

Christopher B Burge

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

85

papers

38,657

citations

55

h-index

96

g-index

96

ext. papers

44,913

ext. citations

18.7

avg, IF

7.47

L-index

#	Paper	IF	Citations
85	Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets. <i>Cell</i> , 2005 , 120, 15-20	56.2	9564
84	Most mammalian mRNAs are conserved targets of microRNAs. <i>Genome Research</i> , 2009 , 19, 92-105	9.7	5919
83	Prediction of mammalian microRNA targets. <i>Cell</i> , 2003 , 115, 787-98	56.2	4144
82	Alternative isoform regulation in human tissue transcriptomes. <i>Nature</i> , 2008 , 456, 470-6	50.4	3526
81	Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals. <i>Journal of Computational Biology</i> , 2004 , 11, 377-94	1.7	1253
80	Proliferating cells express mRNAs with shortened 3' untranslated regions and fewer microRNA target sites. <i>Science</i> , 2008 , 320, 1643-7	33.3	984
79	Analysis and design of RNA sequencing experiments for identifying isoform regulation. <i>Nature Methods</i> , 2010 , 7, 1009-15	21.6	934
78	The microRNAs of <i>Caenorhabditis elegans</i> . <i>Genes and Development</i> , 2003 , 17, 991-1008	12.6	926
77	Predictive identification of exonic splicing enhancers in human genes. <i>Science</i> , 2002 , 297, 1007-13	33.3	867
76	Splicing regulation: from a parts list of regulatory elements to an integrated splicing code. <i>Rna</i> , 2008 , 14, 802-13	5.8	682
75	An abundance of ubiquitously expressed genes revealed by tissue transcriptome sequence data. <i>PLoS Computational Biology</i> , 2009 , 5, e1000598	5	615
74	Evolutionary dynamics of gene and isoform regulation in Mammalian tissues. <i>Science</i> , 2012 , 338, 1593-9	33.3	587
73	Systematic identification and analysis of exonic splicing silencers. <i>Cell</i> , 2004 , 119, 831-45	56.2	522
72	Finding the genes in genomic DNA. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 346-54	8.1	418
71	Variation in alternative splicing across human tissues. <i>Genome Biology</i> , 2004 , 5, R74	18.3	378
70	A postnatal switch of CELF and MBNL proteins reprograms alternative splicing in the developing heart. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 20333-8	11.5	361
69	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-710	10.4	360

68	Transcriptome-wide regulation of pre-mRNA splicing and mRNA localization by muscleblind proteins. <i>Cell</i> , 2012 , 150, 710-24	56.2	347
67	An EMT-driven alternative splicing program occurs in human breast cancer and modulates cellular phenotype. <i>PLoS Genetics</i> , 2011 , 7, e1002218	6	318
66	Biased chromatin signatures around polyadenylation sites and exons. <i>Molecular Cell</i> , 2009 , 36, 245-54	17.6	310
65	Promoter directionality is controlled by U1 snRNP and polyadenylation signals. <i>Nature</i> , 2013 , 499, 360-3	50.4	294
64	Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. <i>Rna</i> , 2007 , 13, 1894-9	11.8	288
63	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	17.6	251
62	Classification of introns: U2-type or U12-type. <i>Cell</i> , 1997 , 91, 875-9	56.2	231
61	Identification and analysis of alternative splicing events conserved in human and mouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 2850-5	11.5	227
60	Widespread regulation of translation by elongation pausing in heat shock. <i>Molecular Cell</i> , 2013 , 49, 439-5	57.6	223
59	The EJC factor eIF4AIII modulates synaptic strength and neuronal protein expression. <i>Cell</i> , 2007 , 130, 179-91	56.2	223
58	SR proteins collaborate with 7SK and promoter-associated nascent RNA to release paused polymerase. <i>Cell</i> , 2013 , 153, 855-68	56.2	222
57	Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. <i>Molecular Cell</i> , 2018 , 70, 854-867.e9	17.6	212
56	RESCUE-ESE identifies candidate exonic splicing enhancers in vertebrate exons. <i>Nucleic Acids Research</i> , 2004 , 32, W187-90	20.1	212
55	A large-scale binding and functional map of human RNA-binding proteins. <i>Nature</i> , 2020 , 583, 711-719	50.4	198
54	Acquisition of a hybrid E/M state is essential for tumorigenicity of basal breast cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 7353-7362	11.5	186
53	Variation in sequence and organization of splicing regulatory elements in vertebrate genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 15700-5	11.5	184
52	Direct measurement of DNA affinity landscapes on a high-throughput sequencing instrument. <i>Nature Biotechnology</i> , 2011 , 29, 659-64	44.5	151
51	Distal Alternative Last Exons Localize mRNAs to Neural Projections. <i>Molecular Cell</i> , 2016 , 61, 821-33	17.6	143

50	Antagonistic regulation of mRNA expression and splicing by CELF and MBNL proteins. <i>Genome Research</i> , 2015 , 25, 858-71	9.7	125
49	3' UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts. <i>Genome Research</i> , 2013 , 23, 2078-90	9.7	123
48	Widespread inhibition of posttranscriptional splicing shapes the cellular transcriptome following heat shock. <i>Cell Reports</i> , 2014 , 7, 1362-1370	10.6	111
47	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. <i>Cell</i> , 2019 , 178, 107-121.e18	56.2	101
46	Patterns of intron gain and loss in fungi. <i>PLoS Biology</i> , 2004 , 2, e422	9.7	101
45	Quantitative visualization of alternative exon expression from RNA-seq data. <i>Bioinformatics</i> , 2015 , 31, 2400-2	7.2	99
44	Alternative splicing regulates vesicular trafficking genes in cardiomyocytes during postnatal heart development. <i>Nature Communications</i> , 2014 , 5, 3603	17.4	98
43	Protein-RNA Networks Regulated by Normal and ALS-Associated Mutant HNRNPA2B1 in the Nervous System. <i>Neuron</i> , 2016 , 92, 780-795	13.9	94
42	Distinct and shared functions of ALS-associated proteins TDP-43, FUS and TAF15 revealed by multisystem analyses. <i>Nature Communications</i> , 2016 , 7, 12143	17.4	94
41	Splice site strength-dependent activity and genetic buffering by poly-G runs. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 1094-100	17.6	92
40	Acidification of Tumor at Stromal Boundaries Drives Transcriptome Alterations Associated with Aggressive Phenotypes. <i>Cancer Research</i> , 2019 , 79, 1952-1966	10.1	86
39	A latent pro-survival function for the mir-290-295 cluster in mouse embryonic stem cells. <i>PLoS Genetics</i> , 2011 , 7, e1002054	6	83
38	A complex network of factors with overlapping affinities represses splicing through intronic elements. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 36-45	17.6	75
37	Enhanced CLIP Uncovers IMP Protein-RNA Targets in Human Pluripotent Stem Cells Important for Cell Adhesion and Survival. <i>Cell Reports</i> , 2016 , 15, 666-679	10.6	75
36	Alternative splicing of RNA triplets is often regulated and accelerates proteome evolution. <i>PLoS Biology</i> , 2012 , 10, e1001229	9.7	74
35	Meta-analysis of RNA-seq expression data across species, tissues and studies. <i>Genome Biology</i> , 2015 , 16, 287	18.3	71
34	RNA Sequence Context Effects Measured In Vitro Predict In Vivo Protein Binding and Regulation. <i>Molecular Cell</i> , 2016 , 64, 294-306	17.6	68
33	Inference of splicing regulatory activities by sequence neighborhood analysis. <i>PLoS Genetics</i> , 2006 , 2, e191	6	65

32	Musashi proteins are post-transcriptional regulators of the epithelial-luminal cell state. <i>ELife</i> , 2014 , 3, e03915	8.9	63
31	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
30	Widespread Shortening of 3' Untranslated Regions and Increased Exon Inclusion Are Evolutionarily Conserved Features of Innate Immune Responses to Infection. <i>PLoS Genetics</i> , 2016 , 12, e1006338	6	53
29	Transcriptome alterations in myotonic dystrophy skeletal muscle and heart. <i>Human Molecular Genetics</i> , 2019 , 28, 1312-1321	5.6	51
28	Assessment of the total number of human transcription units. <i>Genomics</i> , 2001 , 77, 71-8	4.3	49
27	Methods for time series analysis of RNA-seq data with application to human Th17 cell differentiation. <i>Bioinformatics</i> , 2014 , 30, i113-20	7.2	47
26	Recognition of unknown conserved alternatively spliced exons. <i>PLoS Computational Biology</i> , 2005 , 1, 113-22	5	38
25	Muscleblind-like 1 (Mbnl1) regulates pre-mRNA alternative splicing during terminal erythropoiesis. <i>Blood</i> , 2014 , 124, 598-610	2.2	35
24	Widespread Accumulation of Ribosome-Associated Isolated 3' UTRs in Neuronal Cell Populations of the Aging Brain. <i>Cell Reports</i> , 2018 , 25, 2447-2456.e4	10.6	34
23	The kinetics of pre-mRNA splicing in the genome and the influence of gene architecture. <i>ELife</i> , 2017 , 6,	8.9	33
22	A Requirement for Mena, an Actin Regulator, in Local mRNA Translation in Developing Neurons. <i>Neuron</i> , 2017 , 95, 608-622.e5	13.9	30
21	Origins and impacts of new mammalian exons. <i>Cell Reports</i> , 2015 , 10, 1992-2005	10.6	27
20	Exon-Mediated Activation of Transcription Starts. <i>Cell</i> , 2019 , 179, 1551-1565.e17	56.2	27
19	Identification of new branch points and unconventional introns in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2016 , 22, 1522-34	5.8	25
18	Widespread PERK-dependent repression of ER targets in response to ER stress. <i>Scientific Reports</i> , 2019 , 9, 4330	4.9	23
17	RNA Bind-n-Seq: Measuring the Binding Affinity Landscape of RNA-Binding Proteins. <i>Methods in Enzymology</i> , 2015 , 558, 465-493	1.7	18
16	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. <i>Nature Communications</i> , 2019 , 10, 1338	17.4	17
15	MicroRNA target finding by comparative genomics. <i>Methods in Molecular Biology</i> , 2014 , 1097, 457-76	1.4	17

14	Genomic analysis of RNA localization. <i>RNA Biology</i> , 2014 , 11, 1040-50	4.8	16
13	Computational and experimental analysis identifies many novel human genes. <i>Biochemical and Biophysical Research Communications</i> , 2000 , 272, 801-7	3.4	15
12	Alternative RNA splicing in the endothelium mediated in part by Rbfox2 regulates the arterial response to low flow. <i>ELife</i> , 2018 , 7,	8.9	14
11	Concentration-dependent splicing is enabled by Rbfox motifs of intermediate affinity. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 901-912	17.6	13
10	Numerous recursive sites contribute to accuracy of splicing in long introns in flies. <i>PLoS Genetics</i> , 2018 , 14, e1007588	6	9
9	Cotargeting among microRNAs in the brain. <i>Genome Research</i> , 2019 , 29, 1791-1804	9.7	8
8	Loss of LUC7L2 and U1 snRNP subunits shifts energy metabolism from glycolysis to OXPHOS. <i>Molecular Cell</i> , 2021 , 81, 1905-1919.e12	17.6	8
7	Sequence, Structure and Context Preferences of Human RNA Binding Proteins		5
6	Widespread shortening of 3' untranslated regions and increased exon inclusion are evolutionarily conserved features of innate immune responses to infection		2
5	Interactome analysis brings splicing into focus. <i>Genome Biology</i> , 2015 , 16, 135	18.3	1
4	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA		1
3	Secondary motifs enable concentration-dependent regulation by Rbfox family proteins		1
2	Widespread occurrence of hybrid internal-terminal exons in human transcriptomes.. <i>Science Advances</i> , 2022 , 8, eabk1752	14.3	0
1	Identification of mRNA Localization Motifs through Cell Fractionation and Alternative Splicing Analysis. <i>FASEB Journal</i> , 2015 , 29, 562.30	0.9	