Benjamin J Blencowe

List of Publications by Year
in descending order

126	26,140	16437 64	19726 117
papers	citations	h-index	g-index

138	138	138	33048
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Deep surveying of alternative splicing complexity in the human transcriptome by high-throughput sequencing. Nature Genetics, 2008, 40, 1413-1415.	9.4	3,243
2	The Nuclear-Retained Noncoding RNA MALAT1 Regulates Alternative Splicing by Modulating SR Splicing Factor Phosphorylation. Molecular Cell, 2010, 39, 925-938.	4.5	1,906
3	Transcriptomic analysis of autistic brain reveals convergent molecular pathology. Nature, 2011, 474, 380-384.	13.7	1,654
4	A compendium of RNA-binding motifs for decoding gene regulation. Nature, 2013, 499, 172-177.	13.7	1,281
5	The human splicing code reveals new insights into the genetic determinants of disease. Science, 2015, 347, 1254806.	6.0	1,053
6	Alternative Splicing: New Insights from Global Analyses. Cell, 2006, 126, 37-47.	13.5	986
7	Regulation of Alternative Splicing by Histone Modifications. Science, 2010, 327, 996-1000.	6.0	931
8	The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. Science, 2012, 338, 1587-1593.	6.0	905
9	Deciphering the splicing code. Nature, 2010, 465, 53-59.	13.7	781
10	Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism. Nature, 2016, 540, 423-427.	13.7	603
11	Exonic splicing enhancers: mechanism of action, diversity and role in human genetic diseases. Trends in Biochemical Sciences, 2000, 25, 106-110.	3.7	591
12	Widespread intron retention in mammals functionally tunes transcriptomes. Genome Research, 2014, 24, 1774-1786.	2.4	554
13	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. Cell, 2014, 159, 1511-1523.	13.5	546
14	An RNA map predicting Nova-dependent splicing regulation. Nature, 2006, 444, 580-586.	13.7	477
15	Alternative Splicing Regulatory Networks: Functions, Mechanisms, and Evolution. Molecular Cell, 2019, 76, 329-345.	4.5	446
16	Alternative Splicing in the Mammalian Nervous System: Recent Insights into Mechanisms and Functional Roles. Neuron, 2015, 87, 14-27.	3.8	391
17	Dynamic Integration of Splicing within Gene Regulatory Pathways. Cell, 2013, 152, 1252-1269.	13.5	371
18	Tissue-Specific Alternative Splicing Remodels Protein-Protein Interaction Networks. Molecular Cell, 2012, 46, 884-892.	4.5	366

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19	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. Nature, 2013, 498, 241-245.	13.7	326
20	An Alternative Splicing Switch Regulates Embryonic Stem Cell Pluripotency and Reprogramming. Cell, 2011, 147, 132-146.	13.5	325
21	Global Mapping of Human RNA-RNA Interactions. Molecular Cell, 2016, 62, 618-626.	4.5	321
22	An atlas of alternative splicing profiles and functional associations reveals new regulatory programs and genes that simultaneously express multiple major isoforms. Genome Research, 2017, 27, 1759-1768.	2.4	316
23	Revealing Global Regulatory Features of Mammalian Alternative Splicing Using a Quantitative Microarray Platform. Molecular Cell, 2004, 16, 929-941.	4.5	288
24	The functional landscape of mouse gene expression. Journal of Biology, 2004, 3, 21.	2.7	259
25	5-hmC in the brain is abundant in synaptic genes and shows differences at the exon-intron boundary. Nature Structural and Molecular Biology, 2012, 19, 1037-1043.	3.6	221
26	Regulation of Vertebrate Nervous System Alternative Splicing and Development by an SR-Related Protein. Cell, 2009, 138, 898-910.	13.5	195
27	Quantitative microarray profiling provides evidence against widespread coupling of alternative splicing with nonsense-mediated mRNA decay to control gene expression. Genes and Development, 2006, 20, 153-158.	2.7	192
28	Regulation of Multiple Core Spliceosomal Proteins by Alternative Splicing-Coupled Nonsense-Mediated mRNA Decay. Molecular and Cellular Biology, 2008, 28, 4320-4330.	1.1	183
29	Regulation of alternative splicing by the core spliceosomal machinery. Genes and Development, 2011, 25, 373-384.	2.7	181
30	A Comparative Transcriptomic Analysis Reveals Conserved Features of Stem Cell Pluripotency in Planarians and Mammals. Stem Cells, 2012, 30, 1734-1745.	1.4	181
31	QAPA: a new method for the systematic analysis of alternative polyadenylation from RNA-seq data. Genome Biology, 2018, 19, 45.	3.8	176
32	Smg1 is required for embryogenesis and regulates diverse genes via alternative splicing coupled to nonsense-mediated mRNA decay. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12186-12191.	3.3	156
33	Alternative splicing: decoding an expansive regulatory layer. Current Opinion in Cell Biology, 2012, 24, 323-332.	2.6	151
34	Global Profiling and Molecular Characterization of Alternative Splicing Events Misregulated in Lung Cancer. Molecular and Cellular Biology, 2011, 31, 138-150.	1.1	149
35	Brain-expressed exons under purifying selection are enriched for de novo mutations in autism spectrum disorder. Nature Genetics, 2014, 46, 742-747.	9.4	149
36	Global analysis of alternative splicing during T-cell activation. Rna, 2007, 13, 563-572.	1.6	147

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37	Multilayered Control of Alternative Splicing Regulatory Networks by Transcription Factors. Molecular Cell, 2017, 65, 539-553.e7.	4.5	143
38	Current-generation high-throughput sequencing: deepening insights into mammalian transcriptomes. Genes and Development, 2009, 23, 1379-1386.	2.7	140
39	Regulated aggregative multicellularity in a close unicellular relative of metazoa. ELife, 2013, 2, e01287.	2.8	139
40	The Relationship between Alternative Splicing and Proteomic Complexity. Trends in Biochemical Sciences, 2017, 42, 407-408.	3.7	138
41	Genome-wide analysis of alternative splicing in Caenorhabditis elegans. Genome Research, 2011, 21, 342-348.	2.4	137
42	Alternative splicing of conserved exons is frequently species-specific in human and mouse. Trends in Genetics, 2005, 21, 73-77.	2.9	134
43	A Global Regulatory Mechanism for Activating an Exon Network Required for Neurogenesis. Molecular Cell, 2014, 56, 90-103.	4.5	131
44	Global analysis of alternative splicing differences between humans and chimpanzees. Genes and Development, 2007, 21, 2963-2975.	2.7	130
45	An alternative splicing event amplifies evolutionary differences between vertebrates. Science, 2015, 349, 868-873.	6.0	128
46	Autism spectrum disorder: insights into convergent mechanisms from transcriptomics. Nature Reviews Genetics, 2019, 20, 51-63.	7.7	128
47	Cross-Regulation between an Alternative Splicing Activator and a Transcription Repressor Controls Neurogenesis. Molecular Cell, 2011, 43, 843-850.	4.5	124
48	Misregulation of an Activity-Dependent Splicing Network as a Common Mechanism Underlying Autism Spectrum Disorders. Molecular Cell, 2016, 64, 1023-1034.	4.5	121
49	Efficient and Accurate Quantitative Profiling of Alternative Splicing Patterns of Any Complexity on a Laptop. Molecular Cell, 2018, 72, 187-200.e6.	4.5	121
50	Regulatory Expansion in Mammals of Multivalent hnRNP Assemblies that Globally Control Alternative Splicing. Cell, 2017, 170, 324-339.e23.	13.5	119
51	Essential roles for the splicing regulator nSR100/SRRM4 during nervous system development. Genes and Development, 2015, 29, 746-759.	2.7	115
52	The ribosome-engaged landscape of alternative splicing. Nature Structural and Molecular Biology, 2016, 23, 1117-1123.	3.6	115
53	SR-related proteins and the processing of messenger RNA precursors. Biochemistry and Cell Biology, 1999, 77, 277-291.	0.9	111
54	Compound heterozygous mutations in the noncoding RNU4ATAC cause Roifman Syndrome by disrupting minor intron splicing. Nature Communications, 2015, 6, 8718.	5.8	104

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55	The SRm160/300 splicing coactivator subunits. Rna, 2000, 6, 111-120.	1.6	99
56	An extensive program of periodic alternative splicing linked to cell cycle progression. ELife, 2016, 5, .	2.8	99
57	Functional coordination of alternative splicing in the mammalian central nervous system. Genome Biology, 2007, 8, R108.	13.9	97
58	Actionable Cytopathogenic Host Responses of Human Alveolar Type 2 Cells to SARS-CoV-2. Molecular Cell, 2020, 80, 1104-1122.e9.	4.5	94
59	A systematic analysis of intronic sequences downstream of 5â€² splice sites reveals a widespread role for U-rich motifs and TIA1/TIAL1 proteins in alternative splicing regulation. Genome Research, 2008, 18, 1247-1258.	2.4	90
60	Alternative splicing networks regulated by signaling in human T cells. Rna, 2012, 18, 1029-1040.	1.6	90
61	SRm160 Splicing Coactivator Promotes Transcript 3â€²-End Cleavage. Molecular and Cellular Biology, 2002, 22, 148-160.	1.1	87
62	Genome-wide CRISPR-Cas9 Interrogation of Splicing Networks Reveals a Mechanism for Recognition of Autism-Misregulated Neuronal Microexons. Molecular Cell, 2018, 72, 510-524.e12.	4.5	86
63	Genetic interaction mapping and exon-resolution functional genomics with a hybrid Cas9â€“Cas12a platform. Nature Biotechnology, 2020, 38, 638-648.	9.4	85
64	A germline mutation in SRRM2, a splicing factor gene, is implicated in papillary thyroid carcinoma predisposition. Scientific Reports, 2015, 5, 10566.	1.6	83
65	Myc and SAGA rewire an alternative splicing network during early somatic cell reprogramming. Genes and Development, 2015, 29, 803-816.	2.7	73
66	Stromal Fat4 acts non-autonomously with Dachsous1/2 to restrict the nephron progenitor pool. Development (Cambridge), 2015, 142, 2564-73.	1.2	70
67	Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. Molecular Cell, 2020, 77, 1176-1192.e16.	4.5	69
68	SARS-CoV-2 nucleocapsid protein binds host mRNAs and attenuates stress granules to impair host stress response. IScience, 2022, 25, 103562.	1.9	68
69	Epstein-Barr Virus EBNA1 Protein Regulates Viral Latency through Effects on let-7 MicroRNA and Dicer. Journal of Virology, 2014, 88, 11166-11177.	1.5	67
70	Networking in a global world: Establishing functional connections between neural splicing regulators and their target transcripts. Rna, 2011, 17, 775-791.	1.6	65
71	A novel protein domain in an ancestral splicing factor drove the evolution of neural microexons. Nature Ecology and Evolution, 2019, 3, 691-701.	3.4	63
72	Differential contribution of steadyâ€state <scp>RNA</scp> and active transcription in chromatin organization. EMBO Reports, 2019, 20, e48068.	2.0	61

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73	Characterization of disease-associated mutations affecting an exonic splicing enhancer and two cryptic splice sites in exon 13 of the cystic fibrosis transmembrane conductance regulator gene. Human Molecular Genetics, 2003, 12, 2031-2040.	1.4	60
74	Inferring global levels of alternative splicing isoforms using a generative model of microarray data. Bioinformatics, 2006, 22, 606-613.	1.8	57
75	MECP2 Is Post-transcriptionally Regulated during Human Neurodevelopment by Combinatorial Action of RNA-Binding Proteins and miRNAs. Cell Reports, 2016, 17, 720-734.	2.9	54
76	Control of embryonic stem cell self-renewal and differentiation via coordinated alternative splicing and translation of YY2. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12360-12367.	3.3	54
77	The Long Noncoding RNA Pnky Is a Trans-acting Regulator of Cortical Development InÂVivo. Developmental Cell, 2019, 49, 632-642.e7.	3.1	52
78	SnapShot: The Splicing Regulatory Machinery. Cell, 2008, 133, 192-192.e1.	13.5	51
79	The alternative splicing factor Nova2 regulates vascular development and lumen formation. Nature Communications, 2015, 6, 8479.	5.8	50
80	Gomafu lncRNA knockout mice exhibit mild hyperactivity with enhanced responsiveness to the psychostimulant methamphetamine. Scientific Reports, 2016, 6, 27204.	1.6	50
81	Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. ELife, 2016, 5, .	2.8	48
82	SR-related proteins and the processing of messenger RNA precursors. Biochemistry and Cell Biology, 1999, 77, 277-91.	0.9	48
83	Structure and function of the PWI motif: a novel nucleic acid-binding domain that facilitates pre-mRNA processing. Genes and Development, 2003, 17, 461-475.	2.7	47
84	Shifts in Ribosome Engagement Impact Key Gene Sets in Neurodevelopment and Ubiquitination in Rett Syndrome. Cell Reports, 2020, 30, 4179-4196.e11.	2.9	46
85	Major Roles for Pyrimidine Dimers, Nucleotide Excision Repair, and ATR in the Alternative Splicing Response to UV Irradiation. Cell Reports, 2017, 18, 2868-2879.	2.9	41
86	Distinct Factor Requirements for Exonic Splicing Enhancer Function and Binding of U2AF to the Polypyrimidine Tract. Journal of Biological Chemistry, 1999, 274, 35074-35079.	1.6	40
87	Multiple interactions between SRm160 and SR family proteins in enhancer-dependent splicing and development of C. elegans. Current Biology, 2001, 11, 1923-1933.	1.8	38
88	Microexons: at the nexus of nervous system development, behaviour and autism spectrum disorder. Current Opinion in Genetics and Development, 2020, 65, 22-33.	1.5	38
89	An Evolutionarily Conserved Role for SRm160 in 3â€²-End Processing That Functions Independently of Exon Junction Complex Formation. Journal of Biological Chemistry, 2003, 278, 44153-44160.	1.6	33
90	Next-generation RNA Sequencing of Archival Formalin-fixed Paraffin-embedded Urothelial Bladder Cancer. European Urology, 2014, 66, 982-986.	0.9	33

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91	The RNA-binding profile of Acinus, a peripheral component of the exon junction complex, reveals its role in splicing regulation. Rna, 2016, 22, 1411-1426.	1.6	33
92	A multiplexed, next generation sequencing platform for high-throughput detection of SARS-CoV-2. Nature Communications, 2021, 12, 1405.	5.8	33
93	Systematic mapping of nuclear domain-associated transcripts reveals speckles and lamina as hubs of functionally distinct retained introns. Molecular Cell, 2022, 82, 1035-1052.e9.	4.5	31
94	Response to â€œThe Reality of Pervasive Transcriptionâ€• PLoS Biology, 2011, 9, e1001102.	2.6	30
95	Identification of small molecule modulators of HIV-1 Tat and Rev protein accumulation. Retrovirology, 2017, 14, 7.	0.9	30
96	Technologies for the Global Discovery and Analysis of Alternative Splicing. Advances in Experimental Medicine and Biology, 2007, 623, 64-84.	0.8	30
97	Proteomic Analysis of SRm160-containing Complexes Reveals a Conserved Association with Cohesin. Journal of Biological Chemistry, 2005, 280, 42227-42236.	1.6	28
98	The PWI motif: a new protein domain in splicing factors. Trends in Biochemical Sciences, 1999, 24, 179-180.	3.7	25
99	Splicing Regulation: The Cell Cycle Connection. Current Biology, 2003, 13, R149-R151.	1.8	25
100	A Dynamic Splicing Program Ensures Proper Synaptic Connections in the Developing Cerebellum. Cell Reports, 2020, 31, 107703.	2.9	25
101	Nuclear compartmentalization of TERT mRNA and TUG1 lncRNA is driven by intron retention. Nature Communications, 2021, 12, 3308.	5.8	25
102	Model-based detection of alternative splicing signals. Bioinformatics, 2010, 26, i325-i333.	1.8	22
103	The transcriptional and splicing landscape of intestinal organoids undergoing nutrient starvation or endoplasmic reticulum stress. BMC Genomics, 2016, 17, 680.	1.2	21
104	Identification and characterization of RED120: A conserved PWI domain protein with links to splicing and 3â€²-end formation. FEBS Letters, 2007, 581, 3087-3097.	1.3	20
105	Functional Genomics Evidence Unearths New Moonlighting Roles of Outer Ring Coat Nucleoporins. Scientific Reports, 2014, 4, 4655.	1.6	20
106	ARGLU1 is a transcriptional coactivator and splicing regulator important for stress hormone signaling and development. Nucleic Acids Research, 2019, 47, 2856-2870.	6.5	20
107	Differential contribution of transcriptomic regulatory layers in the definition of neuronal identity. Nature Communications, 2021, 12, 335.	5.8	20
108	Transcription: Surprising Role for an Elusive Small Nuclear RNA. Current Biology, 2002, 12, R147-R149.	1.8	17

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109	An exon-centric perspective¹Canadian Society of Molecular Biosciences (CSMB) Senior Investigator Award. Biochemistry and Cell Biology, 2012, 90, 603-612.	0.9	13
110	Neuronal-specific microexon splicing of TAF1 mRNA is directly regulated by SRRM4/nSR100. RNA Biology, 2020, 17, 62-74.	1.5	11
111	An activator of G protein-coupled receptor and MEK1/2-ERK1/2 signaling inhibits HIV-1 replication by altering viral RNA processing. PLoS Pathogens, 2020, 16, e1008307.	2.1	8
112	RNA in control. Nature, 2007, 447, 391-393.	13.7	7
113	Analysis of combinatorial CRISPR screens with the Orthrus scoring pipeline. Nature Protocols, 2021, 16, 4766-4798.	5.5	7
114	Post-transcriptional gene regulation: RNA-protein interactions, RNA processing, mRNA stability and localization. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 545-8.	0.7	6
115	POST-TRANSCRIPTIONAL GENE REGULATION: RNA-PROTEIN INTERACTIONS, RNA PROCESSING, MRNA STABILITY AND LOCALIZATION. , 2008, , .		5
116	Definition of germ layer cell lineage alternative splicing programs reveals a critical role for Quaking in specifying cardiac cell fate. Nucleic Acids Research, 2022, 50, 5313-5334.	6.5	5
117	Orchestrating Ribosomal Subunit Coordination to Control Stem Cell Fate. Cell Stem Cell, 2018, 22, 471-473.	5.2	3
118	Reflections for the 20th anniversary issue ofRNAjournal. Rna, 2015, 21, 573-575.	1.6	2
119	Systematic Genome-Scale Identification of Host Factors for SARS-CoV-2 Infection Across Models Yields a Core Single Gene Dependency; <i>Ace2</i>. SSRN Electronic Journal, 0, , .	0.4	0
120	Alternative Splicing in the Mammalian Nervous System. FASEB Journal, 2009, 23, 422.2.	0.2	0
121	Shifts in Ribosome Engagement Impact Key Gene Sets in Neurodevelopment and Ubiquitination in Rett Syndrome. SSRN Electronic Journal, 0, , .	0.4	0
122	Title is missing!. , 2020, 16, e1008307.		0
123	Title is missing!. , 2020, 16, e1008307.		0
124	Title is missing!. , 2020, 16, e1008307.		0
125	Title is missing!. , 2020, 16, e1008307.		0
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