

# James L Manley

## List of Publications by Year in descending order

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264  
papers

32,960  
citations

2802

94  
h-index

4548

171  
g-index

271  
all docs

271  
docs citations

271  
times ranked

25748  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA-dependent transcription of adenovirus genes in a soluble whole-cell extract.. Proceedings of the National Academy of Sciences of the United States of America, 1980, 77, 3855-3859.	7.1	1,329
2	Mechanisms of alternative splicing regulation: insights from molecular and genomics approaches. Nature Reviews Molecular Cell Biology, 2009, 10, 741-754.	37.0	1,037
3	HnRNP proteins controlled by c-Myc deregulate pyruvate kinase mRNA splicing in cancer. Nature, 2010, 463, 364-368.	27.8	962
4	Alternative polyadenylation of mRNA precursors. Nature Reviews Molecular Cell Biology, 2017, 18, 18-30.	37.0	848
5	Structural basis for signal transduction by the Toll/interleukin-1 receptor domains. Nature, 2000, 408, 111-115.	27.8	714
6	Alternative pre-mRNA splicing regulation in cancer: pathways and programs unhinged. Genes and Development, 2010, 24, 2343-2364.	5.9	697
7	Inactivation of the SR Protein Splicing Factor ASF/SF2 Results in Genomic Instability. Cell, 2005, 122, 365-378.	28.9	655
8	Mechanisms and Consequences of Alternative Polyadenylation. Molecular Cell, 2011, 43, 853-866.	9.7	626
9	Protein-protein interactions and 5'-splice-site recognition in mammalian mRNA precursors. Nature, 1994, 368, 119-124.	27.8	594
10	The RNA polymerase II CTD coordinates transcription and RNA processing. Genes and Development, 2012, 26, 2119-2137.	5.9	513
11	Transcriptional repression of eukaryotic promoters. Cell, 1989, 59, 405-408.	28.9	512
12	A protein factor, ASF, controls cell-specific alternative splicing of SV40 early pre-mRNA in vitro. Cell, 1990, 62, 25-34.	28.9	486
13	A negative element in SMN2 exon 7 inhibits splicing in spinal muscular atrophy. Nature Genetics, 2003, 34, 460-463.	21.4	483
14	The graded distribution of the dorsal morphogen is initiated by selective nuclear transport in Drosophila. Cell, 1989, 59, 1165-1177.	28.9	482
15	Recognition of Trimethylated Histone H3 Lysine 4 Facilitates the Recruitment of Transcription Postinitiation Factors and Pre-mRNA Splicing. Molecular Cell, 2007, 28, 665-676.	9.7	478
16	Molecular Architecture of the Human Pre-mRNA 3' Processing Complex. Molecular Cell, 2009, 33, 365-376.	9.7	475
17	RNA polymerase II and the integration of nuclear events. Genes and Development, 2000, 14, 1415-1429.	5.9	453
18	Polyadenylation factor CPSF-73 is the pre-mRNA 3'-end-processing endonuclease. Nature, 2006, 444, 953-956.	27.8	387

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19	The Polyadenylation Factor CstF-64 Regulates Alternative Processing of IgM Heavy Chain Pre-mRNA during B Cell Differentiation. <i>Cell</i> , 1996, 87, 941-952.	28.9	381
20	Synergistic activation and repression of transcription by Drosophila homeobox proteins. <i>Cell</i> , 1989, 56, 573-583.	28.9	369
21	Primary structure of the human splicing factor asf reveals similarities with drosophila regulators. <i>Cell</i> , 1991, 66, 373-382.	28.9	364
22	R-loop-mediated genomic instability is caused by impairment of replication fork progression. <i>Genes and Development</i> , 2011, 25, 2041-2056.	5.9	361
23	RNA polymerase II is an essential mRNA polyadenylation factor. <i>Nature</i> , 1998, 395, 93-96.	27.8	329
24	ASF/SF2-Regulated CaMKII $\beta$ Alternative Splicing Temporally Reprograms Excitation-Contraction Coupling in Cardiac Muscle. <i>Cell</i> , 2005, 120, 59-72.	28.9	315
25	[35] In Vitro transcription: Whole-cell extract. <i>Methods in Enzymology</i> , 1983, 101, 568-582.	1.0	309
26	Alternative cleavage and polyadenylation: the long and short of it. <i>Trends in Biochemical Sciences</i> , 2013, 38, 312-320.	7.5	297
27	Symplekin and xGLD-2 Are Required for CPEB-Mediated Cytoplasmic Polyadenylation. <i>Cell</i> , 2004, 119, 641-651.	28.9	295
28	The ends of the affair: capping and polyadenylation. , 2000, 7, 838-842.		286
29	Transcription termination by nuclear RNA polymerases. <i>Genes and Development</i> , 2009, 23, 1247-1269.	5.9	280
30	Transcription factor TFIID recruits factor CPSF for formation of 3' end of mRNA. <i>Nature</i> , 1997, 389, 399-402.	27.8	274
31	Misregulation of Pre-mRNA Alternative Splicing in Cancer. <i>Cancer Discovery</i> , 2013, 3, 1228-1237.	9.4	265
32	A rational nomenclature for serine/arginine-rich protein splicing factors (SR proteins): Table 1.. <i>Genes and Development</i> , 2010, 24, 1073-1074.	5.9	262
33	Cell signalling and the control of pre-mRNA splicing. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 727-738.	37.0	257
34	The TET Family of Proteins: Functions and Roles in Disease. <i>Journal of Molecular Cell Biology</i> , 2009, 1, 82-92.	3.3	231
35	The C9ORF72 GGGGCC expansion forms RNA G-quadruplex inclusions and sequesters hnRNP H to disrupt splicing in ALS brains. <i>ELife</i> , 2016, 5, .	6.0	228
36	Base substitution in an intervening sequence of a beta+ thalassaemic human globin gene.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1981, 78, 2455-2459.	7.1	226

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37	The end of the message: multiple protein-RNA interactions define the mRNA polyadenylation site. <i>Genes and Development</i> , 2015, 29, 889-897.	5.9	226
38	Phosphorylation of CPEB by Eg2 Mediates the Recruitment of CPSF into an Active Cytoplasmic Polyadenylation Complex. <i>Molecular Cell</i> , 2000, 6, 1253-1259.	9.7	225
39	Complex Protein Interactions within the Human Polyadenylation Machinery Identify a Novel Component. <i>Molecular and Cellular Biology</i> , 2000, 20, 1515-1525.	2.3	220
40	Systematic Profiling of Poly(A) <sup>+</sup> Transcripts Modulated by Core 3' End Processing and Splicing Factors Reveals Regulatory Rules of Alternative Cleavage and Polyadenylation. <i>PLoS Genetics</i> , 2015, 11, e1005166.	3.5	217
41	Why Is p53 Acetylated?. <i>Cell</i> , 2001, 107, 815-818.	28.9	215
42	Separation and characterization of a poly(A) polymerase and a cleavage/specificity factor required for pre-mRNA polyadenylation. <i>Cell</i> , 1988, 52, 731-742.	28.9	204
43	Dephosphorylated SRp38 acts as a splicing repressor in response to heat shock. <i>Nature</i> , 2004, 427, 553-558.	27.8	202
44	Levels of Polyadenylation Factor CstF-64 Control IgM Heavy Chain mRNA Accumulation and Other Events Associated with B Cell Differentiation. <i>Molecular Cell</i> , 1998, 2, 761-771.	9.7	201
45	Sequence specificity of the human mRNA 5'-adenosine methylase in vitro. <i>Nucleic Acids Research</i> , 1990, 18, 5735-5741.	14.5	200
46	Determinants of SR protein specificity. <i>Current Opinion in Cell Biology</i> , 1999, 11, 358-362.	5.4	199
47	Polyadenylation of mRNA precursors. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1988, 950, 1-12.	2.4	198
48	Splicing-related catalysis by protein-free snRNAs. <i>Nature</i> , 2001, 413, 701-707.	27.8	197
49	The BARD1-CstF-50 Interaction Links mRNA 5' End Formation to DNA Damage and Tumor Suppression. <i>Cell</i> , 2001, 104, 743-753.	28.9	196
50	The Protein Kinase Clk/Sty Directly Modulates SR Protein Activity: Both Hyper- and Hypophosphorylation Inhibit Splicing. <i>Molecular and Cellular Biology</i> , 1999, 19, 6991-7000.	2.3	194
51	CPSF30 and Wdr33 directly bind to AAUAAA in mammalian mRNA 5' end processing. <i>Genes and Development</i> , 2014, 28, 2370-2380.	5.9	193
52	Autoubiquitination of the BRCA1-BARD1 RING Ubiquitin Ligase. <i>Journal of Biological Chemistry</i> , 2002, 277, 22085-22092.	3.4	189
53	Turning on a Fuel Switch of Cancer: hnRNP Proteins Regulate Alternative Splicing of Pyruvate Kinase mRNA. <i>Cancer Research</i> , 2010, 70, 8977-8980.	0.9	189
54	Human Tra2 Proteins Are Sequence-Specific Activators of Pre-mRNA Splicing. <i>Cell</i> , 1998, 93, 139-148.	28.9	186

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55	The SR Protein SRp38 Represses Splicing in M Phase Cells. <i>Cell</i> , 2002, 111, 407-417.	28.9	179
56	Sequence-specific RNA binding by an SR protein requires RS domain phosphorylation: Creation of an SRp40-specific splicing enhancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 1148-1153.	7.1	177
57	Structure and function of the 5'â€²â†'3'â€² exoribonuclease Rat1 and its activating partner Rai1. <i>Nature</i> , 2009, 458, 784-788.	27.8	177
58	RNA-binding proteins in neurodegeneration: mechanisms in aggregate. <i>Genes and Development</i> , 2017, 31, 1509-1528.	5.9	177
59	Base pairing between U2 and U6 snRNAs is necessary for splicing of a mammalian pre-mRNA. <i>Nature</i> , 1991, 352, 818-821.	27.8	176
60	Disease-associated mutation in <i>SRSF2</i> misregulates splicing by altering RNA-binding affinities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4726-34.	7.1	175
61	Phosphorylation-dephosphorylation differentially affects activities of splicing factor ASF/SF2. <i>EMBO Journal</i> , 1998, 17, 6359-6367.	7.8	169
62	hnRNP A1 functions with specificity in repression of SMN2 exon 7 splicing. <i>Human Molecular Genetics</i> , 2007, 16, 3149-3159.	2.9	164
63	Primary structure and expression of bovine poly(A) polymerase. <i>Nature</i> , 1991, 353, 229-234.	27.8	160
64	The RNA polymerase II C-terminal domain promotes splicing activation through recruitment of a U2AF65-Prp19 complex. <i>Genes and Development</i> , 2011, 25, 972-983.	5.9	159
65	Evidence that polyadenylation factor CPSF-73 is the mRNA 3' processing endonuclease. <i>Rna</i> , 2004, 10, 565-573.	3.5	154
66	Cell-cycle related regulation of poly(A) polymerase by phosphorylation. <i>Nature</i> , 1996, 384, 282-285.	27.8	153
67	Functional Interaction of BRCA1-Associated BARD1 with Polyadenylation Factor CstF-50. <i>Science</i> , 1999, 285, 1576-1579.	12.6	152
68	The multifunctional protein p54 <sup>nrb</sup> /PSF recruits the exonuclease XRN2 to facilitate pre-mRNA 3' processing and transcription termination. <i>Genes and Development</i> , 2007, 21, 1779-1789.	5.9	151
69	Pin1 modulates the structure and function of human RNA polymerase II. <i>Genes and Development</i> , 2003, 17, 2765-2776.	5.9	147
70	R Loops and Links to Human Disease. <i>Journal of Molecular Biology</i> , 2017, 429, 3168-3180.	4.2	147
71	Chromatin Binding of SRp20 and ASF/SF2 and Dissociation from Mitotic Chromosomes Is Modulated by Histone H3 Serine 10 Phosphorylation. <i>Molecular Cell</i> , 2009, 33, 450-461.	9.7	145
72	Crystal structure of the human symplekin-Ssu72-CTD phosphopeptide complex. <i>Nature</i> , 2010, 467, 729-733.	27.8	144

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73	A polyadenylation factor subunit is the human homologue of the <i>Drosophila</i> suppressor of forked protein. <i>Nature</i> , 1994, 372, 471-474.	27.8	137
74	RNAP II CTD Phosphorylated on Threonine-4 Is Required for Histone mRNA 3' End Processing. <i>Science</i> , 2011, 334, 683-686.	12.6	136
75	Cotranscriptional processes and their influence on genome stability. <i>Genes and Development</i> , 2006, 20, 1838-1847.	5.9	132
76	ASAP, a Novel Protein Complex Involved in RNA Processing and Apoptosis. <i>Molecular and Cellular Biology</i> , 2003, 23, 2981-2990.	2.3	131
77	Regulation of Plant Developmental Processes by a Novel Splicing Factor. <i>PLoS ONE</i> , 2007, 2, e471.	2.5	131
78	Stability of a PKCI-1-related mRNA is controlled by the splicing factor ASF/SF2: a novel function for SR proteins. <i>Genes and Development</i> , 2002, 16, 594-607.	5.9	128
79	Strange bedfellows: polyadenylation factors at the promoter. <i>Genes and Development</i> , 2003, 17, 1321-1327.	5.9	127
80	BRCA1/BARD1 inhibition of mRNA 3' processing involves targeted degradation of RNA polymerase II. <i>Genes and Development</i> , 2005, 19, 1227-1237.	5.9	126
81	Evolutionarily Conserved Interaction between CstF-64 and PC4 Links Transcription, Polyadenylation, and Termination. <i>Molecular Cell</i> , 2001, 7, 1013-1023.	9.7	125
82	An intronic element contributes to splicing repression in spinal muscular atrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3426-3431.	7.1	123
83	Molecular basis for the recognition of the human AAUAAA polyadenylation signal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1419-E1428.	7.1	121
84	Identification and Functional Characterization of Neo-Poly(A) Polymerase, an RNA Processing Enzyme Overexpressed in Human Tumors. <i>Molecular and Cellular Biology</i> , 2001, 21, 5614-5623.	2.3	120
85	Loss of splicing factor ASF/SF2 induces G2 cell cycle arrest and apoptosis, but inhibits internucleosomal DNA fragmentation. <i>Genes and Development</i> , 2005, 19, 2705-2714.	5.9	120
86	The splicing regulator Sam68 binds to a novel exonic splicing silencer and functions in SMN2 alternative splicing in spinal muscular atrophy. <i>EMBO Journal</i> , 2010, 29, 1235-1247.	7.8	117
87	The tumor suppressor Cdc73 functionally associates with CPSF and CstF mRNA processing factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 755-760.	7.1	116
88	SUMOylation Is an Inhibitory Constraint that Regulates the Prion-like Aggregation and Activity of CPEB3. <i>Cell Reports</i> , 2015, 11, 1694-1702.	6.4	116
89	Mutant p53 cooperates with the SWI/SNF chromatin remodeling complex to regulate <i>VEGFR2</i> in breast cancer cells. <i>Genes and Development</i> , 2015, 29, 1298-1315.	5.9	115
90	Regulation of pre-mRNA splicing in metazoa. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 205-211.	3.3	109

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91	A Complex Signaling Pathway Regulates SRp38 Phosphorylation and Pre-mRNA Splicing in Response to Heat Shock. <i>Molecular Cell</i> , 2007, 28, 79-90.	9.7	108
92	Splicing pathways of SV40 mRNAs in <i>X. laevis</i> oocytes differ in their requirements for snRNPs. <i>Cell</i> , 1984, 37, 927-936.	28.9	107
93	TLS/FUS (translocated in liposarcoma/fused in sarcoma) regulates target gene transcription via single-stranded DNA response elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6030-6035.	7.1	104
94	U1 snRNP-ASF/SF2 interaction and 5' splice site recognition: characterization of required elements. <i>Nucleic Acids Research</i> , 1995, 23, 3260-3267.	14.5	103
95	Splicing of SV40 early pre-mRNA to large T and small t mRNAs utilizes different patterns of lariat branch sites. <i>Cell</i> , 1987, 50, 227-236.	28.9	99
96	Transcriptional Activators Enhance Polyadenylation of mRNA Precursors. <i>Molecular Cell</i> , 2011, 41, 409-418.	9.7	98
97	Structural and biochemical studies of the 5' exoribonuclease Xrn1. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 270-276.	8.2	98
98	An Mtr4/ZFC3H1 complex facilitates turnover of unstable nuclear RNAs to prevent their cytoplasmic transport and global translational repression. <i>Genes and Development</i> , 2017, 31, 1257-1271.	5.9	98
99	Identification of an snRNP-associated kinase activity that phosphorylates arginine/serine rich domains typical of splicing factors. <i>Nucleic Acids Research</i> , 1993, 21, 2815-2822.	14.5	97
100	PP1/PP2A Phosphatases Are Required for the Second Step of Pre-mRNA Splicing and Target Specific snRNP Proteins. <i>Molecular Cell</i> , 2006, 23, 819-829.	9.7	96
101	Terminating the transcript: breaking up is hard to do. <i>Genes and Development</i> , 2006, 20, 1050-1056.	5.9	96
102	Synthesis and degradation of termination and premature-termination fragments of $\beta$ -galactosidase in vitro and in vivo. <i>Journal of Molecular Biology</i> , 1978, 125, 407-432.	4.2	93
103	Accurate and specific polyadenylation of mRNA precursors in a soluble whole-cell lysate. <i>Cell</i> , 1983, 33, 595-605.	28.9	93
104	Inhibition of poly(A) polymerase requires p34cdc2/cyclin B phosphorylation of multiple consensus and non-consensus sites. <i>EMBO Journal</i> , 1998, 17, 1053-1062.	7.8	93
105	Concentration-dependent control of pyruvate kinase M mutually exclusive splicing by hnRNP proteins. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 346-354.	8.2	93
106	A CCAAT box sequence in the adenovirus major late promoter functions as part of an RNA polymerase II termination signal. <i>Cell</i> , 1989, 57, 561-571.	28.9	91
107	Interaction between a transcriptional activator and transcription factor IIB in vivo. <i>Nature</i> , 1993, 362, 549-553.	27.8	91
108	A complex protein assembly catalyzes polyadenylation of mRNA precursors. <i>Current Opinion in Genetics and Development</i> , 1995, 5, 222-228.	3.3	91

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109	XRN2 Links Transcription Termination to DNA Damage and Replication Stress. <i>PLoS Genetics</i> , 2016, 12, e1006107.	3.5	88
110	SRp38 Regulates Alternative Splicing and Is Required for Ca <sup>2+</sup> Handling in the Embryonic Heart. <i>Developmental Cell</i> , 2009, 16, 528-538.	7.0	86
111	A SUMO-dependent interaction between Senataxin and the exosome, disrupted in the neurodegenerative disease AOA2, targets the exosome to sites of transcription-induced DNA damage. <i>Genes and Development</i> , 2013, 27, 2227-2232.	5.9	86
112	Phosphorylation switches the general splicing repressor SRp38 to a sequence-specific activator. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1040-1048.	8.2	85
113	Transcriptome analysis of alternative splicing events regulated by SRSF10 reveals position-dependent splicing modulation. <i>Nucleic Acids Research</i> , 2014, 42, 4019-4030.	14.5	84
114	Disease-Causing Mutations in SF3B1 Alter Splicing by Disrupting Interaction with SUGP1. <i>Molecular Cell</i> , 2019, 76, 82-95.e7.	9.7	84
115	Crystal Structure of Murine CstF-77: Dimeric Association and Implications for Polyadenylation of mRNA Precursors. <i>Molecular Cell</i> , 2007, 25, 863-875.	9.7	83
116	SUMO functions in constitutive transcription and during activation of inducible genes in yeast. <i>Genes and Development</i> , 2010, 24, 1242-1252.	5.9	80
117	Repression of simian virus 40 early transcription by viral DNA replication in human 293 cells. <i>Nature</i> , 1985, 317, 172-175.	27.8	79
118	The transcriptional coactivator PC4/Sub1 has multiple functions in RNA polymerase II transcription. <i>EMBO Journal</i> , 2005, 24, 1009-1020.	7.8	77
119	RBBP6 isoforms regulate the human polyadenylation machinery and modulate expression of mRNAs with AU-rich 3' UTRs. <i>Genes and Development</i> , 2014, 28, 2248-2260.	5.9	76
120	Generation and functional analyses for base-substitution mutants of the adenovirus 2 major late promoter. <i>Nucleic Acids Research</i> , 1984, 12, 9309-9321.	14.5	75
121	Delineating the Structural Blueprint of the Pre-mRNA 3'-End Processing Machinery. <i>Molecular and Cellular Biology</i> , 2014, 34, 1894-1910.	2.3	75
122	Pin1 modulates RNA polymerase II activity during the transcription cycle. <i>Genes and Development</i> , 2007, 21, 2950-2962.	5.9	74
123	TLS Inhibits RNA Polymerase III Transcription. <i>Molecular and Cellular Biology</i> , 2010, 30, 186-196.	2.3	74
124	A human homologue of the <i>Escherichia coli</i> DnaJ heatshock protein. <i>Nucleic Acids Research</i> , 1991, 19, 6645-6645.	14.5	73
125	PARP1 Represses PAP and Inhibits Polyadenylation during Heat Shock. <i>Molecular Cell</i> , 2013, 49, 7-17.	9.7	68
126	A nuclear micrococcal-sensitive, ATP-dependent exoribonuclease degrades uncapped but not capped RNA substrates. <i>Nucleic Acids Research</i> , 1991, 19, 2685-2692.	14.5	67



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127	RNA synthesis in isolated nuclei: Identification and comparison of adenovirus 2 encoded transcripts synthesized in vitro and in vivo. <i>Journal of Molecular Biology</i> , 1979, 135, 171-197.	4.2	66
128	RNA synthesis in isolated nuclei. <i>Journal of Molecular Biology</i> , 1982, 159, 581-599.	4.2	65
129	Cooperation between core promoter elements influences transcriptional activity in vivo.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 1955-1959.	7.1	65
130	Transcriptional repression by p53 involves molecular interactions distinct from those with the TATA box binding protein. <i>Nucleic Acids Research</i> , 1996, 24, 4281-4288.	14.5	65
131	Characterization of the catalytic activity of U2 and U6 snRNAs. <i>Rna</i> , 2003, 9, 892-904.	3.5	65
132	The Prolyl Isomerase Pin1 Functions in Mitotic Chromosome Condensation. <i>Molecular Cell</i> , 2007, 26, 287-300.	9.7	65
133	Structure and function of the S1 nuclease-sensitive site in the adenovirus late promoter. <i>Cell</i> , 1986, 45, 743-751.	28.9	62
134	Physical and functional interactions between Drosophila TRAF2 and Pelle kinase contribute to Dorsal activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8596-8601.	7.1	62
135	Regulation and Substrate Specificity of the SR Protein Kinase Clk/Sty. <i>Molecular and Cellular Biology</i> , 2003, 23, 4139-4149.	2.3	61
136	Nucleotide Binding by the MDM2 RING Domain Facilitates Arf-Independent MDM2 Nucleolar Localization. <i>Molecular Cell</i> , 2003, 12, 875-887.	9.7	60
137	TCF3 alternative splicing controlled by hnRNP H/F regulates E-cadherin expression and hESC pluripotency. <i>Genes and Development</i> , 2018, 32, 1161-1174.	5.9	60
138	Ectopic expression of the Drosophila tramtrack gene results in multiple embryonic defects, including repression of even-skipped and fushi tarazu. <i>Mechanisms of Development</i> , 1992, 38, 183-195.	1.7	57
139	The human papillomavirus type 16 negative regulatory RNA element interacts with three proteins that act at different posttranscriptional levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 4677-4682.	7.1	56
140	RNA Surveillance by the Nuclear RNA Exosome: Mechanisms and Significance. <i>Non-coding RNA</i> , 2018, 4, 8.	2.6	56
141	Synthesis in vitro of an exceptionally long RNA transcript promoted by an AluI sequence. <i>Nature</i> , 1982, 300, 376-379.	27.8	55
142	Even-skipped Represses Transcription by Binding TATA Binding Protein and Blocking the TFIID-TATA Box Interaction. <i>Molecular and Cellular Biology</i> , 1998, 18, 3771-3781.	2.3	55
143	Requirements of the RNA Polymerase II C-Terminal Domain for Reconstituting Pre-mRNA 3' Cleavage. <i>Molecular and Cellular Biology</i> , 2002, 22, 1684-1692.	2.3	55
144	SRSF10 Connects DNA Damage to the Alternative Splicing of Transcripts Encoding Apoptosis, Cell-Cycle Control, and DNA Repair Factors. <i>Cell Reports</i> , 2016, 17, 1990-2003.	6.4	55

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145	Analysis of the Expression of Genes Encoding Animal mRNA by in Vitro Techniques. <i>Progress in Molecular Biology and Translational Science</i> , 1983, 30, 195-244.	1.9	54
146	The RNA binding protein RNPS1 alleviates ASF/SF2 depletion-induced genomic instability. <i>Rna</i> , 2007, 13, 2108-2115.	3.5	53
147	A role for Chk1 in blocking transcriptional elongation of p21 RNA during the S-phase checkpoint. <i>Genes and Development</i> , 2009, 23, 1364-1377.	5.9	53
148	Unexpected similarities between C9ORF72 and sporadic forms of ALS/FTD suggest a common disease mechanism. <i>ELife</i> , 2018, 7, .	6.0	53
149	In vitrosplicing of simian virus 40 early pre mRNA. <i>Nucleic Acids Research</i> , 1986, 14, 1219-1235.	14.5	52
150	Sumoylation regulates multiple aspects of mammalian poly(A) polymerase function. <i>Genes and Development</i> , 2008, 22, 499-511.	5.9	51
151	Sumoylation Modulates the Assembly and Activity of the Pre-mRNA 3' Processing Complex. <i>Molecular and Cellular Biology</i> , 2007, 27, 8848-8858.	2.3	50
152	Sumoylation of transcription factor Gcn4 facilitates its Srb10-mediated clearance from promoters in yeast. <i>Genes and Development</i> , 2012, 26, 350-355.	5.9	49
153	Deregulation of Poly(A) Polymerase Interferes with Cell Growth. <i>Molecular and Cellular Biology</i> , 1998, 18, 5010-5020.	2.3	47
154	The search for alternative splicing regulators: new approaches offer a path to a splicing code. <i>Genes and Development</i> , 2008, 22, 279-285.	5.9	46
155	Function and Control of RNA Polymerase II C-Terminal Domain Phosphorylation in Vertebrate Transcription and RNA Processing. <i>Molecular and Cellular Biology</i> , 2014, 34, 2488-2498.	2.3	46
156	ALS/FTD-associated protein FUS induces mitochondrial dysfunction by preferentially sequestering respiratory chain complex mRNAs. <i>Genes and Development</i> , 2020, 34, 785-805.	5.9	46
157	The End of the Message--Another Link Between Yeast and Mammals. <i>Science</i> , 1996, 274, 1481-1482.	12.6	45
158	Nuclear coupling: RNA processing reaches back to transcription. , 2002, 9, 790-791.		45
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160	Mdm2 and MdmX as Regulators of Gene Expression. <i>Genes and Cancer</i> , 2012, 3, 264-273.	1.9	43
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