John T Lis

List of Publications by Citations

203 papers	23,006 citations	83 h-index	150 g-index
215 ext. papers	26,339 ext. citations	18.5 avg, IF	7.18 L-index

#	Paper	IF	Citations
203	Nascent RNA sequencing reveals widespread pausing and divergent initiation at human promoters. *Science*, **2008**, 322, 1845-8	33.3	1441
202	Promoter-proximal pausing of RNA polymerase II: emerging roles in metazoans. *Nature Reviews Genetics*, **2012**, 13, 720-31	30.1	775
201	The RNA polymerase II molecule at the 5Qend of the uninduced hsp70 gene of D. melanogaster is transcriptionally engaged. *Cell*, **1988**, 54, 795-804	56.2	584
200	Getting up to speed with transcription elongation by RNA polymerase II. *Nature Reviews Molecular Cell Biology*, **2015**, 16, 167-77	48.7	485
199	Precise maps of RNA polymerase reveal how promoters direct initiation and pausing. *Science*, **2013**, 339, 950-3	33.3	466
198	PR-Set7 is a nucleosome-specific methyltransferase that modifies lysine 20 of histone H4 and is associated with silent chromatin. *Molecular Cell*, **2002**, 9, 1201-13	17.6	462
197	Protein traffic on the heat shock promoter: parking, stalling, and trucking along. *Cell*, **1993**, 74, 1-4	56.2	438
196	NAD+-dependent modulation of chromatin structure and transcription by nucleosome binding properties of PARP-1. *Cell*, **2004**, 119, 803-14	56.2	437
195	PARP goes transcription. *Cell*, **2003**, 113, 677-83	56.2	435
194	Stable binding of Drosophila heat shock factor to head-to-head and tail-to-tail repeats of a conserved 5 bp recognition unit. *Cell*, **1989**, 59, 797-806	56.2	423
193	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. *Nature Genetics*, **2014**, 46, 1311-20	36.3	399
192	Defining mechanisms that regulate RNA polymerase II transcription in vivo. *Nature*, **2009**, 461, 186-92	50.4	399
191	Breaking barriers to transcription elongation. *Nature Reviews Molecular Cell Biology*, **2006**, 7, 557-67	48.7	399
190	A rapid, extensive, and transient transcriptional response to estrogen signaling in breast cancer cells. *Cell*, **2011**, 145, 622-34	56.2	377
189	Mechanical disruption of individual nucleosomes reveals a reversible multistage release of DNA. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 1960-5	11.5	368
188	New heat shock puffs and beta-galactosidase activity resulting from transformation of Drosophila with an hsp70-lacZ hybrid gene. *Cell*, **1983**, 35, 403-10	56.2	339
187	Genome-wide dynamics of Pol II elongation and its interplay with promoter proximal pausing, chromatin, and exons. *ELife*, **2014**, 3, e02407	8.9	337

186	The 4D nucleome project. *Nature*, **2017**, 549, 219-226	50.4	332
185	Transcription regulation through promoter-proximal pausing of RNA polymerase II. *Science*, **2008**, 319, 1791-2	33.3	310
184	Phosphorylation of RNA polymerase II C-terminal domain and transcriptional elongation. *Nature*, **1994**, 370, 75-7	50.4	301
183	Determinants of heat shock-induced chromosome puffing. *Cell*, **1985**, 40, 805-17	56.2	294
182	High-resolution dynamic mapping of histone-DNA interactions in a nucleosome. *Nature Structural and Molecular Biology*, **2009**, 16, 124-9	17.6	290
181	Control of transcriptional elongation. *Annual Review of Genetics*, **2013**, 47, 483-508	14.5	285
180	Coordinated effects of sequence variation on DNA binding, chromatin structure, and transcription. *Science*, **2013**, 342, 744-7	33.3	278
179	CDK12 is a transcription elongation-associated CTD kinase, the metazoan ortholog of yeast Ctk1. *Genes and Development*, **2010**, 24, 2303-16	12.6	267
178	Rapid, transcription-independent loss of nucleosomes over a large chromatin domain at Hsp70 loci. *Cell*, **2008**, 134, 74-84	56.2	263
177	Regulating RNA polymerase pausing and transcription elongation in embryonic stem cells. *Genes and Development*, **2011**, 25, 742-54	12.6	243
176	Tracking FACT and the RNA polymerase II elongation complex through chromatin in vivo. *Science*, **2003**, 301, 1094-6	33.3	233
175	Signaling pathways differentially affect RNA polymerase II initiation, pausing, and elongation rate in cells. *Molecular Cell*, **2013**, 50, 212-22	17.6	231
174	Cooperative binding of Drosophila heat shock factor to arrays of a conserved 5 bp unit. *Cell*, **1991**, 64, 585-93	56.2	231
173	P-TEFb kinase recruitment and function at heat shock loci. *Genes and Development*, **2000**, 14, 792-803	12.6	229
172	High-resolution localization of Drosophila Spt5 and Spt6 at heat shock genes in vivo: roles in promoter proximal pausing and transcription elongation. *Genes and Development*, **2000**, 14, 2635-49	12.6	221
171	Elution of DNA from agarose gels after electrophoresis. *Methods in Enzymology*, **1979**, 68, 176-82	1.7	221
170	Mammalian Heat Shock Response and Mechanisms Underlying Its Genome-wide Transcriptional Regulation. *Molecular Cell*, **2016**, 62, 63-78	17.6	213
169	A unified nomenclature for protein subunits of mediator complexes linking transcriptional regulators to RNA polymerase II. *Molecular Cell*, **2004**, 14, 553-7	17.6	209

168	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). *Nature Protocols*, **2016**, 11, 1455-76	18.8	208
167	The RNA processing exosome is linked to elongating RNA polymerase II in Drosophila. *Nature*, **2002**, 420, 837-41	50.4	208
166	Coordination of transcription, RNA processing, and surveillance by P-TEFb kinase on heat shock genes. *Molecular Cell*, **2004**, 13, 55-65	17.6	199
165	Fractionation of DNA fragments by polyethylene glycol induced precipitation. *Methods in Enzymology*, **1980**, 65, 347-53	1.7	199
164	Transcription factor and polymerase recruitment, modification, and movement on dhsp70 in vivo in the minutes following heat shock. *Molecular and Cellular Biology*, **2003**, 23, 7628-37	4.8	192
163	P-TEFb kinase recruitment and function at heat shock loci. *Genes and Development*, **2000**, 14, 792-803	12.6	184
162	Size fractionation of double-stranded DNA by precipitation with polyethylene glycol. *Nucleic Acids Research*, **1975**, 2, 383-9	20.1	171
161	Dynamics of heat shock factor association with native gene loci in living cells. *Nature*, **2006**, 442, 1050-3	50.4	169
160	Defining the status of RNA polymerase at promoters. *Cell Reports*, **2012**, 2, 1025-35	10.6	163
159	Chromatin landscape dictates HSF binding to target DNA elements. *PLoS Genetics*, **2010**, 6, e1001114	6	163
158	Fine structure analyses of the Drosophila and Saccharomyces heat shock factor--heat shock element interactions. *Nucleic Acids Research*, **1994**, 22, 167-73	20.1	161
157	Specific contributions of histone tails and their acetylation to the mechanical stability of nucleosomes. *Journal of Molecular Biology*, **2005**, 346, 135-46	6.5	152
156	A germline transformation analysis reveals flexibility in the organization of heat shock consensus elements. *Nucleic Acids Research*, **1987**, 15, 2971-88	20.1	150
155	X chromosome dosage compensation via enhanced transcriptional elongation in Drosophila. *Nature* , **2011**, 471, 115-8	50.4	149
154	A novel arrangement of tandemly repeated genes at a major heat shock site in D. melanogaster. *Cell*, **1978**, 14, 901-19	56.2	148
153	Transcription properties of a cell type-specific TATA-binding protein, TRF. *Cell*, **1997**, 91, 71-83	56.2	145
152	Single molecule analysis of RNA polymerase elongation reveals uniform kinetic behavior. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 13538-43	11.5	145
151	Peptidylarginine deiminase 2-catalyzed histone H3 arginine 26 citrullination facilitates estrogen receptor target gene activation. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 13331-6	11.5	140

150	Divergent transcription: a new feature of active promoters. *Cell Cycle*, **2009**, 8, 2557-64	4.7	140
149	The Drosophila BRM complex facilitates global transcription by RNA polymerase II. *EMBO Journal*, **2002**, 21, 5245-54	13	140
148	Molecular mechanism of transcription inhibition by peptide antibiotic Microcin J25. *Molecular Cell*, **2004**, 14, 753-62	17.6	140
147	Drosophila Set1 is the major histone H3 lysine 4 trimethyltransferase with role in transcription. *EMBO Journal*, **2011**, 30, 2817-28	13	133
146	Efficient release from promoter-proximal stall sites requires transcript cleavage factor TFIIS. *Molecular Cell*, **2005**, 17, 103-12	17.6	132
145	Physical map of two D. melanogaster DNA segments containing sequences coding for the 70,000 dalton heat shock protein. *Cell*, **1979**, 17, 1-8	56.2	127
144	Condensin controls recruitment of RNA polymerase II to achieve nematode X-chromosome dosage compensation. *ELife*, **2013**, 2, e00808	8.9	123
143	Mediator, not holoenzyme, is directly recruited to the heat shock promoter by HSF upon heat shock. *Molecular Cell*, **2001**, 8, 9-19	17.6	122
142	Identification of active transcriptional regulatory elements from GRO-seq data. *Nature Methods*, **2015**, 12, 433-8	21.6	112
141	Overcoming the nucleosome barrier during transcript elongation. *Trends in Genetics*, **2012**, 28, 285-94	8.5	112
140	New Technologies Provide Quantum Changes in the Scale, Speed, and Success of SELEX Methods and Aptamer Characterization. *Molecular Therapy - Nucleic Acids*, **2014**, 3, e183	10.7	111
139	Genes for the 70,000 dalton heat shock protein in two cloned D. melanogaster DNA segments. *Cell*, **1979**, 17, 9-18	56.2	109
138	Spt6 enhances the elongation rate of RNA polymerase II in vivo. *EMBO Journal*, **2009**, 28, 1067-77	13	108
137	Localization of the hsp83 transcript within a 3292 nucleotide sequence from the 63B heat shock locus of D. melanogaster. *Nucleic Acids Research*, **1983**, 11, 7011-30	20.1	106
136	Molecular mechanisms driving transcriptional stress responses. *Nature Reviews Genetics*, **2018**, 19, 385-397	37.1	103
135	Cotranscriptional folding of a riboswitch at nucleotide resolution. *Nature Structural and Molecular Biology*, **2016**, 23, 1124-1131	17.6	102
134	P-TEFb is critical for the maturation of RNA polymerase II into productive elongation in vivo. *Molecular and Cellular Biology*, **2008**, 28, 1161-70	4.8	101
133	Portable microcomputer software for nucleotide sequence analysis. *Nucleic Acids Research*, **1982**, 10, 6451-63	20.1	100

132	Recruitment timing and dynamics of transcription factors at the Hsp70 loci in living cells. *Molecular Cell*, **2010**, 40, 965-75	17.6	99
131	Drosophila Paf1 modulates chromatin structure at actively transcribed genes. *Molecular and Cellular Biology*, **2006**, 26, 250-60	4.8	98
130	Comprehensive analysis of RNA-protein interactions by high-throughput sequencing-RNA affinity profiling. *Nature Methods*, **2014**, 11, 683-8	21.6	92
129	Intranuclear distribution and local dynamics of RNA polymerase II during transcription activation. *Molecular Cell*, **2007**, 28, 978-90	17.6	92
128	Transcriptional activation independent of TFIIH kinase and the RNA polymerase II mediator in vivo. *Nature*, **1998**, 393, 389-92	50.4	88
127	A TRF1:BRF complex directs Drosophila RNA polymerase III transcription. *Cell*, **2000**, 101, 459-69	56.2	88
126	Activator-induced spread of poly(ADP-ribose) polymerase promotes nucleosome loss at Hsp70. *Molecular Cell*, **2012**, 45, 64-74	17.6	87
125	Dynamics of potentiation and activation: GAGA factor and its role in heat shock gene regulation. *Nucleic Acids Research*, **1997**, 25, 3963-8	20.1	86
124	Optimal heat-induced expression of the Drosophila hsp26 gene requires a promoter sequence containing (CT)n.(GA)n repeats. *Journal of Molecular Biology*, **1990**, 211, 751-61	6.5	84
123	Nascent RNA analyses: tracking transcription and its regulation. *Nature Reviews Genetics*, **2019**, 20, 705-723	53.1	83
122	Genome-wide control of RNA polymerase II activity by cohesin. *PLoS Genetics*, **2013**, 9, e1003382	6	83
121	Probing SWI/SNF remodeling of the nucleosome by unzipping single DNA molecules. *Nature Structural and Molecular Biology*, **2006**, 13, 549-54	17.6	83
120	Promoter sequence containing (CT)n.(GA)n repeats is critical for the formation of the DNase I hypersensitive sites in the Drosophila hsp26 gene. *Journal of Molecular Biology*, **1992**, 225, 985-98	6.5	79
119	Transcriptional response to stress is pre-wired by promoter and enhancer architecture. *Nature Communications*, **2017**, 8, 255	17.4	78
118	Cooperative and competitive protein interactions at the hsp70 promoter. *Journal of Biological Chemistry*, **1997**, 272, 33227-33	5.4	78
117	Selection and elution of aptamers using nanoporous sol-gel arrays with integrated microheaters. *Lab on A Chip*, **2009**, 9, 1206-12	7.2	77
116	Short transcripts of the ternary complex provide insight into RNA polymerase II elongational pausing. *Journal of Molecular Biology*, **1995**, 252, 522-35	6.5	69
115	Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation. *Genes and Development*, **2016**, 30, 1731-46	12.6	68

114	Different cyclic AMP requirements for induction of the arabinose and lactose operons of Escherichia coli. *Journal of Molecular Biology*, **1973**, 79, 149-62	6.5	67
113	Two closely linked transcription units within the 63B heat shock puff locus of D. melanogaster display strikingly different regulation. *Nucleic Acids Research*, **1981**, 9, 5075-92	20.1	66
112	Cloning and characterization of nine heat-shock-induced mRNAs of Drosophila melanogaster. *Gene*, **1981**, 15, 67-80	3.8	65
111	GAGA factor maintains nucleosome-free regions and has a role in RNA polymerase II recruitment to promoters. *PLoS Genetics*, **2015**, 11, e1005108	6	63
110	Minichromosome maintenance helicase paralog MCM9 is dispensible for DNA replication but functions in germ-line stem cells and tumor suppression. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 17702-7	11.5	63
109	Mechanisms by which transcription factors gain access to target sequence elements in chromatin. *Current Opinion in Genetics and Development*, **2013**, 23, 116-23	4.9	61
108	Extensive polymerase pausing during Drosophila axis patterning enables high-level and pliable transcription. *Genes and Development*, **2013**, 27, 1146-58	12.6	61
107	Imaging Drosophila gene activation and polymerase pausing in vivo. *Nature*, **2007**, 450, 198-202	50.4	60
106	Cdk7 is required for full activation of Drosophila heat shock genes and RNA polymerase II phosphorylation in vivo. *Molecular and Cellular Biology*, **2003**, 23, 6876-86	4.8	58
105	A Cdk9-PP1 switch regulates the elongation-termination transition of RNA polymerase II. *Nature*, **2018**, 558, 460-464	50.4	57
104	Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. *Nature Genetics*, **2018**, 50, 1553-1564	36.3	56
103	The upstream activator CTF/NF1 and RNA polymerase II share a common element involved in transcriptional activation. *Nucleic Acids Research*, **1994**, 22, 1966-73	20.1	55
102	Specific SR protein-dependent splicing substrates identified through genomic SELEX. *Nucleic Acids Research*, **2003**, 31, 1955-61	20.1	54
101	A hypersensitive site in hsp70 chromatin requires adjacent not internal DNA sequence. *Nature*, **1985**, 313, 147-9	50.4	54
100	Enhancer transcription: what, where, when, and why?. *Genes and Development*, **2018**, 32, 1-3	12.6	52
99	Divergence of a conserved elongation factor and transcription regulation in budding and fission yeast. *Genome Research*, **2016**, 26, 799-811	9.7	51
98	Nuclear run-on assays: assessing transcription by measuring density of engaged RNA polymerases. *Methods in Enzymology*, **1999**, 304, 351-62	1.7	49
97	Defining NELF-E RNA binding in HIV-1 and promoter-proximal pause regions. *PLoS Genetics*, **2014**, 10, e1004090	6	48

96	RAPID-SELEX for RNA aptamers. *PLoS ONE*, **2013**, 8, e82667	3.7	48
95	DNA distortion and multimerization: novel functions of the glutamine-rich domain of GAGA factor. *Journal of Molecular Biology*, **1999**, 285, 515-25	6.5	48
94	High-Resolution Mapping of RNA Polymerases Identifies Mechanisms of Sensitivity and Resistance to BET Inhibitors in t(8;21) AML. *Cell Reports*, **2016**, 16, 2003-16	10.6	48
93	Single-molecule nascent RNA sequencing identifies regulatory domain architecture at promoters and enhancers. *Nature Genetics*, **2018**, 50, 1533-1541	36.3	48
92	RNA aptamers directed to discrete functional sites on a single protein structural domain. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 3742-6	11.5	47
91	RNA-DNA differences are generated in human cells within seconds after RNA exits polymerase II. *Cell Reports*, **2014**, 6, 906-15	10.6	44
90	Chromatin conformation remains stable upon extensive transcriptional changes driven by heat shock. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 19431-19439	11.5	43
89	Accurate prediction of inducible transcription factor binding intensities in vivo. *PLoS Genetics*, **2012**, 8, e1002610	6	43
88	HSF recruitment and loss at most Drosophila heat shock loci is coordinated and depends on proximal promoter sequences. *Chromosoma*, **1996**, 105, 158-71	2.8	43
87	Human Gene Promoters Are Intrinsically Bidirectional. *Molecular Cell*, **2015**, 60, 346-7	17.6	42
86	Cdk9 regulates a promoter-proximal checkpoint to modulate RNA polymerase II elongation rate in fission yeast. *Nature Communications*, **2018**, 9, 543	17.4	41
85	Phosphorylation of the RNA polymerase II C-terminal domain by TFIIH kinase is not essential for transcription of Saccharomyces cerevisiae genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 14276-80	11.5	41
84	Pol II docking and pausing at growth and stress genes in C. elegans. *Cell Reports*, **2014**, 6, 455-66	10.6	39
83	The polycomb group mutant esc leads to augmented levels of paused Pol II in the Drosophila embryo. *Molecular Cell*, **2011**, 42, 837-44	17.6	39
82	Dynamic evolution of regulatory element ensembles in primate CD4 T cells. *Nature Ecology and Evolution*, **2018**, 2, 537-548	12.3	38
81	Kinetics of promoter Pol II on Hsp70 reveal stable pausing and key insights into its regulation. *Genes and Development*, **2014**, 28, 14-9	12.6	38
80	RNA aptamers that functionally interact with green fluorescent protein and its derivatives. *Nucleic Acids Research*, **2012**, 40, e39	20.1	38
79	An RNA aptamer that interferes with the DNA binding of the HSF transcription activator. *Nucleic Acids Research*, **2006**, 34, 3755-61	20.1	38

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75	CBP Regulates Recruitment and Release of Promoter-Proximal RNA Polymerase II. *Molecular Cell*, **2017**, 68, 491-503.e5	17.6	34
74	Probing TBP interactions in transcription initiation and reinitiation with RNA aptamers that act in distinct modes. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 6934-9	11.5	34
73	Transcription factor TFIIH is required for promoter melting in vivo. *Molecular and Cellular Biology*, **1999**, 19, 5652-8	4.8	34
72	A universal DNA-based protein detection system. *Journal of the American Chemical Society*, **2013**, 135, 14008-11	16.4	32
71	Imaging RNA Polymerase II transcription sites in living cells. *Current Opinion in Genetics and Development*, **2014**, 25, 126-30	4.9	31
70	Targeted H3R26 deimination specifically facilitates estrogen receptor binding by modifying nucleosome structure. *PLoS Genetics*, **2014**, 10, e1004613	6	31
69	The Drosophila 7SK snRNP and the essential role of dHEXIM in development. *Nucleic Acids Research* , **2012**, 40, 5283-97	20.1	30
68	Pre-mRNA splicing by the essential Drosophila protein B52: tissue and target specificity. *Molecular and Cellular Biology*, **2000**, 20, 181-6	4.8	30
67	Direct cloning of DNA that interacts in vivo with a specific protein: application to RNA polymerase II and sites of pausing in Drosophila. *Nucleic Acids Research*, **1998**, 26, 919-24	20.1	28
66	DNA sequences flanking the starts of the hsp 70 and alpha beta heat shock genes are homologous. *Developmental Biology*, **1981**, 83, 291-300	3.1	28
65	Genomic organization and transcription of the alpha beta heat shock DNA in Drosophila melanogaster. *Nucleic Acids Research*, **1981**, 9, 5297-310	20.1	28
64	Inhibiting heat shock factor 1 in human cancer cells with a potent RNA aptamer. *PLoS ONE*, **2014**, 9, e96330	3.7	27
63	Localized heat-shock induction in Drosophila melanogaster. *The Journal of Experimental Zoology*, **1988**, 247, 279-84		27
62	Glycogen synthase phosphatase interacts with heat shock factor to activate CUP1 gene transcription in Saccharomyces cerevisiae. *Molecular and Cellular Biology*, **1999**, 19, 3237-45	4.8	25
61	Chromatin Architecture of the Pitx2 Locus Requires CTCF- and Pitx2-Dependent Asymmetry that Mirrors Embryonic Gut Laterality. *Cell Reports*, **2015**, 13, 337-49	10.6	24

60	Multiplexed microcolumn-based process for efficient selection of RNA aptamers. *Analytical Chemistry*, **2013**, 85, 3417-24	7.8	24
59	A systematic study of the features critical for designing a high avidity multivalent aptamer. *Nucleic Acid Therapeutics*, **2013**, 23, 238-42	4.8	24
58	Fcp1 dephosphorylation of the RNA polymerase II C-terminal domain is required for efficient transcription of heat shock genes. *Molecular and Cellular Biology*, **2012**, 32, 3428-37	4.8	24
57	Indirect immunofluorescent labeling of Drosophila polytene chromosomes: visualizing protein interactions with chromatin in vivo. *Methods in Enzymology*, **2004**, 376, 393-404	1.7	24
56	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. *Genome Research*, **2019**, 29, 223-235	9.7	24
55	Kinetics of -induced gene silencing can be predicted from combinations of epigenetic and genomic features. *Genome Research*, **2019**, 29, 1087-1099	9.7	23
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53	The regulatory region of the L-arabinose operon: its isolation on a 1000 base-pair fragment from DNA heteroduplexes. *Journal of Molecular Biology*, **1975**, 95, 409-16	6.5	23
52	Density-dependent cooperative non-specific binding in solid-phase SELEX affinity selection. *Nucleic Acids Research*, **2013**, 41, 7167-75	20.1	22
51	Imaging transcription dynamics at endogenous genes in living Drosophila tissues. *Methods*, **2008**, 45, 233-41	4.6	22
50	The regulatory region of the L-arabinose operon: a physical, genetic and physiological study. *Journal of Molecular Biology*, **1975**, 95, 417-31	6.5	22
49	Comparison of femtosecond laser and continuous wave UV sources for protein-nucleic acid crosslinking. *Photochemistry and Photobiology*, **2007**, 83, 1394-404	3.6	21
48	Promoter cleavage: a topoIIbeta and PARP-1 collaboration. *Cell*, **2006**, 125, 1225-7	56.2	21
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46	Localization and expression of transformed DNA sequences within heat shock puffs of Drosophila melanogaster. *Chromosoma*, **1985**, 93, 26-30	2.8	20
45	Transcription imparts architecture, function and logic to enhancer units. *Nature Genetics*, **2020**, 52, 1067-1075	36.3	20
44	Paused Pol II captures enhancer activity and acts as a potent insulator. *Genes and Development*, **2009**, 23, 1606-12	12.6	18
43	TFIIB aptamers inhibit transcription by perturbing PIC formation at distinct stages. *Nucleic Acids Research*, **2008**, 36, 3118-27	20.1	18

42	Update for users of the Cornell sequence analysis package. *Nucleic Acids Research*, **1984**, 12, 619-25	20.1	18
41	An RNA aptamer perturbs heat shock transcription factor activity in Drosophila melanogaster. *Nucleic Acids Research*, **2011**, 39, 6729-40	20.1	16
40	Evolutionary dynamics and population control during in vitro selection and amplification with multiple targets. *Rna*, **2002**, 8, 1461-70	5.8	16
39	Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. *Genome Research*, **2017**, 27, 1816-1829	9.7	15
38	Distinct transcriptional responses of RNA polymerases I, II and III to aptamers that bind TBP. *Nucleic Acids Research*, **2005**, 33, 838-45	20.1	15
37	High-throughput binding characterization of RNA aptamer selections using a microplate-based multiplex microcolumn device. *Analytical and Bioanalytical Chemistry*, **2014**, 406, 2727-32	4.4	14
36	Pioneer-like factor GAF cooperates with PBAP (SWI/SNF) and NURF (ISWI) to regulate transcription. *Genes and Development*, **2021**, 35, 147-156	12.6	14
35	The metazoan-specific mediator subunit 26 (Med26) is essential for viability and is found at both active genes and pericentric heterochromatin in Drosophila melanogaster. *Molecular and Cellular Biology*, **2014**, 34, 2710-20	4.8	13
34	A 50 year history of technologies that drove discovery in eukaryotic transcription regulation. *Nature Structural and Molecular Biology*, **2019**, 26, 777-782	17.6	12
33	How does Pol II overcome the nucleosome barrier?. *Molecular Cell*, **2002**, 9, 451-2	17.6	12
32	Quantitative assessment of RNA-protein interactions with high-throughput sequencing-RNA affinity profiling. *Nature Protocols*, **2015**, 10, 1212-33	18.8	11
31	Knocking down gene function with an RNA aptamer expressed as part of an intron. *Nucleic Acids Research*, **2010**, 38, e154	20.1	11
30	Highly Multiplexed RNA Aptamer Selection using a Microplate-based Microcolumn Device. *Scientific Reports*, **2016**, 6, 29771	4.9	10
29	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. *Cell Reports*, **2021**, 34, 108783	10.6	10
28	A rapid, sensitive, scalable method for Precision Run-On sequencing (PRO-seq)		9
27	Chemical roadblocking of DNA transcription for nascent RNA display. *Journal of Biological Chemistry*, **2020**, 295, 6401-6412	5.4	8
26	Use of conditioned media is critical for studies of regulation in response to rapid heat shock. *Cell Stress and Chaperones*, **2017**, 22, 155-162	4	7
25	Expression of the major heat shock gene of Drosophila melanogaster in Saccharomyces cerevisiae. *Nucleic Acids Research*, **1986**, 14, 3587-601	20.1	7

24	Stress-induced transcriptional memory accelerates promoter-proximal pause release and decelerates termination over mitotic divisions. *Molecular Cell*, **2021**, 81, 1715-1731.e6	17.6	7
23	Population-scale study of eRNA transcription reveals bipartite functional enhancer architecture		6
22	RNA polymerase mapping in plants identifies enhancers enriched in causal variants		4
21	A new player in Pol II pausing. *EMBO Journal*, **2013**, 32, 1796-8	13	3
20	Pioneer factor GAF cooperates with PBAP and NURF to regulate transcription		3
19	Chromatin conformation remains stable upon extensive transcriptional changes driven by heat shock		3
18	Prediction of histone post-translational modification patterns based on nascent transcription data.. *Nature Genetics*, **2022**,	36.3	3
17	The H2BG53D oncohistone directly upregulates ANXA3 transcription and enhances cell migration in pancreatic ductal adenocarcinoma. *Signal Transduction and Targeted Therapy*, **2020**, 5, 106	21	2
16	Identifying Transcription Error-Enriched Genomic Loci Using Nuclear Run-on Circular-Sequencing Coupled with Background Error Modeling. *Journal of Molecular Biology*, **2020**, 432, 3933-3949	6.5	2
15	Discovering aptamers by cell-SELEX against human soluble growth factors ectopically expressed on yeast cell surface. *PLoS ONE*, **2014**, 9, e93052	3.7	2
14	HSF recruitment and loss at mostDrosophila heat shock loci is coordinated and depends on proximal promoter sequences **1996**, 105, 158		2
13	A Cdk9-PP1 kinase-phosphatase switch regulates the elongation-termination transition of RNA polymerase II		2
12	Stress-Induced Transcriptional Memory Accelerates Promoter-Proximal Pause-Release and Decelerates Termination over Mitotic Divisions		2
11	RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. *G3: Genes, Genomes, Genetics*, **2021**, 11,	3.2	2
10	RNA aptamer capture of macromolecular complexes for mass spectrometry analysis. *Nucleic Acids Research*, **2020**, 48, e90	20.1	1
9	Improving slide-based assays by stirring: application of liquid-on-liquid mixing to immunofluorescence staining of polytene chromosomes. *Journal of Proteomics*, **2005**, 64, 59-68		1
8	Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation		1
7	Natural Selection has Shaped Coding and Non-coding Transcription in Primate CD4+ T-cells		1

6	Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol		1
5	EmPC-seq: Accurate RNA-sequencing and Bioinformatics Platform to Map RNA Polymerases and Remove Background Error. *Bio-protocol*, **2021**, 11, e3921	0.9	1
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