Christopher B Burge

List of Publications by Year
in descending order

83 papers	48,800 citations	25034 57 h-index	54911 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. Science Advances, 2022, 8, eabk1752.	10.3	10
2	Loss of LUC7L2 and U1 snRNP subunits shifts energy metabolism from glycolysis to OXPHOS. Molecular Cell, 2021, 81, 1905-1919.e12.	9.7	33
3	A large-scale binding and functional map of human RNA-binding proteins. Nature, 2020, 583, 711-719.	27.8	667
4	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
6	Concentration-dependent splicing is enabled by Rbfox motifs of intermediate affinity. Nature Structural and Molecular Biology, 2020, 27, 901-912.	8.2	39
7	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. Cell, 2019, 178, 107-121.e18.	28.9	224
8	Cotargeting among microRNAs in the brain. Genome Research, 2019, 29, 1791-1804.	5.5	27
9	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. Nature Communications, 2019, 10, 1338.	12.8	38
10	Acquisition of a hybrid E/M state is essential for tumorigenicity of basal breast cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7353-7362.	7.1	366
11	Widespread PERK-dependent repression of ER targets in response to ER stress. Scientific Reports, 2019, 9, 4330.	3.3	39
12	Acidification of Tumor at Stromal Boundaries Drives Transcriptome Alterations Associated with Aggressive Phenotypes. Cancer Research, 2019, 79, 1952-1966.	0.9	157
13	Exon-Mediated Activation of Transcription Starts. Cell, 2019, 179, 1551-1565.e17.	28.9	65
14	Transcriptome alterations in myotonic dystrophy skeletal muscle and heart. Human Molecular Genetics, 2019, 28, 1312-1321.	2.9	104
15	Widespread Accumulation of Ribosome-Associated Isolated 3â€² UTRs in Neuronal Cell Populations of the Aging Brain. Cell Reports, 2018, 25, 2447-2456.e4.	6.4	63
16	Numerous recursive sites contribute to accuracy of splicing in long introns in flies. PLoS Genetics, 2018, 14, e1007588.	3.5	18
17	Alternative RNA splicing in the endothelium mediated in part by Rbfox2 regulates the arterial response to low flow. ELife, 2018, 7, .	6.0	25
18	Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. Molecular Cell, 2018, 70, 854-867.e9.	9.7	408

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19	A Requirement for Mena, an Actin Regulator, in Local mRNA Translation in Developing Neurons. Neuron, 2017, 95, 608-622.e5.	8.1	38
20	The kinetics of pre-mRNA splicing in the Drosophila genome and the influence of gene architecture. ELife, 2017, 6, .	6.0	57
21	Distinct and shared functions of ALS-associated proteins TDP-43, FUS and TAF15 revealed by multisystem analyses. Nature Communications, 2016, 7, 12143.	12.8	137
22	Enhanced CLIP Uncovers IMP Protein-RNA Targets in Human Pluripotent Stem Cells Important for Cell Adhesion and Survival. Cell Reports, 2016, 15, 666-679.	6.4	118
23	RNA Sequence Context Effects Measured InÂVitro Predict InÂVivo Protein Binding and Regulation. Molecular Cell, 2016, 64, 294-306.	9.7	110
24	Identification of new branch points and unconventional introns in Saccharomyces cerevisiae. Rna, 2016, 22, 1522-1534.	3.5	32
25	Protein-RNA Networks Regulated by Normal and ALS-Associated Mutant HNRNPA2B1 in the Nervous System. Neuron, 2016, 92, 780-795.	8.1	137
26	Distal Alternative Last Exons Localize mRNAs to Neural Projections. Molecular Cell, 2016, 61, 821-833.	9.7	208
27	Widespread Shortening of 3â€™ Untranslated Regions and Increased Exon Inclusion Are Evolutionarily Conserved Features of Innate Immune Responses to Infection. PLoS Genetics, 2016, 12, e1006338.	3.5	90
28	Interactome analysis brings splicing into focus. Genome Biology, 2015, 16, 135.	8.8	2
29	Meta-analysis of RNA-seq expression data across species, tissues and studies. Genome Biology, 2015, 16, 287.	8.8	122
30	Quantitative visualization of alternative exon expression from RNA-seq data. Bioinformatics, 2015, 31, 2400-2402.	4.1	142
31	RNA Bind-n-Seq. Methods in Enzymology, 2015, 558, 465-493.	1.0	27
32	Origins and Impacts of New Mammalian Exons. Cell Reports, 2015, 10, 1992-2005.	6.4	39
33	Antagonistic regulation of mRNA expression and splicing by CELF and MBNL proteins. Genome Research, 2015, 25, 858-871.	5.5	159
34	Identification of mRNA Localization Motifs through Cell Fractionation and Alternative Splicing Analysis. FASEB Journal, 2015, 29, 562.30.	0.5	0
35	Genomic analysis of RNA localization. RNA Biology, 2014, 11, 1040-1050.	3.1	29
36	Methods for time series analysis of RNA-seq data with application to human Th17 cell differentiation. Bioinformatics, 2014, 30, i113-i120.	4.1	62

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37	Alternative splicing regulates vesicular trafficking genes in cardiomyocytes during postnatal heart development. Nature Communications, 2014, 5, 3603.	12.8	133
38	RNA Bind-n-Seq: Quantitative Assessment of the Sequence and Structural Binding Specificity of RNA Binding Proteins. Molecular Cell, 2014, 54, 887-900.	9.7	346
39	Widespread Inhibition of Posttranscriptional Splicing Shapes the Cellular Transcriptome following Heat Shock. Cell Reports, 2014, 7, 1362-1370.	6.4	169
40	Muscleblind-like 1 (Mbnl1) regulates pre-mRNA alternative splicing during terminal erythropoiesis. Blood, 2014, 124, 598-610.	1.4	46
41	MicroRNA Target Finding by Comparative Genomics. Methods in Molecular Biology, 2014, 1097, 457-476.	0.9	18
42	Musashi proteins are post-transcriptional regulators of the epithelial-luminal cell state. ELife, 2014, 3, e03915.	6.0	88
43	A complex network of factors with overlapping affinities represses splicing through intronic elements. Nature Structural and Molecular Biology, 2013, 20, 36-45.	8.2	90
44	Widespread Regulation of Translation by Elongation Pausing in Heat Shock. Molecular Cell, 2013, 49, 439-452.	9.7	293
45	SR Proteins Collaborate with 7SK and Promoter-Associated Nascent RNA to Release Paused Polymerase. Cell, 2013, 153, 855-868.	28.9	279
46	Promoter directionality is controlled by U1 snRNP and polyadenylation signals. Nature, 2013, 499, 360-363.	27.8	361
47	3â€² UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts. Genome Research, 2013, 23, 2078-2090.	5.5	186
48	Widespread regulation of translation by elongation pausing in heat shock. FASEB Journal, 2013, 27, .	0.5	1
49	Evolutionary Dynamics of Gene and Isoform Regulation in Mammalian Tissues. Science, 2012, 338, 1593-1599.	12.6	853
50	Transcriptome-wide Regulation of Pre-mRNA Splicing and mRNA Localization by Muscleblind Proteins. Cell, 2012, 150, 710-724.	28.9	425
51	Alternative Splicing of RNA Triplets Is Often Regulated and Accelerates Proteome Evolution. PLoS Biology, 2012, 10, e1001229.	5.6	93
52	Direct measurement of DNA affinity landscapes on a high-throughput sequencing instrument. Nature Biotechnology, 2011, 29, 659-664.	17.5	186
53	A Latent Pro-Survival Function for the Mir-290-295 Cluster in Mouse Embryonic Stem Cells. PLoS Genetics, 2011, 7, e1002054.	3.5	110
54	An EMTâ€"Driven Alternative Splicing Program Occurs in Human Breast Cancer and Modulates Cellular Phenotype. PLoS Genetics, 2011, 7, e1002218.	3.5	399

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55	Analysis and design of RNA sequencing experiments for identifying isoform regulation. Nature Methods, 2010, 7, 1009-1015.	19.0	1,224
56	Most mammalian mRNAs are conserved targets of microRNAs. Genome Research, 2009, 19, 92-105.	5.5	7,226
57	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. PLoS Computational Biology, 2009, 5, e1000598.	3.2	777
58	Splice site strengthâ€"dependent activity and genetic buffering by poly-G runs. Nature Structural and Molecular Biology, 2009, 16, 1094-1100.	8.2	112
59	Biased Chromatin Signatures around Polyadenylation Sites and Exons. Molecular Cell, 2009, 36, 245-254.	9.7	347
60	Alternative isoform regulation in human tissue transcriptomes. Nature, 2008, 456, 470-476.	27.8	4,508
61	Proliferating Cells Express mRNAs with Shortened 3' Untranslated Regions and Fewer MicroRNA Target Sites. Science, 2008, 320, 1643-1647.	12.6	1,213
62	Splicing regulation: From a parts list of regulatory elements to an integrated splicing code. Rna, 2008, 14, 802-813.	3.5	829
63	A postnatal switch of CELF and MBNL proteins reprograms alternative splicing in the developing heart. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20333-20338.	7.1	433
64	Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. Rna, 2007, 13, 1894-1910.	3.5	333
65	The EJC Factor eIF4AIII Modulates Synaptic Strength and Neuronal Protein Expression. Cell, 2007, 130, 179-191.	28.9	278
66	Inference of Splicing Regulatory Activities by Sequence Neighborhood Analysis. PLoS Genetics, 2006, 2, e191.	3.5	71
67	Recognition of Unknown Conserved Alternatively Spliced Exons. PLoS Computational Biology, 2005, 1, e15.	3.2	44
68	Identification and analysis of alternative splicing events conserved in human and mouse. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2850-2855.	7.1	263
69	Conserved Seed Pairing, Often Flanked by Adenosines, Indicates that Thousands of Human Genes are MicroRNA Targets. Cell, 2005, 120, 15-20.	28.9	10,880
70	Variation in sequence and organization of splicing regulatory elements in vertebrate genes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15700-15705.	7.1	208
71	Patterns of Intron Gain and Loss in Fungi. PLoS Biology, 2004, 2, e422.	5.6	117
72	RESCUE-ESE identifies candidate exonic splicing enhancers in vertebrate exons. Nucleic Acids Research, 2004, 32, W187-W190.	14.5	251

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73	Maximum Entropy Modeling of Short Sequence Motifs with Applications to RNA Splicing Signals. Journal of Computational Biology, 2004, 11, 377-394.	1.6	1,714
74	Variation in alternative splicing across human tissues. Genome Biology, 2004, 5, R74.	9.6	486
75	Systematic Identification and Analysis of Exonic Splicing Silencers. Cell, 2004, 119, 831-845.	28.9	606
76	Prediction of Mammalian MicroRNA Targets. Cell, 2003, 115, 787-798.	28.9	4,682
77	The microRNAs ofCaenorhabditis elegans. Genes and Development, 2003, 17, 991-1008.	5.9	1,081
78	Predictive Identification of Exonic Splicing Enhancers in Human Genes. Science, 2002, 297, 1007-1013.	12.6	957
79	Assessment of the Total Number of Human Transcription Units. Genomics, 2001, 77, 71-78.	2.9	57
80	Chipping away at the transcriptome. Nature Genetics, 2001, 27, 232-234.	21.4	26
81	Computational and Experimental Analysis Identifies Many Novel Human Genes. Biochemical and Biophysical Research Communications, 2000, 272, 801-807.	2.1	16
82	Finding the genes in genomic DNA. Current Opinion in Structural Biology, 1998, 8, 346-354.	5.7	525
83	Classification of Introns: U2-Type or U12-Type. Cell, 1997, 91, 875-879.	28.9	267