

# Manuel Ares Jr

## List of Publications by Year in Descending Order

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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.

104  
papers

10,924  
citations

53  
h-index

104  
g-index

121  
ext. papers

12,706  
ext. citations

12.4  
avg, IF

6.1  
L-index

#	Paper	IF	Citations
104	Synthesis of modified nucleotide polymers by the poly(U) polymerase Cid1: application to direct RNA sequencing on nanopores. <i>Rna</i> , <b>2021</b> , 27, 1497-1511	5.8	0
103	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. <i>Nature Methods</i> , <b>2020</b> , 17, 481-494	21.6	39
102	The UCSC SARS-CoV-2 Genome Browser. <i>Nature Genetics</i> , <b>2020</b> , 52, 991-998	36.3	44
101	Rapidly evolving protointrons in <i>Saccharomyces</i> genomes revealed by a hungry spliceosome. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008249	6	5
100	Cus2 enforces the first ATP-dependent step of splicing by binding to yeast SF3b1 through a UHM-ULM interaction. <i>Rna</i> , <b>2019</b> , 25, 1020-1037	5.8	12
99	Evidence for convergent evolution of SINE-directed Staufen-mediated mRNA decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 968-973	11.5	26
98	Autogenous cross-regulation of mRNA processing and translation balances functions in splicing and translation. <i>Genes and Development</i> , <b>2017</b> , 31, 1894-1909	12.6	27
97	RNA-binding protein CPEB1 remodels host and viral RNA landscapes. <i>Nature Structural and Molecular Biology</i> , <b>2016</b> , 23, 1101-1110	17.6	24
96	Quaking promotes monocyte differentiation into pro-atherogenic macrophages by controlling pre-mRNA splicing and gene expression. <i>Nature Communications</i> , <b>2016</b> , 7, 10846	17.4	66
95	Protein-RNA Networks Regulated by Normal and ALS-Associated Mutant HNRNPA2B1 in the Nervous System. <i>Neuron</i> , <b>2016</b> , 92, 780-795	13.9	94
94	Distinct and shared functions of ALS-associated proteins TDP-43, FUS and TAF15 revealed by multisystem analyses. <i>Nature Communications</i> , <b>2016</b> , 7, 12143	17.4	94
93	SMITten by the Speed of Splicing. <i>Cell</i> , <b>2016</b> , 165, 265-7	56.2	1
92	Coffee with Ribohipster. <i>Rna</i> , <b>2015</b> , 21, 494-6	5.8	1
91	Intron Invasions Trace Algal Speciation and Reveal Nearly Identical Arctic and Antarctic <i>Micromonas</i> Populations. <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 2219-35	8.3	34
90	Methods for processing high-throughput RNA sequencing data. <i>Cold Spring Harbor Protocols</i> , <b>2014</b> , 2014, 1139-48	1.2	4
89	Basic quantitative polymerase chain reaction using real-time fluorescence measurements. <i>Cold Spring Harbor Protocols</i> , <b>2014</b> , 2014, pdb.prot080903	1.2	2
88	Context-dependent control of alternative splicing by RNA-binding proteins. <i>Nature Reviews Genetics</i> , <b>2014</b> , 15, 689-701	30.1	573

87	Microarray slide hybridization using fluorescently labeled cDNA. <i>Cold Spring Harbor Protocols</i> , <b>2014</b> , 2014, 124-9	1.2	2
86	Scanning microarray slides. <i>Cold Spring Harbor Protocols</i> , <b>2014</b> , 2014, 214-8	1.2	2
85	Methods for processing microarray data. <i>Cold Spring Harbor Protocols</i> , <b>2014</b> , 2014, 225-9	1.2	
84	Tips on hybridizing, washing, and scanning affymetrix microarrays. <i>Cold Spring Harbor Protocols</i> , <b>2014</b> , 2014, 219-24	1.2	2
83	RBPmap: a web server for mapping binding sites of RNA-binding proteins. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W361-7	20.1	253
82	Competition between pre-mRNAs for the splicing machinery drives global regulation of splicing. <i>Molecular Cell</i> , <b>2013</b> , 51, 338-48	17.6	80
81	A high-throughput splicing assay identifies new classes of inhibitors of human and yeast spliceosomes. <i>Journal of Biomolecular Screening</i> , <b>2013</b> , 18, 1110-20		25
80	Genome-wide analysis reveals SR protein cooperation and competition in regulated splicing. <i>Molecular Cell</i> , <b>2013</b> , 50, 223-35	17.6	208
79	Rbfox1 downregulation and altered calpain 3 splicing by FRG1 in a mouse model of Facioscapulohumeral muscular dystrophy (FSHD). <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003186	6	27
78	Quaking and PTB control overlapping splicing regulatory networks during muscle cell differentiation. <i>Rna</i> , <b>2013</b> , 19, 627-38	5.8	105
77	Safer one-pot synthesis of the SHAPE reagent 1-methyl-7-nitroisatoic anhydride (1m7). <i>Rna</i> , <b>2013</b> , 19, 1857-63	5.8	22
76	Fragmentation of whole-transcriptome RNA using E. coli RNase III. <i>Cold Spring Harbor Protocols</i> , <b>2013</b> , 2013, 479-81	1.2	5
75	Analysis of splicing in vitro using extracts of <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Protocols</i> , <b>2013</b> , 2013, 982-5	1.2	1
74	High-yield synthesis of RNA using T7 RNA polymerase and plasmid DNA or oligonucleotide templates. <i>Cold Spring Harbor Protocols</i> , <b>2013</b> , 2013,	1.2	6
73	Bacterial RNA isolation. <i>Cold Spring Harbor Protocols</i> , <b>2012</b> , 2012, 1024-7	1.2	11
72	Integrative genome-wide analysis reveals cooperative regulation of alternative splicing by hnRNP proteins. <i>Cell Reports</i> , <b>2012</b> , 1, 167-78	10.6	322
71	Structural analysis of the quaking homodimerization interface. <i>Journal of Molecular Biology</i> , <b>2012</b> , 423, 766-81	6.5	24
70	Muscleblind-like 2-mediated alternative splicing in the developing brain and dysregulation in myotonic dystrophy. <i>Neuron</i> , <b>2012</b> , 75, 437-50	13.9	234

69	Isolation of total RNA from yeast cell cultures. <i>Cold Spring Harbor Protocols</i> , <b>2012</b> , 2012, 1082-6	1.2	30
68	Muscleblind-like 1 knockout mice reveal novel splicing defects in the myotonic dystrophy brain. <i>PLoS ONE</i> , <b>2012</b> , 7, e33218	3.7	66
67	The splicing regulator Rbfox2 is required for both cerebellar development and mature motor function. <i>Genes and Development</i> , <b>2012</b> , 26, 445-60	12.6	148
66	The splicing regulator Rbfox1 (A2BP1) controls neuronal excitation in the mammalian brain. <i>Nature Genetics</i> , <b>2011</b> , 43, 706-11	36.3	242
65	Role of the ubiquitin-like protein Hub1 in splice-site usage and alternative splicing. <i>Nature</i> , <b>2011</b> , 474, 173-8	50.4	62
64	Alternative splicing variability: exactly how similar are two identical cells?. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 505	12.2	2
63	Competencies: a cure for pre-med curriculum. <i>Science</i> , <b>2011</b> , 334, 760-1	33.3	1
62	Expanding the diversity of mycobacteriophages: insights into genome architecture and evolution. <i>PLoS ONE</i> , <b>2011</b> , 6, e16329	3.7	98
61	Aberrant alternative splicing and extracellular matrix gene expression in mouse models of myotonic dystrophy. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 187-93	17.6	254
60	Integration of a splicing regulatory network within the meiotic gene expression program of <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , <b>2010</b> , 24, 2693-704	12.6	36
59	Purification of RNA using TRIzol (TRI reagent). <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5439	1.2	610
58	Invariant U2 snRNA nucleotides form a stem loop to recognize the intron early in splicing. <i>Molecular Cell</i> , <b>2010</b> , 38, 416-27	17.6	56
57	Determining the yield and quality of purified RNA. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.top82	1.2	10
56	Removal of DNA from RNA. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5443	1.2	16
55	Purification of RNA by SDS solubilization and phenol extraction. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5438	1.2	32
54	Ethanol precipitation of RNA and the use of carriers. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5440	1.2	33
53	Removal of ribosomal subunits (and rRNA) from cytoplasmic extracts before solubilization with SDS and deproteinization. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5442	1.2	5
52	Preparation of cytoplasmic and nuclear RNA from tissue culture cells. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5441	1.2	31

51	Guidelines for the use of RNA purification kits. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.ip79	1.2	10
50	Enrichment of poly(A)+ mRNA using immobilized oligo(dT). <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5454	1.2	13
49	Nondenaturing agarose gel electrophoresis of RNA. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5445	1.2	16
48	Polyacrylamide gel electrophoresis of RNA. <i>Cold Spring Harbor Protocols</i> , <b>2010</b> , 2010, pdb.prot5444	1.2	32
47	Sam68 regulates a set of alternatively spliced exons during neurogenesis. <i>Molecular and Cellular Biology</i> , <b>2009</b> , 29, 201-13	4.8	86
46	Developmental expression profile of quaking, a candidate gene for schizophrenia, and its target genes in human prefrontal cortex and hippocampus shows regional specificity. <i>Journal of Neuroscience Research</i> , <b>2008</b> , 86, 785-96	4.4	22
45	Regulated Alternative Splicing During Myogenesis. <i>FASEB Journal</i> , <b>2008</b> , 22, 602.1	0.9	
44	Sing the genome electric: excited cells adjust their splicing. <i>PLoS Biology</i> , <b>2007</b> , 5, e55	9.7	2
43	Rearrangement of competing U2 RNA helices within the spliceosome promotes multiple steps in splicing. <i>Genes and Development</i> , <b>2007</b> , 21, 811-20	12.6	94
42	A post-transcriptional regulatory switch in polypyrimidine tract-binding proteins reprograms alternative splicing in developing neurons. <i>Genes and Development</i> , <b>2007</b> , 21, 1636-52	12.6	389
41	Structural RNAs of known and unknown function identified in malaria parasites by comparative genomics and RNA analysis. <i>Rna</i> , <b>2007</b> , 13, 1923-39	5.8	75
40	Ultraconserved elements are associated with homeostatic control of splicing regulators by alternative splicing and nonsense-mediated decay. <i>Genes and Development</i> , <b>2007</b> , 21, 708-18	12.6	391
39	Unusual intron conservation near tissue-regulated exons found by splicing microarrays. <i>PLoS Computational Biology</i> , <b>2006</b> , 2, e4	5	165
38	Accumulation of unstable promoter-associated transcripts upon loss of the nuclear exosome subunit Rrp6p in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 3262-7	11.5	194
37	Prp43p is a DEAH-box spliceosome disassembly factor essential for ribosome biogenesis. <i>Molecular and Cellular Biology</i> , <b>2006</b> , 26, 523-34	4.8	88
36	Cell type and culture condition-dependent alternative splicing in human breast cancer cells revealed by splicing-sensitive microarrays. <i>Cancer Research</i> , <b>2006</b> , 66, 1990-9	10.1	71
35	An RNA gene expressed during cortical development evolved rapidly in humans. <i>Nature</i> , <b>2006</b> , 443, 167-70	32.4	691
34	Detection and measurement of alternative splicing using splicing-sensitive microarrays. <i>Methods</i> , <b>2005</b> , 37, 345-59	4.6	82

33	The structure of a rigorously conserved RNA element within the SARS virus genome. <i>PLoS Biology</i> , <b>2005</b> , 3, e5	9.7	97
32	Exploring functional relationships between components of the gene expression machinery. <i>Nature Structural and Molecular Biology</i> , <b>2005</b> , 12, 175-82	17.6	88
31	Mer1p is a modular splicing factor whose function depends on the conserved U2 snRNP protein Snu17p. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 1242-50	20.1	34
30	Genome-wide searching for pseudouridylation guide snoRNAs: analysis of the <i>Saccharomyces cerevisiae</i> genome. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 4281-96	20.1	124
29	A new alpha-helical extension promotes RNA binding by the dsRBD of Rnt1p RNase III. <i>EMBO Journal</i> , <b>2004</b> , 23, 2468-77	13	53
28	Interdisciplinary research and the undergraduate biology student. <i>Nature Structural and Molecular Biology</i> , <b>2004</b> , 11, 1170-2	17.6	15
27	Perturbation of transcription elongation influences the fidelity of internal exon inclusion in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , <b>2003</b> , 9, 993-1006	5.8	130
26	Gene structure-based splice variant deconvolution using a microarray platform. <i>Bioinformatics</i> , <b>2003</b> , 19 Suppl 1, i315-22	7.2	78
25	ATP requirement for Prp5p function is determined by Cus2p and the structure of U2 small nuclear RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 13857-62	11.5	62
24	Genomewide analysis of mRNA processing in yeast using splicing-specific microarrays. <i>Science</i> , <b>2002</b> , 296, 907-10	33.3	332
23	Removal of a single alpha-tubulin gene intron suppresses cell cycle arrest phenotypes of splicing factor mutations in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , <b>2002</b> , 22, 801-15	4.8	64
22	Searching yeast intron data at Ares lab Web site. <i>Methods in Enzymology</i> , <b>2002</b> , 350, 380-92	1.7	38
21	Substrate recognition by a eukaryotic RNase III: the double-stranded RNA-binding domain of Rnt1p selectively binds RNA containing a 5UAGNN-3Utetraloop. <i>Rna</i> , <b>2000</b> , 6, 1142-56	5.8	54
20	Functional Cus1p is found with Hsh155p in a multiprotein splicing factor associated with U2 snRNA. <i>Molecular and Cellular Biology</i> , <b>2000</b> , 20, 2176-85	4.8	27
19	A yeast intronic splicing enhancer and Nam8p are required for Mer1p-activated splicing. <i>Molecular Cell</i> , <b>2000</b> , 6, 329-38	17.6	67
18	Knowledge-based analysis of microarray gene expression data by using support vector machines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2000</b> , 97, 262-7	11.5	1647
17	ATP can be dispensable for prespliceosome formation in yeast. <i>Genes and Development</i> , <b>2000</b> , 14, 97-107	12.6	44
16	Genome-wide bioinformatic and molecular analysis of introns in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , <b>1999</b> , 5, 221-34	5.8	226

15	A handful of intron-containing genes produces the lion's share of yeast mRNA. <i>Rna</i> , <b>1999</b> , 5, 1138-9	5.8	118
14	Depletion of yeast RNase III blocks correct U2 3' end formation and results in polyadenylated but functional U2 snRNA. <i>EMBO Journal</i> , <b>1998</b> , 17, 3738-46	13	102
13	CUS2, a yeast homolog of human Tat-SF1, rescues function of misfolded U2 through an unusual RNA recognition motif. <i>Molecular and Cellular Biology</i> , <b>1998</b> , 18, 5000-9	4.8	69
12	Circular mRNA can direct translation of extremely long repeating-sequence proteins in vivo. <i>Rna</i> , <b>1998</b> , 4, 1047-54	5.8	91
11	Intron self-complementarity enforces exon inclusion in a yeast pre-mRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 12467-72	11.5	70
10	RNase III cleaves eukaryotic preribosomal RNA at a U3 snoRNP-dependent site. <i>Cell</i> , <b>1996</b> , 85, 115-24	56.2	205
9	Rearrangement of snRNA structure during assembly and function of the spliceosome. <i>Progress in Molecular Biology and Translational Science</i> , <b>1995</b> , 50, 131-59		62
8	Mutations define essential and nonessential U2 RNA structures. <i>Molecular Biology Reports</i> , <b>1990</b> , 14, 131-2	2.8	7
7	Internal sequences that distinguish yeast from metazoan U2 snRNA are unnecessary for pre-mRNA splicing. <i>Nature</i> , <b>1988</b> , 334, 450-3	50.4	64
6	U2 RNA from yeast is unexpectedly large and contains homology to vertebrate U4, U5, and U6 small nuclear RNAs. <i>Cell</i> , <b>1986</b> , 47, 49-59	56.2	164
5	Human genes for U2 small nuclear RNA map to a major adenovirus 12 modification site on chromosome 17. <i>Nature</i> , <b>1985</b> , 314, 115-6	50.4	80
4	Sequences required for 3' end formation of human U2 small nuclear RNA. <i>Cell</i> , <b>1985</b> , 42, 193-202	56.2	130
3	Isolation and genetic characterization of a mutation affecting ribosomal resistance to cycloheximide in <i>Tetrahymena</i> . <i>Genetics</i> , <b>1978</b> , 90, 463-74	4	18
2	Autogenous cross-regulation of Quaking mRNA processing and translation balances Quaking functions in splicing and translation		1
1	Rapidly evolving protointrons in <i>Saccharomyces</i> genomes revealed by a hungry spliceosome		2