Manuel Ares Jr

List of Publications by Year
in descending order

105	13,879	28274	29157
papers	citations	55 h-index	104 g-index

121	121	121	17117
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Concerted modification of nucleotides at functional centers of the ribosome revealed by single-molecule RNA modification profiling. ELife, 2022, 11, .	6.0	17
2	Synthesis of modified nucleotide polymers by the poly(U) polymerase Cid1: application to direct RNA sequencing on nanopores. Rna, 2021, 27, 1497-1511.	3.5	12
3	The UCSC SARS-CoV-2 Genome Browser. Nature Genetics, 2020, 52, 991-998.	21.4	79
4	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. Nature Methods, 2020, 17, 481-494.	19.0	97
5	Rapidly evolving protointrons in Saccharomyces genomes revealed by a hungry spliceosome. PLoS Genetics, 2019, 15, e1008249.	3.5	16
6	Cus2 enforces the first ATP-dependent step of splicing by binding to yeast SF3b1 through a UHMâ€“ULM interaction. Rna, 2019, 25, 1020-1037.	3.5	19
7	Evidence for convergent evolution of SINE-directed Staufen-mediated mRNA decay. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 968-973.	7.1	37
8	Autogenous cross-regulation of Quaking mRNA processing and translation balances Quaking functions in splicing and translation. Genes and Development, 2017, 31, 1894-1909.	5.9	40
9	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
10	SMITten by the Speed of Splicing. Cell, 2016, 165, 265-267.	28.9	1
11	RNA-binding protein CPEB1 remodels host and viral RNA landscapes. Nature Structural and Molecular Biology, 2016, 23, 1101-1110.	8.2	40
12	Quaking promotes monocyte differentiation into pro-atherogenic macrophages by controlling pre-mRNA splicing and gene expression. Nature Communications, 2016, 7, 10846.	12.8	87
13	Protein-RNA Networks Regulated by Normal and ALS-Associated Mutant HNRNPA2B1 in the Nervous System. Neuron, 2016, 92, 780-795.	8.1	137
14	Abstract 47: Quaking Post-Transcriptionally Promotes Differentiation of Monocytes Into Pro-Atherogenic Macrophages by Controling Pre-mRNA Splicing and Gene Expression. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, .	2.4	0
15	Coffee with Ribohipster. Rna, 2015, 21, 494-496.	3.5	1
16	Intron Invasions Trace Algal Speciation and Reveal Nearly Identical Arctic and AntarcticMicromonasPopulations. Molecular Biology and Evolution, 2015, 32, 2219-2235.	8.9	48
17	Microarray Slide Hybridization Using Fluorescently Labeled cDNA. Cold Spring Harbor Protocols, 2014, 2014, pdb.prot080135.	0.3	2
18	Scanning Microarray Slides. Cold Spring Harbor Protocols, 2014, 2014, pdb.prot080481.	0.3	2

#	Article	IF	Citations
19	Methods for Processing Microarray Data. Cold Spring Harbor Protocols, 2014, 2014, pdb.prot080507.	0.3	0
20	Tips on Hybridizing, Washing, and Scanning Affymetrix Microarrays. Cold Spring Harbor Protocols, 2014, 2014, pdb.prot080499.	0.3	4
21	RBPmap: a web server for mapping binding sites of RNA-binding proteins. Nucleic Acids Research, 2014, 42, W361-W367.	14.5	409
22	Methods for Processing High-Throughput RNA Sequencing Data. Cold Spring Harbor Protocols, 2014, 2014, pdb.top083352.	0.3	6
23	Basic Quantitative Polymerase Chain Reaction Using Real-Time Fluorescence Measurements. Cold Spring Harbor Protocols, 2014, 2014, pdb.prot080903-pdb.prot080903.	0.3	2
24	Context-dependent control of alternative splicing by RNA-binding proteins. Nature Reviews Genetics, 2014, 15, 689-701.	16.3	854
25	Competition between Pre-mRNAs for the Splicing Machinery Drives Global Regulation of Splicing. Molecular Cell, 2013, 51, 338-348.	9.7	99
26	A High-Throughput Splicing Assay Identifies New Classes of Inhibitors of Human and Yeast Spliceosomes. Journal of Biomolecular Screening, 2013, 18, 1110-1120.	2.6	31
27	Genome-wide Analysis Reveals SR Protein Cooperation and Competition in Regulated Splicing. Molecular Cell, 2013, 50, 223-235.	9.7	261
28	Rbfox1 Downregulation and Altered Calpain 3 Splicing by FRG1 in a Mouse Model of Facioscapulohumeral Muscular Dystrophy (FSHD). PLoS Genetics, 2013, 9, e1003186.	3.5	32
29	Quaking and PTB control overlapping splicing regulatory networks during muscle cell differentiation. Rna, 2013, 19, 627-638.	3.5	137
30	Safer one-pot synthesis of the â€˜SHAPEâ€™ reagent 1-methyl-7-nitroisatoic anhydride (1m7). Rna, 2013, 19, 1857-1863.	3.5	29
31	Fragmentation of Whole-Transcriptome RNA Using E. coli RNase III. Cold Spring Harbor Protocols, 2013, 2013, pdb.prot074369-pdb.prot074369.	0.3	7
32	Analysis of Splicing In Vitro Using Extracts ofSaccharomyces cerevisiae:. Cold Spring Harbor Protocols, 2013, 2013, pdb.prot078121.	0.3	4
33	High-Yield Synthesis of RNA Using T7 RNA Polymerase and Plasmid DNA or Oligonucleotide Templates. Cold Spring Harbor Protocols, 2013, 2013, pdb.prot078535.	0.3	8
34	The splicing regulator Rbfox2 is required for both cerebellar development and mature motor function. Genes and Development, 2012, 26, 445-460.	5.9	186
35	Bacterial RNA Isolation. Cold Spring Harbor Protocols, 2012, 2012, pdb.prot071068.	0.3	17
36	Integrative Genome-wide Analysis Reveals Cooperative Regulation of Alternative Splicing by hnRNP Proteins. Cell Reports, 2012, 1, 167-178.	6.4	420

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37	Structural Analysis of the Quaking Homodimerization Interface. Journal of Molecular Biology, 2012, 423, 766-781.	4.2	26
38	Muscleblind-like 2-Mediated Alternative Splicing in the Developing Brain and Dysregulation in Myotonic Dystrophy. Neuron, 2012, 75, 437-450.	8.1	296
39	Isolation of Total RNA from Yeast Cell Cultures: Figure 1.. Cold Spring Harbor Protocols, 2012, 2012, pdb.prot071456.	0.3	41
40	Muscleblind-Like 1 Knockout Mice Reveal Novel Splicing Defects in the Myotonic Dystrophy Brain. PLoS ONE, 2012, 7, e33218.	2.5	79
41	The splicing regulator Rbfox1 (A2BP1) controls neuronal excitation in the mammalian brain. Nature Genetics, 2011, 43, 706-711.	21.4	297
42	Role of the ubiquitin-like protein Hub1 in splice-site usage and alternative splicing. Nature, 2011, 474, 173-178.	27.8	79
43	Alternative splicing variability: exactly how similar are two identical cells?. Molecular Systems Biology, 2011, 7, 505.	7.2	3
44	Competencies: A Cure for Pre-Med Curriculum. Science, 2011, 334, 760-761.	12.6	2
45	Expanding the Diversity of Mycobacteriophages: Insights into Genome Architecture and Evolution. PLoS ONE, 2011, 6, e16329.	2.5	133
46	Determining the Yield and Quality of Purified RNA. Cold Spring Harbor Protocols, 2010, 2010, pdb.top82.	0.3	10
47	Removal of DNA from RNA. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5443.	0.3	21
48	Purification of RNA by SDS Solubilization and Phenol Extraction. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5438.	0.3	46
49	Ethanol Precipitation of RNA and the Use of Carriers. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5440.	0.3	39
50	Removal of Ribosomal Subunits (and rRNA) from Cytoplasmic Extracts before Solubilization with SDS and Deproteinization. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5442-pdb.prot5442.	0.3	5
51	Preparation of Cytoplasmic and Nuclear RNA from Tissue Culture Cells. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5441.	0.3	42
52	Guidelines for the Use of RNA Purification Kits. Cold Spring Harbor Protocols, 2010, 2010, pdb.ip79.	0.3	13
53	Enrichment of Poly(A)⁺ mRNA Using Immobilized Oligo(dT). Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5454.	0.3	18
54	Nondenaturing Agarose Gel Electrophoresis of RNA. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5445.	0.3	21

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55	Polyacrylamide Gel Electrophoresis of RNA. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5444-pdb.prot5444.	0.3	37
56	Aberrant alternative splicing and extracellular matrix gene expression in mouse models of myotonic dystrophy. Nature Structural and Molecular Biology, 2010, 17, 187-193.	8.2	301
57	Integration of a splicing regulatory network within the meiotic gene expression program of Saccharomyces cerevisiae. Genes and Development, 2010, 24, 2693-2704.	5.9	41
58	Purification of RNA Using TRIzol (TRI Reagent). Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5439.	0.3	1,085
59	Invariant U2 snRNA Nucleotides Form a Stem Loop to Recognize the Intron Early in Splicing. Molecular Cell, 2010, 38, 416-427.	9.7	69
60	Sam68 Regulates a Set of Alternatively Spliced Exons during Neurogenesis. Molecular and Cellular Biology, 2009, 29, 201-213.	2.3	105
61	Developmental expression profile of quaking, a candidate gene for schizophrenia, and its target genes in human prefrontal cortex and hippocampus shows regional specificity. Journal of Neuroscience Research, 2008, 86, 785-796.	2.9	28
62	Stuttering against marginotomy. Nature Structural and Molecular Biology, 2008, 15, 18-19.	8.2	5
63	Regulated Alternative Splicing During Myogenesis. FASEB Journal, 2008, 22, 602.1.	0.5	0
64	Sing the Genome Electric: Excited Cells Adjust Their Splicing. PLoS Biology, 2007, 5, e55.	5.6	3
65	Rearrangement of competing U2 RNA helices within the spliceosome promotes multiple steps in splicing. Genes and Development, 2007, 21, 811-820.	5.9	108
66	A post-transcriptional regulatory switch in polypyrimidine tract-binding proteins reprograms alternative splicing in developing neurons. Genes and Development, 2007, 21, 1636-1652.	5.9	464
67	Structural RNAs of known and unknown function identified in malaria parasites by comparative genomics and RNA analysis. Rna, 2007, 13, 1923-1939.	3.5	89
68	Ultraconserved elements are associated with homeostatic control of splicing regulators by alternative splicing and nonsense-mediated decay. Genes and Development, 2007, 21, 708-718.	5.9	470
69	An RNA gene expressed during cortical development evolved rapidly in humans. Nature, 2006, 443, 167-172.	27.8	884
70	Unusual Intron Conservation near Tissue-Regulated Exons Found by Splicing Microarrays. PLoS Computational Biology, 2006, 2, e4.	3.2	175
71	Accumulation of unstable promoter-associated transcripts upon loss of the nuclear exosome subunit Rrp6p in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3262-3267.	7.1	211
72	Prp43p Is a DEAH-Box Spliceosome Disassembly Factor Essential for Ribosome Biogenesis. Molecular and Cellular Biology, 2006, 26, 523-534.	2.3	102

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73	Cell Type and Culture Conditionâ€“Dependent Alternative Splicing in Human Breast Cancer Cells Revealed by Splicing-Sensitive Microarrays. Cancer Research, 2006, 66, 1990-1999.	0.9	82
74	Exploring functional relationships between components of the gene expression machinery. Nature Structural and Molecular Biology, 2005, 12, 175-182.	8.2	89
75	Detection and measurement of alternative splicing using splicing-sensitive microarrays. Methods, 2005, 37, 345-359.	3.8	89
76	Mer1p is a modular splicing factor whose function depends on the conserved U2 snRNP protein Snu17p. Nucleic Acids Research, 2004, 32, 1242-1250.	14.5	36
77	Genome-wide searching for pseudouridylation guide snoRNAs: analysis of the Saccharomyces cerevisiae genome. Nucleic Acids Research, 2004, 32, 4281-4296.	14.5	139
78	The Structure of a Rigorously Conserved RNA Element within the SARS Virus Genome. PLoS Biology, 2004, 3, e5.	5.6	137
79	A new Î±-helical extension promotes RNA binding by the dsRBD of Rnt1p RNAse III. EMBO Journal, 2004, 23, 2468-2477.	7.8	56
80	Interdisciplinary research and the undergraduate biology student. Nature Structural and Molecular Biology, 2004, 11, 1170-1172.	8.2	16
81	Perturbation of transcription elongation influences the fidelity of internal exon inclusion in Saccharomyces cerevisiae. Rna, 2003, 9, 993-1006.	3.5	146
82	Gene structure-based splice variant deconvolution using a microarry platform. Bioinformatics, 2003, 19, i315-i322.	4.1	88
83	ATP requirement for Prp5p function is determined by Cus2p and the structure of U2 small nuclear RNA. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13857-13862.	7.1	75
84	Genomewide Analysis of mRNA Processing in Yeast Using Splicing-Specific Microarrays. Science, 2002, 296, 907-910.	12.6	359
85	Removal of a Single Î±-Tubulin Gene Intron Suppresses Cell Cycle Arrest Phenotypes of Splicing Factor Mutations in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2002, 22, 801-815.	2.3	69
86	Searching yeast intron data at ares lab web site. Methods in Enzymology, 2002, 350, 380-392.	1.0	45
87	Substrate recognition by a eukaryotic RNase III: The double-stranded RNA-binding domain of Rnt1p selectively binds RNA containing a 5â€²-AGNN-3â€² tetraloop. Rna, 2000, 6, 1142-1156.	3.5	57
88	Functional Cus1p Is Found with Hsh155p in a Multiprotein Splicing Factor Associated with U2 snRNA. Molecular and Cellular Biology, 2000, 20, 2176-2185.	2.3	28
89	A Yeast Intronic Splicing Enhancer and Nam8p Are Required for Mer1p-Activated Splicing. Molecular Cell, 2000, 6, 329-338.	9.7	73
90	Knowledge-based analysis of microarray gene expression data by using support vector machines. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 262-267.	7.1	2,034

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91	ATP can be dispensable for prespliceosome formation in yeast. Genes and Development, 2000, 14, 97-107.	5.9	55
92	Genome-wide bioinformatic and molecular analysis of introns in Saccharomyces cerevisiae. Rna, 1999, 5, 221-234.	3.5	256
93	A handful of intron-containing genes produces the lion's share of yeast mRNA. Rna, 1999, 5, 1138-1139.	3.5	131
94	Depletion of yeast RNase III blocks correct U2 3' end formation and results in polyadenylated but functional U2 snRNA. EMBO Journal, 1998, 17, 3738-3746.	7.8	107
95	CUS2, a Yeast Homolog of Human Tat-SF1, Rescues Function of Misfolded U2 through an Unusual RNA Recognition Motif. Molecular and Cellular Biology, 1998, 18, 5000-5009.	2.3	75
96	Circular mRNA can direct translation of extremely long repeating-sequence proteins in vivo. Rna, 1998, 4, 1047-1054.	3.5	119
97	Intron self-complementarity enforces exon inclusion in a yeast pre-mRNA. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 12467-12472.	7.1	82
98	RNase III Cleaves Eukaryotic Preribosomal RNA at a U3 snoRNP-Dependent Site. Cell, 1996, 85, 115-124.	28.9	215
99	Rearrangement of snRNA Structure during Assembly and Function of the Spliceosome. Progress in Molecular Biology and Translational Science, 1995, 50, 131-159.	1.9	71
100	Mutations define essential and nonessential U2 RNA structures. Molecular Biology Reports, 1990, 14, 131-132.	2.3	7
101	Internal sequences that distinguish yeast from metazoan U2 snRNA are unnecessary for pre-mRNA splicing. Nature, 1988, 334, 450-453.	27.8	65
102	U2 RNA from yeast is unexpectedly large and contains homology to vertebrate U4, U5, and U6 small nuclear RNAs. Cell, 1986, 47, 49-59.	28.9	168
103	Human genes for U2 small nuclear RNA map to a major adenovirus 12 modification site on chromosome 17. Nature, 1985, 314, 115-116.	27.8	89
104	Sequences required for 3â€² end formation of human U2 small nuclear RNA. Cell, 1985, 42, 193-202.	28.9	136
105	ISOLATION AND GENETIC CHARACTERIZATION OF A MUTATION AFFECTING RIBOSOMAL RESISTANCE TO CYCLOHEXIMIDE IN TETRAHYMENA. Genetics, 1978, 90, 463-474.	2.9	21