Christopher B Burge

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/1939242/christopher-b-burge-publications-by-year.pdf
Version: 2024-04-25

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	Widespread occurrence of hybrid internal-terminal exons in human transcriptomes.. *Science Advances*, **2022**, 8, eabk1752	14.3	0
84	Loss of LUC7L2 and U1 snRNP subunits shifts energy metabolism from glycolysis to OXPHOS. *Molecular Cell*, **2021**, 81, 1905-1919.e12	17.6	8
83	A large-scale binding and functional map of human RNA-binding proteins. *Nature*, **2020**, 583, 711-719	50.4	198
82	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
81	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	50.4	360
80	Concentration-dependent splicing is enabled by Rbfox motifs of intermediate affinity. *Nature Structural and Molecular Biology*, **2020**, 27, 901-912	17.6	13
79	Cotargeting among microRNAs in the brain. *Genome Research*, **2019**, 29, 1791-1804	9.7	8
78	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. *Nature Communications*, **2019**, 10, 1338	17.4	17
77	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	11.5	186
76	Widespread PERK-dependent repression of ER targets in response to ER stress. *Scientific Reports*, **2019**, 9, 4330	4.9	23
75	Acidification of Tumor at Stromal Boundaries Drives Transcriptome Alterations Associated with Aggressive Phenotypes. *Cancer Research*, **2019**, 79, 1952-1966	10.1	86
74	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. *Cell*, **2019**, 178, 107-121.e18	56.2	101
73	Exon-Mediated Activation of Transcription Starts. *Cell*, **2019**, 179, 1551-1565.e17	56.2	27
72	Transcriptome alterations in myotonic dystrophy skeletal muscle and heart. *Human Molecular Genetics*, **2019**, 28, 1312-1321	5.6	51
71	Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. *Molecular Cell*, **2018**, 70, 854-867.e9	17.6	212
70	Widespread Accumulation of Ribosome-Associated Isolated 3' UTRs in Neuronal Cell Populations of the Aging Brain. *Cell Reports*, **2018**, 25, 2447-2456.e4	10.6	34
69	Numerous recursive sites contribute to accuracy of splicing in long introns in flies. *PLoS Genetics*, **2018**, 14, e1007588	6	9

68	Alternative RNA splicing in the endothelium mediated in part by Rbfox2 regulates the arterial response to low flow. *ELife*, **2018**, 7,	8.9	14
67	The kinetics of pre-mRNA splicing in the genome and the influence of gene architecture. *ELife*, **2017**, 6,	8.9	33
66	A Requirement for Mena, an Actin Regulator, in Local mRNA Translation in Developing Neurons. *Neuron*, **2017**, 95, 608-622.e5	13.9	30
65	Identification of new branch points and unconventional introns in Saccharomyces cerevisiae. *Rna*, **2016**, 22, 1522-34	5.8	25
64	Protein-RNA Networks Regulated by Normal and ALS-Associated Mutant HNRNPA2B1 in the Nervous System. *Neuron*, **2016**, 92, 780-795	13.9	94
63	Distal Alternative Last Exons Localize mRNAs to Neural Projections. *Molecular Cell*, **2016**, 61, 821-33	17.6	143
62	Widespread Shortening of 3' Untranslated Regions and Increased Exon Inclusion Are Evolutionarily Conserved Features of Innate Immune Responses to Infection. *PLoS Genetics*, **2016**, 12, e1006338	6	53
61	Distinct and shared functions of ALS-associated proteins TDP-43, FUS and TAF15 revealed by multisystem analyses. *Nature Communications*, **2016**, 7, 12143	17.4	94
60	Enhanced CLIP Uncovers IMP Protein-RNA Targets in Human Pluripotent Stem Cells Important for Cell Adhesion and Survival. *Cell Reports*, **2016**, 15, 666-679	10.6	75
59	RNA Sequence Context Effects Measured In Vitro Predict In Vivo Protein Binding and Regulation. *Molecular Cell*, **2016**, 64, 294-306	17.6	68
58	RNA Bind-n-Seq: Measuring the Binding Affinity Landscape of RNA-Binding Proteins. *Methods in Enzymology*, **2015**, 558, 465-493	1.7	18
57	Origins and impacts of new mammalian exons. *Cell Reports*, **2015**, 10, 1992-2005	10.6	27
56	Antagonistic regulation of mRNA expression and splicing by CELF and MBNL proteins. *Genome Research*, **2015**, 25, 858-71	9.7	125
55	Interactome analysis brings splicing into focus. *Genome Biology*, **2015**, 16, 135	18.3	1
54	Meta-analysis of RNA-seq expression data across species, tissues and studies. *Genome Biology*, **2015** , 16, 287	18.3	71
53	Quantitative visualization of alternative exon expression from RNA-seq data. *Bioinformatics*, **2015**, 31, 2400-2	7.2	99
52	Identification of mRNA Localization Motifs through Cell Fractionation and Alternative Splicing Analysis. *FASEB Journal*, **2015**, 29, 562.30	0.9	
51	Alternative splicing regulates vesicular trafficking genes in cardiomyocytes during postnatal heart development. *Nature Communications*, **2014**, 5, 3603	17.4	98

50	RNA Bind-n-Seq: quantitative assessment of the sequence and structural binding specificity of RNA binding proteins. *Molecular Cell*, **2014**, 54, 887-900	17.6	251
49	Widespread inhibition of posttranscriptional splicing shapes the cellular transcriptome following heat shock. *Cell Reports*, **2014**, 7, 1362-1370	10.6	111
48	Muscleblind-like 1 (Mbnl1) regulates pre-mRNA alternative splicing during terminal erythropoiesis. *Blood*, **2014**, 124, 598-610	2.2	35
47	Genomic analysis of RNA localization. *RNA Biology*, **2014**, 11, 1040-50	4.8	16
46	Methods for time series analysis of RNA-seq data with application to human Th17 cell differentiation. *Bioinformatics*, **2014**, 30, i113-20	7.2	47
45	Musashi proteins are post-transcriptional regulators of the epithelial-luminal cell state. *ELife*, **2014**, 3, e03915	8.9	63
44	MicroRNA target finding by comparative genomics. *Methods in Molecular Biology*, **2014**, 1097, 457-76	1.4	17
43	A complex network of factors with overlapping affinities represses splicing through intronic elements. *Nature Structural and Molecular Biology*, **2013**, 20, 36-45	17.6	75
42	Widespread regulation of translation by elongation pausing in heat shock. *Molecular Cell*, **2013**, 49, 439-52	17.6	223
41	SR proteins collaborate with 7SK and promoter-associated nascent RNA to release paused polymerase. *Cell*, **2013**, 153, 855-68	56.2	222
40	Promoter directionality is controlled by U1 snRNP and polyadenylation signals. *Nature*, **2013**, 499, 360-3	50.4	294
39	3' UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts. *Genome Research*, **2013**, 23, 2078-90	9.7	123
38	Evolutionary dynamics of gene and isoform regulation in Mammalian tissues. *Science*, **2012**, 338, 1593-9	33.3	587
37	Transcriptome-wide regulation of pre-mRNA splicing and mRNA localization by muscleblind proteins. *Cell*, **2012**, 150, 710-24	56.2	347
36	Alternative splicing of RNA triplets is often regulated and accelerates proteome evolution. *PLoS Biology*, **2012**, 10, e1001229	9.7	74
35	Direct measurement of DNA affinity landscapes on a high-throughput sequencing instrument. *Nature Biotechnology*, **2011**, 29, 659-64	44.5	151
34	A latent pro-survival function for the mir-290-295 cluster in mouse embryonic stem cells. *PLoS Genetics*, **2011**, 7, e1002054	6	83
33	An EMT-driven alternative splicing program occurs in human breast cancer and modulates cellular phenotype. *PLoS Genetics*, **2011**, 7, e1002218	6	318

32	Analysis and design of RNA sequencing experiments for identifying isoform regulation. *Nature Methods*, **2010**, 7, 1009-15	21.6	934
31	An abundance of ubiquitously expressed genes revealed by tissue transcriptome sequence data. *PLoS Computational Biology*, **2009**, 5, e1000598	5	615
30	Splice site strength-dependent activity and genetic buffering by poly-G runs. *Nature Structural and Molecular Biology*, **2009**, 16, 1094-100	17.6	92
29	Biased chromatin signatures around polyadenylation sites and exons. *Molecular Cell*, **2009**, 36, 245-54	17.6	310
28	Most mammalian mRNAs are conserved targets of microRNAs. *Genome Research*, **2009**, 19, 92-105	9.7	5919
27	Alternative isoform regulation in human tissue transcriptomes. *Nature*, **2008**, 456, 470-6	50.4	3526
26	Proliferating cells express mRNAs with shortened 3' untranslated regions and fewer microRNA target sites. *Science*, **2008**, 320, 1643-7	33.3	984
25	Splicing regulation: from a parts list of regulatory elements to an integrated splicing code. *Rna*, **2008**, 14, 802-13	5.8	682
24	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, 20333-8	11.5	361
23	Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. *Rna*, **2007**, 13, 1894-910	5.8	288
22	The EJC factor eIF4AIII modulates synaptic strength and neuronal protein expression. *Cell*, **2007**, 130, 179-91	56.2	223
21	Inference of splicing regulatory activities by sequence neighborhood analysis. *PLoS Genetics*, **2006**, 2, e191	6	65
20	Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets. *Cell*, **2005**, 120, 15-20	56.2	9564
19	Recognition of unknown conserved alternatively spliced exons. *PLoS Computational Biology*, **2005**, 1, 113-22	5	38
18	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, 2850-5	11.5	227
17	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, 15700-5	11.5	184
16	Patterns of intron gain and loss in fungi. *PLoS Biology*, **2004**, 2, e422	9.7	101
15	RESCUE-ESE identifies candidate exonic splicing enhancers in vertebrate exons. *Nucleic Acids Research*, **2004**, 32, W187-90	20.1	212

14	Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals. *Journal of Computational Biology*, **2004**, 11, 377-94	1.7	1253
13	Variation in alternative splicing across human tissues. *Genome Biology*, **2004**, 5, R74	18.3	378
12	Systematic identification and analysis of exonic splicing silencers. *Cell*, **2004**, 119, 831-45	56.2	522
11	The microRNAs of Caenorhabditis elegans. *Genes and Development*, **2003**, 17, 991-1008	12.6	926
10	Prediction of mammalian microRNA targets. *Cell*, **2003**, 115, 787-98	56.2	4144
9	Predictive identification of exonic splicing enhancers in human genes. *Science*, **2002**, 297, 1007-13	33.3	867
8	Assessment of the total number of human transcription units. *Genomics*, **2001**, 77, 71-8	4.3	49
7	Computational and experimental analysis identifies many novel human genes. *Biochemical and Biophysical Research Communications*, **2000**, 272, 801-7	3.4	15
6	Finding the genes in genomic DNA. *Current Opinion in Structural Biology*, **1998**, 8, 346-54	8.1	418
5	Classification of introns: U2-type or U12-type. *Cell*, **1997**, 91, 875-9	56.2	231
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 shortening of 3′ untranslated regions and increased exon inclusion are evolutionarily conserved features of innate immune responses to infection		2
1	Sequence, Structure and Context Preferences of Human RNA Binding Proteins		5