

# Christopher B Burge

## List of Publications by Year in descending order

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Version: 2024-02-01

83  
papers

48,800  
citations

24978

57  
h-index

54797

84  
g-index

96  
all docs

96  
docs citations

96  
times ranked

56364  
citing authors

#	ARTICLE	IF	CITATIONS
1	Widespread occurrence of hybrid internal-terminal exons in human transcriptomes. <i>Science Advances</i> , 2022, 8, eabk1752.	4.7	10
2	Loss of LUC7L2 and U1 snRNP subunits shifts energy metabolism from glycolysis to OXPHOS. <i>Molecular Cell</i> , 2021, 81, 1905-1919.e12.	4.5	33
3	A large-scale binding and functional map of human RNA-binding proteins. <i>Nature</i> , 2020, 583, 711-719.	13.7	667
4	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
6	Concentration-dependent splicing is enabled by Rbfox motifs of intermediate affinity. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 901-912.	3.6	39
7	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. <i>Cell</i> , 2019, 178, 107-121.e18.	13.5	224
8	Cotargeting among microRNAs in the brain. <i>Genome Research</i> , 2019, 29, 1791-1804.	2.4	27
9	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. <i>Nature Communications</i> , 2019, 10, 1338.	5.8	38
10	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.	3.3	366
11	Widespread PERK-dependent repression of ER targets in response to ER stress. <i>Scientific Reports</i> , 2019, 9, 4330.	1.6	39
12	Acidification of Tumor at Stromal Boundaries Drives Transcriptome Alterations Associated with Aggressive Phenotypes. <i>Cancer Research</i> , 2019, 79, 1952-1966.	0.4	157
13	Exon-Mediated Activation of Transcription Starts. <i>Cell</i> , 2019, 179, 1551-1565.e17.	13.5	65
14	Transcriptome alterations in myotonic dystrophy skeletal muscle and heart. <i>Human Molecular Genetics</i> , 2019, 28, 1312-1321.	1.4	104
15	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.	2.9	63
16	Numerous recursive sites contribute to accuracy of splicing in long introns in flies. <i>PLoS Genetics</i> , 2018, 14, e1007588.	1.5	18
17	Alternative RNA splicing in the endothelium mediated in part by Rbfox2 regulates the arterial response to low flow. <i>ELife</i> , 2018, 7, .	2.8	25
18	Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. <i>Molecular Cell</i> , 2018, 70, 854-867.e9.	4.5	408

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19	A Requirement for Mena, an Actin Regulator, in Local mRNA Translation in Developing Neurons. <i>Neuron</i> , 2017, 95, 608-622.e5.	3.8	38
20	The kinetics of pre-mRNA splicing in the <i>Drosophila</i> genome and the influence of gene architecture. <i>ELife</i> , 2017, 6, .	2.8	57
21	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
22	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.	2.9	118
23	RNA Sequence Context Effects Measured In Vitro Predict In Vivo Protein Binding and Regulation. <i>Molecular Cell</i> , 2016, 64, 294-306.	4.5	110
24	Identification of new branch points and unconventional introns in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2016, 22, 1522-1534.	1.6	32
25	Protein-RNA Networks Regulated by Normal and ALS-Associated Mutant HNRNPA2B1 in the Nervous System. <i>Neuron</i> , 2016, 92, 780-795.	3.8	137
26	Distal Alternative Last Exons Localize mRNAs to Neural Projections. <i>Molecular Cell</i> , 2016, 61, 821-833.	4.5	208
27	Widespread Shortening of 3' UTRs and Increased Exon Inclusion Are Evolutionarily Conserved Features of Innate Immune Responses to Infection. <i>PLoS Genetics</i> , 2016, 12, e1006338.	1.5	90
28	Interactome analysis brings splicing into focus. <i>Genome Biology</i> , 2015, 16, 135.	3.8	2
29	Meta-analysis of RNA-seq expression data across species, tissues and studies. <i>Genome Biology</i> , 2015, 16, 287.	3.8	122
30	Quantitative visualization of alternative exon expression from RNA-seq data. <i>Bioinformatics</i> , 2015, 31, 2400-2402.	1.8	142
31	RNA Bind-n-Seq. <i>Methods in Enzymology</i> , 2015, 558, 465-493.	0.4	27
32	Origins and Impacts of New Mammalian Exons. <i>Cell Reports</i> , 2015, 10, 1992-2005.	2.9	39
33	Antagonistic regulation of mRNA expression and splicing by CELF and MBNL proteins. <i>Genome Research</i> , 2015, 25, 858-871.	2.4	159
34	Identification of mRNA Localization Motifs through Cell Fractionation and Alternative Splicing Analysis. <i>FASEB Journal</i> , 2015, 29, 562.30.	0.2	0
35	Genomic analysis of RNA localization. <i>RNA Biology</i> , 2014, 11, 1040-1050.	1.5	29
36	Methods for time series analysis of RNA-seq data with application to human Th17 cell differentiation. <i>Bioinformatics</i> , 2014, 30, i113-i120.	1.8	62

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37	Alternative splicing regulates vesicular trafficking genes in cardiomyocytes during postnatal heart development. <i>Nature Communications</i> , 2014, 5, 3603.	5.8	133
38	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
39	Widespread Inhibition of Posttranscriptional Splicing Shapes the Cellular Transcriptome following Heat Shock. <i>Cell Reports</i> , 2014, 7, 1362-1370.	2.9	169
40	Muscleblind-like 1 (Mbnl1) regulates pre-mRNA alternative splicing during terminal erythropoiesis. <i>Blood</i> , 2014, 124, 598-610.	0.6	46
41	MicroRNA Target Finding by Comparative Genomics. <i>Methods in Molecular Biology</i> , 2014, 1097, 457-476.	0.4	18
42	Musashi proteins are post-transcriptional regulators of the epithelial-luminal cell state. <i>ELife</i> , 2014, 3, e03915.	2.8	88
43	A complex network of factors with overlapping affinities represses splicing through intronic elements. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 36-45.	3.6	90
44	Widespread Regulation of Translation by Elongation Pausing in Heat Shock. <i>Molecular Cell</i> , 2013, 49, 439-452.	4.5	293
45	SR Proteins Collaborate with 7SK and Promoter-Associated Nascent RNA to Release Paused Polymerase. <i>Cell</i> , 2013, 153, 855-868.	13.5	279
46	Promoter directionality is controlled by U1 snRNP and polyadenylation signals. <i>Nature</i> , 2013, 499, 360-363.	13.7	361
47	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, 2078-2090.	2.4	186
48	Widespread regulation of translation by elongation pausing in heat shock. <i>FASEB Journal</i> , 2013, 27, .	0.2	1
49	Evolutionary Dynamics of Gene and Isoform Regulation in Mammalian Tissues. <i>Science</i> , 2012, 338, 1593-1599.	6.0	853
50	Transcriptome-wide Regulation of Pre-mRNA Splicing and mRNA Localization by Muscleblind Proteins. <i>Cell</i> , 2012, 150, 710-724.	13.5	425
51	Alternative Splicing of RNA Triplets Is Often Regulated and Accelerates Proteome Evolution. <i>PLoS Biology</i> , 2012, 10, e1001229.	2.6	93
52	Direct measurement of DNA affinity landscapes on a high-throughput sequencing instrument. <i>Nature Biotechnology</i> , 2011, 29, 659-664.	9.4	186
53	A Latent Pro-Survival Function for the Mir-290-295 Cluster in Mouse Embryonic Stem Cells. <i>PLoS Genetics</i> , 2011, 7, e1002054.	1.5	110
54	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

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55	Analysis and design of RNA sequencing experiments for identifying isoform regulation. <i>Nature Methods</i> , 2010, 7, 1009-1015.	9.0	1,224
56	Most mammalian mRNAs are conserved targets of microRNAs. <i>Genome Research</i> , 2009, 19, 92-105.	2.4	7,226
57	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000598.	1.5	777
58	Splice site strengthâ€‘dependent activity and genetic buffering by poly-G runs. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1094-1100.	3.6	112
59	Biased Chromatin Signatures around Polyadenylation Sites and Exons. <i>Molecular Cell</i> , 2009, 36, 245-254.	4.5	347
60	Alternative isoform regulation in human tissue transcriptomes. <i>Nature</i> , 2008, 456, 470-476.	13.7	4,508
61	Proliferating Cells Express mRNAs with Shortened 3' Untranslated Regions and Fewer MicroRNA Target Sites. <i>Science</i> , 2008, 320, 1643-1647.	6.0	1,213
62	Splicing regulation: From a parts list of regulatory elements to an integrated splicing code. <i>Rna</i> , 2008, 14, 802-813.	1.6	829
63	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, 20333-20338.	3.3	433
64	Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. <i>Rna</i> , 2007, 13, 1894-1910.	1.6	333
65	The EJC Factor eIF4AIII Modulates Synaptic Strength and Neuronal Protein Expression. <i>Cell</i> , 2007, 130, 179-191.	13.5	278
66	Inference of Splicing Regulatory Activities by Sequence Neighborhood Analysis. <i>PLoS Genetics</i> , 2006, 2, e191.	1.5	71
67	Recognition of Unknown Conserved Alternatively Spliced Exons. <i>PLoS Computational Biology</i> , 2005, 1, e15.	1.5	44
68	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, 2850-2855.	3.3	263
69	Conserved Seed Pairing, Often Flanked by Adenosines, Indicates that Thousands of Human Genes are MicroRNA Targets. <i>Cell</i> , 2005, 120, 15-20.	13.5	10,880
70	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, 15700-15705.	3.3	208
71	Patterns of Intron Gain and Loss in Fungi. <i>PLoS Biology</i> , 2004, 2, e422.	2.6	117
72	RESCUE-ESE identifies candidate exonic splicing enhancers in vertebrate exons. <i>Nucleic Acids Research</i> , 2004, 32, W187-W190.	6.5	251

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73	Maximum Entropy Modeling of Short Sequence Motifs with Applications to RNA Splicing Signals. <i>Journal of Computational Biology</i> , 2004, 11, 377-394.	0.8	1,714
74	Variation in alternative splicing across human tissues. <i>Genome Biology</i> , 2004, 5, R74.	13.9	486
75	Systematic Identification and Analysis of Exonic Splicing Silencers. <i>Cell</i> , 2004, 119, 831-845.	13.5	606
76	Prediction of Mammalian MicroRNA Targets. <i>Cell</i> , 2003, 115, 787-798.	13.5	4,682
77	The microRNAs of <i>Caenorhabditis elegans</i> . <i>Genes and Development</i> , 2003, 17, 991-1008.	2.7	1,081
78	Predictive Identification of Exonic Splicing Enhancers in Human Genes. <i>Science</i> , 2002, 297, 1007-1013.	6.0	957
79	Assessment of the Total Number of Human Transcription Units. <i>Genomics</i> , 2001, 77, 71-78.	1.3	57
80	Chipping away at the transcriptome. <i>Nature Genetics</i> , 2001, 27, 232-234.	9.4	26
81	Computational and Experimental Analysis Identifies Many Novel Human Genes. <i>Biochemical and Biophysical Research Communications</i> , 2000, 272, 801-807.	1.0	16
82	Finding the genes in genomic DNA. <i>Current Opinion in Structural Biology</i> , 1998, 8, 346-354.	2.6	525
83	Classification of Introns: U2-Type or U12-Type. <i>Cell</i> , 1997, 91, 875-879.	13.5	267