

# John T Lis

## List of Publications by Year in descending order

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196  
papers

28,646  
citations

4383

86  
h-index

6294

158  
g-index

215  
all docs

215  
docs citations

215  
times ranked

22280  
citing authors

#	ARTICLE	IF	CITATIONS
1	Nascent RNA Sequencing Reveals Widespread Pausing and Divergent Initiation at Human Promoters. <i>Science</i> , 2008, 322, 1845-1848.	6.0	1,758
2	Promoter-proximal pausing of RNA polymerase II: emerging roles in metazoans. <i>Nature Reviews Genetics</i> , 2012, 13, 720-731.	7.7	1,003
3	Getting up to speed with transcription elongation by RNA polymerase II. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 167-177.	16.1	692
4	Precise Maps of RNA Polymerase Reveal How Promoters Direct Initiation and Pausing. <i>Science</i> , 2013, 339, 950-953.	6.0	683
5	The RNA polymerase II molecule at the 5' end of the uninduced hsp70 gene of <i>D. melanogaster</i> is transcriptionally engaged. <i>Cell</i> , 1988, 54, 795-804.	13.5	658
6	The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.	13.7	579
7	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. <i>Nature Genetics</i> , 2014, 46, 1311-1320.	9.4	572
8	PR-Set7 Is a Nucleosome-Specific Methyltransferase that Modifies Lysine 20 of Histone H4 and Is Associated with Silent Chromatin. <i>Molecular Cell</i> , 2002, 9, 1201-1213.	4.5	525
9	NAD <sup>+</sup> -Dependent Modulation of Chromatin Structure and Transcription by Nucleosome Binding Properties of PARP-1. <i>Cell</i> , 2004, 119, 803-814.	13.5	487
10	Genome-wide dynamics of Pol II elongation and its interplay with promoter proximal pausing, chromatin, and exons. <i>ELife</i> , 2014, 3, e02407.	2.8	484
11	PARP Goes Transcription. <i>Cell</i> , 2003, 113, 677-683.	13.5	478
12	Defining mechanisms that regulate RNA polymerase II transcription in vivo. <i>Nature</i> , 2009, 461, 186-192.	13.7	476
13	Protein traffic on the heat shock promoter: Parking, stalling, and trucking along. <i>Cell</i> , 1993, 74, 1-4.	13.5	474
14	A Rapid, Extensive, and Transient Transcriptional Response to Estrogen Signaling in Breast Cancer Cells. <i>Cell</i> , 2011, 145, 622-634.	13.5	458
15	Stable binding of <i>Drosophila</i> heat shock factor to head-to-head and tail-to-tail repeats of a conserved 5 bp recognition unit. <i>Cell</i> , 1989, 59, 797-806.	13.5	443
16	Mechanical disruption of individual nucleosomes reveals a reversible multistage release of DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1960-1965.	3.3	440
17	Breaking barriers to transcription elongation. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 557-567.	16.1	434
18	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). <i>Nature Protocols</i> , 2016, 11, 1455-1476.	5.5	392

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19	New heat shock puffs and $\beta$ -galactosidase activity resulting from transformation of <i>Drosophila</i> with an hsp70-lacZ hybrid gene. <i>Cell</i> , 1983, 35, 403-410.	13.5	372
20	Coordinated Effects of Sequence Variation on DNA Binding, Chromatin Structure, and Transcription. <i>Science</i> , 2013, 342, 744-747.	6.0	364
21	Control of Transcriptional Elongation. <i>Annual Review of Genetics</i> , 2013, 47, 483-508.	3.2	359
22	High-resolution dynamic mapping of histone-DNA interactions in a nucleosome. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 124-129.	3.6	354
23	Transcription Regulation Through Promoter-Proximal Pausing of RNA Polymerase II. <i>Science</i> , 2008, 319, 1791-1792.	6.0	347
24	Phosphorylation of RNA polymerase II C-terminal domain and transcriptional elongation. <i>Nature</i> , 1994, 370, 75-77.	13.7	326
25	Mammalian Heat Shock Response and Mechanisms Underlying Its Genome-wide Transcriptional Regulation. <i>Molecular Cell</i> , 2016, 62, 63-78.	4.5	322
26	CDK12 is a transcription elongation-associated CTD kinase, the metazoan ortholog of yeast Ctk1. <i>Genes and Development</i> , 2010, 24, 2303-2316.	2.7	320
27	Determinants of heat shock-induced chromosome puffing. <i>Cell</i> , 1985, 40, 805-817.	13.5	314
28	Signaling Pathways Differentially Affect RNA Polymerase II Initiation, Pausing, and Elongation Rate in Cells. <i>Molecular Cell</i> , 2013, 50, 212-222.	4.5	300
29	Rapid, Transcription-Independent Loss of Nucleosomes over a Large Chromatin Domain at Hsp70 Loci. <i>Cell</i> , 2008, 134, 74-84.	13.5	290
30	[10] Elution of DNA from agarose gels after electrophoresis. <i>Methods in Enzymology</i> , 1979, 68, 176-182.	0.4	288
31	Regulating RNA polymerase pausing and transcription elongation in embryonic stem cells. <i>Genes and Development</i> , 2011, 25, 742-754.	2.7	281
32	P-TEFb kinase recruitment and function at heat shock loci. <i>Genes and Development</i> , 2000, 14, 792-803.	2.7	265
33	Tracking FACT and the RNA Polymerase II Elongation Complex Through Chromatin in Vivo. <i>Science</i> , 2003, 301, 1094-1096.	6.0	261
34	Cooperative binding of <i>Drosophila</i> heat shock factor to arrays of a conserved 5 bp unit. <i>Cell</i> , 1991, 64, 585-593.	13.5	254
35	High-resolution localization of <i>Drosophila</i> Spt5 and Spt6 at heat shock genes in vivo: roles in promoter proximal pausing and transcription elongation. <i>Genes and Development</i> , 2000, 14, 2635-2649.	2.7	248
36	P-TEFb kinase recruitment and function at heat shock loci. <i>Genes and Development</i> , 2000, 14, 792-803.	2.7	244

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37	[42] Fractionation of DNA fragments by polyethylene glycol induced precipitation. <i>Methods in Enzymology</i> , 1980, 65, 347-353.	0.4	235
38	A Unified Nomenclature for Protein Subunits of Mediator Complexes Linking Transcriptional Regulators to RNA Polymerase II. <i>Molecular Cell</i> , 2004, 14, 553-557.	4.5	230
39	The RNA processing exosome is linked to elongating RNA polymerase II in <i>Drosophila</i> . <i>Nature</i> , 2002, 420, 837-841.	13.7	228
40	Coordination of Transcription, RNA Processing, and Surveillance by P-TEFb Kinase on Heat Shock Genes. <i>Molecular Cell</i> , 2004, 13, 55-65.	4.5	224
41	Defining the Status of RNA Polymerase at Promoters. <i>Cell Reports</i> , 2012, 2, 1025-1035.	2.9	222
42	Size fractionation of double-stranded DNA by precipitation with polyethylene glycol. <i>Nucleic Acids Research</i> , 1975, 2, 383-390.	6.5	206
43	Molecular mechanisms driving transcriptional stress responses. <i>Nature Reviews Genetics</i> , 2018, 19, 385-397.	7.7	206
44	Transcription Factor and Polymerase Recruitment, Modification, and Movement on dhsp70 In Vivo in the Minutes following Heat Shock. <i>Molecular and Cellular Biology</i> , 2003, 23, 7628-7637.	1.1	202
45	Identification of active transcriptional regulatory elements from GRO-seq data. <i>Nature Methods</i> , 2015, 12, 433-438.	9.0	198
46	Chromatin Landscape Dictates HSF Binding to Target DNA Elements. <i>PLoS Genetics</i> , 2010, 6, e1001114.	1.5	194
47	Dynamics of heat shock factor association with native gene loci in living cells. <i>Nature</i> , 2006, 442, 1050-1053.	13.7	186
48	Fine structure analyses of the <i>Drosophila</i> and <i>Saccharomyces</i> heat shock factor - heat shock element interactions. <i>Nucleic Acids Research</i> , 1994, 22, 167-173.	6.5	184
49	Single molecule analysis of RNA polymerase elongation reveals uniform kinetic behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13538-13543.	3.3	182
50	Specific Contributions of Histone Tails and their Acetylation to the Mechanical Stability of Nucleosomes. <i>Journal of Molecular Biology</i> , 2005, 346, 135-146.	2.0	177
51	Nascent RNA analyses: tracking transcription and its regulation. <i>Nature Reviews Genetics</i> , 2019, 20, 705-723.	7.7	177
52	Peptidylarginine deiminase 2-catalyzed histone H3 arginine 26 citrullination facilitates estrogen receptor $\beta$ target gene activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13331-13336.	3.3	173
53	Divergent transcription: A new feature of active promoters. <i>Cell Cycle</i> , 2009, 8, 2557-2564.	1.3	172
54	X chromosome dosage compensation via enhanced transcriptional elongation in <i>Drosophila</i> . <i>Nature</i> , 2011, 471, 115-118.	13.7	169

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55	<i>Drosophila</i> Set1 is the major histone H3 lysine 4 trimethyltransferase with role in transcription. EMBO Journal, 2011, 30, 2817-2828.	3.5	168
56	Molecular Mechanism of Transcription Inhibition by Peptide Antibiotic Microcin J25. Molecular Cell, 2004, 14, 753-762.	4.5	165
57	Condensin controls recruitment of RNA polymerase II to achieve nematode X-chromosome dosage compensation. ELife, 2013, 2, e00808.	2.8	165
58	Cotranscriptional folding of a riboswitch at nucleotide resolution. Nature Structural and Molecular Biology, 2016, 23, 1124-1131.	3.6	163
59	A novel arrangement of tandemly repeated genes at a major heat shock site in <i>D. melanogaster</i> . Cell, 1978, 14, 901-919.	13.5	160
60	A germline transformation analysis reveals flexibility in the organization of heat shock consensus elements. Nucleic Acids Research, 1987, 15, 2971-2988.	6.5	160
61	Transcription Properties of a Cell Type-Specific TATA-Binding Protein, TRF. Cell, 1997, 91, 71-83.	13.5	159
62	Overcoming the nucleosome barrier during transcript elongation. Trends in Genetics, 2012, 28, 285-294.	2.9	150
63	The <i>Drosophila</i> BRM complex facilitates global transcription by RNA polymerase II. EMBO Journal, 2002, 21, 5245-5254.	3.5	147
64	Efficient Release from Promoter-Proximal Stall Sites Requires Transcript Cleavage Factor TFIIIS. Molecular Cell, 2005, 17, 103-112.	4.5	145
65	New Technologies Provide Quantum Changes in the Scale, Speed, and Success of SELEX Methods and Aptamer Characterization. Molecular Therapy - Nucleic Acids, 2014, 3, e183.	2.3	140
66	Physical map of two <i>D. melanogaster</i> DNA segments containing sequences coding for the 70,000 dalton heat shock protein. Cell, 1979, 17, 1-8.	13.5	138
67	Transcriptional response to stress is pre-wired by promoter and enhancer architecture. Nature Communications, 2017, 8, 255.	5.8	136
68	Mediator, Not Holoenzyme, Is Directly Recruited to the Heat Shock Promoter by HSF upon Heat Shock. Molecular Cell, 2001, 8, 9-19.	4.5	132
69	Spt6 enhances the elongation rate of RNA polymerase II in vivo. EMBO Journal, 2009, 28, 1067-1077.	3.5	131
70	P-TEFb Is Critical for the Maturation of RNA Polymerase II into Productive Elongation In Vivo. Molecular and Cellular Biology, 2008, 28, 1161-1170.	1.1	128
71	Recruitment Timing and Dynamics of Transcription Factors at the Hsp70 Loci in Living Cells. Molecular Cell, 2010, 40, 965-975.	4.5	125
72	Comprehensive analysis of RNA-protein interactions by high-throughput sequencing of RNA affinity profiling. Nature Methods, 2014, 11, 683-688.	9.0	124

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73	Genes for the 70,000 dalton heat shock protein in two cloned <i>D. melanogaster</i> DNA segments. <i>Cell</i> , 1979, 17, 9-18.	13.5	115
74	Localization of the hsp83 transcript within a 3292 nucleotide sequence from the 63B heat shock locus of <i>D. melanogaster</i> . <i>Nucleic Acids Research</i> , 1983, 11, 7011-7030.	6.5	112
75	Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation. <i>Genes and Development</i> , 2016, 30, 1731-1746.	2.7	112
76	Tracking rates of transcription and splicing in vivo. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1123-1124.	3.6	111
77	<i>Drosophila</i> Paf1 Modulates Chromatin Structure at Actively Transcribed Genes. <i>Molecular and Cellular Biology</i> , 2006, 26, 250-260.	1.1	110
78	Intranuclear Distribution and Local Dynamics of RNA Polymerase II during Transcription Activation. <i>Molecular Cell</i> , 2007, 28, 978-990.	4.5	110
79	Portable microcomputer software for nucleotide sequence analysis. <i>Nucleic Acids Research</i> , 1982, 10, 6451-6463.	6.5	109
80	Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. <i>Nature Genetics</i> , 2018, 50, 1553-1564.	9.4	108
81	A Cdk9-PP1 switch regulates the elongation-termination transition of RNA polymerase II. <i>Nature</i> , 2018, 558, 460-464.	13.7	105
82	Dynamics of potentiation and activation: GAGA factor and its role in heat shock gene regulation. <i>Nucleic Acids Research</i> , 1997, 25, 3963-3968.	6.5	102
83	Activator-Induced Spread of Poly(ADP-Ribose) Polymerase Promotes Nucleosome Loss at Hsp70. <i>Molecular Cell</i> , 2012, 45, 64-74.	4.5	101
84	Genome-Wide Control of RNA Polymerase II Activity by Cohesin. <i>PLoS Genetics</i> , 2013, 9, e1003382.	1.5	97
85	Enhancer transcription: what, where, when, and why?. <i>Genes and Development</i> , 2018, 32, 1-3.	2.7	96
86	A TRF1:BRF Complex Directs <i>Drosophila</i> RNA Polymerase III Transcription. <i>Cell</i> , 2000, 101, 459-469.	13.5	93
87	Optimal heat-induced expression of the <i>Drosophila</i> hsp26 gene requires a promoter sequence containing (CT) <sub>n</sub> (GA) <sub>n</sub> repeats. <i>Journal of Molecular Biology</i> , 1990, 211, 751-761.	2.0	92
88	Transcriptional activation independent of TFIIF kinase and the RNA polymerase II mediator in vivo. <i>Nature</i> , 1998, 393, 389-392.	13.7	91
89	Probing SWI/SNF remodeling of the nucleosome by unzipping single DNA molecules. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 549-554.	3.6	89
90	Single-molecule nascent RNA sequencing identifies regulatory domain architecture at promoters and enhancers. <i>Nature Genetics</i> , 2018, 50, 1533-1541.	9.4	89

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91	GAGA Factor Maintains Nucleosome-Free Regions and Has a Role in RNA Polymerase II Recruitment to Promoters. <i>PLoS Genetics</i> , 2015, 11, e1005108.	1.5	87
92	Chromatin conformation remains stable upon extensive transcriptional changes driven by heat shock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19431-19439.	3.3	87
93	Different cyclic AMP requirements for induction of the arabinose and lactose operons of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1973, 79, 149-162.	2.0	85
94	Cooperative and Competitive Protein Interactions at the Hsp70 Promoter. <i>Journal of Biological Chemistry</i> , 1997, 272, 33227-33233.	1.6	84
95	Selection and elution of aptamers using nanoporous sol-gel arrays with integrated microheaters. <i>Lab on A Chip</i> , 2009, 9, 1206.	3.1	83
96	Extensive polymerase pausing during <i>Drosophila</i> axis patterning enables high-level and pliable transcription. <i>Genes and Development</i> , 2013, 27, 1146-1158.	2.7	83
97	Promoter sequence containing (CT) <sub>n</sub> (GA) <sub>n</sub> repeats is critical for the formation of the DNase I hypersensitive sites in the <i>Drosophila</i> hsp26 gene. <i>Journal of Molecular Biology</i> , 1992, 225, 985-998.	2.0	82
98	Mechanisms by which transcription factors gain access to target sequence elements in chromatin. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 116-123.	1.5	77
99	Minichromosome maintenance helicase paralog MCM9 is dispensible for DNA replication but functions in germ-line stem cells and tumor suppression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17702-17707.	3.3	76
100	Divergence of a conserved elongation factor and transcription regulation in budding and fission yeast. <i>Genome Research</i> , 2016, 26, 799-811.	2.4	73
101	Two closely linked transcription units within the 63B heat shock puff locus of <i>D. melanogaster</i> display strikingly different regulation. <i>Nucleic Acids Research</i> , 1981, 9, 5075-5092.	6.5	72
102	Short Transcripts of the Ternary Complex Provide Insight into RNA Polymerase II Elongational Pausing. <i>Journal of Molecular Biology</i> , 1995, 252, 522-535.	2.0	71
103	High-Resolution Mapping of RNA Polymerases Identifies Mechanisms of Sensitivity and Resistance to BET Inhibitors in t(8;21) AML. <i>Cell Reports</i> , 2016, 16, 2003-2016.	2.9	69
104	Cloning and characterization of nine heat-shock-induced mRNAs of <i>Drosophila melanogaster</i> . <i>Gene</i> , 1981, 15, 67-80.	1.0	66
105	Cdk9 regulates a promoter-proximal checkpoint to modulate RNA polymerase II elongation rate in fission yeast. <i>Nature Communications</i> , 2018, 9, 543.	5.8	66
106	Imaging <i>Drosophila</i> gene activation and polymerase pausing in vivo. <i>Nature</i> , 2007, 450, 198-202.	13.7	65
107	Dynamic evolution of regulatory element ensembles in primate CD4+ T cells. <i>Nature Ecology and Evolution</i> , 2018, 2, 537-548.	3.4	65
108	Cdk7 Is Required for Full Activation of <i>Drosophila</i> Heat Shock Genes and RNA Polymerase II Phosphorylation In Vivo. <i>Molecular and Cellular Biology</i> , 2003, 23, 6876-6886.	1.1	61

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109	Pol II Docking and Pausing at Growth and Stress Genes in <i>C.Âlegans</i> . <i>Cell Reports</i> , 2014, 6, 455-466.	2.9	61
110	The upstream activator CTF/NF1 and RNA polymerase II share a common element involved in transcriptional activation. <i>Nucleic Acids Research</i> , 1994, 22, 1966-1973.	6.5	60
111	Transcription imparts architecture, function and logic to enhancer units. <i>Nature Genetics</i> , 2020, 52, 1067-1075.	9.4	60
112	Specific SR protein-dependent splicing substrates identified through genomic SELEX. <i>Nucleic Acids Research</i> , 2003, 31, 1955-1961.	6.5	59
113	CBP Regulates Recruitment and Release of Promoter-Proximal RNA Polymerase II. <i>Molecular Cell</i> , 2017, 68, 491-503.e5.	4.5	59
114	DNA distortion and multimerization: novel functions of the glutamine-rich domain of GAGA factor 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1999, 285, 515-525.	2.0	58
115	RAPID-SELEX for RNA Aptamers. <i>PLoS ONE</i> , 2013, 8, e82667.	1.1	58
116	A hypersensitive site in hsp70 chromatin requires adjacent not internal DNA sequence. <i>Nature</i> , 1985, 313, 147-149.	13.7	57
117	Accurate Prediction of Inducible Transcription Factor Binding Intensities In Vivo. <i>PLoS Genetics</i> , 2012, 8, e1002610.	1.5	56
118	Defining NELF-E RNA Binding in HIV-1 and Promoter-Proximal Pause Regions. <i>PLoS Genetics</i> , 2014, 10, e1004090.	1.5	55
119	Human Gene Promoters Are Intrinsically Bidirectional. <i>Molecular Cell</i> , 2015, 60, 346-347.	4.5	55
120	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021, 34, 108783.	2.9	53
121	Prediction of histone post-translational modification patterns based on nascent transcription data. <i>Nature Genetics</i> , 2022, 54, 295-305.	9.4	53
122	Nuclear run-on assays: Assessing transcription by measuring density of engaged RNA polymerases. <i>Methods in Enzymology</i> , 1999, 304, 351-362.	0.4	52
123	RNA aptamers directed to discrete functional sites on a single protein structural domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3742-3746.	3.3	52
124	RNA-DNA Differences Are Generated in Human Cells within Seconds after RNA Exits Polymerase II. <i>Cell Reports</i> , 2014, 6, 906-915.	2.9	52
125	RNA aptamers that functionally interact with green fluorescent protein and its derivatives. <i>Nucleic Acids Research</i> , 2012, 40, e39-e39.	6.5	47
126	Interactions between subunits of <i>Drosophila</i> Mediator and activator proteins. <i>Trends in Biochemical Sciences</i> , 2005, 30, 245-249.	3.7	46



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127	Kinetics of promoter Pol II on <i>Hsp70</i> reveal stable pausing and key insights into its regulation. <i>Genes and Development</i> , 2014, 28, 14-19.	2.7	46
128	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. <i>Genome Research</i> , 2019, 29, 223-235.	2.4	46
129	Pioneer-like factor GAF cooperates with PBAP (SWI/SNF) and NURF (ISWI) to regulate transcription. <i>Genes and Development</i> , 2021, 35, 147-156.	2.7	46
130	The Polycomb Group Mutant <i>esc</i> Leads to Augmented Levels of Paused Pol II in the <i>Drosophila</i> Embryo. <i>Molecular Cell</i> , 2011, 42, 837-844.	4.5	44
131	Sodium Salicylate and Yeast Heat Shock Gene Transcription. <i>Journal of Biological Chemistry</i> , 1995, 270, 10369-10372.	1.6	43
132	HSF recruitment and loss at most <i>Drosophila</i> heat shock loci is coordinated and depends on proximal promoter sequences. <i>Chromosoma</i> , 1996, 105, 158-171.	1.0	43
133	Targeted H3R26 Deimination Specifically Facilitates Estrogen Receptor Binding by Modifying Nucleosome Structure. <i>PLoS Genetics</i> , 2014, 10, e1004613.	1.5	43
134	Phosphorylation of the RNA polymerase II C-terminal domain by TFIIF kinase is not essential for transcription of <i>Saccharomyces cerevisiae</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14276-14280.	3.3	42
135	The <i>Drosophila</i> 7SK snRNP and the essential role of dHEXIM in development. <i>Nucleic Acids Research</i> , 2012, 40, 5283-5297.	6.5	42
136	Binding of heat shock factor to and transcriptional activation of heat shock genes in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 1995, 23, 4799-4804.	6.5	41
137	Imaging RNA Polymerase II transcription sites in living cells. <i>Current Opinion in Genetics and Development</i> , 2014, 25, 126-130.	1.5	40
138	An RNA aptamer that interferes with the DNA binding of the HSF transcription activator. <i>Nucleic Acids Research</i> , 2006, 34, 3755-3761.	6.5	39
139	Kinetics of <i>Xist</i> -induced gene silencing can be predicted from combinations of epigenetic and genomic features. <i>Genome Research</i> , 2019, 29, 1087-1099.	2.4	38
140	Probing TBP interactions in transcription initiation and reinitiation with RNA aptamers that act in distinct modes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6934-6939.	3.3	37
141	A Universal DNA-Based Protein Detection System. <i>Journal of the American Chemical Society</i> , 2013, 135, 14008-14011.	6.6	35
142	Transcription Factor TFIIF Is Required for Promoter Melting In Vivo. <i>Molecular and Cellular Biology</i> , 1999, 19, 5652-5658.	1.1	34
143	Direct cloning of DNA that interacts in vivo with a specific protein: application to RNA polymerase II and sites of pausing in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 1998, 26, 919-924.	6.5	33
144	Inhibiting Heat Shock Factor 1 in Human Cancer Cells with a Potent RNA Aptamer. <i>PLoS ONE</i> , 2014, 9, e96330.	1.1	32

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145	Localized heat-shock induction in <i>Drosophila melanogaster</i> . <i>The Journal of Experimental Zoology</i> , 1988, 247, 279-284.	1.4	31
146	Pre-mRNA Splicing by the Essential <i>Drosophila</i> Protein B52: Tissue and Target Specificity. <i>Molecular and Cellular Biology</i> , 2000, 20, 181-186.	1.1	31
147	Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. <i>Genome Research</i> , 2017, 27, 1816-1829.	2.4	31
148	Chromatin Architecture of the <i>Pitx2</i> Locus Requires CTCF- and <i>Pitx2</i> -Dependent Asymmetry that Mirrors Embryonic Gut Laterality. <i>Cell Reports</i> , 2015, 13, 337-349.	2.9	30
149	A 50 year history of technologies that drove discovery in eukaryotic transcription regulation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 777-782.	3.6	30
150	DNA sequences flanking the starts of the hsp 70 and $\hat{I}\hat{I}^2$ heat shock genes are homologous. <i>Developmental Biology</i> , 1981, 83, 291-300.	0.9	29
151	Genomic organization and transcription of the $\hat{I}\hat{I}^2$ heat shock DNA in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 1981, 9, 5297-5310.	6.5	29
152	Multiplexed Microcolumn-Based Process for Efficient Selection of RNA Aptamers. <i>Analytical Chemistry</i> , 2013, 85, 3417-3424.	3.2	29
153	Stress-induced transcriptional memory accelerates promoter-proximal pause release and decelerates termination over mitotic divisions. <i>Molecular Cell</i> , 2021, 81, 1715-1731.e6.	4.5	28
154	A comparison of experimental assays and analytical methods for genome-wide identification of active enhancers. <i>Nature Biotechnology</i> , 2022, 40, 1056-1065.	9.4	28
155	Comparison of Femtosecond Laser and Continuous Wave UV Sources for Protein-Nucleic Acid Crosslinking. <i>Photochemistry and Photobiology</i> , 2007, 83, 1394-1404.	1.3	27
156	A Systematic Study of the Features Critical for Designing a High Avidity Multivalent Aptamer. <i>Nucleic Acid Therapeutics</i> , 2013, 23, 238-242.	2.0	27
157	The isolation and characterization of plaque-forming arabinose transducing bacteriophage $\hat{I}$ . <i>Journal of Molecular Biology</i> , 1975, 95, 395-407.	2.0	26
158	The regulatory region of the l-arabinose operon: A physical, genetic and physiological study. <i>Journal of Molecular Biology</i> , 1975, 95, 417-431.	2.0	26
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