Maria Carmo-Fonseca

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Retinoic acid regulates aberrant nuclear localization of PML-RARα in acute promyelocytic leukemia cells. Cell, 1994, 76, 345-356.	13.5	691
2	Mammalian NET-Seq Reveals Genome-wide Nascent Transcription Coupled to RNA Processing. Cell, 2015, 161, 526-540.	13.5	466
3	To be or not to be in the nucleolus. Nature Cell Biology, 2000, 2, E107-E112.	4.6	346
4	Deep intronic mutations and human disease. Human Genetics, 2017, 136, 1093-1111.	1.8	311
5	The C-terminal domain of TAP interacts with the nuclear pore complex and promotes export of specific CTE-bearing RNA substrates. Rna, 2000, 6, 136-158.	1.6	298
6	Dynamic association of RNA-editing enzymes with the nucleolus. Journal of Cell Science, 2003, 116, 1805-1818.	1.2	231
7	Nuclear inclusions in oculopharyngeal muscular dystrophy consist of poly(A) binding protein 2 aggregates which sequester poly(A) RNA. Human Molecular Genetics, 2000, 9, 2321-2328.	1.4	226
8	Vesicular Stomatitis Virus Matrix Protein Inhibits Host Cell Gene Expression by Targeting the Nucleoporin Nup98. Molecular Cell, 2000, 6, 1243-1252.	4.5	226
9	Distinctive Patterns of Transcription and RNA Processing for Human lincRNAs. Molecular Cell, 2017, 65, 25-38.	4.5	222
10	TAP (NXF1) Belongs to a Multigene Family of Putative RNA Export Factors with a Conserved Modular Architecture. Molecular and Cellular Biology, 2000, 20, 8996-9008.	1.1	210
11	The Spinal Muscular Atrophy Disease Gene Product, Smn. Journal of Cell Biology, 1999, 147, 715-728.	2.3	205
12	Splicing enhances recruitment of methyltransferase HYPB/Setd2 and methylation of histone H3 Lys36. Nature Structural and Molecular Biology, 2011, 18, 977-983.	3.6	204
13	Inefficient processing impairs release of RNA from the site of transcription. EMBO Journal, 1999, 18, 2855-2866.	3.5	194
14	Intracellular Macromolecular Mobility Measured by Fluorescence Recovery after Photobleaching with Confocal Laser Scanning Microscopes. Molecular Biology of the Cell, 2004, 15, 4749-4760.	0.9	184
15	Tissue-specific splicing factor gene expression signatures. Nucleic Acids Research, 2008, 36, 4823-4832.	6.5	172
16	The Contribution of Nuclear Compartmentalization to Gene Regulation. Cell, 2002, 108, 513-521.	13.5	171
17	The emerging role of splicing factors in cancer. EMBO Reports, 2008, 9, 1087-1093.	2.0	161
18	Chemical Chaperones Reduce Endoplasmic Reticulum Stress and Prevent Mutant HFE Aggregate Formation. Journal of Biological Chemistry, 2007, 282, 27905-27912.	1.6	150

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19	Live-Cell Visualization of Pre-mRNA Splicing with Single-Molecule Sensitivity. Cell Reports, 2013, 4, 1144-1155.	2.9	149
20	Histone methyltransferase SETD2 coordinates FACT recruitment with nucleosome dynamics during transcription. Nucleic Acids Research, 2013, 41, 2881-2893.	6.5	142
21	Targeting mRNA processing as an anticancer strategy. Nature Reviews Drug Discovery, 2020, 19, 112-129.	21.5	131
22	RNA Polymerase II Phosphorylated on CTD Serine 5 Interacts with the Spliceosome during Co-transcriptional Splicing. Molecular Cell, 2018, 72, 369-379.e4.	4.5	123
23	Clastosome: A Subtype of Nuclear Body Enriched in 19S and 20S Proteasomes, Ubiquitin, and Protein Substrates of Proteasome. Molecular Biology of the Cell, 2002, 13, 2771-2782.	0.9	121
24	Targeting of U2AF65 to Sites of Active Splicing in the Nucleus. Journal of Cell Biology, 1997, 137, 975-987.	2.3	115
25	Precursor RNAs Harboring Nonsense Codons Accumulate Near the Site of Transcription. Molecular Cell, 2001, 8, 33-43.	4.5	115
26	Pervasive transcription read-through promotes aberrant expression of oncogenes and RNA chimeras in renal carcinoma. ELife, 2015, 4, .	2.8	114
27	The intranuclear mobility of messenger RNA binding proteins is ATP dependent and temperature sensitive. Journal of Cell Biology, 2002, 159, 795-805.	2.3	111
28	The rules and roles of nucleocytoplasmic shuttling proteins. FEBS Letters, 2001, 498, 157-163.	1.3	103
29	SUMO-1 Modification Alters ADAR1 Editing Activity. Molecular Biology of the Cell, 2005, 16, 5115-5126.	0.9	102
30	Systematic genome-wide annotation of spliceosomal proteins reveals differential gene family expansion. Genome Research, 2005, 16, 66-77.	2.4	92
31	Deciphering the cellular pathway for transport of poly(A)-binding protein II. Rna, 2000, 6, 245-256.	1.6	91
32	Mammalian NET-seq analysis defines nascent RNA profiles and associated RNA processing genome-wide. Nature Protocols, 2016, 11, 413-428.	5.5	86
33	Transcription Dynamics Prevent RNA-Mediated Genomic Instability through SRPK2-Dependent DDX23 Phosphorylation. Cell Reports, 2017, 18, 334-343.	2.9	86
34	Microinjection of Anti-coilin Antibodies Affects the Structure of Coiled Bodies. Journal of Cell Biology, 1998, 142, 899-912.	2.3	83
35	In vivo recruitment of exon junction complex proteins to transcription sites in mammalian cell nuclei. Rna, 2004, 10, 622-633.	1.6	78
36	Spliceosome assembly is coupled to RNA polymerase II dynamics at the 3′ end of human genes. Nature Structural and Molecular Biology, 2011, 18, 1115-1123.	3.6	76

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37	A Reaction-Diffusion Model to Study RNA Motion by Quantitative Fluorescence Recovery after Photobleaching. Biophysical Journal, 2007, 92, 2694-2703.	0.2	71
38	Macromolecular mobility inside the cell nucleus. Trends in Cell Biology, 2002, 12, 491-495.	3.6	70
39	Genome-wide identification of functionally distinct subsets of cellular mRNAs associated with two nucleocytoplasmic-shuttling mammalian splicing factors. Genome Biology, 2006, 7, R113.	13.9	68
40	Chromosomal G-dark Bands Determine the Spatial Organization of Centromeric Heterochromatin in the Nucleus. Molecular Biology of the Cell, 2001, 12, 3563-3572.	0.9	67
41	Stimulation of an Unfolded Protein Response Impairs MHC Class I Expression. Journal of Immunology, 2007, 178, 3612-3619.	0.4	67
42	Localisation of splicing snRNPs in mammalian cells. Molecular Biology Reports, 1993, 18, 127-133.	1.0	66
43	In vivo aggregation properties of the nuclear poly(A)-binding protein PABPN1. Rna, 2005, 11, 752-762.	1.6	65
44	RNA Interference Knockdown of hU2AF35 Impairs Cell Cycle Progression and Modulates Alternative Splicing of Cdc25 Transcripts. Molecular Biology of the Cell, 2006, 17, 4187-4199.	0.9	65
45	Oculopharyngeal muscular dystrophy-like nuclear inclusions are present in normal magnocellular neurosecretory neurons of the hypothalamus. Human Molecular Genetics, 2004, 13, 829-838.	1.4	58
46	The spliceosome: a self-organized macromolecular machine in the nucleus?. Trends in Cell Biology, 2009, 19, 375-384.	3.6	58
47	Hepatitis delta virus ribonucleoproteins shuttle between the nucleus and the cytoplasm. Rna, 2002, 8, 637-646.	1.6	57
48	In Vivo Requirement of the Small Subunit of U2AF for Recognition of a Weak 3′ Splice Site. Molecular and Cellular Biology, 2006, 26, 8183-8190.	1.1	56
49	A Stochastic View of Spliceosome Assembly and Recycling in the Nucleus. PLoS Computational Biology, 2007, 3, e201.	1.5	56
50	A link between nuclear RNA surveillance, the human exosome and RNA polymerase II transcriptional termination. Nucleic Acids Research, 2010, 38, 8015-8026.	6.5	55
51	Unconstrained mining of transcript data reveals increased alternative splicing complexity in the human transcriptome. Nucleic Acids Research, 2010, 38, 4740-4754.	6.5	55
52	Identification of Two Novel RanGTP-binding Proteins Belonging to the Importin β Superfamily. Journal of Biological Chemistry, 2000, 275, 40163-40168.	1.6	54
53	POINT technology illuminates the processing of polymerase-associated intact nascent transcripts. Molecular Cell, 2021, 81, 1935-1950.e6.	4.5	52
54	New clues to the function of the Cajal body. EMBO Reports, 2002, 3, 726-727.	2.0	51

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55	Design principles of interconnections between chromatin and pre-mRNA splicing. Trends in Biochemical Sciences, 2012, 37, 248-253.	3.7	49
56	Silencing of the lncRNA Zeb2-NAT facilitates reprogramming of aged fibroblasts and safeguards stem cell pluripotency. Nature Communications, 2018, 9, 94.	5.8	49
57	Depletion of the Yeast Nuclear Exosome Subunit Rrp6 Results in Accumulation of Polyadenylated RNAs in a Discrete Domain within the Nucleolus. Molecular and Cellular Biology, 2007, 27, 4157-4165.	1.1	48
58	Diversity of Vertebrate Splicing Factor U2AF35. Journal of Biological Chemistry, 2004, 279, 27039-27049.	1.6	47
59	The CTD role in cotranscriptional RNA processing and surveillance. FEBS Letters, 2008, 582, 1971-1976.	1.3	46
60	Nucleocytoplasmic Shuttling of Heterodimeric Splicing Factor U2AF. Journal of Biological Chemistry, 2001, 276, 13104-13112.	1.6	45
61	Characterization of a Helicase-Like Transcription Factor Involved in the Expression of the Human Plasminogen Activator Inhibitor-1 Gene. DNA and Cell Biology, 1996, 15, 429-442.	0.9	44
62	Triplet repeats, RNA secondary structure and toxic gain-of-function models for pathogenesis. Brain Research Bulletin, 2001, 56, 191-201.	1.4	42
63	Hsp70 Chaperones and Type I PRMTs Are Sequestered at Intranuclear Inclusions Caused by Polyalanine Expansions in PABPN1. PLoS ONE, 2009, 4, e6418.	1.1	42
64	Dynamic transitions in RNA polymerase II density profiles during transcription termination. Genome Research, 2012, 22, 1447-1456.	2.4	42
65	Co-transcriptional splicing and the CTD code. Critical Reviews in Biochemistry and Molecular Biology, 2016, 51, 395-411.	2.3	42
66	Splicing Factors SF1 and U2AF Associate in Extraspliceosomal Complexes. Molecular and Cellular Biology, 2008, 28, 3045-3057.	1.1	40
67	Diversity of human U2AF splicing factors FEBS Journal, 2006, 273, 4807-4816.	2.2	38
68	Cytokeratin filaments are present in golden hamster oocytes and early embryos. Differentiation, 1989, 42, 1-9.	1.0	37
69	Localization of hepatitis delta virus RNA in the nucleus of human cells. Rna, 1998, 4, 680-693.	1.6	33
70	The spatial distribution of human immunoglobulin genes within the nucleus: evidence for gene topography independent of cell type and transcriptional activity. Human Genetics, 1997, 100, 588-594.	1.8	30
71	Splicing- and cleavage-independent requirement of RNA polymerase II CTD for mRNA release from the transcription site. Journal of Cell Biology, 2007, 179, 199-207.	2.3	28
72	Reciprocal regulatory links between cotranscriptional splicing and chromatin. Seminars in Cell and Developmental Biology, 2014, 32, 2-10.	2.3	27

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73	Gene architecture directs splicing outcome in separate nuclear spatial regions. Molecular Cell, 2022, 82, 1021-1034.e8.	4.5	26
74	Pharmacological inhibition of the spliceosome subunit SF3b triggers EJC-independent NMD. Journal of Cell Science, 2017, 130, 1519-1531.	1.2	25
75	Design Principles for Pluripotent Stem Cell-Derived Organoid Engineering. Stem Cells International, 2019, 2019, 1-17.	1.2	25
76	Cryptic Splice-Altering Variants in <i>MYBPC3</i> Are a Prevalent Cause of Hypertrophic Cardiomyopathy. Circulation Genomic and Precision Medicine, 2020, 13, e002905.	1.6	23
77	RNA seeds nuclear bodies. Nature Cell Biology, 2011, 13, 110-112.	4.6	21
78	Frontiers in fluorescence microscopy. International Journal of Developmental Biology, 2009, 53, 1569-1579.	0.3	19
79	Orphan Nuclear Bodies. Cold Spring Harbor Perspectives in Biology, 2010, 2, a000703-a000703.	2.3	19
80	The Topography of Chromosomes and Genes in the Nucleus. Experimental Cell Research, 1996, 229, 247-252.	1.2	18
81	The timing of pre-mRNA splicing visualized in real-time. Nucleus, 2014, 5, 11-14.	0.6	18
82	Regulation of adenovirus alternative RNA splicing correlates with a reorganization of splicing factors in the nucleus. Experimental Cell Research, 2003, 289, 77-85.	1.2	16
83	RNA Splicing Defects in Hypertrophic Cardiomyopathy: Implications for Diagnosis and Therapy. International Journal of Molecular Sciences, 2020, 21, 1329.	1.8	15
84	Differential Isoform Expression and Interaction with the P32 Regulatory Protein Controls the Subcellular Localization of the Splicing Factor U2AF26. Journal of Biological Chemistry, 2008, 283, 19636-19645.	1.6	14
85	Nuclear morphogenesis and the onset of transcriptional activity in early hamster embryos. Chromosoma, 1996, 105, 1-11.	1.0	12
86	Smaug1 membrane-less organelles respond to AMPK and mTOR and affect mitochondrial function. Journal of Cell Science, 2022, 135, .	1.2	12
87	Studies on the role of NonA in mRNA biogenesis. Experimental Cell Research, 2006, 312, 2619-2630.	1.2	11
88	Analysis of Mammalian Native Elongating Transcript sequencing (mNET-seq) high-throughput data. Methods, 2020, 178, 89-95.	1.9	11
89	Transcription and splicing dynamics during early <i>Drosophila</i> development. Rna, 2022, 28, 139-161.	1.6	11
90	Imaging dynamic interactions between spliceosomal proteins and pre-mRNA in living cells. Methods, 2014, 65, 359-366.	1.9	10

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91	How genes find their way inside the cell nucleus. Journal of Cell Biology, 2007, 179, 1093-1094.	2.3	9
92	Nâ€Glycosylation is important for the correct intracellular localization of HFE and its ability to decrease cell surface transferrin binding. FEBS Journal, 2010, 277, 3219-3234.	2.2	9
93	Cytokeratin in early hamster embryogenesis and parthenogenesis: reorganization during mitosis and association with clusters of interchromatinlike granules. Differentiation, 1991, 48, 67-74.	1.0	8
94	Inactivation of Cleavage Factor I Components Rna14p and Rna15p Induces Sequestration of Small Nucleolar Ribonucleoproteins at Discrete Sites in the Nucleus. Molecular Biology of the Cell, 2008, 19, 1499-1508.	0.9	8
95	Transcription-coupled RNA surveillance in human genetic diseases caused by splice site mutations. Human Molecular Genetics, 2015, 24, 2784-2795.	1.4	8
96	Quality control of gene expression in the nucleus. Journal of Cellular and Molecular Medicine, 2001, 5, 267-275.	1.6	7
97	Photobleaching Microscopy Reveals the Dynamics of mRNA-Binding Proteins Inside Live Cell Nuclei. Progress in Molecular and Subcellular Biology, 2008, 35, 119-134.	0.9	7
98	Alternative Splicing and Cancer. Journal of Nucleic Acids, 2012, 2012, 1-2.	0.8	6
99	Understanding nuclear order. Trends in Biochemical Sciences, 2002, 27, 332-334.	3.7	5
100	A single RNA recognition motif in splicing factor ASF/SF2 directs it to nuclear sites of adenovirus transcription. Journal of General Virology, 2004, 85, 603-608.	1.3	5
101	Abundance of the largest subunit of RNA polymerase II in the nucleus is regulated by nucleo-cytoplasmic shuttling. Experimental Cell Research, 2006, 312, 2557-2567.	1.2	5
102	Cotranscriptional RNA checkpoints. Epigenomics, 2010, 2, 449-455.	1.0	5
103	STaQTool: Spot tracking and quantification tool for monitoring splicing of single pre-mRNA molecules in living cells. Methods, 2016, 98, 143-149.	1.9	5
104	Semithin cryosections as a tool to perform high resolution immunofluorescence and in situ hybridization analysis of the nervous tissue: a study in the supraoptic nucleus. Journal of Neuroscience Methods, 1997, 75, 137-145.	1.3	4
105	Single-Molecule Imaging of RNA Splicing in Live Cells. Methods in Enzymology, 2015, 558, 571-585.	0.4	4
106	Nuclear Organization and Splicing Control. Advances in Experimental Medicine and Biology, 2007, 623, 1-13.	0.8	4
107	Interactions of adenovirus with the nucleus of the host cell. Reviews in Medical Virology, 1995, 5, 213-218.	3.9	3
108	Expression Profiling in Ovarian Cancer Reveals Coordinated Regulation of BRCA1/2 and Homologous Recombination Genes. Biomedicines, 2022, 10, 199.	1.4	3

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109	Follow that Messenger: Live-Imaging a Journey out of the Nucleus. Developmental Cell, 2010, 18, 880-882.	3.1	2
110	Single-Molecule Live-Cell Visualization of Pre-mRNA Splicing. Methods in Molecular Biology, 2016, 1358, 335-350.	0.4	2
111	Nuclear morphogenesis and the onset of transcriptional activity in early hamster embryos. Chromosoma, 1996, 105, 1-11.	1.0	2
112	The Potential of Targeting Splicing for Cancer Therapy. Cancer Drug Discovery and Development, 2014, , 313-336.	0.2	1
113	RNA imaging: seeing is believing. Rna, 2015, 21, 580-581.	1.6	1
114	Pseudouridylation: A new player in co-transcriptional splicing regulation. Molecular Cell, 2022, 82, 495-496.	4.5	1
115	In Situ Hybridization for Simultaneous Detection of DNA, RNA, and Protein. , 2006, , 419-427.		0
116	Quantitative Image Analysis of Single-Molecule mRNA Dynamics in Living Cells. Methods in Molecular Biology, 2017, 1563, 229-242.	0.4	0
117	Nuclear Organization of snRNPs and Splicing Factors. Molecular Biology Intelligence Unit, 1995, , 163-171.	0.2	0