

Brenton R Graveley

List of Publications by Year in descending order

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116
papers

20,980
citations

25034
57
h-index

20961
115
g-index

131
all docs

131
docs citations

131
times ranked

25242
citing authors

#	ARTICLE	IF	CITATIONS
1	Expansion of the eukaryotic proteome by alternative splicing. Nature, 2010, 463, 457-463.	27.8	1,787
2	The developmental transcriptome of <i>Drosophila melanogaster</i> . Nature, 2011, 471, 473-479.	27.8	1,379
3	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
4	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. Science, 2010, 330, 1787-1797.	12.6	1,124
5	Alternative splicing: increasing diversity in the proteomic world. Trends in Genetics, 2001, 17, 100-107.	6.7	1,120
6	Sorting out the complexity of SR protein functions. Rna, 2000, 6, 1197-1211.	3.5	922
7	RNA-Guided RNA Cleavage by a CRISPR RNA-Cas Protein Complex. Cell, 2009, 139, 945-956.	28.9	919
8	Genome-wide Analysis of <i>Drosophila</i> Circular RNAs Reveals Their Structural and Sequence Properties and Age-Dependent Neural Accumulation. Cell Reports, 2014, 9, 1966-1980.	6.4	866
9	Codon Optimality Is a Major Determinant of mRNA Stability. Cell, 2015, 160, 1111-1124.	28.9	792
10	A large-scale binding and functional map of human RNA-binding proteins. Nature, 2020, 583, 711-719.	27.8	667
11	Diversity and dynamics of the <i>Drosophila</i> transcriptome. Nature, 2014, 512, 393-399.	27.8	647
12	Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. Molecular Cell, 2018, 70, 854-867.e9.	9.7	408
13	Regulatory divergence in <i>Drosophila</i> revealed by mRNA-seq. Genome Research, 2010, 20, 816-825.	5.5	385
14	Dynamic Integration of Splicing within Gene Regulatory Pathways. Cell, 2013, 152, 1252-1269.	28.9	371
15	Genomewide characterization of non-polyadenylated RNAs. Genome Biology, 2011, 12, R16.	9.6	365
16	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
17	Identification of alternative splicing regulators by RNA interference in <i>Drosophila</i> . Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15974-15979.	7.1	275
18	Essential Features and Rational Design of CRISPR RNAs that Function with the Cas RAMP Module Complex to Cleave RNAs. Molecular Cell, 2012, 45, 292-302.	9.7	275

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19	Mutually Exclusive Splicing of the Insect Dscam Pre-mRNA Directed by Competing Intronic RNA Secondary Structures. <i>Cell</i> , 2005, 123, 65-73.	28.9	271
20	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2011, 21, 301-314.	5.5	235
21	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. <i>Cell</i> , 2019, 178, 107-121.e18.	28.9	224
22	RNA structure and the mechanisms of alternative splicing. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 373-379.	3.3	222
23	Genome-wide analysis of promoter architecture in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011, 21, 182-192.	5.5	211
24	Conservation of an RNA regulatory map between <i>Drosophila</i> and mammals. <i>Genome Research</i> , 2011, 21, 193-202.	5.5	208
25	Distal Alternative Last Exons Localize mRNAs to Neural Projections. <i>Molecular Cell</i> , 2016, 61, 821-833.	9.7	208
26	The PIWI proteins SMEDWI-2 and SMEDWI-3 are required for stem cell function and piRNA expression in planarians. <i>Rna</i> , 2008, 14, 1174-1186.	3.5	207
27	Global Patterns of Tissue-Specific Alternative Polyadenylation in <i>Drosophila</i> . <i>Cell Reports</i> , 2012, 1, 277-289.	6.4	201
28	mRNA Deadenylation Is Coupled to Translation Rates by the Differential Activities of Ccr4-Not Nucleases. <i>Molecular Cell</i> , 2018, 70, 1089-1100.e8.	9.7	182
29	Arginine/Serine-Rich Domains of SR Proteins Can Function as Activators of Pre-mRNA Splicing. <i>Molecular Cell</i> , 1998, 1, 765-771.	9.7	179
30	Tempo and mode of regulatory evolution in <i>Drosophila</i> . <i>Genome Research</i> , 2014, 24, 797-808.	5.5	177
31	Genome-wide identification of zero nucleotide recursive splicing in <i>Drosophila</i> . <i>Nature</i> , 2015, 521, 376-379.	27.8	169
32	Analysis of the Human Neurexin Genes: Alternative Splicing and the Generation of Protein Diversity. <i>Genomics</i> , 2002, 79, 587-597.	2.9	164
33	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , 2016, 17, 74.	8.8	160
34	A systematic analysis of the factors that determine the strength of pre-mRNA splicing enhancers. <i>EMBO Journal</i> , 1998, 17, 6747-6756.	7.8	148
35	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	5.5	147
36	Determining exon connectivity in complex mRNAs by nanopore sequencing. <i>Genome Biology</i> , 2015, 16, 204.	8.8	140

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37	Principles of RNA processing from analysis of enhanced CLIP maps for 150 RNA binding proteins. <i>Genome Biology</i> , 2020, 21, 90.	8.8	136
38	The majority of transcripts in the squid nervous system are extensively recoded by A-to-I RNA editing. <i>ELife</i> , 2015, 4, .	6.0	124
39	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
40	The role of U2AF35 and U2AF65 in enhancer-dependent splicing. <i>Rna</i> , 2001, 7, 806-818.	3.5	121
41	Resources for the Comprehensive Discovery of Functional RNA Elements. <i>Molecular Cell</i> , 2016, 61, 903-913.	9.7	118
42	microRNA-Seq reveals cocaine-regulated expression of striatal microRNAs. <i>Rna</i> , 2011, 17, 1529-1543.	3.5	113
43	The Genome of <i>Anopheles darlingi</i> , the main neotropical malaria vector. <i>Nucleic Acids Research</i> , 2013, 41, 7387-7400.	14.5	102
44	Alternative Splicing of the <i>Drosophila</i> <i>Dscam</i> Pre-mRNA Is Both Temporally and Spatially Regulated. <i>Genetics</i> , 2001, 159, 599-608.	2.9	100
45	Regulation of RNA editing by RNA-binding proteins in human cells. <i>Communications Biology</i> , 2019, 2, 19.	4.4	97
46	Global analysis of <i>trans</i> -splicing in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12975-12979.	7.1	92
47	A regulator of <i>Dscam</i> mutually exclusive splicing fidelity. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1134-1140.	8.2	90
48	RS domains contact the pre-mRNA throughout spliceosome assembly. <i>Trends in Biochemical Sciences</i> , 2005, 30, 115-118.	7.5	88
49	The organization and evolution of the Dipteran and Hymenopteran Down syndrome cell adhesion molecule (<i>Dscam</i>) genes. <i>Rna</i> , 2004, 10, 1499-1506.	3.5	87
50	Cas4 Nucleases Define the PAM, Length, and Orientation of DNA Fragments Integrated at CRISPR Loci. <i>Molecular Cell</i> , 2018, 70, 814-824.e6.	9.7	85
51	Probabilistic Splicing of <i>Dscam1</i> Establishes Identity at the Level of Single Neurons. <i>Cell</i> , 2013, 155, 1166-1177.	28.9	84
52	Gene expression analysis of human induced pluripotent stem cell-derived neurons carrying copy number variants of chromosome 15q11-q13.1. <i>Molecular Autism</i> , 2014, 5, 44.	4.9	83
53	Exon-specific RNAi: A tool for dissecting the functional relevance of alternative splicing. <i>Rna</i> , 2002, 8, 718-724.	3.5	82
54	The origins and implications of Alternative splicing. <i>Trends in Genetics</i> , 2004, 20, 1-4.	6.7	82

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55	The three major types of CRISPR-Cas systems function independently in CRISPR RNA biogenesis in <i>S. thermophilus</i> . Molecular Microbiology, 2014, 93, 98-112.	2.5	81
56	Regulation of alternative splicing in <i>Drosophila</i> by 56 RNA binding proteins. Genome Research, 2015, 25, 1771-1780.	5.5	77
57	Poison Exon Splicing Regulates a Coordinated Network of SR Protein Expression during Differentiation and Tumorigenesis. Molecular Cell, 2020, 80, 648-665.e9.	9.7	76
58	MicroRNAs from the Planarian <i>Schmidtea mediterranea</i> : A model system for stem cell biology. Rna, 2006, 12, 1640-1649.	3.5	71
59	Vex-seq: high-throughput identification of the impact of genetic variation on pre-mRNA splicing efficiency. Genome Biology, 2018, 19, 71.	8.8	66
60	RBP-Maps enables robust generation of splicing regulatory maps. Rna, 2019, 25, 193-204.	3.5	63
61	Power sequencing. Nature, 2008, 453, 1197-1198.	27.8	60
62	Competing RNA secondary structures are required for mutually exclusive splicing of the <i>Dscam</i> exon 6 cluster. Rna, 2011, 17, 222-229.	3.5	54
63	Effects of cocaine and withdrawal on the mouse nucleus accumbens transcriptome. Genes, Brain and Behavior, 2013, 12, 21-33.	2.2	49
64	The iStem, a Long-Range RNA Secondary Structure Element Required for Efficient Exon Inclusion in the <i>Drosophila Dscam</i> Pre-mRNA. Molecular and Cellular Biology, 2005, 25, 10251-10260.	2.3	48
65	Transcriptome Analysis Reveals Strain-Specific and Conserved Stemness Genes in <i>Schmidtea mediterranea</i> . PLoS ONE, 2012, 7, e34447.	2.5	48
66	Three CRISPR-Cas immune effector complexes coexist in <i>Pyrococcus furiosus</i> . Rna, 2015, 21, 1147-1158.	3.5	48
67	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.	5.9	47
68	Deep sequencing identifies new and regulated microRNAs in <i>Schmidtea mediterranea</i> . Rna, 2009, 15, 1483-1491.	3.5	46
69	Sequencing and Structure Probing of Long RNAs Using MarathonRT: A Next-Generation Reverse Transcriptase. Journal of Molecular Biology, 2020, 432, 3338-3352.	4.2	46
70	SR proteins are "locators" of the RNA splicing machinery. Current Biology, 1999, 9, R6-R7.	3.9	44
71	Genomic Imprinting Absent in <i>Drosophila melanogaster</i> Adult Females. Cell Reports, 2012, 2, 69-75.	6.4	44
72	A computational and experimental approach toward a priori identification of alternatively spliced exons. Rna, 2004, 10, 1838-1844.	3.5	41

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73	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. <i>Nature Communications</i> , 2019, 10, 1338.	12.8	38
74	Characterization of U2AF 6 , a Splicing Factor Related to U2AF 35. <i>Molecular and Cellular Biology</i> , 2002, 22, 221-230.	2.3	37
75	Arginine/serine repeats are sufficient to constitute a splicing activation domain. <i>Nucleic Acids Research</i> , 2003, 31, 6502-6508.	14.5	36
76	Massive expansions of <i>Dscam</i> splicing diversity via staggered homologous recombination during arthropod evolution. <i>Rna</i> , 2010, 16, 91-105.	3.5	36
77	Molecular Mechanisms and Evolutionary Processes Contributing to Accelerated Divergence of Gene Expression on the <i>Drosophila</i> X Chromosome. <i>Molecular Biology and Evolution</i> , 2015, 32, 2605-2615.	8.9	35
78	The haplo-spliceo-transcriptome: common variations in alternative splicing in the human population. <i>Trends in Genetics</i> , 2008, 24, 5-7.	6.7	34
79	Programmable plasmid interference by the CRISPR-Cas system in <i>Thermococcus kodakarensis</i> . <i>RNA Biology</i> , 2013, 10, 828-840.	3.1	34
80	Evolution of splicing regulatory networks in <i>Drosophila</i> . <i>Genome Research</i> , 2014, 24, 786-796.	5.5	34
81	Role of free DNA ends and protospacer adjacent motifs for CRISPR DNA uptake in <i>Pyrococcus furiosus</i> . <i>Nucleic Acids Research</i> , 2017, 45, 11281-11294.	14.5	34
82	Complex Alternative Splicing. <i>Advances in Experimental Medicine and Biology</i> , 2007, 623, 50-63.	1.6	34
83	Identification of neoblast- and regeneration-specific miRNAs in the planarian <i>Schmidtea mediterranea</i> . <i>Rna</i> , 2013, 19, 1394-1404.	3.5	33
84	Enhancer-dependent 5' Splice Site Control of fruitless Pre-mRNA Splicing. <i>Journal of Biological Chemistry</i> , 2003, 278, 22740-22747.	3.4	32
85	Sex, AGility, and the Regulation of Alternative Splicing. <i>Cell</i> , 2002, 109, 409-412.	28.9	31
86	Assessing long-distance RNA sequence connectivity via RNA-templated DNA-DNA ligation. <i>ELife</i> , 2015, 4, .	6.0	29
87	Extensive cross-regulation of post-transcriptional regulatory networks in <i>Drosophila</i> . <i>Genome Research</i> , 2015, 25, 1692-1702.	5.5	24
88	RNA Matchmaking: Finding Cellular Pairing Partners. <i>Molecular Cell</i> , 2016, 63, 186-189.	9.7	24
89	Circuitous Route to Transcription Regulation. <i>Molecular Cell</i> , 2013, 51, 705-706.	9.7	23
90	Complete Genome Sequence of Industrial Dairy Strain <i>Streptococcus thermophilus</i> DGCC 7710. <i>Genome Announcements</i> , 2018, 6, .	0.8	22

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91	Alternative splicing: regulation without regulators. Nature Structural and Molecular Biology, 2009, 16, 13-15.	8.2	20
92	Primed CRISPR DNA uptake in Pyrococcus furiosus. Nucleic Acids Research, 2020, 48, 6120-6135.	14.5	20
93	CRISPR repeat sequences and relative spacing specify DNA integration by Pyrococcus furiosus Cas1 and Cas2. Nucleic Acids Research, 2019, 47, 7518-7531.	14.5	18
94	Coordinated control of splicing and translation. Nature Structural and Molecular Biology, 2005, 12, 1022-1023.	8.2	17
95	Restoration of Both Structure and Function to a Defective Poly(A) Site by in Vitro Selection. Journal of Biological Chemistry, 1996, 271, 33654-33663.	3.4	16
96	CRISPR DNA elements controlling site-specific spacer integration and proper repeat length by a Type II CRISPR-Cas system. Nucleic Acids Research, 2019, 47, 8632-8648.	14.5	15
97	Use of RNA interference to dissect the roles of trans-acting factors in alternative pre-mRNA splicing. Methods, 2005, 37, 341-344.	3.8	13
98	New Insights from Existing Sequence Data: Generating Breakthroughs without a Pipette. Molecular Cell, 2013, 49, 605-617.	9.7	12
99	Loss of DNA Mismatch Repair Imparts a Selective Advantage in Planarian Adult Stem Cells. PLoS ONE, 2011, 6, e21808.	2.5	12
100	A Protein Interaction Domain Contacts RNA in the Prespliceosome. Molecular Cell, 2004, 13, 302-304.	9.7	11
101	Exon-Specific RNA Interference: A Tool to Determine the Functional Relevance of Proteins Encoded by Alternatively Spliced mRNAs. , 2005, 309, 273-282.		11
102	Splicing up Pluripotency. Cell, 2011, 147, 22-24.	28.9	11
103	Small molecule control of pre-mRNA splicing. Rna, 2005, 11, 355-358.	3.5	10
104	Transcriptome and in Vitro Differentiation Profile of Human Embryonic Stem Cell Derived NKX2.1-Positive Neural Progenitors. Stem Cell Reviews and Reports, 2016, 12, 744-756.	5.6	9
105	Unique properties of spacer acquisition by the type III-A CRISPR-Cas system. Nucleic Acids Research, 2022, 50, 1562-1582.	14.5	8
106	Direct tracking of reverse-transcriptase speed and template sensitivity: implications for sequencing and analysis of long RNA molecules. Nucleic Acids Research, 2022, 50, 6980-6989.	14.5	8
107	Splicing from the Outside In. Molecular Cell, 2007, 27, 861-862.	9.7	7
108	Type III-A CRISPR systems as a versatile gene knockdown technology. Rna, 2022, 28, 1074-1088.	3.5	7

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109	Sixty years of genome biology. <i>Genome Biology</i> , 2013, 14, 113.	9.6	6
110	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.	0.3	1
111	Complete Genome Sequence of <i>Streptococcus rattus</i> JH145. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
112	Getting the Message Out. <i>Molecular Cell</i> , 2008, 31, 4-6.	9.7	0
113	Getting in the Loop: New Insights into the Mechanism of Poly(A) Site Recognition. <i>Structure</i> , 2011, 19, 279-281.	3.3	0
114	Musings on 20 years of <i>RNA</i> . <i>Rna</i> , 2015, 21, 506-507.	3.5	0
115	RNAs: dynamic and mutable. <i>Genome Biology</i> , 2017, 18, 226.	8.8	0
116	Alternative Splicing of Dscam. <i>FASEB Journal</i> , 2008, 22, 112.3.	0.5	0