD47 axis. Oncogene, 2018, 37, 2394-2409.	2.6	95
2265	Cell-type-resolved alternative splicing patterns in mouse liver. DNA Research, 2018, 25, 265-275.	1.5	14
2266	Electrophiles, Types of. , 2018, , 321-322.		0
2267	microRNA-mediated regulation of splicing factors SRSF1, SRSF2 and hnRNP A1 in context of their alternatively spliced 3' UTRs. Experimental Cell Research, 2018, 363, 208-217.	1.2	26
2268	PolyC-binding proteins enhance expression of the CDK2 cell cycle regulatory protein via alternative splicing. Nucleic Acids Research, 2018, 46, 2030-2044.	6.5	15

#	ARTICLE	IF	CITATIONS
2269	We skip to work: alternative splicing in normal and malignant myelopoiesis. <i>Leukemia</i> , 2018, 32, 1081-1093.	3.3	33
2270	Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 974-992.	2.5	98
2271	Transcription-Associated Mutation Promotes RNA Complexity in Highly Expressed Genes—A Major New Source of Selectable Variation. <i>Molecular Biology and Evolution</i> , 2018, 35, 1104-1119.	3.5	5
2272	PolyA_DB 3 catalogs cleavage and polyadenylation sites identified by deep sequencing in multiple genomes. <i>Nucleic Acids Research</i> , 2018, 46, D315-D319.	6.5	172
2273	Mutually exclusive alternative splicing of pre-mRNAs. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1468.	3.2	47
2274	PAX6 Alternative Splicing and Corneal Development. <i>Stem Cells and Development</i> , 2018, 27, 367-377.	1.1	13
2275	Detection of Proteome Diversity Resulted from Alternative Splicing is Limited by Trypsin Cleavage Specificity. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 422-430.	2.5	75
2276	A Novel Ultrasensitive In Situ Hybridization Approach to Detect Short Sequences and Splice Variants with Cellular Resolution. <i>Molecular Neurobiology</i> , 2018, 55, 6169-6181.	1.9	53
2277	Emerging roles of RNA-binding proteins in diabetes and their therapeutic potential in diabetic complications. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1459.	3.2	42
2278	Gene-based SNP identification and validation in soybean using next-generation transcriptome sequencing. <i>Molecular Genetics and Genomics</i> , 2018, 293, 623-633.	1.0	16
2279	The Y Chromosome Modulates Splicing and Sex-Biased Intron Retention Rates in <i>Drosophila</i> . <i>Genetics</i> , 2018, 208, 1057-1067.	1.2	16
2280	Zinc Deficiency via a Splice Switch in Zinc Importer ZIP2/SLC39A2 Causes Cystic Fibrosis-Associated MUC5AC Hypersecretion in Airway Epithelial Cells. <i>EBioMedicine</i> , 2018, 27, 304-316.	2.7	29
2281	Neuron-specific alternative splicing of transcriptional machineries: Implications for neurodevelopmental disorders. <i>Molecular and Cellular Neurosciences</i> , 2018, 87, 35-45.	1.0	57
2282	Dysregulation of cotranscriptional alternative splicing underlies CHARGE syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E620-E629.	3.3	28
2283	Regulatory Potential of the RNA Processing Machinery: Implications for Human Disease. <i>Trends in Genetics</i> , 2018, 34, 279-290.	2.9	34
2284	Multiple Innovations in Genetic and Epigenetic Mechanisms Cooperate to Underpin Human Brain Evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 263-268.	3.5	8
2285	An engineered RNA binding protein with improved splicing regulation. <i>Nucleic Acids Research</i> , 2018, 46, 3152-3168.	6.5	15
2286	The Expanding Landscape of Alternative Splicing Variation in Human Populations. <i>American Journal of Human Genetics</i> , 2018, 102, 11-26.	2.6	290

#	ARTICLE	IF	CITATIONS
2287	Transcriptome-wide Interrogation of the Functional Intronome by Spliceosome Profiling. <i>Cell</i> , 2018, 173, 1031-1044.e13.	13.5	26
2288	Full-length mRNA sequencing uncovers a widespread coupling between transcription initiation and mRNA processing. <i>Genome Biology</i> , 2018, 19, 46.	3.8	106
2289	Diversification of the muscle proteome through alternative splicing. <i>Skeletal Muscle</i> , 2018, 8, 8.	1.9	63
2290	The complexity of titin splicing pattern in human adult skeletal muscles. <i>Skeletal Muscle</i> , 2018, 8, 11.	1.9	65
2291	Enantioselective Synthesis of Thailanstatin A Methyl Ester and Evaluation of <i>in Vitro</i> Splicing Inhibition. <i>Journal of Organic Chemistry</i> , 2018, 83, 5187-5198.	1.7	21
2292	Bayesian nonparametric discovery of isoforms and individual specific quantification. <i>Nature Communications</i> , 2018, 9, 1681.	5.8	8
2294	CpG Islands in Cancer: Heads, Tails, and Sides. <i>Methods in Molecular Biology</i> , 2018, 1766, 49-80.	0.4	19
2295	Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. <i>Nucleic Acids Research</i> , 2018, 46, 582-592.	6.5	209
2296	Extracellular-Regulated Kinases: Signaling From Ras to ERK Substrates to Control Biological Outcomes. <i>Advances in Cancer Research</i> , 2018, 138, 99-142.	1.9	136
2297	Complementarity of assembly-first and mapping-first approaches for alternative splicing annotation and differential analysis from RNAseq data. <i>Scientific Reports</i> , 2018, 8, 4307.	1.6	31
2298	Identification and characterization of evolutionarily conserved alternative splicing events in a mangrove genus <i>Sonneratia</i> . <i>Scientific Reports</i> , 2018, 8, 4425.	1.6	5
2299	CASH: a constructing comprehensive splice site method for detecting alternative splicing events. <i>Briefings in Bioinformatics</i> , 2018, 19, 905-917.	3.2	47
2300	HNRNPLL, a newly identified colorectal cancer metastasis suppressor, modulates alternative splicing of <i>CD44</i> during epithelial-mesenchymal transition. <i>Gut</i> , 2018, 67, 1103-1111.	6.1	61
2301	Challenges in defining the role of intron retention in normal biology and disease. <i>Seminars in Cell and Developmental Biology</i> , 2018, 75, 40-49.	2.3	51
2302	Differential expression of PARK2 splice isoforms in an in vitro model of dopaminergic-like neurons exposed to toxic insults mimicking Parkinson's disease. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 1062-1073.	1.2	3
2303	The contribution of alternative splicing to genetic risk for psychiatric disorders. <i>Genes, Brain and Behavior</i> , 2018, 17, e12430.	1.1	31
2304	Sparselso: a novel Bayesian approach to identify alternatively spliced isoforms from RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 56-63.	1.8	7
2305	APPRIS 2017: principal isoforms for multiple gene sets. <i>Nucleic Acids Research</i> , 2018, 46, D213-D217.	6.5	134

#	ARTICLE	IF	CITATIONS
2306	Expression of PYCARD gene transcript variant mRNA in peripheral blood mononuclear cells of primary gout patients with different Chinese medicine syndromes. <i>Chinese Journal of Integrative Medicine</i> , 2018, 24, 24-31.	0.7	4
2307	Differential gene expression analysis in ageing muscle and drug discovery perspectives. <i>Ageing Research Reviews</i> , 2018, 41, 53-63.	5.0	20
2308	CHD8short, a naturally-occurring truncated form of a chromatin remodeler lacking the helicase domain, is a potent transcriptional coregulator. <i>Gene</i> , 2018, 641, 303-309.	1.0	12
2309	Rules and tools to predict the splicing effects of exonic and intronic mutations. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1451.	3.2	90
2310	Major splice variants and multiple polyadenylation site utilization in mRNAs encoding human translation initiation factors eIF4E1 and eIF4E3 regulate the translational regulators?. <i>Molecular Genetics and Genomics</i> , 2018, 293, 167-186.	1.0	5
2311	Whole Transcriptome Profiling: An RNA-seq Primer and Implications for Pharmacogenomics Research. <i>Clinical and Translational Science</i> , 2018, 11, 153-161.	1.5	10
2312	Variant snRNPs: New players within the spliceosome system. <i>RNA Biology</i> , 2018, 15, 17-25.	1.5	17
2313	Evaluation and control of miRNA-like off-target repression for RNA interference. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 797-814.	2.4	75
2314	Alternative splicing in cancers: From aberrant regulation to new therapeutics. <i>Seminars in Cell and Developmental Biology</i> , 2018, 75, 13-22.	2.3	99
2315	Systematic profiling of alternative splicing signature reveals prognostic predictor for ovarian cancer. <i>Gynecologic Oncology</i> , 2018, 148, 368-374.	0.6	128
2316	Exploiting differential RNA splicing patterns: a potential new group of therapeutic targets in cancer. <i>Expert Opinion on Therapeutic Targets</i> , 2018, 22, 107-121.	1.5	22
2317	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. <i>Genome Research</i> , 2018, 28, 231-242.	2.4	64
2318	The splicing code. <i>BioSystems</i> , 2018, 164, 39-48.	0.9	59
2319	Targeting splicing abnormalities in cancer. <i>Current Opinion in Genetics and Development</i> , 2018, 48, 67-74.	1.5	72
2320	The Effect of Newly Synthesized Heterosteroids on miRNA34a, 98, and 214 Expression Levels in MCF-7 Breast Cancer Cells. <i>Indian Journal of Clinical Biochemistry</i> , 2018, 33, 328-333.	0.9	3
2321	Genomics of autism spectrum disorder: approach to therapy. <i>F1000Research</i> , 2018, 7, 627.	0.8	6
2322	TAp73 regulates ATP7A: possible implications for ageing-related diseases. <i>Ageing</i> , 2018, 10, 3745-3760.	1.4	4
2323	Different splicing isoforms of ERCC1 affect the expression of its overlapping genes CD3EAP and PPP1R13L, and indicate a potential application in non-small cell lung cancer treatment. <i>International Journal of Oncology</i> , 2018, 52, 2155-2165.	1.4	4

#	ARTICLE	IF	CITATIONS
2324	Joint Prediction of Branchpoint and Splice Acceptor Sites in pre-mRNA Transcripts Using Sequence to Sequence Networks. , 2018, , .		0
2325	Splice-Aware Multiple Sequence Alignment of Protein Isoforms. , 2018, 2018, 200-210.		5
2326	When pitch adds to volume: coregulation of transcript diversity predicts gene function. BMC Genomics, 2018, 19, 926.	1.2	1
2327	Bayesian Modeling Approaches for Temporal Dynamics in RNA-seq Data. , 2018, , .		2
2328	Mammalian Cis-Acting RNA Sequence Elements. , 2018, , .		0
2329	Biomarker Identification from RNA-Seq Data using a Robust Statistical Approach. Bioinformatics, 2018, 14, 153-163.	0.2	10
2331	Detection of Viral RNA Splicing in Diagnostic Virology. , 2018, , 345-402.		1
2332	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of <i>ERAP2</i> transcripts under balancing selection. Genome Research, 2018, 28, 1812-1825.	2.4	66
2333	Deciphering highly similar multigene family transcripts from Iso-Seq data with IsoCon. Nature Communications, 2018, 9, 4601.	5.8	54
2334	Esrp1-Regulated Splicing of Arhgef11 Isoforms Is Required for Epithelial Tight Junction Integrity. Cell Reports, 2018, 25, 2417-2430.e5.	2.9	24
2335	Aberrant RNA Splicing in Cancer and Drug Resistance. Cancers, 2018, 10, 458.	1.7	145
2336	Insulin Receptor Isoforms in Cancer. International Journal of Molecular Sciences, 2018, 19, 3615.	1.8	79
2337	Deep Learning Models Based on Distributed Feature Representations for Alternative Splicing Prediction. IEEE Access, 2018, 6, 58826-58834.	2.6	33
2338	Modeling and Predicting the Activities of Trans-Acting Splicing Factors with Machine Learning. Cell Systems, 2018, 7, 510-520.e4.	2.9	8
2339	The Clinical Application of RNA Sequencing in Genetic Diagnosis of Mendelian Disorders. Advances in Molecular Pathology, 2018, 1, 27-36.	0.2	1
2340	Identification and Characterization of Transcripts Regulated by Circadian Alternative Polyadenylation in Mouse Liver. G3: Genes, Genomes, Genetics, 2018, 8, 3539-3548.	0.8	19
2341	Splicing isoform-specific functional genomic in cancer cells. Applied Cancer Research, 2018, 38, .	1.0	1
2342	Discerning novel splice junctions derived from RNA-seq alignment: a deep learning approach. BMC Genomics, 2018, 19, 971.	1.2	26

#	ARTICLE	IF	CITATIONS
2343	Aberrant expression of alternative isoforms of transcription factors in hepatocellular carcinoma. <i>World Journal of Hepatology</i> , 2018, 10, 645-661.	0.8	8
2344	Transcriptome 3' end organization by PCF11 links alternative polyadenylation to formation and neuronal differentiation of neuroblastoma. <i>Nature Communications</i> , 2018, 9, 5331.	5.8	75
2346	ISOdb: A Comprehensive Database of Full-Length Isoforms Generated by Iso-Seq. <i>International Journal of Genomics</i> , 2018, 2018, 1-6.	0.8	8
2347	SRSF3, a Splicer of the PKM Gene, Regulates Cell Growth and Maintenance of Cancer-Specific Energy Metabolism in Colon Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3012.	1.8	72
2348	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. <i>Nature Genetics</i> , 2018, 50, 1584-1592.	9.4	307
2349	Comparative Study on Alternative Splicing in Human Fungal Pathogens Suggests Its Involvement During Host Invasion. <i>Frontiers in Microbiology</i> , 2018, 9, 2313.	1.5	36
2350	When one becomes many? Alternative splicing in cell function and failure. <i>Diabetes, Obesity and Metabolism</i> , 2018, 20, 77-87.	2.2	32
2351	CRISPR/Cas9-mediated genome editing induces gene knockdown by altering the pre-mRNA splicing in mice. <i>BMC Biotechnology</i> , 2018, 18, 61.	1.7	17
2352	Alternative Splicing Plays a Critical Role in Maintaining Mineral Nutrient Homeostasis in Rice (<i>Oryza sativa</i>). <i>Plant Cell</i> , 2018, 30, 2267-2285.	3.1	121
2353	Quantitative Analysis of BRCA1 and BRCA2 Germline Splicing Variants Using a Novel RNA-Massively Parallel Sequencing Assay. <i>Frontiers in Oncology</i> , 2018, 8, 286.	1.3	23
2354	A Short Tandem Repeat-Enriched RNA Assembles a Nuclear Compartment to Control Alternative Splicing and Promote Cell Survival. <i>Molecular Cell</i> , 2018, 72, 525-540.e13.	4.5	108
2355	Rbfox1 Mediates Cell-type-Specific Splicing in Cortical Interneurons. <i>Neuron</i> , 2018, 100, 846-859.e7.	3.8	92
2356	Landscape of alternative splicing in <i>Capra hircus</i> . <i>Scientific Reports</i> , 2018, 8, 15128.	1.6	3
2357	Characterization of kinase gene expression and splicing profile in prostate cancer with RNA-Seq data. <i>BMC Genomics</i> , 2018, 19, 564.	1.2	6
2358	Single Cell Gene Expression to Understand the Dynamic Architecture of the Heart. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 167.	1.1	16
2359	Systematic evaluation of isoform function in literature reports of alternative splicing. <i>BMC Genomics</i> , 2018, 19, 637.	1.2	35
2360	Comparison of RNA-seq and microarray platforms for splice event detection using a cross-platform algorithm. <i>BMC Genomics</i> , 2018, 19, 703.	1.2	20
2361	Deletion of Long Isoform of Eukaryotic Elongation Factor 1B β Leads to Audiogenic Seizures and Aversive Stimulus-Induced Long-Lasting Activity Suppression in Mice. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 358.	1.4	10

#	ARTICLE	IF	CITATIONS
2362	Regulation of Neuroregeneration by Long Noncoding RNAs. <i>Molecular Cell</i> , 2018, 72, 553-567.e5.	4.5	83
2363	Maximizing the Utility of Cancer Transcriptomic Data. <i>Trends in Cancer</i> , 2018, 4, 823-837.	3.8	32
2364	Modulation of alternative splicing of trafficking genes by genome editing reveals functional consequences in muscle biology. <i>International Journal of Biochemistry and Cell Biology</i> , 2018, 105, 134-143.	1.2	7
2365	Single-cell RNA sequencing reveals gene expression signatures of breast cancer-associated endothelial cells. <i>Oncotarget</i> , 2018, 9, 10945-10961.	0.8	45
2366	<i>Cis</i> -regulated alternative splicing divergence and its potential contribution to environmental responses in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 97, 555-570.	2.8	33
2367	Alternative splicing links histone modifications to stem cell fate decision. <i>Genome Biology</i> , 2018, 19, 133.	3.8	53
2368	Introduction to Microarrays Technology and Data Analysis. <i>Comprehensive Analytical Chemistry</i> , 2018, , 37-69.	0.7	2
2369	<i>PTBP1</i> acts as a dominant repressor of the aberrant tissue-specific splicing of <i>ISCU</i> in hereditary myopathy with lactic acidosis. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 887-897.	0.6	4
2370	Comprehensive off-target analysis of dCas9-SAM-mediated HIV reactivation via long noncoding RNA and mRNA profiling. <i>BMC Medical Genomics</i> , 2018, 11, 78.	0.7	15
2371	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. <i>Frontiers in Genetics</i> , 2018, 9, 433.	1.1	23
2372	Alternative Splicing of Transcription Factors Genes in Muscle Physiology and Pathology. <i>Genes</i> , 2018, 9, 107.	1.0	22
2373	Characterization of cis-acting elements that control oscillating alternative splicing. <i>RNA Biology</i> , 2018, 15, 1-12.	1.5	15
2374	Efficient and Accurate Quantitative Profiling of Alternative Splicing Patterns of Any Complexity on a Laptop. <i>Molecular Cell</i> , 2018, 72, 187-200.e6.	4.5	121
2375	Analysis of alternative cleavage and polyadenylation in mature and differentiating neurons using RNA-seq data. <i>Quantitative Biology</i> , 2018, 6, 253-266.	0.3	28
2376	Chromosome-level reference genome and alternative splicing atlas of moso bamboo (<i>Phyllostachys Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>)	8.3	98
2377	Invention and Early History of Exon Skipping and Splice Modulation. <i>Methods in Molecular Biology</i> , 2018, 1828, 3-30.	0.4	17
2378	Model for breast cancer diversity and spatial heterogeneity. <i>Physical Review E</i> , 2018, 98, .	0.8	5
2379	RANK-c attenuates aggressive properties of ER-negative breast cancer by inhibiting NF- κ B activation and EGFR signaling. <i>Oncogene</i> , 2018, 37, 5101-5114.	2.6	22

#	ARTICLE	IF	CITATIONS
2380	How alternative splicing affects membrane-trafficking dynamics. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	17
2381	Computational identification and validation of alternative splicing in ZSF1 rat RNA-seq data, a preclinical model for type 2 diabetic nephropathy. <i>Scientific Reports</i> , 2018, 8, 7624.	1.6	10
2382	Mechanisms of skeletal muscle wasting in a mouse model for myotonic dystrophy type 1. <i>Human Molecular Genetics</i> , 2018, 27, 2789-2804.	1.4	32
2383	The exonâ€“intron gene structure upstream of the initiation codon predicts translation efficiency. <i>Nucleic Acids Research</i> , 2018, 46, 4575-4591.	6.5	23
2384	The Usage of Exon-Exon Splice Junctions for the Detection of Alternative Splicing using the REIDS model. <i>Scientific Reports</i> , 2018, 8, 8331.	1.6	4
2385	Alternative splicing and cancer metastasis: prognostic and therapeutic applications. <i>Clinical and Experimental Metastasis</i> , 2018, 35, 393-402.	1.7	38
2386	An automated method for detecting alternatively spliced protein domains. <i>Bioinformatics</i> , 2018, 34, 3809-3816.	1.8	0
2387	A survey of transcriptome complexity in <i>Sus scrofa</i> using single-molecule long-read sequencing. <i>DNA Research</i> , 2018, 25, 421-437.	1.5	83
2388	Regulation of alternative <scp>mRNA</scp> splicing: old players and new perspectives. <i>FEBS Letters</i> , 2018, 592, 2987-3006.	1.3	71
2389	SRSF5 functions as a novel oncogenic splicing factor and is upregulated by oncogene SRSF3 in oral squamous cell carcinoma. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2018, 1865, 1161-1172.	1.9	52
2390	Goat Boule: Isoforms identification, mRNA expression in testis and functional study and promoter methylation profiles. <i>Theriogenology</i> , 2018, 116, 53-63.	0.9	5
2391	Genome-Wide Association Analyses Reveal the Importance of Alternative Splicing in Diversifying Gene Function and Regulating Phenotypic Variation in Maize. <i>Plant Cell</i> , 2018, 30, 1404-1423.	3.1	66
2392	Study on the expressions of NLRP3 gene transcript variants in peripheral blood monocytes of primary gout patients. <i>Clinical Rheumatology</i> , 2018, 37, 2547-2555.	1.0	5
2393	Epigenetic Mechanisms of Learning and Memory. , 2018, , 345-382.		16
2394	Rbfox Splicing Factors Maintain Skeletal Muscle Mass by Regulating Calpain3 and Proteostasis. <i>Cell Reports</i> , 2018, 24, 197-208.	2.9	36
2395	Gene Regulatory Network Perturbation by Genetic and Epigenetic Variation. <i>Trends in Biochemical Sciences</i> , 2018, 43, 576-592.	3.7	20
2396	The Novel Short Isoform of Securin Stimulates the Expression of Cyclin D3 and Angiogenesis Factors VEGFA and FGF2, but Does Not Affect the Expression of MYC Transcription Factor. <i>Molecular Biology</i> , 2018, 52, 436-445.	0.4	4
2397	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623

#	ARTICLE	IF	CITATIONS
2398	Alternatively spliced variants in Atlantic cod (<i>Gadus morhua</i>) support response to variable salinity environment. <i>Scientific Reports</i> , 2018, 8, 11607.	1.6	11
2399	Splicing heterogeneity: separating signal from noise. <i>Genome Biology</i> , 2018, 19, 86.	3.8	54
2400	Molecular cloning of novel transcripts of the adaptor-related protein complex 2 alpha 1 subunit (AP2A1) gene, using Next-Generation Sequencing. <i>Gene</i> , 2018, 678, 55-64.	1.0	9
2401	Coregulation of alternative splicing by hnRNPM and ESRP1 during EMT. <i>Rna</i> , 2018, 24, 1326-1338.	1.6	53
2402	Exploring the Crosstalk Between LMNA and Splicing Machinery Gene Mutations in Dilated Cardiomyopathy. <i>Frontiers in Genetics</i> , 2018, 9, 231.	1.1	26
2403	Mutations in voltage-gated L-type calcium channel: implications in cardiac arrhythmia. <i>Channels</i> , 2018, 12, 201-218.	1.5	45
2404	Alternative Splicing of Differentiated Myeloid Cell Transcripts after Infection by <i>Anaplasma phagocytophilum</i> Impacts a Selective Group of Cellular Programs. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 14.	1.8	21
2405	Transcriptome Analysis of Bronchoalveolar Lavage Fluid From Children With <i>Mycoplasma pneumoniae</i> Pneumonia Reveals Natural Killer and T Cell-Proliferation Responses. <i>Frontiers in Immunology</i> , 2018, 9, 1403.	2.2	27
2406	Alternative Splicing in Neurogenesis and Brain Development. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 12.	1.6	141
2407	Olfactory Receptors as Biomarkers in Human Breast Carcinoma Tissues. <i>Frontiers in Oncology</i> , 2018, 8, 33.	1.3	52
2408	Development of Neuroendocrine Prostate Cancers by the Ser/Arg Repetitive Matrix 4-Mediated RNA Splicing Network. <i>Frontiers in Oncology</i> , 2018, 8, 93.	1.3	16
2409	Proper splicing contributes to visual function in the aging <i>Drosophila</i> eye. <i>Aging Cell</i> , 2018, 17, e12817.	3.0	35
2410	Signaling Pathways Driving Aberrant Splicing in Cancer Cells. <i>Genes</i> , 2018, 9, 9.	1.0	53
2411	Characterization of TTN Novex Splicing Variants across Species and the Role of RBM20 in Novex-Specific Exon Splicing. <i>Genes</i> , 2018, 9, 86.	1.0	7
2412	Modulation of VEGF-A Alternative Splicing as a Novel Treatment in Chronic Kidney Disease. <i>Genes</i> , 2018, 9, 98.	1.0	15
2413	Alternative Splicing in the Hippo Pathway—Implications for Disease and Potential Therapeutic Targets. <i>Genes</i> , 2018, 9, 161.	1.0	16
2414	Therapeutic Applications of Targeted Alternative Splicing to Cancer Treatment. <i>International Journal of Molecular Sciences</i> , 2018, 19, 75.	1.8	44
2415	Alternative Splicing as a Target for Cancer Treatment. <i>International Journal of Molecular Sciences</i> , 2018, 19, 545.	1.8	114

#	ARTICLE	IF	CITATIONS
2416	The Role of scaRNAs in Adjusting Alternative mRNA Splicing in Heart Development. <i>Journal of Cardiovascular Development and Disease</i> , 2018, 5, 26.	0.8	18
2417	Transcriptome Analysis of Epithelioma Papulosum Cyprini Cells Infected by Reovirus Isolated from Allogynogenetic Silver Crucian Carp. <i>Viruses</i> , 2018, 10, 135.	1.5	3
2418	RNA-seq analysis reveals alternative splicing under salt stress in cotton, <i>Gossypium davidsonii</i> . <i>BMC Genomics</i> , 2018, 19, 73.	1.2	72
2419	TSVdb: a web-tool for TCGA splicing variants analysis. <i>BMC Genomics</i> , 2018, 19, 405.	1.2	78
2420	Increased Alternative Splicing as a Host Response to <i>Edwardsiella ictaluri</i> Infection in Catfish. <i>Marine Biotechnology</i> , 2018, 20, 729-738.	1.1	55
2421	Role of fibroblast growth factor receptor-2 splicing in normal and cancer cells. <i>Frontiers in Bioscience - Landmark</i> , 2018, 23, 626-639.	3.0	39
2422	The importance of DNA methylation of exons on alternative splicing. <i>Rna</i> , 2018, 24, 1351-1362.	1.6	119
2423	Transcriptome analysis of alternative splicing in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2018, 18, 139.	1.6	21
2424	Regulation of Neuronal Differentiation, Function, and Plasticity by Alternative Splicing. <i>Annual Review of Cell and Developmental Biology</i> , 2018, 34, 451-469.	4.0	108
2425	Differential expression of mRNA isoforms in the skeletal muscle of pigs with distinct growth and fatness profiles. <i>BMC Genomics</i> , 2018, 19, 145.	1.2	43
2426	QAPA: a new method for the systematic analysis of alternative polyadenylation from RNA-seq data. <i>Genome Biology</i> , 2018, 19, 45.	3.8	176
2427	HNRNPH1 is required for rhabdomyosarcoma cell growth and survival. <i>Oncogenesis</i> , 2018, 7, 9.	2.1	21
2428	Developmental dynamics of gene expression and alternative polyadenylation in the <i>Caenorhabditis elegans</i> germline. <i>Genome Biology</i> , 2018, 19, 8.	3.8	31
2429	SUPPA2: fast, accurate, and uncertainty-aware differential splicing analysis across multiple conditions. <i>Genome Biology</i> , 2018, 19, 40.	3.8	408
2430	Identify Down syndrome transcriptome associations using integrative analysis of microarray database and correlation-interaction network. <i>Human Genomics</i> , 2018, 12, 2.	1.4	14
2431	Splicing QTL of human adipose-related traits. <i>Scientific Reports</i> , 2018, 8, 318.	1.6	9
2432	Extensive Differential Splicing Underlies Phenotypically Plastic Aphid Morphs. <i>Molecular Biology and Evolution</i> , 2018, 35, 1934-1946.	3.5	42
2433	Decoding a cancer-relevant splicing decision in the RON proto-oncogene using high-throughput mutagenesis. <i>Nature Communications</i> , 2018, 9, 3315.	5.8	46

#	ARTICLE	IF	CITATIONS
2434	Identification of novel transcripts and peptides in developing murine lens. <i>Scientific Reports</i> , 2018, 8, 11162.	1.6	5
2435	Glycogen synthase kinase β and alternative splicing. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1501.	3.2	20
2436	Stress in the Educational System as a Potential Source of Epigenetic Influences on Children's Development and Behavior. <i>Frontiers in Behavioral Neuroscience</i> , 2018, 12, 143.	1.0	4
2437	A compendium of conserved cleavage and polyadenylation events in mammalian genes. <i>Genome Research</i> , 2018, 28, 1427-1441.	2.4	81
2438	Quantitative Analysis of Alternative Pre-mRNA Splicing in Mouse Brain Sections Using RNA <i>In Situ</i> Hybridization Assay. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	6
2439	The Role of Noncoding mRNA Isoforms in the Regulation of Gene Expression. <i>Russian Journal of Genetics</i> , 2018, 54, 879-887.	0.2	1
2440	JUM is a computational method for comprehensive annotation-free analysis of alternative pre-mRNA splicing patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8181-E8190.	3.3	53
2441	Single-cell RNAseq for the study of isoforms—how is that possible?. <i>Genome Biology</i> , 2018, 19, 110.	3.8	100
2442	Transcriptome-wide analysis of alternative mRNA splicing signature in the diagnosis and prognosis of stomach adenocarcinoma. <i>Oncology Reports</i> , 2018, 40, 2014-2022.	1.2	35
2443	The Cancer Spliceome: Reprograming of Alternative Splicing in Cancer. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 80.	1.6	192
2444	Alternative Splicing of Alpha- and Beta-Synuclein Genes Plays Differential Roles in Synucleinopathies. <i>Genes</i> , 2018, 9, 63.	1.0	25
2445	Isoform-Level Interpretation of High-Throughput Proteomics Data Enabled by Deep Integration with RNA-seq. <i>Journal of Proteome Research</i> , 2018, 17, 3431-3444.	1.8	23
2446	Comparative performance of the BGISEQ-500 and Illumina HiSeq4000 sequencing platforms for transcriptome analysis in plants. <i>Plant Methods</i> , 2018, 14, 69.	1.9	128
2447	Alternative splicing in prostate cancer. <i>Nature Reviews Clinical Oncology</i> , 2018, 15, 663-675.	12.5	142
2448	Open questions: How many genes do we have?. <i>BMC Biology</i> , 2018, 16, 94.	1.7	127
2449	The Human Transcriptome. , 2018, , 135-164.		4
2450	Construction of lentiviral RNAi vector of PPAR β gene in cashmere goats and comparison with the transcriptome analysis of adipose cells treatments. <i>Small Ruminant Research</i> , 2018, 164, 87-93.	0.6	2
2451	Precise temporal regulation of alternative splicing during neural development. <i>Nature Communications</i> , 2018, 9, 2189.	5.8	155

#	ARTICLE	IF	CITATIONS
2452	Cellular and Molecular Biology Fundamentals. , 2018, , 59-78.		0
2454	Pig StAR: mRNA expression and alternative splicing in testis and Leydig cells, and association analyses with testicular morphology traits. <i>Theriogenology</i> , 2018, 118, 46-56.	0.9	13
2455	Isolation and characterization of porcine PILRB gene and its alternative splicing variants. <i>Gene</i> , 2018, 672, 8-15.	1.0	3
2456	Cellular stress alters 3'UTR landscape through alternative polyadenylation and isoform-specific degradation. <i>Nature Communications</i> , 2018, 9, 2268.	5.8	104
2457	The Human Genome and Neonatal Care. , 2018, , 180-189.e2.		0
2458	Alternative Splicing in Genetic Diseases: Improved Diagnosis and Novel Treatment Options. <i>International Review of Cell and Molecular Biology</i> , 2018, 335, 85-141.	1.6	23
2459	Nuclear PTEN safeguards pre-mRNA splicing to link Golgi apparatus for its tumor suppressive role. <i>Nature Communications</i> , 2018, 9, 2392.	5.8	47
2460	Analysis of RNA-Seq datasets reveals enrichment of tissue-specific splice variants for nuclear envelope proteins. <i>Nucleus</i> , 2018, 9, 410-430.	0.6	10
2461	Proteoforms: Methods of Analysis and Clinical Prospects. <i>Molecular Biology</i> , 2018, 52, 335-349.	0.4	6
2462	Inactivation of Citron Kinase Inhibits Medulloblastoma Progression by Inducing Apoptosis and Cell Senescence. <i>Cancer Research</i> , 2018, 78, 4599-4612.	0.4	24
2463	Bioinformatics Approaches for Studying Alternative Splicing. , 2019, , 221-234.		6
2464	Physiological and druggable skipping of immunoglobulin variable exons in plasma cells. <i>Cellular and Molecular Immunology</i> , 2019, 16, 810-819.	4.8	11
2465	A Novel Serine/Arginine-Rich Like Protein GjSR45a in <i>Gardenia jasminoides</i> . <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 242, 042004.	0.2	0
2466	Multiple Plasticity Regulators Reveal Targets Specifying an Induced Predatory Form in Nematodes. <i>Molecular Biology and Evolution</i> , 2019, 36, 2387-2399.	3.5	20
2467	2,3,7,8-Tetrachlorodibenzo-p-dioxin modifies alternative splicing in mouse liver. <i>PLoS ONE</i> , 2019, 14, e0219747.	1.1	7
2468	Pan-cancer analysis of clinical relevance of alternative splicing events in 31 human cancers. <i>Oncogene</i> , 2019, 38, 6678-6695.	2.6	58
2469	Depletion of Hemoglobin Transcripts and Long-Read Sequencing Improves the Transcriptome Annotation of the Polar Bear (<i>Ursus maritimus</i>). <i>Frontiers in Genetics</i> , 2019, 10, 643.	1.1	23
2470	Splicing the Clock to Maintain and Entrain Circadian Rhythms. <i>Journal of Biological Rhythms</i> , 2019, 34, 584-595.	1.4	13

#	ARTICLE	IF	CITATIONS
2471	TCF3 mutually exclusive alternative splicing is controlled by long-range cooperative actions between hnRNPH1 and PTBP1. <i>Rna</i> , 2019, 25, 1497-1508.	1.6	14
2472	Sequence and Evolutionary Features for the Alternatively Spliced Exons of Eukaryotic Genes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3834.	1.8	11
2473	Proteomics analysis of proteins interacting with heat shock factor 1 in squamous cell carcinoma of the cervix. <i>Oncology Letters</i> , 2019, 18, 2568-2575.	0.8	8
2474	A Computational Analysis of Alternative Splicing across Mammalian Tissues Reveals Circadian and Ultradian Rhythms in Splicing Events. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3977.	1.8	26
2475	RNA components of the spliceosome regulate tissue- and cancer-specific alternative splicing. <i>Genome Research</i> , 2019, 29, 1591-1604.	2.4	96
2476	A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. <i>Nature Communications</i> , 2019, 10, 3359.	5.8	164
2477	Alternative splicing is required for stage differentiation in malaria parasites. <i>Genome Biology</i> , 2019, 20, 151.	3.8	29
2478	RNA sequencing: the teenage years. <i>Nature Reviews Genetics</i> , 2019, 20, 631-656.	7.7	1,192
2479	The Grass Carp Genomic Visualization Database (GCCVD): an informational platform for genome biology of grass carp. <i>International Journal of Biological Sciences</i> , 2019, 15, 2119-2127.	2.6	10
2480	High-throughput targeted long-read single cell sequencing reveals the clonal and transcriptional landscape of lymphocytes. <i>Nature Communications</i> , 2019, 10, 3120.	5.8	202
2481	Repeat-associated RNA structure and aberrant splicing. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 194405.	0.9	23
2482	Small non-coding RNA within the endogenous spliceosome and alternative splicing regulation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 194406.	0.9	17
2483	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. <i>Bioinformatics</i> , 2019, 35, i284-i294.	1.8	28
2484	Molecular cloning and characterization of farnesyl pyrophosphate synthase gene from <i>Panax sokpayensis</i> , a new <i>Panax</i> species from Sikkim Himalaya. <i>Journal of Applied Research on Medicinal and Aromatic Plants</i> , 2019, 14, 100215.	0.9	0
2485	Getting the Entire Message: Progress in Isoform Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 709.	1.1	39
2486	Isoforms of Base Excision Repair Enzymes Produced by Alternative Splicing. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3279.	1.8	12
2487	Comprehensive Transcriptome Reveals an Opposite Regulatory Effect of Plant Growth Retardants in Controlling Seedling Overgrowth between Roots and Shoots. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3307.	1.8	4
2488	Alternative splicing regulates stochastic NLRP3 activity. <i>Nature Communications</i> , 2019, 10, 3238.	5.8	44

#	ARTICLE	IF	CITATIONS
2489	Aberrant DNA methylation defines isoform usage in cancer, with functional implications. <i>PLoS Computational Biology</i> , 2019, 15, e1007095.	1.5	16
2490	Large Scale Profiling of Protein Isoforms Using Label-Free Quantitative Proteomics Revealed the Regulation of Nonsense-Mediated Decay in Moso Bamboo (<i>Phyllostachys edulis</i>). <i>Cells</i> , 2019, 8, 744.	1.8	13
2491	Multi-level remodeling of transcriptional landscapes in aging and longevity. <i>BMB Reports</i> , 2019, 52, 86-108.	1.1	42
2492	Networks of mRNA Processing and Alternative Splicing Regulation in Health and Disease. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1157, 1-27.	0.8	9
2493	Genetic basis of functional variability in adhesion G protein-coupled receptors. <i>Scientific Reports</i> , 2019, 9, 11036.	1.6	27
2494	A bioinformatic analysis identifies circadian expression of splicing factors and time-dependent alternative splicing events in the HD-MY-Z cell line. <i>Scientific Reports</i> , 2019, 9, 11062.	1.6	11
2495	Improving Silkworm Genome Annotation Using a Proteogenomics Approach. <i>Journal of Proteome Research</i> , 2019, 18, 3009-3019.	1.8	11
2496	Cardioprotective mechanisms of salvianic acid A sodium in rats with myocardial infarction based on proteome and transcriptome analysis. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 1513-1522.	2.8	10
2497	Comparative Transcriptome Analysis Reveals Molecular Basis Underlying Fast Growth of the Selectively Bred Pacific Oyster, <i>Crassostrea gigas</i> . <i>Frontiers in Genetics</i> , 2019, 10, 610.	1.1	30
2498	Functional Genetic Variant of Long Pentraxin 3 Gene Is Associated With Clinical Aspects of Oral Cancer in Male Patients. <i>Frontiers in Oncology</i> , 2019, 9, 581.	1.3	9
2499	The d16HER2 Splice Variant: A Friend or Foe of HER2-Positive Cancers?. <i>Cancers</i> , 2019, 11, 902.	1.7	21
2500	Combinatorial regulation of alternative splicing. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 194392.	0.9	39
2501	Body's Own Epitopes among Foreign Ones: T Cells and Autoantigens. <i>Molecular Biology</i> , 2019, 53, 748-757.	0.4	0
2502	mountainClimber Identifies Alternative Transcription Start and Polyadenylation Sites in RNA-Seq. <i>Cell Systems</i> , 2019, 9, 393-400.e6.	2.9	15
2503	The RNA binding protein QKI controls alternative splicing as a model of vascular therapies. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	19
2504	Ultrafast Flash Energy Conductance at MXene's Surfactant Interface and Its Molecular Origins. <i>Advanced Materials Interfaces</i> , 2019, 6, 1901461.	1.9	17
2505	Ten years of the horse reference genome: insights into equine biology, domestication and population dynamics in the post-genome era. <i>Animal Genetics</i> , 2019, 50, 569-597.	0.6	43
2506	Alternative Splicing Regulatory Networks: Functions, Mechanisms, and Evolution. <i>Molecular Cell</i> , 2019, 76, 329-345.	4.5	446

#	ARTICLE	IF	CITATIONS
2507	Informing disease modelling with brain-relevant functional genomic annotations. <i>Brain</i> , 2019, 142, 3694-3712.	3.7	8
2508	The UGTome: The expanding diversity of UDP glycosyltransferases and its impact on small molecule metabolism. , 2019, 204, 107414.		32
2509	Alternatively spliced down syndrome cell adhesion molecule (Dscam) controls innate immunity in crab. <i>Journal of Biological Chemistry</i> , 2019, 294, 16440-16450.	1.6	35
2510	A missense mutation in SNRPE linked to non-syndromal microcephaly interferes with U snRNP assembly and pre-mRNA splicing. <i>PLoS Genetics</i> , 2019, 15, e1008460.	1.5	18
2511	Ultra-deep sequencing reveals pre-mRNA splicing as a sequence driven high-fidelity process. <i>PLoS ONE</i> , 2019, 14, e0223132.	1.1	3
2512	RNA-Seq Perspectives to Improve Clinical Diagnosis. <i>Frontiers in Genetics</i> , 2019, 10, 1152.	1.1	72
2513	Splicing in the pathogenesis, diagnosis and treatment of ciliopathies. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 194433.	0.9	25
2514	Keep calm: the intestinal barrier at the interface of peace and war. <i>Cell Death and Disease</i> , 2019, 10, 849.	2.7	98
2515	Prognostic Potential of Alternative Splicing Markers in Endometrial Cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 1039-1048.	2.3	13
2516	Dietary-phytochemical mediated reversion of cancer-specific splicing inhibits Warburg effect in head and neck cancer. <i>BMC Cancer</i> , 2019, 19, 1031.	1.1	21
2517	Identification of Prognostic and Metastatic Alternative Splicing Signatures in Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 270.	2.0	55
2518	Intronic RNA: Adâ€junkâ€™ mediator of post-transcriptional gene regulation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 194439.	0.9	11
2519	Bioinformatic analysis of a novel <i>Echinococcus granulosus</i> nuclear receptor with two DNA binding domains. <i>PLoS ONE</i> , 2019, 14, e0224703.	1.1	8
2520	Comparative analysis of the accelerated aged seed transcriptome profiles of two maize chromosome segment substitution lines. <i>PLoS ONE</i> , 2019, 14, e0216977.	1.1	8
2521	A Novel Missense Variant Associated with A Splicing Defect in A Myopathic Form of PGK1 Deficiency in The Spanish Population. <i>Genes</i> , 2019, 10, 785.	1.0	11
2522	The functional mechanisms of mutations in myelodysplastic syndrome. <i>Leukemia</i> , 2019, 33, 2779-2794.	3.3	28
2523	Could circRNA be a new biomarker for preâ€eclampsia?. <i>Molecular Reproduction and Development</i> , 2019, 86, 1773-1780.	1.0	52
2524	Long Read Single-Molecule Real-Time Sequencing Elucidates Transcriptome-Wide Heterogeneity and Complexity in Esophageal Squamous Cells. <i>Frontiers in Genetics</i> , 2019, 10, 915.	1.1	12

#	ARTICLE	IF	CITATIONS
2525	Modeling allele-specific expression at the gene and SNP levels simultaneously by a Bayesian logistic mixed regression model. <i>BMC Bioinformatics</i> , 2019, 20, 530.	1.2	7
2526	Pig Hsd17b3: Alternative splice variants expression, insertion/deletion (indel) in promoter region and their associations with male reproductive traits. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 195, 105483.	1.2	13
2527	Identification of prognosis-related alternative splicing events in kidney renal clear cell carcinoma. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 7762-7772.	1.6	14
2528	Genome-Wide Analysis of Alternative Splicing Provides Insights Into Stress Response of the Pacific White Shrimp <i>Litopenaeus vannamei</i> . <i>Frontiers in Genetics</i> , 2019, 10, 845.	1.1	30
2529	The mutation of Transportin 3 gene that causes limb girdle muscular dystrophy 1F induces protection against HIV-1 infection. <i>PLoS Pathogens</i> , 2019, 15, e1007958.	2.1	22
2530	Modulation of <i>PDCD1</i> exon 3 splicing. <i>RNA Biology</i> , 2019, 16, 1794-1805.	1.5	18
2531	Alternative splicing of P2RX7 pre-messenger RNA in health and diseases: Myth or reality?. <i>Biomedical Journal</i> , 2019, 42, 141-154.	1.4	30
2532	Identification of novel alternative splice variants of the human L-DOPA decarboxylase (DDC) gene in human cancer cells, using high-throughput sequencing approaches. <i>Gene</i> , 2019, 719, 144075.	1.0	10
2533	Transcriptome variation in human populations and its potential application in forensics. <i>Journal of Applied Genetics</i> , 2019, 60, 319-328.	1.0	3
2534	Survival-Associated Alternative Messenger RNA Splicing Signatures in Pancreatic Ductal Adenocarcinoma: A Study Based on RNA-Sequencing Data. <i>DNA and Cell Biology</i> , 2019, 38, 1207-1222.	0.9	7
2535	Srrm234, but not canonical SR and hnRNP proteins, drive inclusion of <i>Dscam</i> exon 9 variable exons. <i>Rna</i> , 2019, 25, 1353-1365.	1.6	16
2536	SRSF3-Regulated RNA Alternative Splicing Promotes Glioblastoma Tumorigenicity by Affecting Multiple Cellular Processes. <i>Cancer Research</i> , 2019, 79, 5288-5301.	0.4	63
2537	UPF1/SMG7-dependent microRNA-mediated gene regulation. <i>Nature Communications</i> , 2019, 10, 4181.	5.8	20
2538	Zika virus noncoding sRNAs sequester multiple host-derived RNA-binding proteins and modulate mRNA decay and splicing during infection. <i>Journal of Biological Chemistry</i> , 2019, 294, 16282-16296.	1.6	53
2540	Genome-Wide Profiling of Prognostic Alternative Splicing Pattern in Pancreatic Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 773.	1.3	27
2541	Classes of non-conventional tetraspanins defined by alternative splicing. <i>Scientific Reports</i> , 2019, 9, 14075.	1.6	16
2542	Temporal dynamics in meta longitudinal RNA-Seq data. <i>Scientific Reports</i> , 2019, 9, 763.	1.6	4
2543	A 54kDa short variant of DHX33 functions in regulating mRNA translation. <i>Journal of Cellular Physiology</i> , 2019, 234, 15308-15319.	2.0	1

#	ARTICLE	IF	CITATIONS
2544	B52 promotes alternative splicing of Dscam in Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Fish and Shellfish Immunology</i> , 2019, 87, 460-469.	1.6	11
2545	High-throughput RNAi screening reveals cancer-selective lethal targets in the RNA spliceosome. <i>Oncogene</i> , 2019, 38, 4142-4153.	2.6	18
2546	ARGLU1 is a transcriptional coactivator and splicing regulator important for stress hormone signaling and development. <i>Nucleic Acids Research</i> , 2019, 47, 2856-2870.	6.5	20
2547	A high-throughput screen identifies small molecule modulators of alternative splicing by targeting RNA G-quadruplexes. <i>Nucleic Acids Research</i> , 2019, 47, 3667-3679.	6.5	49
2548	Tissue-specific epigenetics of atherosclerosis-related <i>ANGPT</i> and <i>ANGPTL</i> genes. <i>Epigenomics</i> , 2019, 11, 169-186.	1.0	30
2549	Deterministic splicing of <i>Dscam2</i> is regulated by Muscleblind. <i>Science Advances</i> , 2019, 5, eaav1678.	4.7	8
2550	Expression of NOTCH3 exon 16 differentiates Diffuse Large B-cell Lymphoma into molecular subtypes and is associated with prognosis. <i>Scientific Reports</i> , 2019, 9, 335.	1.6	7
2551	Oncogene SRSF3 suppresses autophagy via inhibiting BECN1 expression. <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 966-972.	1.0	18
2552	Constitutive splicing and economies of scale in gene expression. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 424-432.	3.6	41
2553	Alternative Splicing and Protein Diversity: Plants Versus Animals. <i>Frontiers in Plant Science</i> , 2019, 10, 708.	1.7	136
2554	Alternative splicing and insect ryanodine receptor. <i>Archives of Insect Biochemistry and Physiology</i> , 2019, 102, e21590.	0.6	5
2555	<i>HnRNPL</i> promotes Wilms tumor progression by regulating the p53 and Bcl2 pathways. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 4269-4279.	1.0	15
2556	Two Separation-of-Function Isoforms of Human TPP1 Dictate Telomerase Regulation in Somatic and Germ Cells. <i>Cell Reports</i> , 2019, 27, 3511-3521.e7.	2.9	20
2557	Chemokines in Alzheimer's Disease: New Insights Into Prokineticins, Chemokine-Like Proteins. <i>Frontiers in Pharmacology</i> , 2019, 10, 622.	1.6	44
2558	The role of proteomics in assessing beta-cell dysfunction and death in type 1 diabetes. <i>Expert Review of Proteomics</i> , 2019, 16, 569-582.	1.3	8
2559	Emerging roles of histone modifications and HDACs in RNA splicing. <i>Nucleic Acids Research</i> , 2019, 47, 4911-4926.	6.5	64
2560	CFIm25 and alternative polyadenylation: Conflicting roles in cancer. <i>Cancer Letters</i> , 2019, 459, 112-121.	3.2	25
2561	Increased FLYWCH1 Expression is Negatively Correlated with Wnt/ β -catenin Target Gene Expression in Acute Myeloid Leukemia Cells. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2739.	1.8	7

#	ARTICLE	IF	CITATIONS
2562	The complexity of alternative splicing and landscape of tissue-specific expression in lotus (<i>Nelumbo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 2019, 26, 301-311.	1.5	28
2563	QuaPra: Efficient transcript assembly and quantification using quadratic programming with Apriori algorithm. <i>Science China Life Sciences</i> , 2019, 62, 937-946.	2.3	14
2564	The LL-100 panel: 100 cell lines for blood cancer studies. <i>Scientific Reports</i> , 2019, 9, 8218.	1.6	74
2565	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	1.0	25
2566	Profound analgesia is associated with a truncated peptide resulting from tissue specific alternative splicing of DRG CA8-204 regulated by an exon-level cis-eQTL. <i>PLoS Genetics</i> , 2019, 15, e1008226.	1.5	4
2567	The carboxy-terminus, a key regulator of protein function. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2019, 54, 85-102.	2.3	42
2568	A Method Based on Differential Entropy-Like Function for Detecting Differentially Expressed Genes Across Multiple Conditions in RNA-Seq Studies. <i>Entropy</i> , 2019, 21, 242.	1.1	1
2569	Intron retention as an alternative splice variant of the cattle ANGPTL6 gene. <i>Gene</i> , 2019, 709, 17-24.	1.0	6
2570	Alternative polyadenylation of single cells delineates cell types and serves as a prognostic marker in early stage breast cancer. <i>PLoS ONE</i> , 2019, 14, e0217196.	1.1	23
2571	SCAF4 and SCAF8, mRNA Anti-Terminator Proteins. <i>Cell</i> , 2019, 177, 1797-1813.e18.	13.5	85
2572	SpliceV: analysis and publication quality printing of linear and circular RNA splicing, expression and regulation. <i>BMC Bioinformatics</i> , 2019, 20, 231.	1.2	10
2573	Post-transcriptional regulation through alternative splicing after infection with <i>Flavobacterium columnare</i> in channel catfish (<i>Ictalurus punctatus</i>). <i>Fish and Shellfish Immunology</i> , 2019, 91, 188-193.	1.6	25
2574	Genetic variations within alternative splicing associated genes are associated with breast cancer susceptibility in Chinese women. <i>Gene</i> , 2019, 706, 140-145.	1.0	7
2575	ALG-1 Influences Accurate mRNA Splicing Patterns in the <i>Caenorhabditis elegans</i> Intestine and Body Muscle Tissues by Modulating Splicing Factor Activities. <i>Genetics</i> , 2019, 212, 931-951.	1.2	8
2576	PASS: A Proteomics Alternative Splicing Screening Pipeline. <i>Proteomics</i> , 2019, 19, e1900041.	1.3	6
2577	IL-4 subverts mycobacterial containment in <i>Mycobacterium tuberculosis</i> -infected human macrophages. <i>European Respiratory Journal</i> , 2019, 54, 1802242.	3.1	22
2578	Insights into Telomerase/hTERT Alternative Splicing Regulation Using Bioinformatics and Network Analysis in Cancer. <i>Cancers</i> , 2019, 11, 666.	1.7	26
2579	Effects of intron retention on properties of Î²-glucosidase in <i>Aspergillus niger</i> . <i>Fungal Biology</i> , 2019, 123, 465-470.	1.1	2

#	ARTICLE	IF	CITATIONS
2580	Platform-Independent Classification System to Predict Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. <i>JCO Clinical Cancer Informatics</i> , 2019, 3, 1-9.	1.0	18
2581	Novel insights into PARPs in gene expression: regulation of RNA metabolism. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 3283-3299.	2.4	32
2582	Identification of DNA-Methylated CpG Islands Associated With Gene Silencing in the Adult Body Tissues of the Ogye Chicken Using RNA-Seq and Reduced Representation Bisulfite Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 346.	1.1	37
2583	Viral modulation of cellular RNA alternative splicing: A new key player in virus-host interactions?. <i>Wiley Interdisciplinary Reviews RNA</i> , 2019, 10, e1543.	3.2	56
2584	Netrin Family: Role for Protein Isoforms in Cancer. <i>Journal of Nucleic Acids</i> , 2019, 2019, 1-9.	0.8	19
2585	BRCA1-“No Matter How You Splice It. <i>Cancer Research</i> , 2019, 79, 2091-2098.	0.4	16
2586	Circular RNAs and RNA Splice Variants as Biomarkers for Prognosis and Therapeutic Response in the Liquid Biopsies of Lung Cancer Patients. <i>Frontiers in Genetics</i> , 2019, 10, 390.	1.1	68
2587	Development of PCR markers specific to <i>Dasypyrum villosum</i> genome based on transcriptome data and their application in breeding <i>Triticum aestivum</i> -D. villosum#4 alien chromosome lines. <i>BMC Genomics</i> , 2019, 20, 289.	1.2	15
2588	TransLiG: a de novo transcriptome assembler that uses line graph iteration. <i>Genome Biology</i> , 2019, 20, 81.	3.8	30
2589	SNAP-25 isoforms differentially regulate synaptic transmission and long-term synaptic plasticity at central synapses. <i>Scientific Reports</i> , 2019, 9, 6403.	1.6	40
2590	Sequencing and curation strategies for identifying candidate glioblastoma treatments. <i>BMC Medical Genomics</i> , 2019, 12, 56.	0.7	7
2591	The emerging roles and functions of circular RNAs and their generation. <i>Journal of Biomedical Science</i> , 2019, 26, 29.	2.6	297
2592	Postmortem brain tissue as an underutilized resource to study the molecular pathology of neuropsychiatric disorders across different ethnic populations. <i>Neuroscience and Biobehavioral Reviews</i> , 2019, 102, 195-207.	2.9	9
2593	ELP1 Splicing Correction Reverses Proprioceptive Sensory Loss in Familial Dysautonomia. <i>American Journal of Human Genetics</i> , 2019, 104, 638-650.	2.6	32
2594	Identification of candidate genes of growth traits in pigs using RNA-sequencing. <i>Italian Journal of Animal Science</i> , 2019, 18, 279-286.	0.8	4
2595	PTBP1 contributes to spermatogenesis through regulation of proliferation in spermatogonia. <i>Journal of Reproduction and Development</i> , 2019, 65, 37-46.	0.5	11
2596	Regulation of Intronic Polyadenylation by PCF11 Impacts mRNA Expression of Long Genes. <i>Cell Reports</i> , 2019, 26, 2766-2778.e6.	2.9	77
2597	A cytosine-rich splice regulatory determinant enforces functional processing of the human β -globin gene transcript. <i>Blood</i> , 2019, 133, 2338-2347.	0.6	4

#	ARTICLE	IF	CITATIONS
2598	Combinatorial Pattern of Histone Modifications in Exon Skipping Event. <i>Frontiers in Genetics</i> , 2019, 10, 122.	1.1	5
2599	Novel alternative splice variants of the human protein arginine methyltransferase 1 (PRMT1) gene, discovered using next-generation sequencing. <i>Gene</i> , 2019, 699, 135-144.	1.0	14
2600	Identification, evolution and alternative splicing profile analysis of the splicing factor 30 (SPF30) in plant species. <i>Planta</i> , 2019, 249, 1997-2014.	1.6	7
2601	RNA-sequencing in ophthalmology research: considerations for experimental design and analysis. <i>Therapeutic Advances in Ophthalmology</i> , 2019, 11, 251584141983546.	0.8	6
2602	Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 317.	1.1	611
2603	Polyadenylation sites and their characteristics in the genome of channel catfish (<i>Ictalurus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 <i>Genomics and Proteomics</i> , 2019, 30, 248-255.	0.4	0
2604	Genotoxic stress causes the accumulation of DNA-dependent protein kinase catalytic subunit phosphorylated at serine 2056 at nuclear speckles and alters pre-mRNA alternative splicing. <i>FEBS Open Bio</i> , 2019, 9, 304-314.	1.0	5
2605	RNA Splicing: A New Paradigm in Host-Pathogen Interactions. <i>Journal of Molecular Biology</i> , 2019, 431, 1565-1575.	2.0	59
2606	The Epstein-Barr virus EBNA1 protein modulates the alternative splicing of cellular genes. <i>Virology Journal</i> , 2019, 16, 29.	1.4	23
2607	A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. <i>Frontiers in Genetics</i> , 2019, 10, 155.	1.1	48
2608	Temporal Splicing Switches in Elements of the TNF-Pathway Identified by Computational Analysis of Transcriptome Data for Human Cell Lines. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1182.	1.8	7
2609	Full-Length Transcriptome Sequencing and the Discovery of New Transcripts in the Unfertilized Eggs of Zebrafish (<i>Danio rerio</i>). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1831-1838.	0.8	14
2610	Serine/Arginine-rich protein family of splicing regulators: New approaches to study splice isoform functions. <i>Plant Science</i> , 2019, 283, 127-134.	1.7	27
2611	Interplay between coding and exonic splicing regulatory sequences. <i>Genome Research</i> , 2019, 29, 711-722.	2.4	14
2612	Inhibition of SF3b1 by pladienolide B evokes cycle arrest, apoptosis induction and p73 splicing in human cervical carcinoma cells. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2019, 47, 1273-1280.	1.9	34
2613	A Combined in silico, in vitro and Clinical Approach to Characterize Novel Pathogenic Missense Variants in PRPF31 in Retinitis Pigmentosa. <i>Frontiers in Genetics</i> , 2019, 10, 248.	1.1	7
2614	<i>Brassica napus</i> Infected with <i>Leptosphaeria maculans</i> . <i>Genes</i> , 2019, 10, 296.	1.0	8
2615	Production of an aberrant splice variant of CCL5 is not caused by genetic mutation in the mammary glands of mastitis-infected Holstein cows. <i>Molecular Medicine Reports</i> , 2019, 19, 4159-4166.	1.1	6

#	ARTICLE	IF	CITATIONS
2616	Prognostic alternative mRNA splicing signature in hepatocellular carcinoma: a study based on large-scale sequencing data. <i>Carcinogenesis</i> , 2019, 40, 1077-1085.	1.3	34
2617	RNA-binding proteins in hematopoiesis and hematological malignancy. <i>Blood</i> , 2019, 133, 2365-2373.	0.6	52
2618	Transcriptomic Analysis of Seed Germination Under Salt Stress in Two Desert Sister Species (<i>Populus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 TF	1.1	32
2619	Clinical application of next-generation sequencing to the practice of neurology. <i>Lancet Neurology</i> , The, 2019, 18, 492-503.	4.9	76
2620	Defining the genetic and evolutionary architecture of alternative splicing in response to infection. <i>Nature Communications</i> , 2019, 10, 1671.	5.8	52
2621	A statistical normalization method and differential expression analysis for RNA-seq data between different species. <i>BMC Bioinformatics</i> , 2019, 20, 163.	1.2	24
2622	An alternative CTCF isoform antagonizes canonical CTCF occupancy and changes chromatin architecture to promote apoptosis. <i>Nature Communications</i> , 2019, 10, 1535.	5.8	39
2623	Alternative splicing, RNA-seq and drug discovery. <i>Drug Discovery Today</i> , 2019, 24, 1258-1267.	3.2	55
2624	Differential isoform expression and alternative splicing in sex determination in mice. <i>BMC Genomics</i> , 2019, 20, 202.	1.2	23
2625	The germ cell marker dead end reveals alternatively spliced transcripts with dissimilar expression. <i>Scientific Reports</i> , 2019, 9, 2407.	1.6	4
2626	Oncogenic splicing factor SRSF3 regulates ILF3 alternative splicing to promote cancer cell proliferation and transformation. <i>Rna</i> , 2019, 25, 630-644.	1.6	47
2627	Dynamic stacking of an expected branch point adenosine in duplexes containing pseudouridine-modified or unmodified U2 snRNA sites. <i>Biochemical and Biophysical Research Communications</i> , 2019, 511, 416-421.	1.0	12
2628	RNAs in the spliceosome: Insight from cryoEM structures. <i>Wiley Interdisciplinary Reviews RNA</i> , 2019, 10, e1523.	3.2	21
2629	Identification of exon skipping events associated with Alzheimer's disease in the human hippocampus. <i>BMC Medical Genomics</i> , 2019, 12, 13.	0.7	17
2630	Predictive models of subcellular localization of long RNAs. <i>Rna</i> , 2019, 25, 557-572.	1.6	75
2631	S-CAP extends pathogenicity prediction to genetic variants that affect RNA splicing. <i>Nature Genetics</i> , 2019, 51, 755-763.	9.4	56
2632	RNA-seq based elucidation of mechanism underlying <i>Ganoderma atrum</i> polysaccharide induced immune activation of murine myeloid-derived dendritic cells. <i>Journal of Functional Foods</i> , 2019, 55, 104-116.	1.6	25
2633	An ancient germ cell-specific RNA-binding protein protects the germline from cryptic splice site poisoning. <i>ELife</i> , 2019, 8, .	2.8	22

#	ARTICLE	IF	CITATIONS
2634	Conserved functions of RNA-binding proteins in muscle. <i>International Journal of Biochemistry and Cell Biology</i> , 2019, 110, 29-49.	1.2	19
2635	Long-Read Sequencing – A Powerful Tool in Viral Transcriptome Research. <i>Trends in Microbiology</i> , 2019, 27, 578-592.	3.5	76
2636	Alternative splicing of the <i>Izumo1</i> gene ensures triggering gamete fusion in mice. <i>Scientific Reports</i> , 2019, 9, 3151.	1.6	5
2637	De novo characterization of placental transcriptome in the Eurasian beaver (<i>Castor fiber</i> L.). <i>Functional and Integrative Genomics</i> , 2019, 19, 421-435.	1.4	4
2638	Alternative Splicing in Apicomplexan Parasites. <i>MBio</i> , 2019, 10, .	1.8	19
2639	Physiological functions of Wilms’s tumor 1-associated protein and its role in tumorigenesis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 10884-10892.	1.2	17
2640	Using BRIE to Detect and Analyze Splicing Isoforms in scRNA-Seq Data. <i>Methods in Molecular Biology</i> , 2019, 1935, 175-185.	0.4	2
2641	Structural-Functional Diversity of p53 Proteoforms. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2019, 13, 293-307.	0.2	0
2642	Circular RNAs as diagnostic tool for renal transplant patients with acute rejection. <i>Annals of Translational Medicine</i> , 2019, 7, S302-S302.	0.7	0
2643	U1 snRNP Telescripting Roles in Transcription and Its Mechanism. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019, 84, 115-122.	2.0	17
2644	Combined Statistics for Differential Expression Analysis of RNA-Sequencing Data. , 2019, , .		0
2645	Modified protocol for RNA isolation from different parts of field-grown jute plant suitable for NGS data generation and quantitative real-time RT-PCR. <i>African Journal of Biotechnology</i> , 2019, 18, 647-658.	0.3	6
2646	Role for the splicing factor TCERG1 in Cajal body integrity and snRNP assembly. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	5
2647	The Bellerophon pipeline, improving de novo transcriptomes and removing chimeras. <i>Ecology and Evolution</i> , 2019, 9, 10513-10521.	0.8	14
2648	Differentiating isoform functions with collaborative matrix factorization. <i>Bioinformatics</i> , 2020, 36, 1864-1871.	1.8	24
2649	Inclusion of hnRNP L Alternative Exon 7 Is Associated with Good Prognosis and Inhibited by Oncogene SRSF3 in Head and Neck Squamous Cell Carcinoma. <i>BioMed Research International</i> , 2019, 2019, 1-11.	0.9	10
2650	Food-Derived Compounds Apigenin and Luteolin Modulate mRNA Splicing of Introns with Weak Splice Sites. <i>IScience</i> , 2019, 22, 336-352.	1.9	15
2651	Broad regulation of gene isoform expression by Wnt signaling in cancer. <i>Rna</i> , 2019, 25, 1696-1713.	1.6	5

#	ARTICLE	IF	CITATIONS
2652	Deep profiling and custom databases improve detection of proteoforms generated by alternative splicing. <i>Genome Research</i> , 2019, 29, 2046-2055.	2.4	23
2653	Cloud accelerated alignment and assembly of full-length single-cell RNA-seq data using Falco. <i>BMC Genomics</i> , 2019, 20, 927.	1.2	2
2654	Transcriptome assembly from long-read RNA-seq alignments with StringTie2. <i>Genome Biology</i> , 2019, 20, 278.	3.8	897
2655	Single-molecule real-time sequencing facilitates the analysis of transcripts and splice isoforms of anthers in Chinese cabbage (<i>Brassica rapa</i> L. ssp. <i>pekinensis</i>). <i>BMC Plant Biology</i> , 2019, 19, 517.	1.6	16
2656	Gene Expression Profiles Controlled by the Alternative Splicing Factor Nova2 in Endothelial Cells. <i>Cells</i> , 2019, 8, 1498.	1.8	10
2657	Characterization of Full-Length Transcriptome Sequences and Splice Variants of <i>Lateolabrax maculatus</i> by Single-Molecule Long-Read Sequencing and Their Involvement in Salinity Regulation. <i>Frontiers in Genetics</i> , 2019, 10, 1126.	1.1	29
2658	Transcriptome analysis of the almond moth, <i>Cadra cautella</i> , female abdominal tissues and identification of reproduction control genes. <i>BMC Genomics</i> , 2019, 20, 883.	1.2	4
2659	PsyMuKB: An Integrative De Novo Variant Knowledge Base for Developmental Disorders. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 453-464.	3.0	10
2660	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. <i>Nature Communications</i> , 2019, 10, 5712.	5.8	27
2661	Genome-wide human brain eQTLs: In-depth analysis and insights using the UKBEC dataset. <i>Scientific Reports</i> , 2019, 9, 19201.	1.6	15
2662	Splice-Junction-Based Mapping of Alternative Isoforms in the Human Proteome. <i>Cell Reports</i> , 2019, 29, 3751-3765.e5.	2.9	64
2663	RNA Expression Profile and Alternative Splicing Signatures of Genistein-Treated Breeder Hens Revealed by Hepatic Transcriptomic Analysis. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-19.	1.9	3
2664	Neuroblastoma RAS viral oncogene homolog mRNA is differentially spliced to give five distinct isoforms: implications for melanoma therapy. <i>Melanoma Research</i> , 2019, 29, 491-500.	0.6	6
2665	Regulatory genes and pathways disrupted in autism spectrum disorders. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2019, 89, 57-64.	2.5	29
2666	Time Course of Disease Progression of PRPF31-mediated Retinitis Pigmentosa. <i>American Journal of Ophthalmology</i> , 2019, 200, 76-84.	1.7	25
2667	Advances in Analyzing Virus-Induced Alterations of Host Cell Splicing. <i>Trends in Microbiology</i> , 2019, 27, 268-281.	3.5	49
2668	Guided Reconstruction of Full-Length Isoforms from Short Reads by CIDANE. <i>Methods in Molecular Biology</i> , 2019, 1870, 199-208.	0.4	1
2669	RNA splicing analysis in genomic medicine. <i>International Journal of Biochemistry and Cell Biology</i> , 2019, 108, 61-71.	1.2	21

#	ARTICLE	IF	CITATIONS
2670	A Sam68-dependent alternative splicing program shapes postsynaptic protein complexes. <i>European Journal of Neuroscience</i> , 2019, 49, 1436-1453.	1.2	12
2671	mQC: A post-mapping data exploration tool for ribosome profiling. <i>Computer Methods and Programs in Biomedicine</i> , 2019, 181, 104806.	2.6	12
2672	RNA Splicing and Disease: Animal Models to Therapies. <i>Trends in Genetics</i> , 2019, 35, 68-87.	2.9	154
2673	Heat stress induced alternative splicing in catfish as determined by transcriptome analysis. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 166-172.	0.4	36
2674	Targeted deletion of an NRL- and CRX-regulated alternative promoter specifically silences FERM and PDZ domain containing 1 (Frmpl1) in rod photoreceptors. <i>Human Molecular Genetics</i> , 2019, 28, 804-817.	1.4	9
2675	RNA-binding proteins RBM20 and PTBP1 regulate the alternative splicing of FHOD3. <i>International Journal of Biochemistry and Cell Biology</i> , 2019, 106, 74-83.	1.2	19
2676	OTUB2 stabilizes U2AF2 to promote the Warburg effect and tumorigenesis via the AKT/mTOR signaling pathway in non-small cell lung cancer. <i>Theranostics</i> , 2019, 9, 179-195.	4.6	93
2677	Hybrid sequencing-based personal full-length transcriptomic analysis implicates proteostatic stress in metastatic ovarian cancer. <i>Oncogene</i> , 2019, 38, 3047-3060.	2.6	6
2678	Predicting Splicing from Primary Sequence with Deep Learning. <i>Cell</i> , 2019, 176, 535-548.e24.	13.5	1,305
2679	Spatial proteomics: a powerful discovery tool for cell biology. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 285-302.	16.1	316
2680	Genome-wide identification and comparative analysis of alternative splicing across four legume species. <i>Planta</i> , 2019, 249, 1133-1142.	1.6	16
2681	The expression of FOXP3 and its role in human cancers. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2019, 1871, 170-178.	3.3	50
2682	Transcriptional landscape of alternative splicing during peripheral nerve injury. <i>Journal of Cellular Physiology</i> , 2019, 234, 6876-6885.	2.0	13
2683	Autism spectrum disorder: insights into convergent mechanisms from transcriptomics. <i>Nature Reviews Genetics</i> , 2019, 20, 51-63.	7.7	128
2684	CancerSplicingQTL: a database for genome-wide identification of splicing QTLs in human cancer. <i>Nucleic Acids Research</i> , 2019, 47, D909-D916.	6.5	61
2685	DeepIsoFun: a deep domain adaptation approach to predict isoform functions. <i>Bioinformatics</i> , 2019, 35, 2535-2544.	1.8	20
2687	RBP-Maps enables robust generation of splicing regulatory maps. <i>Rna</i> , 2019, 25, 193-204.	1.6	63
2688	Survival-associated alternative splicing signatures in esophageal carcinoma. <i>Carcinogenesis</i> , 2019, 40, 121-130.	1.3	66

#	ARTICLE	IF	CITATIONS
2689	PacBio full-length cDNA sequencing integrated with RNA-seq reads drastically improves the discovery of splicing transcripts in rice. <i>Plant Journal</i> , 2019, 97, 296-305.	2.8	90
2690	psichomics: graphical application for alternative splicing quantification and analysis. <i>Nucleic Acids Research</i> , 2019, 47, e7-e7.	6.5	36
2691	A benchmarking of workflows for detecting differential splicing and differential expression at isoform level in human RNA-seq studies. <i>Briefings in Bioinformatics</i> , 2019, 20, 471-481.	3.2	31
2692	Upstream analysis of alternative splicing: a review of computational approaches to predict context-dependent splicing factors. <i>Briefings in Bioinformatics</i> , 2019, 20, 1358-1375.	3.2	53
2693	Beyond genome-wide significance: integrative approaches to the interpretation and extension of GWAS findings for alcohol use disorder. <i>Addiction Biology</i> , 2019, 24, 275-289.	1.4	15
2694	IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 938-948.	1.9	4
2695	Multiplexed primer extension sequencing: A targeted RNA-seq method that enables high-precision quantitation of mRNA splicing isoforms and rare pre-mRNA splicing intermediates. <i>Methods</i> , 2020, 176, 34-45.	1.9	8
2696	Alternative splicing events during adipogenesis from hMSCs. <i>Journal of Cellular Physiology</i> , 2020, 235, 304-316.	2.0	10
2698	Tumor-Based Genetic Testing and Familial Cancer Risk. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020, 10, a036590.	2.9	27
2699	Targeting mRNA processing as an anticancer strategy. <i>Nature Reviews Drug Discovery</i> , 2020, 19, 112-129.	21.5	131
2700	A network-based variable selection approach for identification of modules and biomarker genes associated with end-stage kidney disease. <i>Nephrology</i> , 2020, 25, 775-784.	0.7	5
2701	Epigenetic requisites of the Cambrian explosion. , 2020, , 71-136.		0
2702	A survey on identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1261-1276.	3.2	33
2703	Identification of novel alternative transcripts of the human Ribonuclease P (RNASEK) gene using 3' RACE and high-throughput sequencing approaches. <i>Genomics</i> , 2020, 112, 943-951.	1.3	3
2704	Isoform function prediction based on bi-random walks on a heterogeneous network. <i>Bioinformatics</i> , 2020, 36, 303-310.	1.8	27
2705	Detection of a novel CFBF-MYH11 fusion transcript in acute myeloid leukemia M1 with inv(16)(p13q22). <i>Cancer Genetics</i> , 2020, 241, 72-76.	0.2	2
2706	Genome-wide analysis of alternative splicing events during response to drought stress in tomato (<i>Solanum lycopersicum</i> L.). <i>Journal of Horticultural Science and Biotechnology</i> , 2020, 95, 286-293.	0.9	9
2707	The Expression of CNS-Specific PPARGC1A Transcripts Is Regulated by Hypoxia and a Variable GT Repeat Polymorphism. <i>Molecular Neurobiology</i> , 2020, 57, 752-764.	1.9	10

#	ARTICLE	IF	CITATIONS
2708	Compressed and Penalized Linear Regression. <i>Journal of Computational and Graphical Statistics</i> , 2020, 29, 309-322.	0.9	2
2709	Identification of a prognostic alternative splicing signature in oral squamous cell carcinoma. <i>Journal of Cellular Physiology</i> , 2020, 235, 4804-4813.	2.0	27
2710	In silico analysis of alternative splicing on drug-target gene interactions. <i>Scientific Reports</i> , 2020, 10, 134.	1.6	11
2711	Genome-wide analysis reveals the association between alternative splicing and DNA methylation across human solid tumors. <i>BMC Medical Genomics</i> , 2020, 13, 4.	0.7	20
2712	Alternative splicing programming of axon formation. <i>Wiley Interdisciplinary Reviews RNA</i> , 2020, 11, e1585.	3.2	23
2713	Accurate quantification of circular RNAs identifies extensive circular isoform switching events. <i>Nature Communications</i> , 2020, 11, 90.	5.8	140
2714	RNA isoform screens uncover the essentiality and tumor-suppressor activity of ultraconserved poison exons. <i>Nature Genetics</i> , 2020, 52, 84-94.	9.4	70
2715	Alternative Splicing of the <i>SLCO1B1</i> Gene: An Exploratory Analysis of Isoform Diversity in Pediatric Liver. <i>Clinical and Translational Science</i> , 2020, 13, 509-519.	1.5	9
2716	Systematic analysis of survival-associated alternative splicing signatures in clear cell renal cell carcinoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 4074-4084.	1.2	47
2717	<i>Immuno-Oncology. Methods in Pharmacology and Toxicology</i> , 2020, , .	0.1	4
2718	Functional Analysis of Sheep <i>POU2F3</i> Isoforms. <i>Biochemical Genetics</i> , 2020, 58, 335-347.	0.8	6
2719	Alternative splicing coupled with transcript degradation modulates <i>OAS1g</i> antiviral activity. <i>Rna</i> , 2020, 26, 126-136.	1.6	15
2720	Systematic evaluation of differential splicing tools for RNA-seq studies. <i>Briefings in Bioinformatics</i> , 2020, 21, 2052-2065.	3.2	124
2721	Genome-wide analysis of mammary gland shows modulation of transcriptome landscape with alternative splice variants in <i>Staphylococcus aureus</i> mastitis in mice. <i>Gene</i> , 2020, 735, 144278.	1.0	6
2722	Understanding aberrant RNA splicing to facilitate cancer diagnosis and therapy. <i>Oncogene</i> , 2020, 39, 2231-2242.	2.6	53
2723	Alternative splicing in aging and longevity. <i>Human Genetics</i> , 2020, 139, 357-369.	1.8	108
2724	The Function of Pre-mRNA Alternative Splicing in Mammal Spermatogenesis. <i>International Journal of Biological Sciences</i> , 2020, 16, 38-48.	2.6	45
2725	RNA Splicing by the Spliceosome. <i>Annual Review of Biochemistry</i> , 2020, 89, 359-388.	5.0	357

#	ARTICLE	IF	CITATIONS
2726	Global identification of alternative splicing in <i>Shiraia bambusicola</i> and analysis of its regulation in hypocrellin biosynthesis. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 211-223.	1.7	8
2727	Splicing Dysregulation as Oncogenic Driver and Passenger Factor in Brain Tumors. <i>Cells</i> , 2020, 9, 10.	1.8	21
2728	An Intricate Connection between Alternative Splicing and Phenotypic Plasticity in Development and Cancer. <i>Cells</i> , 2020, 9, 34.	1.8	21
2729	PTPN21â€CDS long isoform inhibits the response of acute lymphoblastic leukemia cells to NKâ€Cmediated lysis via the KIR/HLAâ€C axis. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 3298-3312.	1.2	3
2730	Characterization and prognostic significance of alternative splicing events in lowerâ€Cgrade diffuse gliomas. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 13171-13180.	1.6	4
2731	An Improved CRISPR/dCas9 Interference Tool for Neuronal Gene Suppression. <i>Frontiers in Genome Editing</i> , 2020, 2, 9.	2.7	23
2732	An Overview of Alternative Splicing Defects Implicated in Myotonic Dystrophy Type I. <i>Genes</i> , 2020, 11, 1109.	1.0	66
2733	Transcriptome analysis of alternative splicing in the pathogen life cycle in human foreskin fibroblasts infected with <i>Trypanosoma cruzi</i> . <i>Scientific Reports</i> , 2020, 10, 17481.	1.6	4
2734	Alternative Splicing Enhances the Transcriptome Complexity of <i>Liriodendron chinense</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 578100.	1.7	14
2735	Adult-Onset Myopathy with Constitutive Activation of Akt following the Loss of hnRNP-U. <i>IScience</i> , 2020, 23, 101319.	1.9	5
2736	seekCRIT: Detecting and characterizing differentially expressed circular RNAs using high-throughput sequencing data. <i>PLoS Computational Biology</i> , 2020, 16, e1008338.	1.5	14
2737	Synergistic apoptotic effects in cancer cells by the combination of CLK and Bcl-2 family inhibitors. <i>PLoS ONE</i> , 2020, 15, e0240718.	1.1	10
2738	An analysis of tissue-specific alternative splicing at the protein level. <i>PLoS Computational Biology</i> , 2020, 16, e1008287.	1.5	55
2739	Changes in Alternative Splicing in Response to Domestication and Polyploidization in Wheat. <i>Plant Physiology</i> , 2020, 184, 1955-1968.	2.3	34
2740	Development of a nomogram for prognostic prediction of lowerâ€Cgrade glioma based on alternative splicing signatures. <i>Cancer Medicine</i> , 2020, 9, 9266-9281.	1.3	6
2741	Alternative Splicing for Improving Abiotic Stress Tolerance and Agronomic Traits in Crop Plants. <i>Journal of Plant Biology</i> , 2020, 63, 409-420.	0.9	7
2742	Aberrant RNA Splicing Events Driven by Mutations of RNA-Binding Proteins as Indicators for Skin Cutaneous Melanoma Prognosis. <i>Frontiers in Oncology</i> , 2020, 10, 568469.	1.3	4
2743	Comprehensive Analysis of Prognostic Alternative Splicing Signatures in Oral Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 1740.	1.3	12

#	ARTICLE	IF	CITATIONS
2744	WT1 activates transcription of the splice factor kinase SRPK1 gene in PC3 and K562 cancer cells in the absence of corepressor BASP1. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194642.	0.9	14
2745	Action, program, metaphor. <i>Interdisciplinary Science Reviews</i> , 2020, 45, 344-359.	1.0	1
2746	Innovative Therapeutic and Delivery Approaches Using Nanotechnology to Correct Splicing Defects Underlying Disease. <i>Frontiers in Genetics</i> , 2020, 11, 731.	1.1	14
2747	A long-read RNA-seq approach to identify novel transcripts of very large genes. <i>Genome Research</i> , 2020, 30, 885-897.	2.4	29
2748	A multi-view classification and feature selection method via sparse low-rank regression analysis. <i>International Journal of Data Mining and Bioinformatics</i> , 2020, 24, 140.	0.1	0
2749	SRRM4 Expands the Repertoire of Circular RNAs by Regulating Microexon Inclusion. <i>Cells</i> , 2020, 9, 2488.	1.8	8
2750	Alternative Polyadenylation: a new frontier in post transcriptional regulation. <i>Biomarker Research</i> , 2020, 8, 67.	2.8	48
2751	Archetypes and the "Impoverished Genome"™ argument: updates from evolutionary genetics. <i>Journal of Analytical Psychology</i> , 2020, 65, 911-931.	0.1	9
2752	An alternative splicing signature model for predicting hepatocellular carcinoma-specific survival. <i>Journal of Gastrointestinal Oncology</i> , 2020, 11, 1054-1064.	0.6	3
2753	Profiling Novel Alternative Splicing within Multiple Tissues Provides Useful Insights into Porcine Genome Annotation. <i>Genes</i> , 2020, 11, 1405.	1.0	3
2754	Alternative Splicing: Expanding the Landscape of Cancer Biomarkers and Therapeutics. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9032.	1.8	28
2755	Alternative splicing in endothelial cells: novel therapeutic opportunities in cancer angiogenesis. <i>Journal of Experimental and Clinical Cancer Research</i> , 2020, 39, 275.	3.5	17
2756	Differences in Alternative Splicing between Yellow and Black-Seeded Rapeseed. <i>Plants</i> , 2020, 9, 977.	1.6	10
2757	Alternative splicing and cancer: insights, opportunities, and challenges from an expanding view of the transcriptome. <i>Genes and Development</i> , 2020, 34, 1005-1016.	2.7	61
2758	Global profiling of the alternative splicing landscape reveals transcriptomic diversity during the early phase of enterovirus 71 infection. <i>Virology</i> , 2020, 548, 213-225.	1.1	8
2759	Splicing-accessible coding 3'UTRs control protein stability and interaction networks. <i>Genome Biology</i> , 2020, 21, 186.	3.8	13
2760	Transcriptome-wide stability analysis uncovers LARP4-mediated NF- κ B1 mRNA stabilization during T β cell activation. <i>Nucleic Acids Research</i> , 2020, 48, 8724-8739.	6.5	10
2761	Differential tissue specific expression of Kif23 alternative transcripts in mice with the human mutation causing congenital dyserythropoietic anemia type III. <i>Blood Cells, Molecules, and Diseases</i> , 2020, 85, 102483.	0.6	4

#	ARTICLE	IF	CITATIONS
2762	Improving the diversity of captured full-length isoforms using a normalized single-molecule RNA-sequencing method. <i>Communications Biology</i> , 2020, 3, 403.	2.0	9
2763	RNA-Seq Analysis Reveals Localization-Associated Alternative Splicing across 13 Cell Lines. <i>Genes</i> , 2020, 11, 820.	1.0	11
2764	Isolation, identification, expression and subcellular localization of PPARG gene in buffalo mammary gland. <i>Gene</i> , 2020, 759, 144981.	1.0	3
2765	Cryo-EM snapshots of the human spliceosome reveal structural adaptations for splicing regulation. <i>Current Opinion in Structural Biology</i> , 2020, 65, 139-148.	2.6	21
2766	An Alternative Splicing Program for Mouse Craniofacial Development. <i>Frontiers in Physiology</i> , 2020, 11, 1099.	1.3	12
2767	Splice variants of RASâ€™ translational significance. <i>Cancer and Metastasis Reviews</i> , 2020, 39, 1039-1049.	2.7	12
2768	Global regulatory features of alternative splicing across tissues and within the nervous system of <i>C. elegans</i> . <i>Genome Research</i> , 2020, 30, 1766-1780.	2.4	8
2769	Alternative Splicing During the <i>Chlamydomonas reinhardtii</i> Cell Cycle. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3797-3810.	0.8	15
2770	Evolutionary Biologyâ€™ A Transdisciplinary Approach. , 2020, , .		5
2771	CELF2 regulates the species-specific alternative splicing of TREM2. <i>Scientific Reports</i> , 2020, 10, 17995.	1.6	14
2772	Identification of Survival-Associated Alternative Splicing Signatures in Lung Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 587343.	1.3	12
2773	A new mechanism for a familiar mutation â€™ bovine DGAT1 K232A modulates gene expression through multi-junction exon splice enhancement. <i>BMC Genomics</i> , 2020, 21, 591.	1.2	15
2774	Integrative bioinformatics analysis of prognostic alternative splicing signatures in gastric cancer. <i>Journal of Gastrointestinal Oncology</i> , 2020, 11, 685-694.	0.6	3
2775	NineTeen Complex-subunit Salsa is required for efficient splicing of a subset of introns and dorsalâ€™ventral patterning. <i>Rna</i> , 2020, 26, 1935-1956.	1.6	2
2776	PTBP3 Induced Inhibition of Differentiation of Gastric Cancer Cells Through Alternative Splicing of Id1. <i>Frontiers in Oncology</i> , 2020, 10, 1477.	1.3	6
2777	Features of alternative splicing in stomach adenocarcinoma and their clinical implication: a research based on massive sequencing data. <i>BMC Genomics</i> , 2020, 21, 580.	1.2	8
2778	The Construction of Bone Metastasis-Specific Prognostic Model and Co-expressed Network of Alternative Splicing in Breast Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 790.	1.8	6
2779	Plant 3â€™ Regulatory Regions From mRNA-Encoding Genes and Their Uses to Modulate Expression. <i>Frontiers in Plant Science</i> , 2020, 11, 1252.	1.7	30

#	ARTICLE	IF	CITATIONS
2780	The roles of long noncoding RNAs in breast cancer metastasis. <i>Cell Death and Disease</i> , 2020, 11, 749.	2.7	48
2781	The biological function and clinical significance of SF3B1 mutations in cancer. <i>Biomarker Research</i> , 2020, 8, 38.	2.8	47
2782	Targeting Alternative Splicing as a Potential Therapy for Episodic Ataxia Type 2. <i>Biomedicines</i> , 2020, 8, 332.	1.4	13
2784	Systematic characterization of the branch point binding protein, splicing factor 1, gene family in plant development and stress responses. <i>BMC Plant Biology</i> , 2020, 20, 379.	1.6	5
2785	Dynamic nanopore long-read sequencing analysis of HIV-1 splicing events during the early steps of infection. <i>Retrovirology</i> , 2020, 17, 25.	0.9	23
2786	Modulation of hepatitis B virus pregenomic RNA stability and splicing by histone deacetylase 5 enhances viral biosynthesis. <i>PLoS Pathogens</i> , 2020, 16, e1008802.	2.1	6
2787	Loss of ESRP1 blocks mouse oocyte development and leads to female infertility. <i>Development (Cambridge)</i> , 2020, 148, .	1.2	10
2788	Evidence of BK _{Ca} Channelopathy-Driven Breast Cancer Metastasis to Brain. , 0, , .		0
2789	Perspective in Alternative Splicing Coupled to Nonsense-Mediated mRNA Decay. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9424.	1.8	39
2790	A variant of H19 transcript regulates EMT and oral cancer progression. <i>Oral Diseases</i> , 2022, 28, 116-124.	1.5	7
2791	Titration of SF3B1 Activity Reveals Distinct Effects on the Transcriptome and Cell Physiology. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9641.	1.8	2
2792	DNA Methylation Regulates Alternative Polyadenylation via CTCF and the Cohesin Complex. <i>Molecular Cell</i> , 2020, 78, 752-764.e6.	4.5	62
2793	Single-cell RNA counting at allele and isoform resolution using Smart-seq3. <i>Nature Biotechnology</i> , 2020, 38, 708-714.	9.4	399
2794	Gene expression dynamics are a proxy for selective pressures on alternatively polyadenylated isoforms. <i>Nucleic Acids Research</i> , 2020, 48, 5926-5938.	6.5	11
2795	tappAS: a comprehensive computational framework for the analysis of the functional impact of differential splicing. <i>Genome Biology</i> , 2020, 21, 119.	3.8	40
2796	High-resolution profile of transcriptomes reveals a role of alternative splicing for modulating response to nitrogen in maize. <i>BMC Genomics</i> , 2020, 21, 353.	1.2	21
2797	ORF Capture-Seq as a versatile method for targeted identification of full-length isoforms. <i>Nature Communications</i> , 2020, 11, 2326.	5.8	19
2798	Emerging Functions of Plant Serine/Arginine-Rich (SR) Proteins: Lessons from Animals. <i>Critical Reviews in Plant Sciences</i> , 2020, 39, 173-194.	2.7	19

#	ARTICLE	IF	CITATIONS
2799	Assessing heterogeneity among single embryos and single blastomeres using open microfluidic design. <i>Science Advances</i> , 2020, 6, eaay1751.	4.7	16
2800	From Gene to Protein—How Bacterial Virulence Factors Manipulate Host Gene Expression During Infection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3730.	1.8	34
2801	PRKCSH Alternative Splicing Involves in Silica-Induced Expression of Epithelial—Mesenchymal Transition Markers and Cell Proliferation. <i>Dose-Response</i> , 2020, 18, 155932582092382.	0.7	9
2802	RNA-Seq reveals skipping of exon 3 in a breast cancer patient carrying G118D PIK3CA mutation. <i>Gene Reports</i> , 2020, 20, 100704.	0.4	0
2803	CRISPR-Cas9 gene editing causes alternative splicing of the targeting mRNA. <i>Biochemical and Biophysical Research Communications</i> , 2020, 528, 54-61.	1.0	9
2804	Heterogeneity in mRNA Translation. <i>Trends in Cell Biology</i> , 2020, 30, 606-618.	3.6	54
2805	A combinatorially regulated RNA splicing signature predicts breast cancer EMT states and patient survival. <i>Rna</i> , 2020, 26, 1257-1267.	1.6	16
2806	Comprehensive analysis of prognostic alternative splicing signature in cervical cancer. <i>Cancer Cell International</i> , 2020, 20, 221.	1.8	20
2807	Novel Insights Into Triple-Negative Breast Cancer Prognosis by Comprehensive Characterization of Aberrant Alternative Splicing. <i>Frontiers in Genetics</i> , 2020, 11, 534.	1.1	10
2808	CRISPR artificial splicing factors. <i>Nature Communications</i> , 2020, 11, 2973.	5.8	70
2809	SURF: integrative analysis of a compendium of RNA-seq and CLIP-seq datasets highlights complex governing of alternative transcriptional regulation by RNA-binding proteins. <i>Genome Biology</i> , 2020, 21, 139.	3.8	5
2810	The Role of Alternative RNA Splicing in the Regulation of hTERT, Telomerase, and Telomeres: Implications for Cancer Therapeutics. <i>Cancers</i> , 2020, 12, 1514.	1.7	14
2811	Microexons: at the nexus of nervous system development, behaviour and autism spectrum disorder. <i>Current Opinion in Genetics and Development</i> , 2020, 65, 22-33.	1.5	38
2812	Handling multi-mapped reads in RNA-seq. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1569-1576.	1.9	44
2813	Emerging Roles of RNA 3'-end Cleavage and Polyadenylation in Pathogenesis, Diagnosis and Therapy of Human Disorders. <i>Biomolecules</i> , 2020, 10, 915.	1.8	46
2814	Emerging Roles of Activity-Dependent Alternative Splicing in Homeostatic Plasticity. <i>Frontiers in Cellular Neuroscience</i> , 2020, 14, 104.	1.8	16
2815	Hallmarks of Splicing Defects in Cancer: Clinical Applications in the Era of Personalized Medicine. <i>Cancers</i> , 2020, 12, 1381.	1.7	14
2816	RNA Splicing and Cancer. <i>Trends in Cancer</i> , 2020, 6, 631-644.	3.8	140

#	ARTICLE	IF	CITATIONS
2817	Silencing Core Spliceosome Sm Gene Expression Induces a Cytotoxic Splicing Switch in the Proteasome Subunit Beta 3 mRNA in Non-Small Cell Lung Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4192.	1.8	13
2818	Heterozygous loss of Rbm24 in the adult mouse heart increases sarcomere slack length but does not affect function. <i>Scientific Reports</i> , 2020, 10, 7687.	1.6	3
2819	Identification of novel alternative splicing isoform biomarkers and their association with overall survival in colorectal cancer. <i>BMC Gastroenterology</i> , 2020, 20, 171.	0.8	23
2820	The Genetic Regulation of Alternative Splicing in <i>Populus deltoides</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 590.	1.7	5
2821	Asian Zika Virus Isolate Significantly Changes the Transcriptional Profile and Alternative RNA Splicing Events in a Neuroblastoma Cell Line. <i>Viruses</i> , 2020, 12, 510.	1.5	25
2823	Pattern of alternative splicing different associated with difference in rooting depth in rice. <i>Plant and Soil</i> , 2020, 449, 233-248.	1.8	4
2824	BANDITS: Bayesian differential splicing accounting for sample-to-sample variability and mapping uncertainty. <i>Genome Biology</i> , 2020, 21, 69.	3.8	17
2825	Regulation of Cancer Immune Checkpoints. <i>Advances in Experimental Medicine and Biology</i> , 2020, , .	0.8	7
2826	CuAS: a database of annotated transcripts generated by alternative splicing in cucumbers. <i>BMC Plant Biology</i> , 2020, 20, 119.	1.6	8
2827	Isoform-resolved correlation analysis between $\langle scp \rangle$ mRNA $\langle /scp \rangle$ abundance regulation and protein level degradation. <i>Molecular Systems Biology</i> , 2020, 16, e9170.	3.2	42
2828	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2020, 26, 3597-3607.	3.2	26
2829	Srsf7 Establishes the Juvenile Transcriptome through Age-Dependent Alternative Splicing in Mice. <i>IScience</i> , 2020, 23, 100929.	1.9	21
2830	Miliefy: visualizing cell-to-cell heterogeneity in read coverage of single-cell RNA sequencing datasets. <i>BMC Genomics</i> , 2020, 21, 177.	1.2	5
2831	Regulating Divergent Transcriptomes through mRNA Splicing and Its Modulation Using Various Small Compounds. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2026.	1.8	8
2832	Cellular, transcriptomic and isoform heterogeneity of breast cancer cell line revealed by full-length single-cell RNA sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 676-685.	1.9	26
2833	Specific expression and alternative splicing of mouse genes during spermatogenesis. <i>Molecular Omics</i> , 2020, 16, 258-267.	1.4	6
2834	<p>Novel Alternatively Spliced Variants of Smad4 Expressed in TGF- β 2-Induced EMT Regulating Proliferation and Migration of A549 Cells</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 2203-2213.	1.0	10
2835	Expression Changes Confirm Genomic Variants Predicted to Result in Allele-Specific, Alternative mRNA Splicing. <i>Frontiers in Genetics</i> , 2020, 11, 109.	1.1	19

#	ARTICLE	IF	CITATIONS
2836	UGT1A1 Variants c.864+5G>T and c.996+2_996+5del of a Crigler-Najjar Patient Induce Aberrant Splicing in Minigene Assays. <i>Frontiers in Genetics</i> , 2020, 11, 169.	1.1	9
2837	Proteomic and interactomic insights into the molecular basis of cell functional diversity. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 327-340.	16.1	156
2838	Systemic Analysis of RNA Alternative Splicing Signals Related to the Prognosis for Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 87.	1.3	7
2839	Isobaric tags for relative and absolute quantitation (iTRAQ)-based proteomic analysis of mRNA splicing relevant proteins in aging HSPCs. <i>Aging Clinical and Experimental Research</i> , 2021, 33, 3123-3134.	1.4	2
2840	Identification of Prognostic Signatures of Alternative Splicing in Glioma. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1484-1492.	1.1	8
2841	A tumor-associated splice-isoform of <i>MAP2K7</i> drives dedifferentiation in MBNL1-low cancers via JNK activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16391-16400.	3.3	23
2842	Circular RNAs in Sepsis: Biogenesis, Function, and Clinical Significance. <i>Cells</i> , 2020, 9, 1544.	1.8	47
2843	Regional Variation of Splicing QTLs in Human Brain. <i>American Journal of Human Genetics</i> , 2020, 107, 196-210.	2.6	26
2844	Epigenome-based splicing prediction using a recurrent neural network. <i>PLoS Computational Biology</i> , 2020, 16, e1008006.	1.5	16
2845	Alternative splicing is highly variable among <i>Daphnia pulex</i> lineages in response to acute copper exposure. <i>BMC Genomics</i> , 2020, 21, 433.	1.2	15
2846	Antisense oligonucleotide modulation of non-productive alternative splicing upregulates gene expression. <i>Nature Communications</i> , 2020, 11, 3501.	5.8	103
2847	A role for alternative splicing in circadian control of exocytosis and glucose homeostasis. <i>Genes and Development</i> , 2020, 34, 1089-1105.	2.7	22
2848	mRNA Editing, Processing and Quality Control in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2020, 215, 531-568.	1.2	24
2849	Germ Cell-Specific Gene 1-Like Protein Regulated by Splicing Factor CUGBP Elav-Like Family Member 5 and Primary Bile Acid Biosynthesis are Prognostic in Glioblastoma Multiforme. <i>Frontiers in Genetics</i> , 2019, 10, 1380.	1.1	6
2850	Opportunities and challenges in long-read sequencing data analysis. <i>Genome Biology</i> , 2020, 21, 30.	3.8	1,536
2851	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. <i>Current Bioinformatics</i> , 2020, 15, 2-16.	0.7	9
2852	Tissue transglutaminase variant 2 transduced mesenchymal stem cells and their chondrogenic potential. <i>Biotechnology and Bioengineering</i> , 2020, 117, 1839-1852.	1.7	1
2853	Developmental Time Course of SNAP-25 Isoforms Regulate Hippocampal Long-Term Synaptic Plasticity and Hippocampus-Dependent Learning. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1448.	1.8	9

#	ARTICLE	IF	CITATIONS
2854	A Novel Prognostic Index Based on Alternative Splicing in Papillary Renal Cell Carcinoma. <i>Frontiers in Genetics</i> , 2020, 10, 1333.	1.1	3
2855	Transcriptsâ€™ Evolutionary History and Structural Dynamics Give Mechanistic Insights into the Functional Diversity of the JNK Family. <i>Journal of Molecular Biology</i> , 2020, 432, 2121-2140.	2.0	7
2856	Contributions of alternative splicing to muscle type development and function. <i>Seminars in Cell and Developmental Biology</i> , 2020, 104, 65-80.	2.3	33
2857	Global Analysis of Alternative Splicing Difference in Peripheral Immune Organs between Tongcheng Pigs and Large White Pigs Artificially Infected with PRRSV <i>In Vivo</i> . <i>BioMed Research International</i> , 2020, 2020, 1-14.	0.9	6
2858	An activator of G protein-coupled receptor and MEK1/2-ERK1/2 signaling inhibits HIV-1 replication by altering viral RNA processing. <i>PLoS Pathogens</i> , 2020, 16, e1008307.	2.1	8
2859	Alternative Splicing and DNA Damage Response in Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 91.	1.7	20
2860	RNA Splicing Defects in Hypertrophic Cardiomyopathy: Implications for Diagnosis and Therapy. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1329.	1.8	15
2861	Goat CMTM2: mRNA expression profiles of different alternative spliced variants and associations analyses with growth traits. <i>3 Biotech</i> , 2020, 10, 131.	1.1	6
2862	Real-time detection of mRNA splicing variants with specifically designed reverse-transcription loop-mediated isothermal amplification. <i>RSC Advances</i> , 2020, 10, 6271-6276.	1.7	2
2863	Altered chromatin landscape and enhancer engagement underlie transcriptional dysregulation in MED12 mutant uterine leiomyomas. <i>Nature Communications</i> , 2020, 11, 1019.	5.8	34
2864	Roles of Splicing Factors in Hormone-Related Cancer Progression. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1551.	1.8	16
2865	Amniotic fluid cell-free transcriptome: a glimpse into fetal development and placental cellular dynamics during normal pregnancy. <i>BMC Medical Genomics</i> , 2020, 13, 25.	0.7	25
2866	Single-cell alternative splicing analysis reveals dominance of single transcript variant. <i>Genomics</i> , 2020, 112, 2418-2425.	1.3	19
2867	Comprehensive identification of alternative back-splicing in human tissue transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, 1779-1789.	6.5	33
2868	Genome-wide analysis of alternative splicing differences between oocyte and zygoteâ€. <i>Biology of Reproduction</i> , 2020, 102, 999-1010.	1.2	7
2869	iPAC: a genome-guided assembler of isoforms via phasing and combing paths. <i>Bioinformatics</i> , 2020, 36, 2712-2717.	1.8	5
2871	SMRT sequencing of a full-length transcriptome reveals transcript variants involved in C18 unsaturated fatty acid biosynthesis and metabolism pathways at chilling temperature in <i>Pennisetum giganteum</i> . <i>BMC Genomics</i> , 2020, 21, 52.	1.2	16
2872	Omics and the molecular exercise physiology. <i>Advances in Clinical Chemistry</i> , 2020, 96, 55-84.	1.8	22

#	ARTICLE	IF	CITATIONS
2873	3â€™Pool-seq: an optimized cost-efficient and scalable method of whole-transcriptome gene expression profiling. <i>BMC Genomics</i> , 2020, 21, 64.	1.2	12
2874	Retinoic Acid Induces Embryonic Stem Cells (ESCs) Transition to 2 Cell-Like State Through a Coordinated Expression of Dux and Duxbl1. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 385.	1.8	24
2875	Antiviral, Immunomodulatory and Antiproliferative Activities of Recombinant Soluble IFNAR2 without IFN-Î³ Mediation. <i>Journal of Clinical Medicine</i> , 2020, 9, 959.	1.0	4
2876	Subphysiological temperature induces pervasive alternative splicing in Chinese hamster ovary cells. <i>Biotechnology and Bioengineering</i> , 2020, 117, 2489-2503.	1.7	6
2877	Pathogenic diversity of RNA variants and RNA variation-associated factors in cancer development. <i>Experimental and Molecular Medicine</i> , 2020, 52, 582-593.	3.2	10
2878	Cytokine stimulation of the choriocarcinoma cell line JEG-3 leads to alterations in the HLA-G expression profile. <i>Cellular Immunology</i> , 2020, 352, 104110.	1.4	17
2879	The Interaction Between lncRNA SNHG6 and hnRNPA1 Contributes to the Growth of Colorectal Cancer by Enhancing Aerobic Glycolysis Through the Regulation of Alternative Splicing of PKM. <i>Frontiers in Oncology</i> , 2020, 10, 363.	1.3	61
2880	Discrete functional and mechanistic roles of chromodomain Y-like 2 (CDYL2) transcript variants in breast cancer growth and metastasis. <i>Theranostics</i> , 2020, 10, 5242-5258.	4.6	14
2881	Specific histone modifications associate with alternative exon selection during mammalian development. <i>Nucleic Acids Research</i> , 2020, 48, 4709-4724.	6.5	19
2882	A functional network of gastric-cancer-associated splicing events controlled by dysregulated splicing factors. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa013.	1.5	5
2883	Obstacles to detecting isoforms using full-length scRNA-seq data. <i>Genome Biology</i> , 2020, 21, 74.	3.8	36
2884	hnRNP A1 Regulates Alternative Splicing of Tau Exon 10 by Targeting 3â€™ Splice Sites. <i>Cells</i> , 2020, 9, 936.	1.8	11
2885	Alternative splicing (AS) mechanism plays important roles in response to different salinity environments in spotted sea bass. <i>International Journal of Biological Macromolecules</i> , 2020, 155, 50-60.	3.6	18
2886	Roles and mechanisms of alternative splicing in cancer â€” implications for care. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 457-474.	12.5	400
2887	Genome-Wide Characterization of Alternative Splicing Events and Their Responses to Cold Stress in Tilapia. <i>Frontiers in Genetics</i> , 2020, 11, 244.	1.1	25
2888	Modulator-Dependent RBPs Changes Alternative Splicing Outcomes in Kidney Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 265.	1.1	22
2890	Next-generation sequencing reveals alternative L-DOPA decarboxylase (DDC) splice variants bearing novel exons, in human hepatocellular and lung cancer cells. <i>Gene</i> , 2021, 768, 145262.	1.0	10
2891	B7-H3 is spliced by SRSF3 in colorectal cancer. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 311-321.	2.0	16

#	ARTICLE	IF	CITATIONS
2892	Overview of PAX gene family: analysis of human tissue-specific variant expression and involvement in human disease. <i>Human Genetics</i> , 2021, 140, 381-400.	1.8	25
2893	Systematics for types and effects of RNA variations. <i>RNA Biology</i> , 2021, 18, 481-498.	1.5	8
2894	IntAPT: integrated assembly of phenotype-specific transcripts from multiple RNA-seq profiles. <i>Bioinformatics</i> , 2021, 37, 650-658.	1.8	1
2895	Splicing to Keep Cycling: The Importance of Pre-mRNA Splicing during the Cell Cycle. <i>Trends in Genetics</i> , 2021, 37, 266-278.	2.9	26
2896	RNA in cancer. <i>Nature Reviews Cancer</i> , 2021, 21, 22-36.	12.8	655
2897	Intron retention and its impact on gene expression and protein diversity: A review and a practical guide. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021, 12, e1631.	3.2	33
2898	Holding on to Junk Bonds: Intron Retention in Cancer and Therapy. <i>Cancer Research</i> , 2021, 81, 779-789.	0.4	19
2899	RNA splicing alteration in the response to platinum chemotherapy in ovarian cancer: A possible biomarker and therapeutic target. <i>Medicinal Research Reviews</i> , 2021, 41, 586-615.	5.0	6
2900	Towards Decoding the Sequence-Based Grammar Governing the Functions of Intrinsically Disordered Protein Regions. <i>Journal of Molecular Biology</i> , 2021, 433, 166724.	2.0	29
2901	RJunBase: a database of RNA splice junctions in human normal and cancerous tissues. <i>Nucleic Acids Research</i> , 2021, 49, D201-D211.	6.5	12
2902	RNA-binding motif protein 39 (RBM39): An emerging cancer target. <i>British Journal of Pharmacology</i> , 2022, 179, 2795-2812.	2.7	31
2903	Anything but Ordinary – Emerging Splicing Mechanisms in Eukaryotic Gene Regulation. <i>Trends in Genetics</i> , 2021, 37, 355-372.	2.9	64
2904	Identification of Dominant Transcripts in Oxidative Stress Response by a Full-Length Transcriptome Analysis. <i>Molecular and Cellular Biology</i> , 2021, 41, .	1.1	7
2905	Splicing factors: Insights into their regulatory network in alternative splicing in cancer. <i>Cancer Letters</i> , 2021, 501, 83-104.	3.2	22
2906	UniProt: the universal protein knowledgebase in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D480-D489.	6.5	4,709
2907	A splice acceptor variant in <i>HLA-DRA</i> affects the conformation and cellular localization of the class II DR alpha-chain. <i>Immunology</i> , 2021, 162, 194-207.	2.0	3
2908	Genome-wide alternative splicing profiling in the fungal plant pathogen <i>Sclerotinia sclerotiorum</i> during the colonization of diverse host families. <i>Molecular Plant Pathology</i> , 2021, 22, 31-47.	2.0	25
2909	RNA structure probing to characterize RNA-protein interactions on low abundance pre-mRNA in living cells. <i>Rna</i> , 2021, 27, 343-358.	1.6	6

#	ARTICLE	IF	CITATIONS
2910	Genome-wide alternative splicing variation and its potential contribution to maize immature-ear heterosis. <i>Crop Journal</i> , 2021, 9, 476-486.	2.3	5
2911	Novel Variant of OCT4, Named OCT4B5, is Highly Expressed in Human Pluripotent Cells. <i>Stem Cell Reviews and Reports</i> , 2021, 17, 1068-1073.	1.7	5
2912	<i>Ctcf</i> haploinsufficiency mediates intron retention in a tissue-specific manner. <i>RNA Biology</i> , 2021, 18, 93-103.	1.5	12
2913	Determination of isoform-specific RNA structure with nanopore long reads. <i>Nature Biotechnology</i> , 2021, 39, 336-346.	9.4	72
2914	LncAS2Cancer: a comprehensive database for alternative splicing of lncRNAs across human cancers. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
2915	Regulation of RNA degradation pathways during the lipopolysaccharide response in Macrophages. <i>Journal of Leukocyte Biology</i> , 2021, 109, 593-603.	1.5	2
2916	Gene co-expression and alternative splicing analysis of key metabolic tissues to unravel the regulatory signatures of fatty acid composition in cattle. <i>RNA Biology</i> , 2021, 18, 854-862.	1.5	13
2917	TREND-DB—a transcriptome-wide atlas of the dynamic landscape of alternative polyadenylation. <i>Nucleic Acids Research</i> , 2021, 49, D243-D253.	6.5	23
2918	RNA structures in alternative splicing and backsplicing. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021, 12, e1626.	3.2	37
2919	Iso-Seq Long Read Transcriptome Sequencing. , 2021, , 486-500.		2
2920	QKI is a critical pre-mRNA alternative splicing regulator of cardiac myofibrillogenesis and contractile function. <i>Nature Communications</i> , 2021, 12, 89.	5.8	47
2921	Simultaneous studies of gene expression and alternative polyadenylation in primary human immune cells. <i>Methods in Enzymology</i> , 2021, 655, 349-399.	0.4	2
2922	Alternative splicing modulates cancer aggressiveness: role in EMT/metastasis and chemoresistance. <i>Molecular Biology Reports</i> , 2021, 48, 897-914.	1.0	26
2923	Targeting alternative splicing by RNAi: from the differential impact on splice variants to triggering artificial pre-mRNA splicing. <i>Nucleic Acids Research</i> , 2021, 49, 1133-1151.	6.5	12
2924	Allele-specific alternative splicing and its functional genetic variants in human tissues. <i>Genome Research</i> , 2021, 31, 359-371.	2.4	17
2927	DeepIDA: Predicting Isoform-Disease Associations by Data Fusion and Deep Neural Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2166-2176.	1.9	8
2928	Regulation of splicing in cardiovascular disease. , 2021, , 163-186.		1
2929	Target-capture full-length double-strand cDNA sequencing for alternative splicing analysis. <i>RNA Biology</i> , 2021, 18, 1600-1607.	1.5	7

#	ARTICLE	IF	CITATIONS
2931	Biological Aspects of Cancer Health Disparities. Annual Review of Medicine, 2021, 72, 229-241.	5.0	10
2932	Deconvolution of expression for nascent RNA-sequencing data (DENR) highlights pre-RNA isoform diversity in human cells. Bioinformatics, 2021, 37, 4727-4736.	1.8	4
2933	RAP: A Web Tool for RNA-Seq Data Analysis. Methods in Molecular Biology, 2021, 2284, 393-415.	0.4	0
2934	Simultaneous profiling of Arabidopsis thaliana and Vibrio vulnificus MO6-24/O transcriptomes by dual RNA-seq analysis. Computational and Structural Biotechnology Journal, 2021, 19, 2084-2096.	1.9	5
2935	Methods for Characterization of Alternative RNA Splicing. Methods in Molecular Biology, 2021, 2372, 209-222.	0.4	5
2936	Identification of prognostic and bone metastatic alternative splicing signatures in bladder cancer. Bioengineered, 2021, 12, 5289-5304.	1.4	10
2937	High-resolution analysis of cell-state transitions in yeast suggests widespread transcriptional tuning by alternative starts. Genome Biology, 2021, 22, 34.	3.8	30
2938	Alternative splicing landscapes in Arabidopsis thaliana across tissues and stress conditions highlight major functional differences with animals. Genome Biology, 2021, 22, 35.	3.8	93
2939	Tissue Specificity Based Isoform Function Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 3048-3059.	1.9	0
2940	The landscape of alternative splicing reveals novel events associated with tumorigenesis and the immune microenvironment in gastric cancer. Aging, 2021, 13, 4317-4334.	1.4	2
2941	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. Nature Communications, 2021, 12, 463.	5.8	109
2942	Cancer DEIso: An integrative analysis platform for investigating differentially expressed gene-level and isoform-level human cancer markers. Computational and Structural Biotechnology Journal, 2021, 19, 5149-5159.	1.9	5
2943	Genetics of Cardiomyopathy: Clinical and Mechanistic Implications for Heart Failure. Korean Circulation Journal, 2021, 51, 797.	0.7	13
2944	TRENDseq—A highly multiplexed high throughput RNA 3' end sequencing for mapping alternative polyadenylation. Methods in Enzymology, 2021, 655, 37-72.	0.4	6
2945	Androgen receptor and its splice variant, AR-V7, differentially induce mRNA splicing in prostate cancer cells. Scientific Reports, 2021, 11, 1393.	1.6	10
2946	Single-Cell RNA Sequencing Analysis: A Step-by-Step Overview. Methods in Molecular Biology, 2021, 2284, 343-365.	0.4	65
2947	QuickIsoSeq for Isoform Quantification in Large-Scale RNA Sequencing. Methods in Molecular Biology, 2021, 2284, 135-145.	0.4	1
2948	Splicing-associated chromatin signatures: a combinatorial and position-dependent role for histone marks in splicing definition. Nature Communications, 2021, 12, 682.	5.8	43

#	ARTICLE	IF	CITATIONS
2949	Hypoxia-induced alternative splicing in human diseases: the pledge, the turn, and the prestige. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 2729-2747.	2.4	12
2950	Alternative Splicing Increases Sirtuin Gene Family Diversity and Modulates Their Subcellular Localization and Function. <i>International Journal of Molecular Sciences</i> , 2021, 22, 473.	1.8	13
2951	Roles of developmentally regulated KIF2A alternative isoforms in cortical neuron migration and differentiation. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	10
2952	Splicing alterations in healthy aging and disease. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021, 12, e1643.	3.2	29
2953	A Prognostic Model Based on RNA Binding Protein Predicts Clinical Outcomes in Hepatocellular Carcinoma Patients. <i>Frontiers in Oncology</i> , 2020, 10, 613102.	1.3	6
2954	Alternative RNA Splicing in Fatty Liver Disease. <i>Frontiers in Endocrinology</i> , 2021, 12, 613213.	1.5	19
2955	CADD-Splice“improving genome-wide variant effect prediction using deep learning-derived splice scores. <i>Genome Medicine</i> , 2021, 13, 31.	3.6	375
2956	A Mechanism Leading to Changes in Copy Number Variations Affected by Transcriptional Level Might Be Involved in Evolution, Embryonic Development, Senescence, and Oncogenesis Mediated by Retrotransposons. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 618113.	1.8	2
2957	The Atypical Kinase R1OK3 Limits RVFV Propagation and Is Regulated by Alternative Splicing. <i>Viruses</i> , 2021, 13, 367.	1.5	6
2958	The Chloroplast Trans-Splicing RNA“Protein Supercomplex from the Green Alga <i>Chlamydomonas reinhardtii</i> . <i>Cells</i> , 2021, 10, 290.	1.8	11
2960	The Alter Retina: Alternative Splicing of Retinal Genes in Health and Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1855.	1.8	19
2961	Genome“wide discovery of natural variation in pre“mRNA splicing and prioritising causal alternative splicing to salt stress response in rice. <i>New Phytologist</i> , 2021, 230, 1273-1287.	3.5	20
2962	Fast and furious: insights of back splicing regulation during nascent RNA synthesis. <i>Science China Life Sciences</i> , 2021, 64, 1050-1061.	2.3	1
2963	Development and validation of an individual alternative splicing prognostic signature in gastric cancer. <i>Aging</i> , 2021, 13, 5824-5844.	1.4	3
2964	Alternatively Splicing Interactomes Identify Novel Isoform-Specific Partners for NSD2. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 612019.	1.8	0
2966	Prediction of RNA-binding protein and alternative splicing event associations during epithelial“mesenchymal transition based on inductive matrix completion. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
2967	Differential Splicing of Skipped Exons Predicts Drug Response in Cancer Cell Lines. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 901-912.	3.0	0
2968	2passtools: two-pass alignment using machine-learning-filtered splice junctions increases the accuracy of intron detection in long-read RNA sequencing. <i>Genome Biology</i> , 2021, 22, 72.	3.8	16

#	ARTICLE	IF	CITATIONS
2969	A Comprehensive Map of mRNAs and Their Isoforms across All 14 Renal Tubule Segments of Mouse. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 897-912.	3.0	110
2970	The methyltransferase SETD2 couples transcription and splicing by engaging mRNA processing factors through its SHI domain. <i>Nature Communications</i> , 2021, 12, 1443.	5.8	42
2971	Testis-expressed protein 33 is not essential for spermiogenesis and fertility in mice. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	3
2972	NCK-associated protein 1 like (nckap1l) minor splice variant regulates intrahepatic biliary network morphogenesis. <i>PLoS Genetics</i> , 2021, 17, e1009402.	1.5	3
2973	Cleavage and Polyadenylation Specific Factor 1 Promotes Tumor Progression via Alternative Polyadenylation and Splicing in Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 616835.	1.8	17
2974	CaMKII δ Splice Variants in the Healthy and Diseased Heart. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 644630.	1.8	13
2975	Epigenetic Regulation of Alternative Splicing: How LncRNAs Tailor the Message. <i>Non-coding RNA</i> , 2021, 7, 21.	1.3	33
2976	Pancreatic cancer driver mutations are targetable through distant alternative RNA splicing dependencies. <i>Oncotarget</i> , 2021, 12, 525-533.	0.8	4
2977	MTSplice predicts effects of genetic variants on tissue-specific splicing. <i>Genome Biology</i> , 2021, 22, 94.	3.8	23
2978	Single-cell transcriptomics dissects hematopoietic cell destruction and T-cell engagement in aplastic anemia. <i>Blood</i> , 2021, 138, 23-33.	0.6	33
2980	SRSF9 Regulates Cassette Exon Splicing of Caspase-2 by Interacting with Its Downstream Exon. <i>Cells</i> , 2021, 10, 679.	1.8	7
2981	Selective Activation of CNS and Reference PPARGC1A Promoters Is Associated with Distinct Gene Programs Relevant for Neurodegenerative Diseases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3296.	1.8	5
2982	A Novel Titin Truncation Variant Linked to Familial Dilated Cardiomyopathy Found in a Japanese Family and Its Functional Analysis in Genome-Edited Model Cells. <i>International Heart Journal</i> , 2021, 62, 359-366.	0.5	6
2983	An <i>in vitro</i> reconstituted U1 snRNP allows the study of the disordered regions of the particle and the interactions with proteins and ligands. <i>Nucleic Acids Research</i> , 2021, 49, e63-e63.	6.5	12
2984	Complexity and graded regulation of neuronal cell-type-specific alternative splicing revealed by single-cell RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	33
2986	Alternative splicing events implicated in carcinogenesis and prognosis of thyroid gland cancer. <i>Scientific Reports</i> , 2021, 11, 4841.	1.6	8
2987	An alternative splicing hypothesis for neuropathology of schizophrenia: evidence from studies on historical candidate genes and multi-omics data. <i>Molecular Psychiatry</i> , 2022, 27, 95-112.	4.1	19
2988	Advances in Proteomics Allow Insights Into Neuronal Proteomes. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 647451.	1.4	8

#	ARTICLE	IF	CITATIONS
2989	Loss of splicing factor IK impairs normal skeletal muscle development. <i>BMC Biology</i> , 2021, 19, 44.	1.7	5
2990	Translation of single-cell transcriptomic analysis of uveal melanomas to clinical oncology. <i>Progress in Retinal and Eye Research</i> , 2021, 85, 100968.	7.3	13
2991	Abelson interactor 1 splice isoform-L plays an anti-oncogenic role in colorectal carcinoma through interactions with WAVE2 and full-length Abelson interactor 1. <i>World Journal of Gastroenterology</i> , 2021, 27, 1595-1615.	1.4	3
2992	The Role of RNA-Sequencing as a New Genetic Diagnosis Tool. <i>Current Genetic Medicine Reports</i> , 2021, 9, 13-21.	1.9	12
2993	Alternative Splicing of Pre-mRNA in the Control of Immune Activity. <i>Genes</i> , 2021, 12, 574.	1.0	19
2995	Assessing the functional relevance of splice isoforms. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab044.	1.5	13
2996	Nanomaterials in Wound Healing and Infection Control. <i>Antibiotics</i> , 2021, 10, 473.	1.5	63
2997	Efficient splicing-based RNA regulators for tetracycline-inducible gene expression in human cell culture and <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2021, 49, e71-e71.	6.5	14
2999	Cotranscriptional and Posttranscriptional Features of the Transcriptome in Soybean Shoot Apex and Leaf. <i>Frontiers in Plant Science</i> , 2021, 12, 649634.	1.7	6
3001	Alternative Splicing Dynamics of the Hypothalamus-Pituitary-Ovary Axis During Pubertal Transition in Gilts. <i>Frontiers in Genetics</i> , 2021, 12, 592669.	1.1	4
3002	Comparative Genome-Wide Alternative Splicing Analysis of Longissimus Dorsi Muscles Between Japanese Black (Wagyu) and Chinese Red Steppes Cattle. <i>Frontiers in Veterinary Science</i> , 2021, 8, 634577.	0.9	10
3003	An extended catalogue of tandem alternative splice sites in human tissue transcriptomes. <i>PLoS Computational Biology</i> , 2021, 17, e1008329.	1.5	7
3004	Impact of Ribosome Activity on SARS-CoV-2 LNP-Based mRNA Vaccines. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 654866.	1.6	10
3005	Computing the Role of Alternative Splicing in Cancer. <i>Trends in Cancer</i> , 2021, 7, 347-358.	3.8	19
3006	RNA alternative splicing prediction with discrete compositional energy network. , 2021, , .		2
3007	PD-L1 lncRNA splice isoform promotes lung adenocarcinoma progression via enhancing c-Myc activity. <i>Genome Biology</i> , 2021, 22, 104.	3.8	42
3008	RNA Epigenetics: Fine-Tuning Chromatin Plasticity and Transcriptional Regulation, and the Implications in Human Diseases. <i>Genes</i> , 2021, 12, 627.	1.0	12
3009	MCPIP1-mediated NFIC alternative splicing inhibits proliferation of triple-negative breast cancer via cyclin D1-Rb-E2F1 axis. <i>Cell Death and Disease</i> , 2021, 12, 370.	2.7	24

#	ARTICLE	IF	CITATIONS
3011	Systematic Identification of Survival-Associated Alternative Splicing Events in Kidney Renal Clear Cell Carcinoma. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-10.	0.7	2
3012	FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab057.	1.5	3
3013	Direct Nanopore Sequencing of mRNA Reveals Landscape of Transcript Isoforms in Apicomplexan Parasites. <i>MSystems</i> , 2021, 6, .	1.7	31
3014	Regulatory roles and mechanisms of alternative RNA splicing in adipogenesis and human metabolic health. <i>Cell and Bioscience</i> , 2021, 11, 66.	2.1	26
3016	Post-transcriptional control of cell cytokine production: Implications for cancer therapy. <i>Immunology</i> , 2021, 164, 57-72.	2.0	3
3017	TieBrush: an efficient method for aggregating and summarizing mapped reads across large datasets. <i>Bioinformatics</i> , 2021, 37, 3650-3651.	1.8	9
3018	RBM10: Structure, functions, and associated diseases. <i>Gene</i> , 2021, 783, 145463.	1.0	27
3019	Personalized Proteome: Comparing Proteogenomics and Open Variant Search Approaches for Single Amino Acid Variant Detection. <i>Journal of Proteome Research</i> , 2021, 20, 3353-3364.	1.8	10
3020	Insulin-like androgenic gland hormone from the shrimp <i>Fenneropenaeus merguensis</i> : Expression, gene organization and transcript variants. <i>Gene</i> , 2021, 782, 145529.	1.0	13
3021	A drug-repositioning screen using splicing-sensitive fluorescent reporters identifies novel modulators of VEGF-A splicing with anti-angiogenic properties. <i>Oncogenesis</i> , 2021, 10, 36.	2.1	5
3022	The RNA-Binding Protein HuD Regulates Alternative Splicing and Alternative Polyadenylation in the Mouse Neocortex. <i>Molecules</i> , 2021, 26, 2836.	1.7	12
3023	Alternative Splicing of Human Telomerase Reverse Transcriptase (hTERT) and Its Implications in Physiological and Pathological Processes. <i>Biomedicines</i> , 2021, 9, 526.	1.4	11
3024	Splicing factor SRSF1 promotes breast cancer progression via oncogenic splice switching of PTPMT1. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 171.	3.5	42
3025	The Detection and Bioinformatic Analysis of Alternative 3' UTR Isoforms as Potential Cancer Biomarkers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5322.	1.8	5
3026	Deep sequencing of pre-translational mRNPs reveals hidden flux through evolutionarily conserved alternative splicing nonsense-mediated decay pathways. <i>Genome Biology</i> , 2021, 22, 132.	3.8	14
3027	Large-Scale Multiplexing Permits Full-Length Transcriptome Annotation of 32 Bovine Tissues From a Single Nanopore Flow Cell. <i>Frontiers in Genetics</i> , 2021, 12, 664260.	1.1	18
3028	Polyadenylation-related isoform switching in human evolution revealed by full-length transcript structure. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
3030	Nanopore Sequencing Unveils Diverse Transcript Variants of the Epithelial Cell-Specific Transcription Factor Elf-3 in Human Malignancies. <i>Genes</i> , 2021, 12, 839.	1.0	6

#	ARTICLE	IF	CITATIONS
3031	A new non-aggregative splicing isoform of human Tau is decreased in Alzheimer's disease. <i>Acta Neuropathologica</i> , 2021, 142, 159-177.	3.9	20
3032	A prometastatic splicing program regulated by SNRPA1 interactions with structured RNA elements. <i>Science</i> , 2021, 372, .	6.0	37
3033	Influence of Age on Skeletal Muscle Hypertrophy and Atrophy Signaling: Established Paradigms and Unexpected Links. <i>Genes</i> , 2021, 12, 688.	1.0	6
3035	saturn: A Scalable analysis of differential transcript usage for bulk and single-cell RNA-sequencing applications. <i>F1000Research</i> , 0, 10, 374.	0.8	17
3036	A comparison of alternative mRNA splicing in the CD4 and CD8 T cell lineages. <i>Molecular Immunology</i> , 2021, 133, 53-62.	1.0	9
3039	Splicing regulation in hematopoiesis. <i>Current Opinion in Hematology</i> , 2021, 28, 277-283.	1.2	2
3040	LncRNA <i>ctcflos</i> orchestrates transcription and alternative splicing in thermogenic adipogenesis. <i>EMBO Reports</i> , 2021, 22, e51289.	2.0	19
3041	Splicing factor SRSF6 mediates pleural fibrosis. <i>JCI Insight</i> , 2021, 6, .	2.3	6
3042	Inflammation drives alternative first exon usage to regulate immune genes including a novel iron-regulated isoform of Aim2. <i>ELife</i> , 2021, 10, .	2.8	23
3043	Differential alternative RNA splicing and transcription events between tumors from African American and White patients in The Cancer Genome Atlas. <i>Genomics</i> , 2021, 113, 1234-1246.	1.3	10
3044	Biology of the mRNA Splicing Machinery and Its Dysregulation in Cancer Providing Therapeutic Opportunities. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5110.	1.8	20
3046	Computational comparison of common event-based differential splicing tools: practical considerations for laboratory researchers. <i>BMC Bioinformatics</i> , 2021, 22, 347.	1.2	12
3048	CD44 alternative splicing senses intragenic DNA methylation in tumors via direct and indirect mechanisms. <i>Nucleic Acids Research</i> , 2021, 49, 6213-6237.	6.5	12
3049	The pan-cancer lncRNA PLANE regulates an alternative splicing program to promote cancer pathogenesis. <i>Nature Communications</i> , 2021, 12, 3734.	5.8	33
3050	Alternative Promoter Use Governs the Expression of IgLON Cell Adhesion Molecules in Histogenetic Fields of the Embryonic Mouse Brain. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6955.	1.8	33
3052	Prognostic Alternative Splicing Signatures in Esophageal Carcinoma. <i>Cancer Management and Research</i> , 2021, Volume 13, 4509-4527.	0.9	4
3053	Correlations Between the Characteristics of Alternative Splicing Events, Prognosis, and the Immune Microenvironment in Breast Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 686298.	1.1	3
3054	Insights into the role of alternative splicing in plant temperature response. <i>Journal of Experimental Botany</i> , 2021, , .	2.4	17

#	ARTICLE	IF	CITATIONS
3055	Two RECK Splice Variants (Long and Short) Are Differentially Expressed in Patients with Stable and Unstable Coronary Artery Disease: A Pilot Study. <i>Genes</i> , 2021, 12, 939.	1.0	3
3056	The Emerging Roles of the RNA Binding Protein QKI in Cardiovascular Development and Function. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 668659.	1.8	14
3057	Dynamics of alternative splicing during somatic cell reprogramming reveals functions for RNA-binding proteins CPSF3, hnRNP U1, and TIA1. <i>Genome Biology</i> , 2021, 22, 171.	3.8	12
3058	Alternative splicing perturbation landscape identifies RNA binding proteins as potential therapeutic targets in cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 792-806.	2.3	15
3059	Regulatory and Functional Involvement of Long Non-Coding RNAs in DNA Double-Strand Break Repair Mechanisms. <i>Cells</i> , 2021, 10, 1506.	1.8	16
3060	lncRNA TRMP-S directs dual mechanisms to regulate p27-mediated cellular senescence. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 971-985.	2.3	13
3061	Transcript isoforms of Reep6 have distinct functions in the retina. <i>Human Molecular Genetics</i> , 2021, 30, 1907-1918.	1.4	6
3062	IKK μ isoform switching governs the immune response against EV71 infection. <i>Communications Biology</i> , 2021, 4, 663.	2.0	7
3063	Global Alternative Splicing Defects in Human Breast Cancer Cells. <i>Cancers</i> , 2021, 13, 3071.	1.7	6
3064	A deep learning approach to identify gene targets of a therapeutic for human splicing disorders. <i>Nature Communications</i> , 2021, 12, 3332.	5.8	26
3065	Significance of PD1 Alternative Splicing in Celiac Disease as a Novel Source for Diagnostic and Therapeutic Target. <i>Frontiers in Immunology</i> , 2021, 12, 678400.	2.2	5
3066	LIQA: long-read isoform quantification and analysis. <i>Genome Biology</i> , 2021, 22, 182.	3.8	49
3067	The landscape and biological relevance of aberrant alternative splicing events in esophageal squamous cell carcinoma. <i>Oncogene</i> , 2021, 40, 4184-4197.	2.6	8
3068	LABRAT reveals association of alternative polyadenylation with transcript localization, RNA binding protein expression, transcription speed, and cancer survival. <i>BMC Genomics</i> , 2021, 22, 476.	1.2	29
3069	How Machine Learning and Statistical Models Advance Molecular Diagnostics of Rare Disorders Via Analysis of RNA Sequencing Data. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 647277.	1.6	12
3070	Functional analysis of CASK transcript variants expressed in human brain. <i>PLoS ONE</i> , 2021, 16, e0253223.	1.1	8
3071	SpliceViNCI: Visualizing the splicing of non-canonical introns through recurrent neural networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2150014.	0.3	2
3072	Assessing conservation of alternative splicing with evolutionary splicing graphs. <i>Genome Research</i> , 2021, 31, 1462-1473.	2.4	8

#	ARTICLE	IF	CITATIONS
3073	Mechanistic Insights of Aberrant Splicing with Splicing Factor Mutations Found in Myelodysplastic Syndromes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7789.	1.8	6
3074	Activation of CRF 1 receptors expressed in brainstem autonomic nuclei stimulates colonic enteric neurons and secretomotor function in male rats. <i>Neurogastroenterology and Motility</i> , 2021, 33, e14189.	1.6	2
3075	Alternative splicing and gene co-expression network-based analysis of dizygotic twins with autism-spectrum disorder and their parents. <i>Genomics</i> , 2021, 113, 2561-2571.	1.3	4
3076	Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes. <i>Nature Communications</i> , 2021, 12, 4203.	5.8	24
3077	A pan-cancer analysis of alternative splicing of splicing factors in 6904 patients. <i>Oncogene</i> , 2021, 40, 5441-5450.	2.6	12
3079	Identification of altered cell signaling pathways using proteomic profiling in stable and progressive chronic lymphocytic leukemia. <i>Journal of Leukocyte Biology</i> , 2022, 111, 313-325.	1.5	2
3080	Alternative splicing of mRNA in colorectal cancer: new strategies for tumor diagnosis and treatment. <i>Cell Death and Disease</i> , 2021, 12, 752.	2.7	16
3081	A global survey of alternative splicing of HBV transcriptome using long-read sequencing. <i>Journal of Hepatology</i> , 2022, 76, 234-236.	1.8	5
3083	The clinical importance of tandem exon duplication-derived substitutions. <i>Nucleic Acids Research</i> , 2021, 49, 8232-8246.	6.5	11
3084	Alternative Polyadenylation in Stem Cell Self-Renewal and Differentiation. <i>Trends in Molecular Medicine</i> , 2021, 27, 660-672.	3.5	27
3085	Srsf3 mediates alternative RNA splicing downstream of PDGFR β signaling in the facial mesenchyme. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	10
3086	Alteration of protein expression and spliceosome pathway activity during Barrett's carcinogenesis. <i>Journal of Gastroenterology</i> , 2021, 56, 791-807.	2.3	1
3087	capCLIP: a new tool to probe translational control in human cells through capture and identification of the eIF4E-mRNA interactome. <i>Nucleic Acids Research</i> , 2021, 49, e105-e105.	6.5	15
3089	IntSplice2: Prediction of the Splicing Effects of Intronic Single-Nucleotide Variants Using LightGBM Modeling. <i>Frontiers in Genetics</i> , 2021, 12, 701076.	1.1	6
3090	Nanopore sequencing reveals full-length Tropomyosin 1 isoforms and their regulation by RNA-binding proteins during rat heart development. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 8352-8362.	1.6	15
3091	Alternative RNA Splicing: The Trojan Horse of Cancer Cells in Chemotherapy. <i>Genes</i> , 2021, 12, 1085.	1.0	13
3092	Role of Alternative Splicing in Regulating Host Response to Viral Infection. <i>Cells</i> , 2021, 10, 1720.	1.8	16
3093	Statistical Approach of Gene Set Analysis with Quantitative Trait Loci for Crop Gene Expression Studies. <i>Entropy</i> , 2021, 23, 945.	1.1	1

#	ARTICLE	IF	CITATIONS
3095	Alternative 3' UTRs play a widespread role in translation-independent mRNA association with the endoplasmic reticulum. <i>Cell Reports</i> , 2021, 36, 109407.	2.9	14
3097	CRISPR gene editing in pluripotent stem cells reveals the function of MBNL proteins during human <i>in vitro</i> myogenesis. <i>Human Molecular Genetics</i> , 2021, 31, 41-56.	1.4	15
3098	Therapeutic manipulation of IKBKAP mis-splicing with a small molecule to cure familial dysautonomia. <i>Nature Communications</i> , 2021, 12, 4507.	5.8	21
3099	Integrative analysis reveals the prognostic value and functions of splicing factors implicated in hepatocellular carcinoma. <i>Scientific Reports</i> , 2021, 11, 15175.	1.6	8
3100	HP1 ^β binding pre-mRNA intronic repeats modulates RNA splicing decisions. <i>EMBO Reports</i> , 2021, 22, e52320.	2.0	12
3101	Understanding small ORF diversity through a comprehensive transcription feature classification. <i>DNA Research</i> , 2021, 28, .	1.5	17
3102	Nonsense-Mediated RNA Decay Is a Unique Vulnerability of Cancer Cells Harboring <i>SF3B1</i> or <i>U2AF1</i> Mutations. <i>Cancer Research</i> , 2021, 81, 4499-4513.	0.4	28
3103	Regulation of Alternative Splicing during Epithelial-Mesenchymal Transition. <i>Cells Tissues Organs</i> , 2022, 211, 238-251.	1.3	7
3104	Time-sequenced transcriptomes of developing distal mouse limb buds: A comparative tissue layer analysis. <i>Developmental Dynamics</i> , 2021, , .	0.8	7
3105	A ligand-insensitive <i>UNC5B</i> splicing isoform regulates angiogenesis by promoting apoptosis. <i>Nature Communications</i> , 2021, 12, 4872.	5.8	17
3106	AGTAR: A novel approach for transcriptome assembly and abundance estimation using an adapted genetic algorithm from RNA-seq data. <i>Computers in Biology and Medicine</i> , 2021, 135, 104646.	3.9	1
3107	Transcriptome programs involved in the development and structure of the cerebellum. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 6431-6451.	2.4	9
3108	RNA regulatory mechanisms that control antiviral innate immunity. <i>Immunological Reviews</i> , 2021, 304, 77-96.	2.8	14
3109	Variety of Non-Coding RNAs in Eukaryotic Genomes. <i>Mathematical Biology and Bioinformatics</i> , 2021, 16, 256-298.	0.1	2
3110	IsoDA: Isoform Disease Association Prediction by Multiomics Data Fusion. <i>Journal of Computational Biology</i> , 2021, 28, 804-819.	0.8	1
3111	SRp20: A potential therapeutic target for human tumors. <i>Pathology Research and Practice</i> , 2021, 224, 153444.	1.0	4
3112	Human oocyte meiotic maturation is associated with a specific profile of alternatively spliced transcript isoforms. <i>Molecular Reproduction and Development</i> , 2021, 88, 605-617.	1.0	4
3113	A synthetic small molecule stalls pre-mRNA splicing by promoting an early-stage <i>U2AF2</i> -RNA complex. <i>Cell Chemical Biology</i> , 2021, 28, 1145-1157.e6.	2.5	24

#	ARTICLE	IF	CITATIONS
3114	Matrix factorization-based data fusion for the prediction of RNA-binding proteins and alternative splicing event associations during epithelialâ€”mesenchymal transition. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	11
3115	Unstructural Biology of TRP Ion Channels: The Role of Intrinsically Disordered Regions in Channel Function and Regulation. <i>Journal of Molecular Biology</i> , 2021, 433, 166931.	2.0	31
3116	Isoform Age - Splice Isoform Profiling Using Long-Read Technologies. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 711733.	1.6	31
3117	Enriched Alternative Splicing in Islets of Diabetes-Susceptible Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8597.	1.8	7
3118	Epsteinâ€”Barr virus EBNA2 phase separation regulates cancerâ€”associated alternative RNA splicing patterns. <i>Clinical and Translational Medicine</i> , 2021, 11, e504.	1.7	8
3119	The three as: Alternative splicing, alternative polyadenylation and their impact on apoptosis in immune function. <i>Immunological Reviews</i> , 2021, 304, 30-50.	2.8	20
3120	SDE2 is an essential gene required for ribosome biogenesis and the regulation of alternative splicing. <i>Nucleic Acids Research</i> , 2021, 49, 9424-9443.	6.5	5
3121	Full-length isoform transcriptome of the developing human brain provides further insights into autism. <i>Cell Reports</i> , 2021, 36, 109631.	2.9	23
3123	Comprehensive Characterization of RNA Processing Factors in Gastric Cancer Identifies a Prognostic Signature for Predicting Clinical Outcomes and Therapeutic Responses. <i>Frontiers in Immunology</i> , 2021, 12, 719628.	2.2	19
3124	Global Survey of Alternative Splicing in Rice by Direct RNA Sequencing During Reproductive Development: Landscape and Genetic Regulation. <i>Rice</i> , 2021, 14, 75.	1.7	10
3125	TFâ€”RBPâ€”AS Triplet Analysis Reveals the Mechanisms of Aberrant Alternative Splicing Events in Kidney Cancer: Implications for Their Possible Clinical Use as Prognostic and Therapeutic Biomarkers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8789.	1.8	7
3126	The Expanding Role of Alternative Splicing in Vascular Smooth Muscle Cell Plasticity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10213.	1.8	7
3127	Position Specific Alternative Splicing and Gene Expression Profiles Along the Tonotopic Axis of Chick Cochlea. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 726976.	1.6	3
3128	Neuronal Cell-type Engineering by Transcriptional Activation. <i>Frontiers in Genome Editing</i> , 2021, 3, 715697.	2.7	5
3129	Role of long non-coding RNAs in Down syndrome patients: a transcriptome analysis study. <i>Human Cell</i> , 2021, 34, 1662-1670.	1.2	4
3130	Alternative splicing regulation of cell-cycle genes by SPF45/SR140/CHERP complex controls cell proliferation. <i>Rna</i> , 2021, 27, 1557-1576.	1.6	14
3131	Transcriptome analysis reveals the molecular mechanisms of heterosis on thermal resistance in hybrid abalone. <i>BMC Genomics</i> , 2021, 22, 650.	1.2	24
3132	Detection of Alu Exonization Events in Human Frontal Cortex From RNA-Seq Data. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 727537.	1.6	7

#	ARTICLE	IF	CITATIONS
3133	Alternative polyadenylation: An enigma of transcript length variation in health and disease. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1692.	3.2	15
3134	Splice and Dice: Intronic microRNAs, Splicing and Cancer. Biomedicines, 2021, 9, 1268.	1.4	8
3135	Wilmsâ€™ tumor 1-associating protein complex regulates alternative splicing and polyadenylation at potential G-quadruplex-forming splice site sequences. Journal of Biological Chemistry, 2021, 297, 101248.	1.6	16
3136	Global Transcriptome Characterization and Assembly of the Thermophilic Ascomycete Chaetomium thermophilum. Genes, 2021, 12, 1549.	1.0	3
3137	SON drives oncogenic RNA splicing in glioblastoma by regulating PTBP1/PTBP2 switching and RBFOX2 activity. Nature Communications, 2021, 12, 5551.	5.8	17
3138	Alternative splicing and liver disease. Annals of Hepatology, 2021, 26, 100534.	0.6	8
3140	A molecular perspective on identifying TRPV1 thermosensitive regions and disentangling polymodal activation. Temperature, 2023, 10, 67-101.	1.7	4
3141	Transcriptional Landscapes of Long Non-coding RNAs and Alternative Splicing in Pyricularia oryzae Revealed by RNA-Seq. Frontiers in Plant Science, 2021, 12, 723636.	1.7	3
3142	Systematic analysis of the relationship between ovarian cancer prognosis and alternative splicing. Journal of Ovarian Research, 2021, 14, 120.	1.3	3
3143	Do Fragile X Syndrome and Other Intellectual Disorders Converge at Aberrant Pre-mRNA Splicing?. Frontiers in Psychiatry, 2021, 12, 715346.	1.3	5
3144	Role of Alternative Splicing in Sex Determination in Vertebrates. Sexual Development, 2021, 15, 381-391.	1.1	13
3145	Development of Cdc2-like Kinase 2 Inhibitors: Achievements and Future Directions. Journal of Medicinal Chemistry, 2021, 64, 13191-13211.	2.9	10
3147	Genome-Wide Analysis of Light-Regulated Alternative Splicing in Artemisia annua L.. Frontiers in Plant Science, 2021, 12, 733505.	1.7	4
3148	Differences in gene expression and variable splicing events of ovaries between large and small litter size in Chinese Xiang pigs. Porcine Health Management, 2021, 7, 52.	0.9	5
3149	Splice variants of metabolic nuclear receptors: Relevance for metabolic disease and therapeutic targeting. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2021, 1867, 166183.	1.8	10
3150	Full-length transcriptomic analysis reveals osmoregulatory mechanisms in Coilia nasus eyes reared under hypotonic and hyperosmotic stress. Science of the Total Environment, 2021, 799, 149333.	3.9	8
3151	Genes for RNA-binding proteins involved in neural-specific functions and diseases are downregulated in Rubinstein-Taybi iNeurons. Neural Regeneration Research, 2022, 17, 5.	1.6	5
3152	Structural Aspects of Proteinâ€™Protein Interactions. , 2021, , 61-112.		1

#	ARTICLE	IF	CITATIONS
3153	Differential contribution of transcriptomic regulatory layers in the definition of neuronal identity. Nature Communications, 2021, 12, 335.	5.8	20
3154	Prpf31 is essential for the survival and differentiation of retinal progenitor cells by modulating alternative splicing. Nucleic Acids Research, 2021, 49, 2027-2043.	6.5	18
3155	Analysis of Prognostic Associated Alternative Splicing Signatures in Breast Cancer. Statistics and Applications, 2021, 10, 355-364.	0.0	0
3156	Design and synthesis of herboxidiene derivatives that potently inhibit <i>in vitro</i> splicing. Organic and Biomolecular Chemistry, 2021, 19, 1365-1377.	1.5	3
3157	Prediction of Alzheimer's disease-specific phospholipase c gamma-1 SNV by deep learning-based approach for high-throughput screening. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
3158	An integrated approach in gene-expression landscape profiling to identify housekeeping and tissue-specific genes in cattle. Animal Production Science, 2021, , .	0.6	1
3161	Genome-Wide Association Studies (GWAS). , 2013, , 25-50.		4
3162	Is Transcription the Dominant Force During Dynamic Changes in Gene Expression?. Advances in Experimental Medicine and Biology, 2011, 780, 1-13.	0.8	12
3163	Expression and Functions of the Star Proteins Sam68 and t-star in Mammalian Spermatogenesis. Advances in Experimental Medicine and Biology, 2010, 693, 67-81.	0.8	8
3164	Alternative Splicing in Stem Cell Self-Renewal and Differentiation. Advances in Experimental Medicine and Biology, 2010, 695, 92-104.	0.8	10
3165	Biotechnology for Drought and Salinity Tolerance of Crops. , 2014, , 97-113.		3
3166	Radiolabeled Semi-quantitative RT-PCR Assay for the Analysis of Alternative Splicing of Interleukin Genes. Methods in Molecular Biology, 2014, 1172, 343-362.	0.4	3
3167	Genome-Wide Mapping of RNA Pol-II Promoter Usage in Mouse Tissues by ChIP-Seq. Methods in Molecular Biology, 2014, 1176, 1-9.	0.4	3
3168	Splicing Code Modeling. Advances in Experimental Medicine and Biology, 2014, 825, 451-466.	0.8	4
3169	Genetic Variation and RNA Binding Proteins: Tools and Techniques to Detect Functional Polymorphisms. Advances in Experimental Medicine and Biology, 2014, 825, 227-266.	0.8	22
3170	Fractionation of Non-polyadenylated and Ribosomal-Free RNAs from Mammalian Cells. Methods in Molecular Biology, 2015, 1206, 69-80.	0.4	16
3171	ASPicDB: A Database Web Tool for Alternative Splicing Analysis. Methods in Molecular Biology, 2015, 1269, 365-378.	0.4	5
3172	Quality Control of RNA-Seq Experiments. Methods in Molecular Biology, 2015, 1269, 137-146.	0.4	51

#	ARTICLE	IF	CITATIONS
3173	RNA Sequencing for Transcript 5â€²-End Mapping in Mycobacteria. <i>Methods in Molecular Biology</i> , 2015, 1285, 31-45.	0.4	14
3174	A High-Throughput Screening Assay for the Functional Delivery of Splice-Switching Oligonucleotides in Human Melanoma Cells. <i>Methods in Molecular Biology</i> , 2015, 1297, 187-196.	0.4	3
3175	Methods for Characterization of Alternative RNA Splicing. <i>Methods in Molecular Biology</i> , 2016, 1402, 229-241.	0.4	38
3176	Design of RNA-Binding Proteins: Manipulate Alternative Splicing in Human Cells with Artificial Splicing Factors. <i>Methods in Molecular Biology</i> , 2016, 1421, 227-241.	0.4	2
3177	Role of Alternative Splicing of the 5-HT _{2C} Receptor in the Prader-Willi Syndrome. <i>Receptors</i> , 2011, , 413-427.	0.2	1
3178	Yeast Systems Biology: The Challenge of Eukaryotic Complexity. <i>Methods in Molecular Biology</i> , 2011, 759, 3-28.	0.4	10
3179	Identifying Differential Alternative Splicing Events from RNA Sequencing Data Using RNASeq-MATS. <i>Methods in Molecular Biology</i> , 2013, 1038, 171-179.	0.4	64
3180	Accurate Mapping of Cleavage and Polyadenylation Sites by 3â€² Region Extraction and Deep Sequencing. <i>Methods in Molecular Biology</i> , 2014, 1125, 119-129.	0.4	20
3181	Diversity and Evolution of Spliceosomal Systems. <i>Methods in Molecular Biology</i> , 2014, 1126, 13-33.	0.4	11
3182	Medium Throughput Analysis of Alternative Splicing by Fluorescently Labeled RT-PCR. <i>Methods in Molecular Biology</i> , 2014, 1126, 299-313.	0.4	6
3183	Mechanisms of Spliceosomal Assembly. <i>Methods in Molecular Biology</i> , 2014, 1126, 35-43.	0.4	5
3184	Alternative Pre-mRNA Splicing. <i>Methods in Molecular Biology</i> , 2014, 1126, 45-54.	0.4	15
3185	Regulation of Alternative Pre-mRNA Splicing. <i>Methods in Molecular Biology</i> , 2014, 1126, 55-82.	0.4	19
3186	Chromatin and Splicing. <i>Methods in Molecular Biology</i> , 2014, 1126, 97-113.	0.4	19
3187	Role of Alternative Splicing in Prostate Cancer Aggressiveness and Drug Resistance in African Americans. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1164, 119-139.	0.8	14
3188	Isoform-Disease Association Prediction by Data Fusion. <i>Lecture Notes in Computer Science</i> , 2020, , 44-55.	1.0	2
3189	Modified Antisense Oligonucleotides and Their Analogs in Therapy of Neuromuscular Diseases. <i>RNA Technologies</i> , 2016, , 243-271.	0.2	4
3190	Discriminant Analysis and Normalization Methods for Next-Generation Sequencing Data. <i>ICSA Book Series in Statistics</i> , 2018, , 365-384.	0.0	1

#	ARTICLE	IF	CITATIONS
3191	Inference of Isoforms from Short Sequence Reads. Lecture Notes in Computer Science, 2010, , 138-157.	1.0	18
3192	Estimation of Alternative Splicing isoform Frequencies from RNA-Seq Data. Lecture Notes in Computer Science, 2010, , 202-214.	1.0	17
3193	Statistical and Computational Studies on Alternative Splicing. , 2011, , 31-53.		4
3194	The MicroArray Quality Control (MAQC) Project and Cross-Platform Analysis of Microarray Data. , 2011, , 171-192.		6
3195	A Robust Method for Transcript Quantification with RNA-seq Data. Lecture Notes in Computer Science, 2012, , 127-147.	1.0	1
3196	Detection of Alternatively Spliced or Processed RNAs in Cancer Using Oligonucleotide Microarray. Cancer Treatment and Research, 2013, 158, 25-40.	0.2	1
3197	Alternative Splicing of Tumor Suppressors and Oncogenes. Cancer Treatment and Research, 2013, 158, 95-117.	0.2	6
3198	Oligonucleotide Therapeutics in Cancer. Cancer Treatment and Research, 2013, 158, 213-233.	0.2	17
3199	A Polynomial Delay Algorithm for the Enumeration of Bubbles with Length Constraints in Directed Graphs and Its Application to the Detection of Alternative Splicing in RNA-seq Data. Lecture Notes in Computer Science, 2013, , 99-111.	1.0	6
3200	Current Thinking About Nature and Nurture. History, Philosophy and Theory of the Life Sciences, 2013, , 629-652.	0.4	7
3201	Global Approaches to Alternative Splicing and Its Regulation—Recent Advances and Open Questions. Translational Bioinformatics, 2016, , 37-71.	0.0	2
3203	Regulations on Messenger RNA: Wires and Nodes. Advances in Experimental Medicine and Biology, 2020, 1248, 251-263.	0.8	2
3204	Splicing dysfunction and disease: The case of granulopoiesis. Seminars in Cell and Developmental Biology, 2018, 75, 23-39.	2.3	8
3205	SCCE isoform characterization and expression in human brain: implications for myoclonus—dystonia pathogenesis?. , 0, .		1
3207	Incomplete cryptic splicing by an intronic mutation of OCRL in patients with partial phenotypes of Lowe syndrome. Journal of Human Genetics, 2020, 65, 831-839.	1.1	4
3208	A novel isoform of cryptochrome 4 (Cry4b) is expressed in the retina of a night-migratory songbird. Scientific Reports, 2020, 10, 15794.	1.6	21
3209	Transcriptomes of cochlear inner and outer hair cells from adult mice. Scientific Data, 2018, 5, 180199.	2.4	101
3210	Identification and characterization of adipose surface epitopes. Biochemical Journal, 2020, 477, 2509-2541.	1.7	9

#	ARTICLE	IF	CITATIONS
3211	Linking transcription, RNA polymerase II elongation and alternative splicing. <i>Biochemical Journal</i> , 2020, 477, 3091-3104.	1.7	24
3212	Comprehensive analysis of long noncoding RNA and mRNA in five colorectal cancer tissues and five normal tissues. <i>Bioscience Reports</i> , 2020, 40, .	1.1	4
3213	Prognostic alternative splicing signature in cervical squamous cell carcinoma. <i>IET Systems Biology</i> , 2020, 14, 314-322.	0.8	5
3215	RNA-Seq-based identification of potential resistance mechanism against the soybean cyst nematode (<i>Heterodera glycines</i>) HG Type 0 in soybean (<i>Glycine max</i>) cv. Dongnong L-204. <i>Crop and Pasture Science</i> , 2020, 71, 539.	0.7	9
3216	Approaches to Fungal Genome Annotation. <i>Mycology</i> , 2011, 2, 118-141.	2.0	109
3217	FXR1 splicing is important for muscle development and biomolecular condensates in muscle cells. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	30
3218	Multiple competing RNA structures dynamically control alternative splicing in the human ATE1 gene. <i>Nucleic Acids Research</i> , 2021, 49, 479-490.	6.5	22
3292	SYSTEMS BIOLOGY ANALYSES OF GENE EXPRESSION AND GENOME WIDE ASSOCIATION STUDY DATA IN OBSTRUCTIVE SLEEP APNEA. , 2010, , 14-25.		25
3293	Posttranslational Regulation of the Exon Skipping Machinery Controls Aberrant Splicing in Leukemia. <i>Cancer Discovery</i> , 2020, 10, 1388-1409.	7.7	37
3294	RNA processing genes characterize RNA splicing and further stratify lower-grade glioma. <i>JCI Insight</i> , 2019, 5, .	2.3	20
3295	Living or dying by RNA processing: caspase expression in NSCLC. <i>Journal of Clinical Investigation</i> , 2010, 120, 3798-3801.	3.9	9
3296	Lineage-specific splicing of a brain-enriched alternative exon promotes glioblastoma progression. <i>Journal of Clinical Investigation</i> , 2014, 124, 2861-2876.	3.9	83
3297	RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. <i>Journal of Clinical Investigation</i> , 2014, 124, 3419-3430.	3.9	176
3298	WHEAT GENOMICS: PRESENT STATUS AND FUTURE PROSPECTS. , 2014, , 129-196.		2
3299	RSEM. , 2014, , 41-74.		31
3300	RNA-binding protein Ptbp1 regulates alternative splicing and transcriptome in spermatogonia and maintains spermatogenesis in concert with Nanos3. <i>Journal of Reproduction and Development</i> , 2020, 66, 459-467.	0.5	3
3301	Complete epigenomic and genomic analysis of transcriptome modulation within skin cutaneous melanoma. <i>Medical Science Monitor</i> , 2020, 26, e921133.	0.5	12
3302	Systematic Profiling of Alternative Splicing for Sarcoma Patients Reveals Novel Prognostic Biomarkers Associated with Tumor Microenvironment and Immune Cells. <i>Medical Science Monitor</i> , 2020, 26, e924126.	0.5	7

#	ARTICLE	IF	CITATIONS
3303	Systematic Analysis of Alternative Splicing Landscape in Pancreatic Adenocarcinoma Reveals Regulatory Network Associated with Tumorigenesis and Immune Response. <i>Medical Science Monitor</i> , 2020, 26, e925733.	0.5	6
3304	RNA and Proteins: Mutual Respect. <i>F1000Research</i> , 2017, 6, 345.	0.8	8
3305	Androgen-dependent alternative mRNA isoform expression in prostate cancer cells. <i>F1000Research</i> , 2018, 7, 1189.	0.8	16
3306	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. <i>F1000Research</i> , 2013, 2, 188.	0.8	372
3307	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. <i>F1000Research</i> , 2013, 2, 188.	0.8	293
3308	DRIMSeq: a Dirichlet-multinomial framework for multivariate count outcomes in genomics. <i>F1000Research</i> , 2016, 5, 1356.	0.8	66
3309	DRIMSeq: a Dirichlet-multinomial framework for multivariate count outcomes in genomics. <i>F1000Research</i> , 2016, 5, 1356.	0.8	139
3310	Advances in analyzing RNA diversity in eukaryotic transcriptomes: peering through the Omics lens. <i>F1000Research</i> , 2016, 5, 2668.	0.8	3
3311	Most "Dark Matter" Transcripts Are Associated With Known Genes. <i>PLoS Biology</i> , 2010, 8, e1000371.	2.6	377
3312	Alternative Splicing of RNA Triplets Is Often Regulated and Accelerates Proteome Evolution. <i>PLoS Biology</i> , 2012, 10, e1001229.	2.6	93
3313	Single Nucleotide Polymorphisms Can Create Alternative Polyadenylation Signals and Affect Gene Expression through Loss of MicroRNA-Regulation. <i>PLoS Computational Biology</i> , 2012, 8, e1002621.	1.5	49
3314	Mutations in the <i>Caenorhabditis elegans</i> U2AF Large Subunit UAF-1 Alter the Choice of a 3' Splice Site In Vivo. <i>PLoS Genetics</i> , 2009, 5, e1000708.	1.5	19
3315	Emergence, Retention and Selection: A Trilogy of Origination for Functional De Novo Proteins from Ancestral LncRNAs in Primates. <i>PLoS Genetics</i> , 2015, 11, e1005391.	1.5	45
3316	Haploinsufficiency for Core Exon Junction Complex Components Disrupts Embryonic Neurogenesis and Causes p53-Mediated Microcephaly. <i>PLoS Genetics</i> , 2016, 12, e1006282.	1.5	92
3317	A Novel Protein Isoform of the Multicopy Human NAIP Gene Derives from Intragenic Alu SINE Promoters. <i>PLoS ONE</i> , 2009, 4, e5761.	1.1	47
3318	Genome-Wide Analysis of Immune Activation in Human T and B Cells Reveals Distinct Classes of Alternatively Spliced Genes. <i>PLoS ONE</i> , 2009, 4, e7906.	1.1	35
3319	Exon-Level Transcriptome Profiling in Murine Breast Cancer Reveals Splicing Changes Specific to Tumors with Different Metastatic Abilities. <i>PLoS ONE</i> , 2010, 5, e11981.	1.1	23
3320	SAW: A Method to Identify Splicing Events from RNA-Seq Data Based on Splicing Fingerprints. <i>PLoS ONE</i> , 2010, 5, e12047.	1.1	7

#	ARTICLE	IF	CITATIONS
3321	Caenorhabditis elegans Operons Contain a Higher Proportion of Genes with Multiple Transcripts and Use 3â€² Splice Sites Differentially. PLoS ONE, 2010, 5, e12456.	1.1	6
3322	Ratio-Based Analysis of Differential mRNA Processing and Expression of a Polyadenylation Factor Mutant pcfs4 Using Arabidopsis Tiling Microarray. PLoS ONE, 2011, 6, e14719.	1.1	5
3323	Detection and Removal of Biases in the Analysis of Next-Generation Sequencing Reads. PLoS ONE, 2011, 6, e16685.	1.1	81
3324	Alternative Splicing and Nonsense-Mediated RNA Decay Contribute to the Regulation of SHOX Expression. PLoS ONE, 2011, 6, e18115.	1.1	36
3325	Expression of a Dominant Negative CELF Protein In Vivo Leads to Altered Muscle Organization, Fiber Size, and Subtype. PLoS ONE, 2011, 6, e19274.	1.1	19
3326	An shRNA-Based Screen of Splicing Regulators Identifies SFRS3 as a Negative Regulator of IL-1Î² Secretion. PLoS ONE, 2011, 6, e19829.	1.1	10
3327	Variation in Human Recombination Rates and Its Genetic Determinants. PLoS ONE, 2011, 6, e20321.	1.1	101
3328	Comparative Analysis of Serine/Arginine-Rich Proteins across 27 Eukaryotes: Insights into Sub-Family Classification and Extent of Alternative Splicing. PLoS ONE, 2011, 6, e24542.	1.1	69
3329	Optimal Deconvolution of Transcriptional Profiling Data Using Quadratic Programming with Application to Complex Clinical Blood Samples. PLoS ONE, 2011, 6, e27156.	1.1	130
3330	Comparative Analysis of Human Protein-Coding and Noncoding RNAs between Brain and 10 Mixed Cell Lines by RNA-Seq. PLoS ONE, 2011, 6, e28318.	1.1	27
3331	A Novel Conserved Isoform of the Ubiquitin Ligase UFD2a/UBE4B Is Expressed Exclusively in Mature Striated Muscle Cells. PLoS ONE, 2011, 6, e28861.	1.1	13
3332	Preservation of Ranking Order in the Expression of Human Housekeeping Genes. PLoS ONE, 2011, 6, e29314.	1.1	10
3333	Fast Computation and Applications of Genome Mappability. PLoS ONE, 2012, 7, e30377.	1.1	458
3334	Transcriptome Analysis of the Model Protozoan, Tetrahymena thermophila, Using Deep RNA Sequencing. PLoS ONE, 2012, 7, e30630.	1.1	111
3335	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	1.1	7
3336	Complex Control of GABA(A) Receptor Subunit mRNA Expression: Variation, Covariation, and Genetic Regulation. PLoS ONE, 2012, 7, e34586.	1.1	65
3337	Bovine ncRNAs Are Abundant, Primarily Intergenic, Conserved and Associated with Regulatory Genes. PLoS ONE, 2012, 7, e42638.	1.1	64
3338	Hypoxia-Induced Alternative Splicing in Endothelial Cells. PLoS ONE, 2012, 7, e42697.	1.1	72

#	ARTICLE	IF	CITATIONS
3339	Transcriptome Analysis of the Silkworm (<i>Bombyx mori</i>) by High-Throughput RNA Sequencing. PLoS ONE, 2012, 7, e43713.	1.1	42
3340	Possible Role of the WDR3 Gene on Genome Stability in Thyroid Cancer Patients. PLoS ONE, 2012, 7, e44288.	1.1	4
3341	Accumulation of Splice Variants and Transcripts in Response to PI3K Inhibition in T Cells. PLoS ONE, 2013, 8, e50695.	1.1	2
3342	Functional Modulation of Vascular Adhesion Protein-1 by a Novel Splice Variant. PLoS ONE, 2013, 8, e54151.	1.1	9
3343	Analysis of Genetic Interaction Networks Shows That Alternatively Spliced Genes Are Highly Versatile. PLoS ONE, 2013, 8, e55671.	1.1	1
3344	Characterization of FUS Mutations in Amyotrophic Lateral Sclerosis Using RNA-Seq. PLoS ONE, 2013, 8, e60788.	1.1	21
3345	Genome-Wide Analysis of Alternative Splicing during Dendritic Cell Response to a Bacterial Challenge. PLoS ONE, 2013, 8, e61975.	1.1	26
3346	Characterization of Transcriptional Complexity during Longissimus Muscle Development in Bovines Using High-Throughput Sequencing. PLoS ONE, 2013, 8, e64356.	1.1	57
3347	Dissecting the Characteristics and Dynamics of Human Protein Complexes at Transcriptome Cascade Using RNA-Seq Data. PLoS ONE, 2013, 8, e66521.	1.1	4
3348	Dietary Alleviation of Maternal Obesity and Diabetes: Increased Resistance to Diet-Induced Obesity Transcriptional and Epigenetic Signatures. PLoS ONE, 2013, 8, e66816.	1.1	43
3349	Alternative Splice Variants in TIM Barrel Proteins from Human Genome Correlate with the Structural and Evolutionary Modularity of this Versatile Protein Fold. PLoS ONE, 2013, 8, e70582.	1.1	7
3350	The Relationship between Gene Isoform Multiplicity, Number of Exons and Protein Divergence. PLoS ONE, 2013, 8, e72742.	1.1	5
3351	The Venom Gland Transcriptome of <i>Latrodectus tredecimguttatus</i> Revealed by Deep Sequencing and cDNA Library Analysis. PLoS ONE, 2013, 8, e81357.	1.1	60
3352	A Gene Expression and Pre-mRNA Splicing Signature That Marks the Adenoma-Adenocarcinoma Progression in Colorectal Cancer. PLoS ONE, 2014, 9, e87761.	1.1	56
3353	Human Transporter Database: Comprehensive Knowledge and Discovery Tools in the Human Transporter Genes. PLoS ONE, 2014, 9, e88883.	1.1	24
3354	CMT: A Constrained Multi-Level Thresholding Approach for ChIP-Seq Data Analysis. PLoS ONE, 2014, 9, e93873.	1.1	3
3355	RNA Sequencing Analysis of the Gametophyte Transcriptome from the Liverwort, <i>Marchantia polymorpha</i> . PLoS ONE, 2014, 9, e97497.	1.1	40
3356	Characterization of Natural Antisense Transcript, Sclerotia Development and Secondary Metabolism by Strand-Specific RNA Sequencing of <i>Aspergillus flavus</i> . PLoS ONE, 2014, 9, e97814.	1.1	13

#	ARTICLE	IF	CITATIONS
3357	Detection of SRSF2-P95 Mutation by High-Resolution Melting Curve Analysis and Its Effect on Prognosis in Myelodysplastic Syndrome. PLoS ONE, 2014, 9, e115693.	1.1	25
3358	Functional Genomics Screening Utilizing Mutant Mouse Embryonic Stem Cells Identifies Novel Radiation-Response Genes. PLoS ONE, 2015, 10, e0120534.	1.1	5
3359	Differential Effects of Tra2 ^Δ Isoforms on HIV-1 RNA Processing and Expression. PLoS ONE, 2015, 10, e0125315.	1.1	10
3360	Widespread Polycistronic Transcripts in Fungi Revealed by Single-Molecule mRNA Sequencing. PLoS ONE, 2015, 10, e0132628.	1.1	340
3361	Boundary Associated Long Noncoding RNA Mediates Long-Range Chromosomal Interactions. PLoS ONE, 2015, 10, e0136104.	1.1	7
3362	Tissue Restricted Splice Junctions Originate Not Only from Tissue-Specific Gene Loci, but Gene Loci with a Broad Pattern of Expression. PLoS ONE, 2015, 10, e0144302.	1.1	20
3363	Specific Tandem 3'UTR Patterns and Gene Expression Profiles in Mouse Thy1+ Germline Stem Cells. PLoS ONE, 2015, 10, e0145417.	1.1	7
3364	MiasDB: A Database of Molecular Interactions Associated with Alternative Splicing of Human Pre-mRNAs. PLoS ONE, 2016, 11, e0155443.	1.1	12
3365	Prediction and Quantification of Splice Events from RNA-Seq Data. PLoS ONE, 2016, 11, e0156132.	1.1	102
3366	Deciphering Transcriptome and Complex Alternative Splicing Transcripts in Mammary Gland Tissues from Cows Naturally Infected with Staphylococcus aureus Mastitis. PLoS ONE, 2016, 11, e0159719.	1.1	66
3367	Decoding the Regulatory Landscape of Ageing in Musculoskeletal Engineered Tissues Using Genome-Wide DNA Methylation and RNASeq. PLoS ONE, 2016, 11, e0160517.	1.1	26
3368	Iron Content Affects Lipogenic Gene Expression in the Muscle of Nelore Beef Cattle. PLoS ONE, 2016, 11, e0161160.	1.1	28
3369	Identification of Claudin 1 Transcript Variants in Human Invasive Breast Cancer. PLoS ONE, 2016, 11, e0163387.	1.1	11
3370	Bayesian Correlation Analysis for Sequence Count Data. PLoS ONE, 2016, 11, e0163595.	1.1	10
3371	Transcriptomic Variation during Spermiogenesis in Mouse Germ Cells. PLoS ONE, 2016, 11, e0164874.	1.1	13
3372	Computational Identification of Tissue-Specific Splicing Regulatory Elements in Human Genes from RNA-Seq Data. PLoS ONE, 2016, 11, e0166978.	1.1	17
3373	A Hypothesis Testing Based Method for Normalization and Differential Expression Analysis of RNA-Seq Data. PLoS ONE, 2017, 12, e0169594.	1.1	8
3374	Optimized approach for Ion Proton RNA sequencing reveals details of RNA splicing and editing features of the transcriptome. PLoS ONE, 2017, 12, e0176675.	1.1	17

#	ARTICLE	IF	CITATIONS
3375	Identification and characterization of new isoforms of human fas apoptotic inhibitory molecule (FAIM). PLoS ONE, 2017, 12, e0185327.	1.1	6
3376	Aberrant expression of CPSF1 promotes head and neck squamous cell carcinoma via regulating alternative splicing. PLoS ONE, 2020, 15, e0233380.	1.1	13
3377	Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis. PLoS ONE, 2020, 15, e0239711.	1.1	5
3378	A splicing factor switch controls hematopoietic lineage specification of pluripotent stem cells. EMBO Reports, 2021, 22, e50535.	2.0	9
3379	An expanded mouse testis transcriptome and mass spectrometry defines novel proteins. Reproduction, 2020, 159, 15-26.	1.1	12
3380	Exploring the Impact of Cleavage and Polyadenylation Factors on Pre-mRNA Splicing Across Eukaryotes. G3: Genes, Genomes, Genetics, 2017, 7, 2107-2114.	0.8	6
3381	Experimental procedures to identify and validate specific mRNA targets of miRNAs. EXCLI Journal, 2015, 14, 758-90.	0.5	20
3382	Identification of survival-associated alternative splicing events and signatures in adrenocortical carcinoma based on TCGA SpliceSeq data. Aging, 2020, 12, 4996-5009.	1.4	7
3383	Characterization of RON protein isoforms in pancreatic cancer: implications for biology and therapeutics. Oncotarget, 2016, 7, 45959-45975.	0.8	24
3384	MACC1 is post-transcriptionally regulated by miR-218 in colorectal cancer. Oncotarget, 2016, 7, 53443-53458.	0.8	27
3385	Variant 2 of KIAA0101, antagonizing its oncogenic variant 1, might be a potential therapeutic strategy in hepatocellular carcinoma. Oncotarget, 2017, 8, 43990-44003.	0.8	7
3386	Genomic variants link to hepatitis C racial disparities. Oncotarget, 2017, 8, 59455-59475.	0.8	5
3387	Transcriptional signature of lymphoblastoid cell lines of <i>BRCA1</i> and <i>BRCA2</i> and non- <i>BRCA1/2</i> high risk breast cancer families. Oncotarget, 2017, 8, 78691-78712.	0.8	8
3388	Radiation-induced alternative transcripts as detected in total and polysome-bound mRNA. Oncotarget, 2018, 9, 691-705.	0.8	6
3389	CFIm25 inhibits hepatocellular carcinoma metastasis by suppressing the p38 and JNK/c-Jun signaling pathways. Oncotarget, 2018, 9, 11783-11793.	0.8	17
3390	Splicing regulatory factors in breast cancer hallmarks and disease progression. Oncotarget, 2019, 10, 6021-6037.	0.8	19
3391	Transcriptome-wide identification and study of cancer-specific splicing events across multiple tumors. Oncotarget, 2015, 6, 6825-6839.	0.8	36
3392	The impact of RNA binding motif protein 4-regulated splicing cascade on the progression and metabolism of colorectal cancer cells. Oncotarget, 2015, 6, 38046-38060.	0.8	19

#	ARTICLE	IF	CITATIONS
3393	RNA-binding protein CELF1 promotes tumor growth and alters gene expression in oral squamous cell carcinoma. <i>Oncotarget</i> , 2015, 6, 43620-43634.	0.8	29
3394	Expression of androgen receptor splice variants in clinical breast cancers. <i>Oncotarget</i> , 2015, 6, 44728-44744.	0.8	77
3395	Pre-mRNA splicing and its regulation in <i>Caenorhabditis elegans</i> . <i>WormBook</i> , 2012, , 1-21.	5.3	31
3396	hnRNP E1 at the crossroads of translational regulation of epithelial-mesenchymal transition. <i>Journal of Cancer Metastasis and Treatment</i> , 2019, 2019, .	0.5	8
3397	Alternative Splicing in Prostate and Breast Cancer. <i>The Open Cancer Journal</i> , 2010, 3, 62-76.	0.2	5
3398	Alternative Polyadenylation and Its Impact on Cellular Processes. <i>MicroRNA (Sharjah, United Arab)</i> Tj ETQq1 1 0.784314 rgBT /Overl	0.6	23
3399	Construction and Cloning of Minigenes for in vivo Analysis of Potential Splice Mutations. <i>Bio-protocol</i> , 2018, 8, e2760.	0.2	4
3400	Comparative Proteomic Analysis of Tumor Mesenchymal-Like Stem Cells Derived from High Grade versus Low Grade Gliomas. <i>Cell Journal</i> , 2017, 19, 250-258.	0.2	6
3401	Allele-specific expression and alternative splicing in horse \times monkey and cattle \times yak hybrids. <i>Zoological Research</i> , 2019, 40, 293-304.	0.9	18
3402	Sequence variations affecting AU-rich element function and disease. <i>Frontiers in Bioscience - Landmark</i> , 2012, 17, 1846.	3.0	21
3403	RNA-Binding Proteins: Splicing Factors and Disease. <i>Biomolecules</i> , 2015, 5, 893-909.	1.8	74
3404	Recent advances in RNA sequence analysis. <i>F1000 Biology Reports</i> , 2010, 2, 64.	4.0	13
3405	How do RNA sequence, DNA sequence, and chromatin properties regulate splicing?. <i>F1000 Biology Reports</i> , 2010, 2, 74.	4.0	5
3406	A Review on The Processing and Analysis of Next-generation RNA-seq Data*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 834-846.	0.3	8
3407	Impairment of pre-mRNA splicing in liver disease: Mechanisms and consequences. <i>World Journal of Gastroenterology</i> , 2010, 16, 3091.	1.4	40
3408	Alternative splicing of <i>VEGFA</i> , <i>APP</i> and <i>NUMB</i> genes in colorectal cancer. <i>World Journal of Gastroenterology</i> , 2015, 21, 6550.	1.4	23
3409	Systematic profiling of a novel prognostic alternative splicing signature in hepatocellular carcinoma. <i>Oncology Reports</i> , 2019, 42, 2450-2472.	1.2	12
3410	SRSF6 regulates alternative splicing of genes involved in DNA damage response and DNA repair in HeLa cells. <i>Oncology Reports</i> , 2020, 44, 1851-1862.	1.2	13

#	ARTICLE	IF	CITATIONS
3411	Transcriptomics to Metabolomics. Advances in Bioinformatics and Biomedical Engineering Book Series, 2018, , 188-206.	0.2	5
3412	Transcriptomics to Metabolomics. , 2019, , 361-379.		1
3413	Alternative Splicing and Nonsense Mediated Decay in Mitochondrial Complex-I Biogenesis and its Implication in Human Diseases. Journal of Bioanalysis & Biomedicine, 2013, s3, .	0.1	2
3414	Making Use of Aberrant and Nonsense: Aberrant Splicing and Nonsense-Mediated Decay as Targets for Personalized Medicine. International Journal of Genomic Medicine, 2013, 1, .	0.0	1
3415	Management of High-Throughput DNA Sequencing Projects: Alpheus. Journal of Computer Science and Systems Biology, 2008, 01, 132.	0.0	65
3416	Diversity in the Interactions of Isoforms Linked to Clustered Transcripts: A Systematic Literature Analysis. Journal of Proteomics and Bioinformatics, 2011, 4, .	0.4	2
3417	Comparative Analysis of the Exon-Intron Structure in Eukaryotic Genomes. Yangtze Medicine, 2017, 01, 50-64.	0.1	10
3418	Alternative splicing: An important mechanism in stem cell biology. World Journal of Stem Cells, 2015, 7, 1.	1.3	40
3419	A penalized likelihood approach for robust estimation of isoform expression. Statistics and Its Interface, 2015, 8, 437-445.	0.2	11
3420	Association of survivin splice variants with prognosis and treatment of breast cancer. World Journal of Clinical Oncology, 2014, 5, 883.	0.9	24
3421	Modulators of alternative splicing as novel therapeutics in cancer. World Journal of Clinical Oncology, 2015, 6, 92.	0.9	5
3422	Molecular cloning and characterization of novel human JNK2 (MAPK9) transcript variants that show different stimulation activities on AP-1. BMB Reports, 2010, 43, 738-743.	1.1	9
3423	An integrated bioinformatics analysis of mouse testis protein profiles with new understanding. BMB Reports, 2011, 44, 347-351.	1.1	9
3424	Analyses of alternative polyadenylation: from old school biochemistry to high-throughput technologies. BMB Reports, 2017, 50, 201-207.	1.1	14
3425	Alternative Splicing and Its Impact as a Cancer Diagnostic Marker. Genomics and Informatics, 2012, 10, 74.	0.4	20
3426	Analysis of Whole Transcriptome Sequencing Data: Workflow and Software. Genomics and Informatics, 2015, 13, 119.	0.4	58
3427	Assessing long-distance RNA sequence connectivity via RNA-templated DNA-DNA ligation. ELife, 2015, 4, .	2.8	29
3428	An extensive program of periodic alternative splicing linked to cell cycle progression. ELife, 2016, 5, .	2.8	99

#	ARTICLE	IF	CITATIONS
3429	Tunable protein synthesis by transcript isoforms in human cells. <i>ELife</i> , 2016, 5, .	2.8	238
3430	An alternative splicing program promotes adipose tissue thermogenesis. <i>ELife</i> , 2016, 5, .	2.8	55
3431	Transcription of a 5â€™™ extended mRNA isoform directs dynamic chromatin changes and interference of a downstream promoter. <i>ELife</i> , 2017, 6, .	2.8	68
3432	Striking circadian neuron diversity and cycling of <i>Drosophila</i> alternative splicing. <i>ELife</i> , 2018, 7, .	2.8	24
3433	A novel L1CAM isoform with angiogenic activity generated by NOVA2-mediated alternative splicing. <i>ELife</i> , 2019, 8, .	2.8	38
3434	Srsf10 and the minor spliceosome control tissue-specific and dynamic SR protein expression. <i>ELife</i> , 2020, 9, .	2.8	18
3435	Modulation of transcriptional activity in brain lower grade glioma by alternative splicing. <i>PeerJ</i> , 2018, 6, e4686.	0.9	6
3436	Single-molecule real-time sequencing identifies massive full-length cDNAs and alternative-splicing events that facilitate comparative and functional genomics study in the hexaploid crop sweet potato. <i>PeerJ</i> , 2019, 7, e7933.	0.9	3
3437	Systematic analysis and prediction model construction of alternative splicing events in hepatocellular carcinoma: a study on the basis of large-scale splice-seq data from The Cancer Genome Atlas. <i>PeerJ</i> , 2019, 7, e8245.	0.9	10
3438	APPRIS: selecting functionally important isoforms. <i>Nucleic Acids Research</i> , 2022, 50, D54-D59.	6.5	29
3439	Heterozygous <i>Tropomodulin 3</i> mice have improved lung vascularization after chronic hypoxia. <i>Human Molecular Genetics</i> , 2022, 31, 1130-1140.	1.4	0
3441	Alternative RNA splicing in stem cells and cancer stem cells: Importance of transcript-based expression analysis. <i>World Journal of Stem Cells</i> , 2021, 13, 1394-1416.	1.3	4
3442	mRNA alternative polyadenylation (APA) in regulation of gene expression and diseases. <i>Genes and Diseases</i> , 2023, 10, 165-174.	1.5	5
3443	AI applications in functional genomics. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5762-5790.	1.9	34
3444	PIC-Me: paralogs and isoforms classifier based on machine-learning approaches. <i>BMC Bioinformatics</i> , 2021, 22, 311.	1.2	0
3445	RNA Targeting in Inherited Neuromuscular Disorders: Novel Therapeutic Strategies to Counteract Mis-Splicing. <i>Cells</i> , 2021, 10, 2850.	1.8	3
3446	Molecular Profiling of DNA Methylation and Alternative Splicing of Genes in Skeletal Muscle of Obese Rabbits. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1558-1575.	1.0	2
3447	Improved prediction of smoking status via isoform-aware RNA-seq deep learning models. <i>PLoS Computational Biology</i> , 2021, 17, e1009433.	1.5	7

#	ARTICLE	IF	CITATIONS
3448	Methylation Modification, Alternative Splicing, and Noncoding RNA Play a Role in Cancer Metastasis through Epigenetic Regulation. <i>BioMed Research International</i> , 2021, 2021, 1-13.	0.9	9
3449	Impact of alternative splicing on mechanisms of resistance to anticancer drugs. <i>Biochemical Pharmacology</i> , 2021, 193, 114810.	2.0	14
3450	Genome-Wide Profiling Reveals Alternative Polyadenylation of Innate Immune-Related mRNA in Patients With COVID-19. <i>Frontiers in Immunology</i> , 2021, 12, 756288.	2.2	17
3451	The SR Splicing Factors: Providing Perspectives on Their Evolution, Expression, Alternative Splicing, and Function in <i>Populus trichocarpa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 11369.	1.8	18
3452	Dynamic transcriptional reprogramming leads to immunotherapeutic vulnerabilities in myeloma. <i>Nature Cell Biology</i> , 2021, 23, 1199-1211.	4.6	22
3453	Gills full-length transcriptomic analysis of osmoregulatory adaptive responses to salinity stress in <i>Coilia nasus</i> . <i>Ecotoxicology and Environmental Safety</i> , 2021, 226, 112848.	2.9	8
3454	Human genes are multitaskers. <i>Nature</i> , 2008, 456, 9.	13.7	2
3455	Applications of high-throughput sequencing to chromatin structure and function in mammals. <i>F1000 Biology Reports</i> , 2009, 1, 32.	4.0	0
3458	New Tools for Expression Alternative Splicing Validation. <i>Communications in Computer and Information Science</i> , 2010, , 222-231.	0.4	0
3459	Analysis of Mutations that Influence Pre-mRNA Splicing. <i>Methods in Molecular Biology</i> , 2011, 703, 137-160.	0.4	0
3463	Quantifying Alternatively Spliced mRNA via Capillary Electrophoresis. <i>Methods in Molecular Biology</i> , 2011, 712, 69-77.	0.4	1
3464	Recent Advances in Understanding of Alternative Splicing in Neuronal Pathogenesis. , 0, , .		0
3465	Preclinical Considerations for Development of Antibody-Based Therapeutics in Oncology. , 2012, , 183-240.		0
3466	Visual Screening for the Natural Compounds That Affect the Formation of Nuclear Structures. , 2012, , 183-192.		0
3467	Splicing Mechanisms and Mutations in the NF1 Gene. , 2012, , 135-150.		0
3468	Case study: C-It, knowledge database for screening evolutionarily conserved, tissue-enriched, uncharacterized genes. , 2012, , 75-94.		0
3469	Alzheimer's Disease: Approaches to Pathogenesis in the Genomic Age. , 0, , .		0
3470	Role of alternative splicing in modulating protein-protein interactions. <i>EMBnet Journal</i> , 2012, 18, 86.	0.2	0

#	ARTICLE	IF	CITATIONS
3471	Paired SAGE-microarray Expression Data Sets Reveal Antisense Transcripts Differentially Expressed in Embryonic Stem Cell Differentiation. , 2012, , 193-215.		0
3472	Toward Revealing the Complexity of Androgen-Responsive Protein and Noncoding Transcripts in Prostate Cancer. , 2013, , 117-134.		0
3473	Evaluation of RNA-Seq software in gene expression quantification. Journal of Biomedical Science and Engineering, 2013, 06, 473-477.	0.2	0
3474	Isoform Inference From RNA-Seq Samples Based on Gene Structures on Chromosomes. Journal of Biosciences and Medicines, 2013, 01, 1-5.	0.1	0
3475	Transcriptome Sequencing. , 2013, , 2259-2259.		0
3477	Analysis of fusion gene expression in prostate tumors by using single-end reads. Genetics and Molecular Research, 2013, 12, 2886-2894.	0.3	0
3478	The Identification of a Novel Transcript Variant of Chicken <i>Lmbr1</i> and the Sequence Variation Analysis. Journal of Poultry Science, 2013, 50, 104-113.	0.7	0
3480	Genetic Control of pre-mRNA Splicing and Diseases. Enliven Journal of Genetics Molecular and Cellular Biology, 2014, 01, .	0.0	0
3481	Expression Assessment. , 2014, , 1-4.		0
3482	dSpliceType: A Multivariate Model for Detecting Various Types of Differential Splicing Events Using RNA-Seq. Lecture Notes in Computer Science, 2014, , 322-333.	1.0	3
3485	Next-Generation Sequencing or the Dilemma of Large-Scale Data Analysis: Opportunities, Insights, and Challenges to Translational, Preventive and Personalized Medicine. Journal of Investigative Genomics, 2014, 1, .	0.2	0
3491	Decoding Abnormal Splicing Code in Human Diseases. Journal of Investigative Genomics, 2015, 2, .	0.2	1
3493	FOXP3+ Treg Cells and Systems Biology Approaches to Studying Their Function. Translational Bioinformatics, 2015, , 73-93.	0.0	0
3499	Codon Usage Bias is not Significantly Different between the High and the Low Expression Genes in Human. International Journal of Molecular Genetics and Gene Therapy, 2016, 1, .	0.1	1
3501	Gene Extraction Based on Sparse Singular Value Decomposition. Lecture Notes in Computer Science, 2016, , 285-293.	1.0	1
3511	IsoTree: De Novo Transcriptome Assembly from RNA-Seq Reads. Lecture Notes in Computer Science, 2017, , 71-83.	1.0	1
3525	Sex-Specific Development in Haplodiploid Honeybee is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic lncRNAs. SSRN Electronic Journal, 0, , .	0.4	0
3526	Working with (too) Few Samples. Studies in Systems, Decision and Control, 2018, , 337-346.	0.8	0

#	ARTICLE	IF	CITATIONS
3529	Expression Assessment. , 2018, , 383-386.		0
3548	Alternative Splicing. , 2019, , 1-8.		0
3558	Tumor Heterogeneity Uncovered by HLA-G Isoforms Expression. , 0, , .		0
3563	Power-law Behavior of the Alternative Splicing of Exons in Human Transcriptome. Annual Research & Review in Biology, 0, , 1-13.	0.4	0
3564	Construction of a model to predict the prognosis of patients with cholangiocarcinoma using alternative splicing events. Oncology Letters, 2019, 18, 4677-4690.	0.8	3
3565	Platform-Independent Gene-Expression Based Classification-System for Molecular Sub-typing of Cancer. Computers in Health Care, 2020, , 151-160.	0.2	0
3573	Identification and functional analysis of a novel splice variant of AC3â€™33 in breast cancer. Experimental and Therapeutic Medicine, 2020, 19, 183-191.	0.8	3
3574	QTL Analysis Beyond eQTLs. Methods in Molecular Biology, 2020, 2082, 201-210.	0.4	4
3578	Genomic profiling of Nipah virus using NGS driven RNA-Seq expression data. Bioinformatics, 2019, 15, 853-862.	0.2	2
3579	Real-Time PCR Assay for the Analysis of Alternative Splicing of Immune Mediators in Cancer. Methods in Molecular Biology, 2020, 2108, 241-258.	0.4	0
3580	Novel Approaches to Profile Functional Long Noncoding RNAs Associated with Stem Cell Pluripotency. Current Genomics, 2020, 21, 37-45.	0.7	2
3589	The Clinical Application of RNA Sequencing in Genetic Diagnosis of Mendelian Disorders. Clinics in Laboratory Medicine, 2020, 40, 121-133.	0.7	19
3590	Circular RNA: the rings of power over cell. Biopolymers and Cell, 2020, 36, 163-181.	0.1	1
3592	Wideâ€™ranging analysis of survivalâ€™related alternative splicing events in invasive breast carcinoma. Oncology Letters, 2020, 20, 1866-1878.	0.8	1
3595	Dissecting the role of alternative splicing in the regulation of autophagy: a narrative review. Journal of Bio-X Research, 2020, 3, 104-108.	0.3	0
3597	Application of third-generation sequencing in cancer research. Medical Review, 2021, 1, 150-171.	0.3	6
3598	Systematic Genome-Wide Profiles Reveal Alternative Splicing Landscape and Implications of Splicing Regulator DExD-Box Helicase 21 in Aggressive Progression of Adrenocortical Carcinoma. Phenomics, 2021, 1, 243-256.	0.9	13
3599	Ral GEF with the PH Domain and SH3 Binding Motif 1 Regulated by Splicing Factor Junction Plakoglobin and Pyrimidine Metabolism Are Prognostic in Uterine Carcinosarcoma. Disease Markers, 2021, 2021, 1-17.	0.6	1

#	ARTICLE	IF	CITATIONS
3600	Alternative splicing during fruit development among fleshy fruits. BMC Genomics, 2021, 22, 762.	1.2	9
3601	Maternal methionine supplementation during gestation alters alternative splicing and DNA methylation in bovine skeletal muscle. BMC Genomics, 2021, 22, 780.	1.2	9
3602	Mass spectrometry-based targeted proteomics for analysis of protein mutations. Mass Spectrometry Reviews, 2023, 42, 796-821.	2.8	19
3603	Maximizing the Utility of Transcriptomics Data in Inflammatory Skin Diseases. Frontiers in Immunology, 2021, 12, 761890.	2.2	9
3609	Distant coupling between RNA editing and alternative splicing of the osmosensitive cation channel Tmem63b. Journal of Biological Chemistry, 2020, 295, 18199-18212.	1.6	14
3611	Identification and comparative study of melanoma differentiation-associated gene 5 homologues of triploid hybrid fish and its parents. Developmental and Comparative Immunology, 2022, 127, 104294.	1.0	1
3612	Functional categories of RNA regulation. , 2020, , 59-83.		0
3613	The Quest for the Next-Generation of Tumor Targets: Discovery and Prioritization in the Genomics Era. Methods in Pharmacology and Toxicology, 2020, , 239-253.	0.1	0
3614	Interactive Alternative Splicing Analysis of Human Stem Cells Using psichomics. Methods in Molecular Biology, 2020, 2117, 179-205.	0.4	0
3615	Orthology: Promises and Challenges. , 2020, , 203-228.		10
3616	Expression Analysis of Apocheima cinerarius Ershoff from Different Geographical Populations through Illumina RNA-seq. Pakistan Journal of Zoology, 2020, 52, .	0.1	0
3617	Alternative Splicing and Aging. , 2020, , 125-139.		0
3620	Chemical Probes to Control RNA Function. Chemical Biology, 2020, , 214-246.	0.1	0
3621	The Role of Alternative mRNA Splicing in Heart Development. , 2020, , 339-351.		1
3622	Splicing and Alternative Splicing and the Impact of Mechanics. Biological and Medical Physics Series, 2020, , 509-593.	0.3	0
3626	Structural basis of the interaction between SETD2 methyltransferase and hnRNP L paralogs for governing co-transcriptional splicing. Nature Communications, 2021, 12, 6452.	5.8	12
3627	Immunological functional differentiation of two transmembrane variants of Dscam in Chinese mitten crab. Developmental and Comparative Immunology, 2022, 128, 104313.	1.0	3
3628	Long non-coding RNAs are involved in alternative splicing and promote cancer progression. British Journal of Cancer, 2022, 126, 1113-1124.	2.9	53

#	ARTICLE	IF	CITATIONS
3629	Aberrant Post-Transcriptional Regulation of Protein Expression in the Development of Chronic Obstructive Pulmonary Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11963.	1.8	4
3630	Cigarette smoking-associated isoform switching and 3' UTR lengthening via alternative polyadenylation. <i>Genomics</i> , 2021, 113, 4184-4195.	1.3	3
3631	RBFOX2 is critical for maintaining alternative polyadenylation patterns and mitochondrial health in rat myoblasts. <i>Cell Reports</i> , 2021, 37, 109910.	2.9	13
3639	Cancer Epigenomics and Beyond: Advancing the Precision Oncology Paradigm. <i>Journal of Immunotherapy and Precision Oncology</i> , 2020, 3, 147-156.	0.6	0
3640	Dynamic Transcriptome, DNA Methylome, and DNA Hydroxymethylome Networks During T-Cell Lineage Commitment. <i>Molecules and Cells</i> , 2018, 41, 953-963.	1.0	5
3642	HuB/C/D, nPTB, REST4, and miR-124 regulators of neuronal cell identity are also utilized in the lens. <i>Molecular Vision</i> , 2010, 16, 2301-16.	1.1	26
3646	Current Understandings of Molecular Biology of <i>Echinococcus multilocularis</i> , a Pathogen for Alveolar Echinococcosis in Humans- a Narrative Review Article. <i>Iranian Journal of Parasitology</i> , 2015, 10, 329-37.	0.6	3
3647	Cloning and sequence analysis of SLC25A13 transcripts in human amniocytes. <i>Translational Pediatrics</i> , 2012, 1, 85-90.	0.5	2
3648	DNA Hypomethylation in Intragenic and Intergenic Enhancer Chromatin of Muscle-Specific Genes Usually Correlates with their Expression. <i>Yale Journal of Biology and Medicine</i> , 2016, 89, 441-455.	0.2	22
3650	A Novel Variant of Entitled OCT4B3 is Expressed in Human Bladder Cancer and Astrocytoma Cell Lines. <i>Avicenna Journal of Medical Biotechnology</i> , 2017, 9, 142-145.	0.2	6
3651	Genetic variation affecting exon skipping contributes to brain structural atrophy in Alzheimer's disease. <i>AMIA Summits on Translational Science Proceedings</i> , 2018, 2017, 124-131.	0.4	6
3652	Comprehensive Analysis of Alternative Splicing Signature in Gastric Cancer Prognosis Based on The Cancer Genome Atlas (TCGA) and SpliceSeq Databases. <i>Medical Science Monitor</i> , 2020, 26, e925772.	0.5	0
3653	Single-cell transcriptomic profiling provides insights into retinal endothelial barrier properties. <i>Molecular Vision</i> , 2020, 26, 766-779.	1.1	2
3654	Alternative splicing of lncRNAs in human diseases. <i>American Journal of Cancer Research</i> , 2021, 11, 624-639.	1.4	4
3655	Sex-Specific Development in Haplodiploid Honeybee Is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic lncRNAs. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 690167.	1.8	0
3656	Dynamic intron retention modulates gene expression in the monocytic differentiation pathway. <i>Immunology</i> , 2022, 165, 274-286.	2.0	7
3657	Comprehensive Analysis of Large-Scale Transcriptomes from Multiple Cancer Types. <i>Genes</i> , 2021, 12, 1865.	1.0	3
3658	RNA-seq Analysis Reveals Alternative Splicing Under Heat Stress in Rainbow Trout (<i>Oncorhynchus</i>) Tj ETQq1 1 0.784314 rgBT ₁₁ /Overlook	1.1	11

#	ARTICLE	IF	CITATIONS
3659	Identification of tumour immune microenvironment-related alternative splicing events for the prognostication of pancreatic adenocarcinoma. <i>BMC Cancer</i> , 2021, 21, 1211.	1.1	7
3660	Alternative splicing level related to intron size and organism complexity. <i>BMC Genomics</i> , 2021, 22, 853.	1.2	8
3661	Circular RNA—Is the Circle Perfect?. <i>Biomolecules</i> , 2021, 11, 1755.	1.8	24
3662	Biological function and molecular mechanism of SRSF3 in cancer and beyond (Review). <i>Oncology Letters</i> , 2021, 23, 21.	0.8	6
3663	Full-length transcript sequencing of human and mouse cerebral cortex identifies widespread isoform diversity and alternative splicing. <i>Cell Reports</i> , 2021, 37, 110022.	2.9	79
3664	Pseudoxon activation in disease by non-splice site deep intronic sequence variation—wild type pseudoxons constitute high-risk sites in the human genome. <i>Human Mutation</i> , 2022, 43, 103-127.	1.1	17
3665	Roles of Major RNA Adenosine Modifications in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Pharmacology</i> , 2021, 12, 779779.	1.6	3
3667	Accurate expression quantification from nanopore direct RNA sequencing with NanoCount. <i>Nucleic Acids Research</i> , 2022, 50, e19-e19.	6.5	44
3668	Case Report: A Synonymous Mutation in NF1 Located at the Non-canonical Splicing Site Leading to Exon 45 Skipping. <i>Frontiers in Genetics</i> , 2021, 12, 772958.	1.1	5
3669	Genome annotation with long RNA reads reveals new patterns of gene expression and improves single-cell analyses in an ant brain. <i>BMC Biology</i> , 2021, 19, 254.	1.7	11
3670	Exploring the Diverse Functional and Regulatory Consequences of Alternative Splicing in Development and Disease. <i>Frontiers in Genetics</i> , 2021, 12, 775395.	1.1	9
3672	Genome-Wide Analysis of Alternative Splicing during Host-Virus Interactions in Chicken. <i>Viruses</i> , 2021, 13, 2409.	1.5	3
3673	Effects of Different Molecular Weight Polysaccharides From <i>Dendrobium officinale</i> Kimura & Migo on Human Colorectal Cancer and Transcriptome Analysis of Differentially Expressed Genes. <i>Frontiers in Pharmacology</i> , 2021, 12, 704486.	1.6	15
3674	A short sequence within <i>Alu</i> Sx induces downstream exon skipping in an <i>ACAT1</i> minigene model. <i>International Journal of Transgender Health</i> , 2021, 14, 869-873.	1.1	1
3677	Uncovering the impacts of alternative splicing on the proteome with current omics techniques. <i>Wiley Interdisciplinary Reviews RNA</i> , 2022, 13, e1707.	3.2	22
3678	Subcutaneous adipose tissue splice quantitative trait loci reveal differences in isoform usage associated with cardiometabolic traits. <i>American Journal of Human Genetics</i> , 2022, 109, 66-80.	2.6	13
3679	Genetic Regulation of Transcription in the Endometrium in Health and Disease. <i>Frontiers in Reproductive Health</i> , 2022, 3, .	0.6	8
3680	Genome-wide profiling of the expression of serum derived exosomal circRNAs in patients with hepatic alveolar echinococcosis. <i>Gene</i> , 2022, 814, 146161.	1.0	3

#	ARTICLE	IF	CITATIONS
3681	Comprehensive Analysis of Alternative Splicing Signature in Gastric Cancer Prognosis Based on The Cancer Genome Atlas (TCGA) and SpliceSeq Databases. <i>Medical Science Monitor</i> , 2020, 26, e925772.	0.5	1
3682	Alternative splicing regulation of membrane trafficking genes during myogenesis. <i>Rna</i> , 2022, 28, 523-540.	1.6	4
3683	Genomic studies controvert the existence of the CUX1 p75 isoform. <i>Scientific Reports</i> , 2022, 12, 151.	1.6	1
3685	Direct analysis of ribosome targeting illuminates thousand-fold regulation of translation initiation. <i>Cell Systems</i> , 2022, 13, 256-264.e3.	2.9	20
3688	USP15 and USP4 facilitate lung cancer cell proliferation by regulating the alternative splicing of SRSF1. <i>Cell Death Discovery</i> , 2022, 8, 24.	2.0	9
3689	Comparative transcriptome profiles of <i>Schistosoma japonicum</i> larval stages: Implications for parasite biology and host invasion. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0009889.	1.3	5
3690	Using machine learning to detect the differential usage of novel gene isoforms. <i>BMC Bioinformatics</i> , 2022, 23, 45.	1.2	1
3691	<i>Bmp</i> influences wing morphology by regulating anterior-posterior and proximal-distal axes development. <i>Insect Science</i> , 2022, 29, 1569-1582.	1.5	0
3692	Switched alternative splicing events as attractive features in lung squamous cell carcinoma. <i>Cancer Cell International</i> , 2022, 22, 5.	1.8	2
3693	Clinical Significance and Regulation of ERK5 Expression and Function in Cancer. <i>Cancers</i> , 2022, 14, 348.	1.7	14
3694	CellRank for directed single-cell fate mapping. <i>Nature Methods</i> , 2022, 19, 159-170.	9.0	286
3696	Shaping the Innate Immune Response Through Post-Transcriptional Regulation of Gene Expression Mediated by RNA-Binding Proteins. <i>Frontiers in Immunology</i> , 2021, 12, 796012.	2.2	10
3697	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	11
3698	How paediatric drug development and use could benefit from OMICs: A c4c expert group white paper. <i>British Journal of Clinical Pharmacology</i> , 2022, , .	1.1	3
3700	Characterization of Alternative Splicing Events in Porcine Skeletal Muscles with Different Intramuscular Fat Contents. <i>Biomolecules</i> , 2022, 12, 154.	1.8	10
3701	Widespread occurrence of hybrid internal-terminal exons in human transcriptomes. <i>Science Advances</i> , 2022, 8, eabk1752.	4.7	10
3703	Heat shock induces premature transcript termination and reconfigures the human transcriptome. <i>Molecular Cell</i> , 2022, 82, 1573-1588.e10.	4.5	27
3704	Full-Length Transcriptome of the Whale Shark (<i>Rhincodon typus</i>) Facilitates the Genome Information. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	2

#	ARTICLE	IF	CITATIONS
3705	Full-length coding moth transcriptome atlas revealed by single-molecule real-time sequencing. <i>Genomics</i> , 2022, 114, 110299.	1.3	2
3706	In silico prediction of HIV-1-host molecular interactions and their directionality. <i>PLoS Computational Biology</i> , 2022, 18, e1009720.	1.5	0
3707	Human embryonic genome activation initiates at the one-cell stage. <i>Cell Stem Cell</i> , 2022, 29, 209-216.e4.	5.2	71
3708	Targeting a novel inducible GPX4 alternative isoform to alleviate ferroptosis and treat metabolic-associated fatty liver disease. <i>Acta Pharmaceutica Sinica B</i> , 2022, 12, 3650-3666.	5.7	31
3709	Fixing the GAP: The role of RhoGAPs in cancer. <i>European Journal of Cell Biology</i> , 2022, 101, 151209.	1.6	20
3710	The role of alternative splicing in human cancer progression. <i>American Journal of Cancer Research</i> , 2021, 11, 4642-4667.	1.4	3
3712	Role of transcription factors in hepatocellular carcinoma. , 2022, , 149-163.		0
3713	Ptbp1-Activated Co-Transcriptional Splicing Controls Epigenetic Status of Pluripotent Stem Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3714	Systems Biology on Acetogenic Bacteria for Utilizing C1 Feedstocks. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2022, , 1.	0.6	0
3715	A guide for the diagnosis of rare and undiagnosed disease: beyond the exome. <i>Genome Medicine</i> , 2022, 14, 23.	3.6	101
3716	The SWI/SNF subunit BRG1 affects alternative splicing by changing RNA binding factor interactions with nascent RNA. <i>Molecular Genetics and Genomics</i> , 2022, 297, 463-484.	1.0	11
3717	DNA Hydroxymethylation in Smoking-Associated Cancers. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2657.	1.8	7
3718	Recent Progress in Drug Repurposing Using Protein Variants and Amino Acids in Disease Phenotypes/Disorders. , 0, , .		0
3719	Chemerin Impact on Alternative mRNA Transcription in the Porcine Luteal Cells. <i>Cells</i> , 2022, 11, 715.	1.8	7
3720	Tinker, Tailor, Tumour Suppressor: The Many Functions of PRP4K. <i>Frontiers in Genetics</i> , 2022, 13, 839963.	1.1	1
3721	A novel role for nucleolin in splice site selection. <i>RNA Biology</i> , 2022, 19, 333-352.	1.5	3
3722	Effects of Serine/Arginine Enriched Protein BmUP on the Development of Male Silkworm Reproductive Organs. <i>Current Issues in Molecular Biology</i> , 2022, 44, 928-941.	1.0	0
3723	DJExpress: An Integrated Application for Differential Splicing Analysis and Visualization. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	5

#	ARTICLE	IF	CITATIONS
3724	The Splicing of the Mitochondrial Calcium Uniporter Genuine Activator MICU1 Is Driven by RBFOX2 Splicing Factor during Myogenic Differentiation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2517.	1.8	2
3726	Co-transcriptional splicing efficiency is a gene-specific feature that can be regulated by TGF β 2. <i>Communications Biology</i> , 2022, 5, 277.	2.0	4
3729	SRSF1 governs progenitor-specific alternative splicing to maintain adult epithelial tissue homeostasis and renewal. <i>Developmental Cell</i> , 2022, 57, 624-637.e4.	3.1	9
3730	Reprogramming RNA processing: an emerging therapeutic landscape. <i>Trends in Pharmacological Sciences</i> , 2022, 43, 437-454.	4.0	14
3731	A Quality Control Mechanism of Splice Site Selection Abrogated under Stress and in Cancer. <i>Cancers</i> , 2022, 14, 1750.	1.7	2
3732	Beyond Genes: Inclusion of Alternative Splicing and Alternative Polyadenylation to Assess the Genetic Architecture of Predisposition to Voluntary Alcohol Consumption in Brain of the HXB/BXH Recombinant Inbred Rat Panel. <i>Frontiers in Genetics</i> , 2022, 13, 821026.	1.1	2
3733	Improved Reference Genome Annotation of Brassica rapa by Pacific Biosciences RNA Sequencing. <i>Frontiers in Plant Science</i> , 2022, 13, 841618.	1.7	20
3735	Single molecule, long-read Apoer2 sequencing identifies conserved and species-specific splicing patterns. <i>Genomics</i> , 2022, 114, 110318.	1.3	7
3737	Splice-disrupt genomic variants in prostate cancer. <i>Molecular Biology Reports</i> , 2022, , 1.	1.0	2
3738	Predicting exon criticality from protein sequence. <i>Nucleic Acids Research</i> , 2022, 50, 3128-3141.	6.5	1
3740	Splicing in Cancer. , 0, , .		0
3741	The Arabidopsis cyclophilin CYP18-1 facilitates PRP18 dephosphorylation and the splicing of introns retained under heat stress. <i>Plant Cell</i> , 2022, 34, 2383-2403.	3.1	10
3743	Enhanced protein isoform characterization through long-read proteogenomics. <i>Genome Biology</i> , 2022, 23, 69.	3.8	33
3744	Single-nuclei isoform RNA sequencing unlocks barcoded exon connectivity in frozen brain tissue. <i>Nature Biotechnology</i> , 2022, 40, 1082-1092.	9.4	52
3745	Sequencing of individual barcoded cDNAs using Pacific Biosciences and Oxford Nanopore Technologies reveals platform-specific error patterns. <i>Genome Research</i> , 2022, 32, 726-737.	2.4	13
3747	PTBP1 is a Novel Poor Prognostic Factor for Glioma. <i>BioMed Research International</i> , 2022, 2022, 1-11.	0.9	3
3749	Identifying genes with conserved splicing structure and orthologous isoforms in human, mouse and dog. <i>BMC Genomics</i> , 2022, 23, 216.	1.2	1
3750	Transcriptome Analysis Reveals the Alternative Splicing Changes in the Immune-Related Genes of the Giant Panda (<i>Ailuropoda melanoleuca</i>), in Response to the Canine Distemper Vaccine. <i>Zoological Science</i> , 2022, 39, .	0.3	3

#	ARTICLE	IF	CITATIONS
3751	Protein speciation is likely to increase the chance of proteins to be determined in 2â€œDE/MS. Electrophoresis, 2022, , .	1.3	1
3752	CHD8 haploinsufficiency links autism to transient alterations in excitatory and inhibitory trajectories. Cell Reports, 2022, 39, 110615.	2.9	40
3754	Aberrant RNA Splicing Is a Primary Link between Genetic Variation and Pancreatic Cancer Risk. Cancer Research, 2022, 82, 2084-2096.	0.4	14
3755	Chicken CDS2 isoforms presented distinct spatio-temporal expression pattern and regulated by insulin in a breed-specific manner. Poultry Science, 2022, 101, 101893.	1.5	0
3756	Key pituitary miRNAs mediate the expression of pig GHRHR splice variants by regulating splice factors. International Journal of Biological Macromolecules, 2022, 208, 208-218.	3.6	0
3757	m6A-induced repression of SIAH1 facilitates alternative splicing of androgen receptor variant 7 by regulating CPSF1. Molecular Therapy - Nucleic Acids, 2022, 28, 219-230.	2.3	7
3758	Deciphering alternative splicing patterns in multiple tissues of Ginkgo biloba important secondary metabolites. Industrial Crops and Products, 2022, 181, 114812.	2.5	4
3760	Impact of Alternative Splicing Variants on Liver Cancer Biology. Cancers, 2022, 14, 18.	1.7	11
3761	Comprehensive Analysis of Alternative Splicing in Gastric Cancer Identifies Epithelialâ€œMesenchymal Transition Subtypes Associated with Survival. Cancer Research, 2022, 82, 543-555.	0.4	12
3762	Combined Quantitative (Phospho)proteomics and Mass Spectrometry Imaging Reveal Temporal and Spatial Protein Changes in Human Intestinal Ischemiaâ€œReperfusion. Journal of Proteome Research, 2022, 21, 49-66.	1.8	11
3763	Soluble Receptor Isoform of IFN-Beta (sIFNAR2) in Multiple Sclerosis Patients and Their Association With the Clinical Response to IFN-Beta Treatment. Frontiers in Immunology, 2021, 12, 778204.	2.2	5
3764	Transcript-Specific Loss-of-Function Variants in <i>VPS16</i> Are Enriched in Patients With Dystonia. Neurology: Genetics, 2022, 8, e644.	0.9	9
3765	Mammalian splicing divergence is shaped by drift, buffering in <i>trans</i>, and a scaling law. Life Science Alliance, 2022, 5, e202101333.	1.3	3
3766	Estimating Cell Type Composition Using Isoform Expression One Gene at a Time. Biometrics, 2023, 79, 854-865.	0.8	0
3767	Differential fates of introns in gene expression due to global alternative splicing. Human Genetics, 2022, 141, 31-47.	1.8	14
3768	Identification of an mRNA isoform switch for HNRNPA1 in breast cancers. Scientific Reports, 2021, 11, 24444.	1.6	5
3769	RNA metabolism and links to inflammatory regulation and disease. Cellular and Molecular Life Sciences, 2022, 79, 21.	2.4	3
3771	Long-read isoform sequencing reveals tissue-specific isoform expression between active and hibernating brown bears (<i>Ursus arctos</i>). G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7

#	ARTICLE	IF	CITATIONS
3773	Pre-mRNA splicing factor U2AF2 recognizes distinct conformations of nucleotide variants at the center of the pre-mRNA splice site signal. <i>Nucleic Acids Research</i> , 2022, 50, 5299-5312.	6.5	8
3774	Abnormal global alternative RNA splicing in COVID-19 patients. <i>PLoS Genetics</i> , 2022, 18, e1010137.	1.5	21
3775	SRSF6 Regulates the Alternative Splicing of the Apoptotic Fas Gene by Targeting a Novel RNA Sequence. <i>Cancers</i> , 2022, 14, 1990.	1.7	6
3776	An Alternatively Spliced Variant of METTL3 Mediates Tumor Suppression in Hepatocellular Carcinoma. <i>Genes</i> , 2022, 13, 669.	1.0	7
3777	Placental Transcription Profiling in 6â€“23 Weeksâ€™ Gestation Reveals Differential Transcript Usage in Early Development. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4506.	1.8	3
3779	<sc><i>U2AF1</i></sc> mutation connects <sc>DNA</sc> damage to the alternative splicing of <sc><i>RAD51</i></sc> in lung adenocarcinomas. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2022, 49, 740-747.	0.9	3
3780	Two Different Aging Paths in Human Blood Revealed by Integrated Analysis of Gene Expression, Mutation and Alternative Splicing. <i>Gene</i> , 2022, 829, 146501.	1.0	0
3781	DEK modulates both expression and alternative splicing of cancerâ€™related genes. <i>Oncology Reports</i> , 2022, 47, .	1.2	2
3783	A comparison of mRNA sequencing (RNA-Seq) library preparation methods for transcriptome analysis. <i>BMC Genomics</i> , 2022, 23, 303.	1.2	10
3989	Tissue-specific expression of IL-15RA alternative splicing transcripts and its regulation by DNA methylation. <i>European Cytokine Network</i> , 2010, 21, 308-18.	1.1	8
3990	Knowledge enrichment analysis for human tissue-specific genes uncover new biological insights. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 194.	1.0	1
3991	Sex-Specific Development in Haplodiploid Honeybee Is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic LncRNAs. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 690167.	1.8	0
3992	Peak identification for ChIP-seq data with no controls. <i>Zoological Research</i> , 2012, 33, E121-8.	0.6	3
3994	Fast, Flexible, andâ€Exact Minimum Flow Decompositions viaâ€ILP. <i>Lecture Notes in Computer Science</i> , 2022, , 230-245.	1.0	4
3995	SRTdb: an omnibus for human tissue and cancer-specific RNA transcripts. <i>Biomarker Research</i> , 2022, 10, 27.	2.8	5
3996	Emerging Function of Ecotype-Specific Splicing in the Recruitment of Commensal Microbiome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4860.	1.8	4
3997	Recent Advances in Research on Molecular Mechanisms of Fungal Signaling. <i>Encyclopedia</i> , 2022, 2, 840-863.	2.4	4
3998	Mechanisms of action of intranuclear microRNAs. Part 2. MicroRNA-mediated regulation of ncRNA transcriptome and alternative splicing. <i>Zdorovâ€™e Rebenka</i> , 2022, 17, 48-53.	0.0	0

#	ARTICLE	IF	CITATIONS
3999	The Deubiquitinase USP39 Promotes Esophageal Squamous Cell Carcinoma Malignancy as a Splicing Factor. <i>Genes</i> , 2022, 13, 819.	1.0	4
4000	Transcriptome analysis of clock disrupted cancer cells reveals differential alternative splicing of cancer hallmarks genes. <i>Npj Systems Biology and Applications</i> , 2022, 8, 17.	1.4	4
4001	Ubiquitination and Ubiquitin-Like Modifications as Mediators of Alternative Pre-mRNA Splicing in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	0
4002	Where protein structure and cell diversity meet. <i>Trends in Cell Biology</i> , 2022, 32, 996-1007.	3.6	10
4003	TDP43 promotes stemness of breast cancer stem cells through CD44 variant splicing isoforms. <i>Cell Death and Disease</i> , 2022, 13, 428.	2.7	7
4004	Alternative splicing modulation by G-quadruplexes. <i>Nature Communications</i> , 2022, 13, 2404.	5.8	38
4005	Translational suppression via IFG-1/eIF4G inhibits stress-induced RNA alternative splicing in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2022, 221, .	1.2	6
4006	Characterization and clustering of kinase isoform expression in metastatic melanoma. <i>PLoS Computational Biology</i> , 2022, 18, e1010065.	1.5	4
4007	NSrp70 suppresses metastasis in triple-negative breast cancer by modulating Numb/TÎ²R1/EMT axis. <i>Oncogene</i> , 2022, 41, 3409-3422.	2.6	2
4008	Alternative splicing as a key player in the fine-tuning of the immunity response in <i>Arabidopsis</i> . <i>Molecular Plant Pathology</i> , 2022, 23, 1226-1238.	2.0	12
4009	Gene expression adjustment of inflammatory mechanisms in dairy cow mammary gland parenchyma during host defense against staphylococci. <i>Annals of Animal Science</i> , 2022, .	0.6	1
4010	Autophagy regulation by RNA alternative splicing and implications in human diseases. <i>Nature Communications</i> , 2022, 13, 2735.	5.8	12
4011	Biogenesis and Regulatory Roles of Circular RNAs. <i>Annual Review of Cell and Developmental Biology</i> , 2022, 38, 263-289.	4.0	75
4013	Secondary structures in RNA synthesis, splicing and translation. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2871-2884.	1.9	13
4014	Tissue-Specific Analysis of Alternative Splicing Events and Differential Isoform Expression in Large Yellow Croaker (<i>Larimichthys crocea</i>) After <i>Cryptocaryon irritans</i> Infection. <i>Marine Biotechnology</i> , 2022, 24, 640-654.	1.1	3
4015	Transcriptional Basis of Psoriasis from Large Scale Gene Expression Studies: The Importance of Moving towards a Precision Medicine Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6130.	1.8	8
4016	Use of CRISPR/Cas9 with homology-directed repair to silence the human topoisomerase III α intron-19 5' splice site: Generation of etoposide resistance in human leukemia K562 cells. <i>PLoS ONE</i> , 2022, 17, e0265794.	1.1	3
4018	Identification of Protein Isoforms Using Reference Databases Built from Long and Short Read RNA-Sequencing. <i>Journal of Proteome Research</i> , 2022, 21, 1628-1639.	1.8	4

#	ARTICLE	IF	CITATIONS
4019	Alternative splicing diversifies the skeletal muscle transcriptome during prolonged spaceflight. <i>Skeletal Muscle</i> , 2022, 12, .	1.9	3
4020	Dysregulation and therapeutic targeting of RNA splicing in cancer. <i>Nature Cancer</i> , 2022, 3, 536-546.	5.7	65
4021	Splicing mutations in the CFTR gene as therapeutic targets. <i>Gene Therapy</i> , 2022, 29, 399-406.	2.3	6
4022	Efficient Detection of the Alternative Spliced Human Proteome Using Translatome Sequencing. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	1.6	2
4023	The Isolation and Full-Length Transcriptome Sequencing of a Novel Nidovirus and Response of Its Infection in Japanese Flounder (<i>Paralichthys olivaceus</i>). <i>Viruses</i> , 2022, 14, 1216.	1.5	2
4024	Sensitive and accurate analysis of gene expression signatures enabled by oligonucleotide-labelled cDNA. <i>RNA Biology</i> , 2022, 19, 774-780.	1.5	1
4025	CI-SpliceAI™ Improving machine learning predictions of disease causing splicing variants using curated alternative splice sites. <i>PLoS ONE</i> , 2022, 17, e0269159.	1.1	15
4026	Improved transcriptome assembly using a hybrid of long and short reads with StringTie. <i>PLoS Computational Biology</i> , 2022, 18, e1009730.	1.5	94
4029	Proteogenomic, Epigenetic, and Clinical Implications of Recurrent Aberrant Splice Variants in Clear Cell Renal Cell Carcinoma. <i>European Urology</i> , 2022, 82, 354-362.	0.9	13
4030	Carnosol, a diterpene present in rosemary, increases ELP1 levels in familial dysautonomia patient-derived cells and healthy adults: a possible therapy for FD. <i>Human Molecular Genetics</i> , 2022, 31, 3521-3538.	1.4	1
4031	Temporal Analysis of Gene Expression and Isoform Switching in Brown Bears (<i>Ursus arctos</i>). <i>Integrative and Comparative Biology</i> , 0, , .	0.9	3
4032	SAPFIR: A webserver for the identification of alternative protein features. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	0
4033	Transcript Complexity and New Insights of Restorer Line in CMS-D8 Cotton Through Full-Length Transcriptomic Analysis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
4034	Genome-wide alternative splicing profile in the posterior kidney of brown trout (<i>Salmo trutta</i>) during proliferative kidney disease. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
4035	Derivation of splice junction-specific antibodies using a unique hapten targeting strategy and directed evolution. <i>New Biotechnology</i> , 2022, 71, 1-10.	2.4	5
4036	Dynamics and functional roles of splicing factor autoregulation. <i>Cell Reports</i> , 2022, 39, 110985.	2.9	9
4037	Selective ablation of 3' RNA ends and processive RTs facilitate direct cDNA sequencing of full-length host cell and viral transcripts. <i>Nucleic Acids Research</i> , 2022, 50, e98-e98.	6.5	4
4038	A Transcriptomic Atlas Underlying Developmental Plasticity of Seasonal Forms of <i>Bicyclus anynana</i> Butterflies. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9

#	ARTICLE	IF	CITATIONS
4039	A bioinformatics framework for targeted gene expression assay design: Application to in vitro developmental neurotoxicity screening in a rat model. <i>Regulatory Toxicology and Pharmacology</i> , 2022, 133, 105211.	1.3	0
4040	N6-methyladenosine (m6A) regulator expression pattern correlates with the immune landscape in lung adenocarcinoma. <i>Gene</i> , 2022, 836, 146639.	1.0	2
4042	Smooth muscle diversity in the vascular system. , 2022, , 45-55.		1
4043	FishExp: A comprehensive database and analysis platform for gene expression and alternative splicing of fish species. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3676-3684.	1.9	3
4044	Intronic Polyadenylation in Acquired Cancer Drug Resistance Circumvented by Utilizing CRISPR/Cas9 with Homology-Directed Repair: The Tale of Human DNA Topoisomerase III±. <i>Cancers</i> , 2022, 14, 3148.	1.7	2
4045	Deciphering associations between three RNA splicing-related genetic variants and lung cancer risk. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	1
4047	The Long Read Transcriptome of Rice (<i>Oryza sativa</i> ssp. japonica var. Nipponbare) Reveals Novel Transcripts. <i>Rice</i> , 2022, 15, .	1.7	2
4048	<i>ggtranscript</i> : an R package for the visualization and interpretation of transcript isoforms using <i>ggplot2</i> . <i>Bioinformatics</i> , 2022, 38, 3844-3846.	1.8	76
4049	Development of a Prognostic Alternative Splicing Signature Associated With Tumor Microenvironment Immune Profiles in Lung Adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
4051	The splicing factor RBM17 drives leukemic stem cell maintenance by evading nonsense-mediated decay of pro-leukemic factors. <i>Nature Communications</i> , 2022, 13, .	5.8	3
4052	Alternative splicing patterns reveal prognostic indicator in muscle-invasive bladder cancer. <i>World Journal of Surgical Oncology</i> , 2022, 20, .	0.8	2
4053	Identification of the prognostic signature based on genomic instability-related alternative splicing in colorectal cancer and its regulatory network. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	1
4054	Human FOXP3 and tumour microenvironment. <i>Immunology</i> , 2023, 168, 248-255.	2.0	33
4055	APEX1 regulates alternative splicing of key tumorigenesis genes in non-small-cell lung cancer. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	6
4056	Splicing dysregulation in human hematologic malignancies: beyond splicing mutations. <i>Trends in Immunology</i> , 2022, 43, 674-686.	2.9	7
4057	Transcriptomic analysis reveals the key role of histone deacetylation via mediating different phytohormone signalings in fiber initiation of cotton. <i>Cell and Bioscience</i> , 2022, 12, .	2.1	5
4058	Alternative splicing as a source of phenotypic diversity. <i>Nature Reviews Genetics</i> , 2022, 23, 697-710.	7.7	120
4059	Dysregulated minor intron splicing in cancer. <i>Cancer Science</i> , 2022, 113, 2934-2942.	1.7	7

#	ARTICLE	IF	CITATIONS
4060	Quantum tunneling of three-spine solitons through excentric barriers. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2022, 448, 128319.	0.9	3
4062	A powerful global test for spliceQTL effects. <i>Biometrical Journal</i> , 0, , .	0.6	0
4063	Impaired type I interferon signaling activity implicated in the peripheral blood transcriptome of preclinical Alzheimer's disease. <i>EBioMedicine</i> , 2022, 82, 104175.	2.7	15
4064	Identifying cell state-associated alternative splicing events and their coregulation. <i>Genome Research</i> , 2022, 32, 1385-1397.	2.4	3
4066	Decoding the concealed transcriptional signature of the apoptosis-related BCL2 antagonist/killer 1 (BAK1) gene in human malignancies. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 0, , .	2.2	0
4067	Alternatively Spliced Isoforms of the P2X7 Receptor: Structure, Function and Disease Associations. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8174.	1.8	8
4070	scGENA: A Single-Cell Gene Coexpression Network Analysis Framework for Clustering Cell Types and Revealing Biological Mechanisms. <i>Bioengineering</i> , 2022, 9, 353.	1.6	5
4071	UHRF1 interacts with snRNAs and regulates alternative splicing in mouse spermatogonial stem cells. <i>Stem Cell Reports</i> , 2022, 17, 1859-1873.	2.3	5
4072	Bridging the splicing gap in human genetics with long-read RNA sequencing: finding the protein isoform drivers of disease. <i>Human Molecular Genetics</i> , 2022, 31, R123-R136.	1.4	10
4073	Splice modulating oligomers as cancer therapeutics. <i>Genes and Cancer</i> , 2022, 13, 46-48.	0.6	0
4074	Quantitative trait locus (xQTL) approaches identify risk genes and drug targets from non-coding genome findings. <i>Human Molecular Genetics</i> , 0, , .	1.4	2
4075	Novel Method of Full-Length RNA-seq That Expands the Identification of Non-Polyadenylated RNAs Using Nanopore Sequencing. <i>Analytical Chemistry</i> , 2022, 94, 12342-12351.	3.2	2
4076	Failure of diet-induced transcriptional adaptations in alpha-synuclein transgenic mice. <i>Human Molecular Genetics</i> , 0, , .	1.4	0
4080	To kill a cancer: Targeting the immune inhibitory checkpoint molecule, B7-H3. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2022, 1877, 188783.	3.3	14
4081	satuRn: Scalable analysis of differential transcript usage for bulk and single-cell RNA-sequencing applications. <i>F1000Research</i> , 0, 10, 374.	0.8	1
4083	lluminating the dark protein-protein interactome. <i>Cell Reports Methods</i> , 2022, 2, 100275.	1.4	10
4084	Myocardin regulates exon usage in smooth muscle cells through induction of splicing regulatory factors. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	6
4085	Prognostic alternative splicing events related splicing factors define the tumor microenvironment and pharmacogenomic landscape in lung adenocarcinoma. <i>Aging</i> , 2022, 14, 6689-6715.	1.4	2

#	ARTICLE	IF	CITATIONS
4086	A widespread length-dependent splicing dysregulation in cancer. <i>Science Advances</i> , 2022, 8, .	4.7	7
4087	Use of animal models to understand titin physiology and pathology. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 5103-5112.	1.6	6
4088	Role of WTAP in Cancer: From Mechanisms to the Therapeutic Potential. <i>Biomolecules</i> , 2022, 12, 1224.	1.8	10
4089	Integrative analysis of synovial sarcoma transcriptome reveals different types of transcriptomic changes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
4090	CYCLIN K down-regulation induces androgen receptor gene intronic polyadenylation, variant expression and PARP inhibitor vulnerability in castration-resistant prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	6
4091	Harnessing gene fusion-derived neoantigens for "cold" breast and prostate tumor immunotherapy. <i>Immunotherapy</i> , 2022, 14, 1165-1179.	1.0	4
4092	Analysis of RANK-c interaction partners identifies TRAF3 as a critical regulator of breast cancer aggressiveness. <i>Neoplasia</i> , 2022, 33, 100836.	2.3	1
4093	Post-transcriptional gene regulation in solid tumors. , 2022, , 119-148.		0
4094	Expression and characterisation of Fmr1 splice variants during folliculogenesis in the rat. <i>Reproduction, Fertility and Development</i> , 2022, , .	0.1	0
4095	Two-Color Fluorescent Reporters for Analysis of Alternative Splicing. <i>Methods in Molecular Biology</i> , 2022, , 211-229.	0.4	0
4096	TEx-MST: tissue expression profiles of MANE select transcripts. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	0
4097	Strategies for Enhancement of Transgene Expression. , 2022, , 75-106.		0
4098	Quantitative Detection of Protein Splice Variants by Selected Reaction Monitoring (SRM) Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2022, , 231-246.	0.4	1
4099	Targeting Alternative Splicing for Therapeutic Interventions. <i>Methods in Molecular Biology</i> , 2022, , 21-36.	0.4	1
4100	Analysis of Splicing Regulation by Third-Generation Sequencing. <i>Methods in Molecular Biology</i> , 2022, , 81-95.	0.4	0
4101	Computational Analysis of Alternative Splicing Using VAST-TOOLS and the VastDB Framework. <i>Methods in Molecular Biology</i> , 2022, , 97-128.	0.4	2
4102	Functional Annotation of Custom Transcriptomes. <i>Methods in Molecular Biology</i> , 2022, , 149-172.	0.4	3
4103	Identification and Quantification of Microexons Using Bulk and Single-Cell RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2022, , 129-147.	0.4	1

#	ARTICLE	IF	CITATIONS
4104	Post-transcriptional regulation. , 2022, , 89-104.		0
4105	DNA Technologies in Precision Medicine and Pharmacogenetics. , 2022, , 129-149.		0
4106	Eomes function is conserved between zebrafish and mouse and controls left-right organiser progenitor gene expression via interlocking feedforward loops. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	1
4108	Full and D-BOX-Deficient PTTG1 Isoforms: Effects on Cell Proliferation. <i>Molecular Biology</i> , 0, , .	0.4	0
4109	Comprehensive Transcriptome Analysis Reveals Sex-Specific Alternative Splicing Events in Zebrafish Gonads. <i>Life</i> , 2022, 12, 1441.	1.1	2
4110	Alternative splicing signature of alveolar type II epithelial cells of Tibetan pigs under hypoxia-induced. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	1
4111	Insights into established and emerging roles of <scp>SR</scp> protein family in plants and animals. <i>Wiley Interdisciplinary Reviews RNA</i> , 2023, 14, .	3.2	5
4113	Diverse cell-specific patterns of alternative polyadenylation in <i>Drosophila</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	13
4114	HOX-Gene Cluster Organization and Genome Duplications in Fishes and Mammals: Transcript Variant Distribution along the Anteriorâ€“Posterior Axis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9990.	1.8	1
4115	Integrated omics analysis identified genes and their splice variants involved in fruit development and metabolites production in <i>Capsicum</i> species. <i>Functional and Integrative Genomics</i> , 2022, 22, 1189-1209.	1.4	7
4116	The alternative splicing of intersectin 1 regulated by PTBP1 promotes human glioma progression. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	5
4117	Stretching muscle cells induces transcriptional and splicing transitions and changes in SR proteins. <i>Communications Biology</i> , 2022, 5, .	2.0	2
4118	<scp>mRNA</scp> isoform balance in neuronal development and disease. <i>Wiley Interdisciplinary Reviews RNA</i> , 2023, 14, .	3.2	4
4119	Comprehensive and scalable quantification of splicing differences with MntJULiP. <i>Genome Biology</i> , 2022, 23, .	3.8	1
4120	RNA velocity unraveled. <i>PLoS Computational Biology</i> , 2022, 18, e1010492.	1.5	65
4123	Insights into sweet potato SR proteins: from evolution to species-specific expression and alternative splicing. <i>Planta</i> , 2022, 256, .	1.6	3
4124	CPEB2 m6A methylation regulates bloodâ€“tumor barrier permeability by regulating splicing factor SRSF5 stability. <i>Communications Biology</i> , 2022, 5, .	2.0	17
4125	Alternative splicing in bladder cancer: potential strategies for cancer diagnosis, prognosis, and treatment. <i>Wiley Interdisciplinary Reviews RNA</i> , 2023, 14, .	3.2	2

#	ARTICLE	IF	CITATIONS
4126	Targeting acetylcholine signaling modulates persistent drug tolerance in EGFR-mutant lung cancer and impedes tumor relapse. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	17
4127	Integrating machine learning to construct aberrant alternative splicing event related classifiers to predict prognosis and immunotherapy response in patients with hepatocellular carcinoma. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
4128	From multitude to singularity: An up-to-date overview of scRNA-seq data generation and analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
4130	The oncogenic role of SNRPB in human tumors: A pan-cancer analysis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
4131	Sex and the basal <scp>mRNA</scp> synthesis machinery. <i>Wiley Interdisciplinary Reviews RNA</i> , 0, , .	3.2	2
4132	RNA Metabolism in T Lymphocytes. <i>Immune Network</i> , 2022, 22, .	1.6	3
4133	The physiology of alternative splicing. <i>Nature Reviews Molecular Cell Biology</i> , 2023, 24, 242-254.	16.1	84
4134	Transcriptome-Based Analysis of the Response Mechanism of Leopard Coralgroupers Liver at Different Flow Velocities. <i>Fishes</i> , 2022, 7, 279.	0.7	0
4135	Splicing factor SRSF3 promotes the progression of cervical cancer through regulating DDX5. <i>Molecular Carcinogenesis</i> , 2023, 62, 210-223.	1.3	3
4136	The regulation of totipotency transcription: Perspective from in vitro and in vivo totipotency. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	5
4137	DAZAP1 facilitates the alternative splicing of KITLG to promote multiple myeloma cell proliferation via ERK signaling pathway. <i>Aging</i> , 2022, 14, 7972-7985.	1.4	0
4138	Differential alternative splicing genes and isoform co-expression networks of Brassica napus under multiple abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
4139	Efficient Minimum Flow Decomposition via Integer Linear Programming. <i>Journal of Computational Biology</i> , 2022, 29, 1252-1267.	0.8	4
4140	Alternative Transcription Start Site Usage and Functional Implications in Pathogenic Fungi. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1044.	1.5	2
4141	Alternative Splicing Landscape of Placental Decidual Cells during Physiological Pregnancy. <i>Russian Journal of Genetics</i> , 2022, 58, 1257-1265.	0.2	0
4142	Clinical variant interpretation and biologically relevant reference transcripts. <i>Npj Genomic Medicine</i> , 2022, 7, .	1.7	2
4143	Identification of a novel alternatively spliced isoform of the ribosomal uL10 protein. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2023, 1866, 194890.	0.9	0
4145	Blood transcriptome analysis and identification of genes associated with supernumerary teats in Chinese Holstein cows. <i>Journal of Dairy Science</i> , 2022, , .	1.4	1

#	ARTICLE	IF	CITATIONS
4146	Posttranscriptional regulation of neurofilament proteins and tau in health and disease. <i>Brain Research Bulletin</i> , 2023, 192, 115-127.	1.4	4
4147	Alternative splicing in plants: current knowledge and future directions for assessing the biological relevance of splice variants. <i>Journal of Experimental Botany</i> , 2023, 74, 2251-2272.	2.4	13
4148	Alternative splicing reprogramming in fungal pathogen <i>Sclerotinia sclerotiorum</i> at different infection stages on <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
4149	The Difference in Structural States between Canonical Proteins and Their Isoforms Established by Proteome-Wide Bioinformatics Analysis. <i>Biomolecules</i> , 2022, 12, 1610.	1.8	11
4150	DeepASmRNA: Reference-free prediction of alternative splicing events with a scalable and interpretable deep learning model. <i>IScience</i> , 2022, 25, 105345.	1.9	3
4151	Identification of sex-specific splicing via comparative transcriptome analysis of gonads from sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101031.	0.4	0
4152	Genetic and epigenetic regulation of growth, reproduction, disease resistance and stress responses in aquaculture. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	13
4153	FOXK2 transcription factor and its roles in tumorigenesis (Review). <i>Oncology Letters</i> , 2022, 24, .	0.8	0
4154	Identification of alternative transcripts of NSD1 gene in Sotos Syndrome patients and healthy subjects. <i>Gene</i> , 2023, 851, 146970.	1.0	3
4155	Sequence and expression regulation of the BCL2L2 gene in pigs. <i>Gene</i> , 2023, 851, 146992.	1.0	1
4157	A molecular brake that modulates spliceosome pausing at detained introns contributes to neurodegeneration. <i>Protein and Cell</i> , 0, , .	4.8	0
4158	Origins and Evolution of Human Tandem Duplicated Exon Substitution Events. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	1
4159	TARDBP promotes ovarian cancer progression by altering vascular endothelial growth factor splicing. <i>Oncogene</i> , 2023, 42, 49-61.	2.6	2
4160	Combining genetic constraint with predictions of alternative splicing to prioritize deleterious splicing in rare disease studies. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	7
4161	Characterization of alternative mRNA splicing in cultured cell populations representing progressive stages of human fetal kidney development. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
4162	SRSF10 is essential for progenitor spermatogonia expansion by regulating alternative splicing. <i>ELife</i> , 0, 11, .	2.8	5
4164	Deciphering the impact of genetic variation on human polyadenylation using APARENT2. <i>Genome Biology</i> , 2022, 23, .	3.8	12
4165	Systematic characterization of cancer transcriptome at transcript resolution. <i>Nature Communications</i> , 2022, 13, .	5.8	7

#	ARTICLE	IF	CITATIONS
4166	Retained introns in long RNA-seq reads are not reliably detected in sample-matched short reads. <i>Genome Biology</i> , 2022, 23, .	3.8	7
4167	SETD2 transcriptional control of ATG14L/S isoforms regulates autophagosome-lysosome fusion. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	7
4168	Alternative splicing downstream of EMT enhances phenotypic plasticity and malignant behavior in colon cancer. <i>ELife</i> , 0, 11, .	2.8	5
4169	DNA replication initiation shapes the mutational landscape and expression of the human genome. <i>Science Advances</i> , 2022, 8, .	4.7	4
4170	Comparative Analysis of Alternative Splicing in Two Contrasting Apple Cultivars Defense against <i>Alternaria alternata</i> Apple Pathotype Infection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14202.	1.8	4
4171	IntroVerse: a comprehensive database of introns across human tissues. <i>Nucleic Acids Research</i> , 2023, 51, D167-D178.	6.5	5
4173	Splice Variants of G Protein-Coupled Receptors Expressed in Cancers: Effective Targeting with Monoclonal Antibodies and Antibody-Like Scaffolds As Ligands Irrespective of the Pharmacological Status of Isoforms. , 2022, , 1-45.		0
4174	Effect of selenium nanoparticles on alternative splicing in heat-stressed rainbow trout primary hepatocytes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101042.	0.4	0
4175	Defining the characteristics of interferon-alpha-stimulated human genes: insight from expression data and machine learning. <i>GigaScience</i> , 2022, 11, .	3.3	1
4176	Time-course RNA-Seq profiling reveals isoform-level gene expression dynamics of the cGAS-STING pathway. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 6490-6500.	1.9	0
4177	Multi-omics approach to identifying isoform variants as therapeutic targets in cancer patients. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
4178	RNA-based drug discovery for spinal muscular atrophy: a story of small molecules and antisense oligonucleotides. <i>Expert Opinion on Drug Discovery</i> , 2023, 18, 181-192.	2.5	1
4179	Brain Region-Dependent Alternative Splicing of Alzheimer Disease (AD)-Risk Genes Is Associated With Neuropathological Features in AD. <i>International Neurourology Journal</i> , 2022, 26, S126-136.	0.5	6
4180	SRSF6 balances mitochondrial-driven innate immune outcomes through alternative splicing of BAX. <i>ELife</i> , 0, 11, .	2.8	5
4181	The PtoTCP20-miR396d-PtoGRF15 module regulates secondary vascular development in <i>Populus</i> . <i>Plant Communications</i> , 2023, 4, 100494.	3.6	6
4183	Cell-type-specific alternative splicing in the <i>Arabidopsis</i> germline. <i>Plant Physiology</i> , 2023, 192, 85-101.	2.3	3
4185	Comprehensive analysis of pre-mRNA alternative splicing regulated by m6A methylation in pig oxidative and glycolytic skeletal muscles. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
4188	The Role of Alternative Splicing Factors, DDB2-Related Ageing and DNA Damage Repair in the Progression and Prognosis of Stomach Adenocarcinoma Patients. <i>Genes</i> , 2023, 14, 39.	1.0	3

#	ARTICLE	IF	CITATIONS
4189	Promoter-Adjacent DNA Hypermethylation Can Downmodulate Gene Expression: TBX15 in the Muscle Lineage. <i>Epigenomes</i> , 2022, 6, 43.	0.8	0
4190	Characterization of an RNA binding protein interactome reveals a context-specific post-transcriptional landscape of MYC-amplified medulloblastoma. <i>Nature Communications</i> , 2022, 13, .	5.8	5
4191	Regulation of pre-mRNA splicing: roles in physiology and disease, and therapeutic prospects. <i>Nature Reviews Genetics</i> , 2023, 24, 251-269.	7.7	39
4192	Global Landscape of Alternative Splicing in Maize Response to Low Temperature. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 15715-15725.	2.4	6
4193	Arm race between Rift Valley fever virus and host. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
4194	Structure-guided isoform identification for the human transcriptome. <i>ELife</i> , 0, 11, .	2.8	14
4195	Freddie: annotation-independent detection and discovery of transcriptomic alternative splicing isoforms using long-read sequencing. <i>Nucleic Acids Research</i> , 2023, 51, e11-e11.	6.5	3
4197	Alternative pre-mRNA splicing as a mechanism for terminating Toll-like Receptor signaling. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
4199	MALAT1 modulates alternative splicing by cooperating with the splicing factors PTBP1 and PSF. <i>Science Advances</i> , 2022, 8, .	4.7	6
4200	Liver RBFOX2 regulates cholesterol homeostasis via Scarb1 alternative splicing in mice. <i>Nature Metabolism</i> , 2022, 4, 1812-1829.	5.1	12
4202	Broad misappropriation of developmental splicing profile by cancer in multiple organs. <i>Nature Communications</i> , 2022, 13, .	5.8	3
4203	Knowledge mapping of alternative splicing of cancer from 2012 to 2021: A bibliometric analysis. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
4204	High throughput sequencing revealed enhanced cell cycle signaling in SLE patients. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
4205	PTBP1-activated co-transcriptional splicing controls epigenetic status of pluripotent stem cells. <i>Molecular Cell</i> , 2023, 83, 203-218.e9.	4.5	7
4206	The variables on RNA molecules: concert or cacophony? Answers in long-read sequencing. <i>Nature Methods</i> , 2023, 20, 20-24.	9.0	9
4207	Transcriptomics for Clinical and Experimental Biology Research: Hang on a Seq. <i>Genetics & Genomics Next</i> , 2023, 4, .	0.8	5
4209	Genetic Mutations and Alternative Splicing in Schizophrenia. , 2023, , 15-31.		0
4210	RNA splicing factors in normal hematopoiesis and hematologic malignancies: novel therapeutic targets and strategies. <i>Journal of Leukocyte Biology</i> , 0, , .	1.5	1

#	ARTICLE	IF	CITATIONS
4211	RNA splicing dysregulation and the hallmarks of cancer. <i>Nature Reviews Cancer</i> , 2023, 23, 135-155.	12.8	73
4212	Long non-coding RNAs reveal new regulatory mechanisms controlling gene expression. <i>Comptes Rendus - Biologies</i> , 2022, 345, 15-39.	0.1	1
4215	Alternative splicing is not a key source of chemerin isoforms diversity. <i>Molecular Biology Reports</i> , 0, , .	1.0	0
4216	Alternatively Spliced Isoforms of MUC4 and ADAM12 as Biomarkers for Colorectal Cancer Metastasis. <i>Journal of Personalized Medicine</i> , 2023, 13, 135.	1.1	0
4217	Reovirus $\hat{1}/4$ Protein Impairs Translation to Reduce U5 snRNP Protein Levels. <i>International Journal of Molecular Sciences</i> , 2023, 24, 727.	1.8	0
4218	De Novo Transcriptome Profiling of <i>Naegleria fowleri</i> Trophozoites and Cysts via RNA Sequencing. <i>Pathogens</i> , 2023, 12, 174.	1.2	0
4219	Alternative splicing in multiple myeloma is associated with the non-homologous end joining pathway. <i>Blood Cancer Journal</i> , 2023, 13, .	2.8	3
4220	LncRNA BC promotes lung adenocarcinoma progression by modulating IMPAD1 alternative splicing. <i>Clinical and Translational Medicine</i> , 2023, 13, .	1.7	9
4221	Identification of Alternative Splicing in Proteomes of Human Melanoma Cell Lines without RNA Sequencing Data. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2466.	1.8	0
4223	Full-length transcriptome sequencing analysis reveals differential skin color regulation in snakeheads fish <i>Channa argus</i> . <i>Aquaculture and Fisheries</i> , 2023, , .	1.2	2
4224	Position-dependent effects of RNA-binding proteins in the context of co-transcriptional splicing. <i>Npj Systems Biology and Applications</i> , 2023, 9, .	1.4	3
4225	Alternative splicing: a new breakthrough for understanding tumorigenesis and potential clinical applications. <i>Genes and Genomics</i> , 0, , .	0.5	1
4226	Epigenetic modifications and alternative pre-mRNA splicing in cancer. , 2023, , 123-146.		0
4227	CAFuncAPA: a knowledgebase for systematic functional annotations of APA events in human cancers. <i>NAR Cancer</i> , 2023, 5, .	1.6	1
4228	Alternative RNA Splicing in the Retina: Insights and Perspectives. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2023, 13, a041313.	2.9	3
4229	Understanding the Nature of Cancerâ€™General Principles. , 2023, , 3-26.		0
4230	Improved Annotation of the Peach (<i>Prunus persica</i>) Genome and Identification of Tissue- or Development Stage-Specific Alternative Splicing through the Integration of Iso-Seq and RNA-Seq Data. <i>Horticulturae</i> , 2023, 9, 175.	1.2	1
4231	Alternative splicing of <i>PSMD13</i> mediated by genetic variants is significantly associated with endometrial cancer risk. <i>Journal of Gynecologic Oncology</i> , 2023, 34, .	1.0	2

#	ARTICLE	IF	CITATIONS
4232	Current perspective of transcriptional regulators in human health and diseases. , 2023, , 3-16.		0
4233	SRSF3-Mediated Ki67 Exon 7-Inclusion Promotes Head and Neck Squamous Cell Carcinoma Progression via Repressing AKR1C2. International Journal of Molecular Sciences, 2023, 24, 3872.	1.8	2
4235	Failure of ALL recognition by CAR T cells: a review of CD 19-negative relapses after anti-CD 19 CAR-T treatment in B-ALL. Frontiers in Immunology, 0, 14, .	2.2	6
4236	A comprehensive benchmarking of differential splicing tools for RNA-seq analysis at the event level. Briefings in Bioinformatics, 2023, 24, .	3.2	9
4237	Differential splicing of neuronal genes in a Trem2 ^{*R47H} mouse model mimics alterations associated with Alzheimer's disease. BMC Genomics, 2023, 24, .	1.2	2
4238	CD44 occurring alternative splicing promotes cisplatin resistance and evokes tumor immune response in oral squamous cell carcinoma cells. Translational Oncology, 2023, 31, 101644.	1.7	1
4239	Distinct regulatory functions and biological roles of lncRNA splice variants. Molecular Therapy - Nucleic Acids, 2023, 32, 127-143.	2.3	5
4240	All differential on the splicing front: Host alternative splicing alters the landscape of virus-host conflict. Seminars in Cell and Developmental Biology, 2023, 146, 40-56.	2.3	0
4243	METTL3 regulates breast cancer-associated alternative splicing switches. Oncogene, 2023, 42, 911-925.	2.6	12
4244	Relationship between NUDT21 mediated alternative polyadenylation process and tumor. Frontiers in Oncology, 0, 13, .	1.3	1
4245	The Functional Meaning of 5'UTR in Protein-Coding Genes. International Journal of Molecular Sciences, 2023, 24, 2976.	1.8	11
4246	Re-evaluating the impact of alternative RNA splicing on proteomic diversity. Frontiers in Genetics, 0, 14, .	1.1	2
4247	Pancreatic microexons regulate islet function and glucose homeostasis. Nature Metabolism, 2023, 5, 219-236.	5.1	4
4248	RNA epitranscriptomics dysregulation: A major determinant for significantly increased risk of ASD pathogenesis. Frontiers in Neuroscience, 0, 17, .	1.4	1
4249	SPHINX-Based Combination Therapy as a Potential Novel Treatment Strategy for Acute Myeloid Leukaemia. , 0, 80, .		2
4250	UHRF1/DNMT1-MZF1 axis-modulated intragenic site-specific CpG methylation confers divergent expression and opposing functions of PRSS3 isoforms in lung cancer. Acta Pharmaceutica Sinica B, 2023, 13, 2086-2106.	5.7	3
4252	Alternative splicing in shaping the molecular landscape of the cochlea. Frontiers in Cell and Developmental Biology, 0, 11, .	1.8	0
4253	DELongSeq for efficient detection of differential isoform expression from long-read RNA-seq data. NAR Genomics and Bioinformatics, 2023, 5, .	1.5	0

#	ARTICLE	IF	CITATIONS
4254	MYC-driven U2SURP regulates alternative splicing of SAT1 to promote triple-negative breast cancer progression. <i>Cancer Letters</i> , 2023, 560, 216124.	3.2	5
4256	Transcriptomic Analysis Reveals mRNA and Alternative Splicing Events in Ovine Skeletal Muscle Satellite Cells during Proliferation and Differentiation. <i>Animals</i> , 2023, 13, 1076.	1.0	2
4257	PCB: A pseudotemporal causality-based Bayesian approach to identify EMT-associated regulatory relationships of AS events and RBPs during breast cancer progression. <i>PLoS Computational Biology</i> , 2023, 19, e1010939.	1.5	1
4258	BORIS variant SF2(C2/A4) promotes the malignant development of liver cancer by activating epithelial-mesenchymal transition and hepatic stellate cells. <i>Molecular Carcinogenesis</i> , 2023, 62, 731-742.	1.3	2
4259	Alternative mRNA Splicing and Promising Therapies in Cancer. <i>Biomolecules</i> , 2023, 13, 561.	1.8	4
4260	Genome-Wide Splicing Quantitative Expression Locus Analysis Identifies Causal Risk Variants for Non-Small Cell Lung Cancer. <i>Cancer Research</i> , 2023, 83, 1742-1756.	0.4	1
4261	Control of RNA degradation in cell fate decision. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	3
4262	Post-transcriptional control of hemostatic genes: mechanisms and emerging therapeutic concepts in thrombo-inflammatory disorders. <i>Cardiovascular Research</i> , 0, , .	1.8	3
4263	Global detection of human variants and isoforms by deep proteome sequencing. <i>Nature Biotechnology</i> , 2023, 41, 1776-1786.	9.4	43
4266	An ancient testis-specific IQ motif-containing H gene regulates specific transcript isoform expression during spermatogenesis. <i>Development (Cambridge)</i> , 2023, 150, .	1.2	1
4267	Abnormalities in intron retention characterize patients with systemic lupus erythematosus. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
4268	Identification of a comprehensive alternative splicing function during epithelial-mesenchymal transition. <i>IScience</i> , 2023, 26, 106517.	1.9	1
4269	p53 and p63 Proteoforms Derived from Alternative Splicing Possess Differential Seroreactivity in Colorectal Cancer with Distinct Diagnostic Ability from the Canonical Proteins. <i>Cancers</i> , 2023, 15, 2102.	1.7	9
4270	Comparison of alternative splicing (AS) events in adipose tissue of polled dorset versus small tail han sheep. <i>Heliyon</i> , 2023, 9, e14938.	1.4	2
4271	De novo full-length transcriptome analysis of two ecotypes of <i>Phragmites australis</i> (swamp reed and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf adaptation to desert environments. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
4272	Splicing complexity as a pivotal feature of alternative exons in mammalian species. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
4273	SRSF5 Regulates the Expression of BQ323636.1 to Modulate Tamoxifen Resistance in ER-Positive Breast Cancer. <i>Cancers</i> , 2023, 15, 2271.	1.7	1
4274	Definition of the transcriptional units of inherited retinal disease genes by meta-analysis of human retinal transcriptome data. <i>BMC Genomics</i> , 2023, 24, .	1.2	0

#	ARTICLE	IF	CITATIONS
4276	Large-scale long terminal repeat insertions produced a significant set of novel transcripts in cotton. <i>Science China Life Sciences</i> , 2023, 66, 1711-1724.	2.3	3
4282	Deciphering DNA variant-associated aberrant splicing with the aid of RNA sequencing. <i>Nature Genetics</i> , 2023, 55, 732-733.	9.4	0
4294	The Human Genome and Neonatal Care. , 2024, , 309-321.e4.		0
4312	Fortuna Detects Novel Splicing in Drosophila scRNASeq Data. , 2023, , .		0
4315	Alternative Splicing and Cancer. , 2023, , 61-104.		0
4386	Reference-guided search for open reading frames. <i>Nature Computational Science</i> , 2023, 3, 667-668.	3.8	0
4403	Post-transcriptional regulation of myeloid cell-mediated inflammatory responses. <i>Advances in Immunology</i> , 2023, , .	1.1	0
4419	Decoding the role of aberrant RNA alternative splicing in hepatocellular carcinoma: a comprehensive review. <i>Journal of Cancer Research and Clinical Oncology</i> , 2023, 149, 17691-17708.	1.2	0
4421	Revisiting the development of cerebellar inhibitory interneurons in the light of single-cell genetic analyses. <i>Histochemistry and Cell Biology</i> , 0, , .	0.8	1
4426	The function of alternative splicing in the proteome: rewiring protein interactomes to put old functions into new contexts. <i>Nature Structural and Molecular Biology</i> , 2023, 30, 1844-1856.	3.6	0
4465	Rigor and reproducibility of RNA sequencing analyses. , 2024, , 211-245.		0
4467	Review of gene expression using microarray and RNA-seq. , 2024, , 159-187.		0
4479	RNA-mediated pathogenic mechanisms in Huntington's disease. , 2024, , 135-158.		0
4503	RNA binding proteins in cardiovascular development and disease. <i>Current Topics in Developmental Biology</i> , 2024, , 51-119.	1.0	0
4507	Dissecting the Immune System through Gene Regulation. <i>Advances in Experimental Medicine and Biology</i> , 2024, , 219-235.	0.8	0