

John T Lis

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Prediction of histone post-translational modification patterns based on nascent transcription data.. <i>Nature Genetics</i> , 2022 ,	36.3	3
202	Stress-induced transcriptional memory accelerates promoter-proximal pause release and decelerates termination over mitotic divisions. <i>Molecular Cell</i> , 2021 , 81, 1715-1731.e6	17.6	7
201	Pioneer-like factor GAF cooperates with PBAP (SWI/SNF) and NURF (ISWI) to regulate transcription. <i>Genes and Development</i> , 2021 , 35, 147-156	12.6	14
200	EmPC-seq: Accurate RNA-sequencing and Bioinformatics Platform to Map RNA Polymerases and Remove Background Error. <i>Bio-protocol</i> , 2021 , 11, e3921	0.9	1
199	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021 , 34, 108783	10.6	10
198	RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	2
197	Chemical roadblocking of DNA transcription for nascent RNA display. <i>Journal of Biological Chemistry</i> , 2020 , 295, 6401-6412	5.4	8
196	The H2BG53D oncohistone directly upregulates ANXA3 transcription and enhances cell migration in pancreatic ductal adenocarcinoma. <i>Signal Transduction and Targeted Therapy</i> , 2020 , 5, 106	21	2
195	RNA aptamer capture of macromolecular complexes for mass spectrometry analysis. <i>Nucleic Acids Research</i> , 2020 , 48, e90	20.1	1
194	Identifying Transcription Error-Enriched Genomic Loci Using Nuclear Run-on Circular-Sequencing Coupled with Background Error Modeling. <i>Journal of Molecular Biology</i> , 2020 , 432, 3933-3949	6.5	2
193	An improved 4Qaminomethyltrioxsalen-based nucleic acid crosslinker for biotinylation of double-stranded DNA or RNA.. <i>RSC Advances</i> , 2020 , 10, 39870-39874	3.7	0
192	Transcription imparts architecture, function and logic to enhancer units. <i>Nature Genetics</i> , 2020 , 52, 1067-1075	30.75	20
191	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	11.543	43
190	Kinetics of -induced gene silencing can be predicted from combinations of epigenetic and genomic features. <i>Genome Research</i> , 2019 , 29, 1087-1099	9.7	23
189	Nascent RNA analyses: tracking transcription and its regulation. <i>Nature Reviews Genetics</i> , 2019 , 20, 705-721	32.1	83
188	A 50 year history of technologies that drove discovery in eukaryotic transcription regulation. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 777-782	17.6	12
187	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. <i>Genome Research</i> , 2019 , 29, 223-235	9.7	24

186	Cdk9 regulates a promoter-proximal checkpoint to modulate RNA polymerase II elongation rate in fission yeast. <i>Nature Communications</i> , 2018 , 9, 543	17.4	41
185	Dynamic evolution of regulatory element ensembles in primate CD4 T cells. <i>Nature Ecology and Evolution</i> , 2018 , 2, 537-548	12.3	38
184	Enhancer transcription: what, where, when, and why?. <i>Genes and Development</i> , 2018 , 32, 1-3	12.6	52
183	Molecular mechanisms driving transcriptional stress responses. <i>Nature Reviews Genetics</i> , 2018 , 19, 385-397	37.1	103
182	A Cdk9-PP1 switch regulates the elongation-termination transition of RNA polymerase II. <i>Nature</i> , 2018 , 558, 460-464	50.4	57
181	Single-molecule nascent RNA sequencing identifies regulatory domain architecture at promoters and enhancers. <i>Nature Genetics</i> , 2018 , 50, 1533-1541	36.3	48
180	Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. <i>Nature Genetics</i> , 2018 , 50, 1553-1564	36.3	56
179	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	9.7	15
178	CBP Regulates Recruitment and Release of Promoter-Proximal RNA Polymerase II. <i>Molecular Cell</i> , 2017 , 68, 491-503.e5	17.6	34
177	The 4D nucleome project. <i>Nature</i> , 2017 , 549, 219-226	50.4	332
176	Transcriptional response to stress is pre-wired by promoter and enhancer architecture. <i>Nature Communications</i> , 2017 , 8, 255	17.4	78
175	Use of conditioned media is critical for studies of regulation in response to rapid heat shock. <i>Cell Stress and Chaperones</i> , 2017 , 22, 155-162	4	7
174	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). <i>Nature Protocols</i> , 2016 , 11, 1455-76	18.8	208
173	Cotranscriptional folding of a riboswitch at nucleotide resolution. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 1124-1131	17.6	102
172	Mammalian Heat Shock Response and Mechanisms Underlying Its Genome-wide Transcriptional Regulation. <i>Molecular Cell</i> , 2016 , 62, 63-78	17.6	213
171	Highly Multiplexed RNA Aptamer Selection using a Microplate-based Microcolumn Device. <i>Scientific Reports</i> , 2016 , 6, 29771	4.9	10
170	Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation. <i>Genes and Development</i> , 2016 , 30, 1731-46	12.6	68
169	Divergence of a conserved elongation factor and transcription regulation in budding and fission yeast. <i>Genome Research</i> , 2016 , 26, 799-811	9.7	51

168	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, 2003-16	10.6	48
167	GAGA factor maintains nucleosome-free regions and has a role in RNA polymerase II recruitment to promoters. <i>PLoS Genetics</i> , 2015 , 11, e1005108	6	63
166	Quantitative assessment of RNA-protein interactions with high-throughput sequencing-RNA affinity profiling. <i>Nature Protocols</i> , 2015 , 10, 1212-33	18.8	11
165	Identification of active transcriptional regulatory elements from GRO-seq data. <i>Nature Methods</i> , 2015 , 12, 433-8	21.6	112
164	Human Gene Promoters Are Intrinsically Bidirectional. <i>Molecular Cell</i> , 2015 , 60, 346-7	17.6	42
163	Chromatin Architecture of the Pitx2 Locus Requires CTCF- and Pitx2-Dependent Asymmetry that Mirrors Embryonic Gut Laterality. <i>Cell Reports</i> , 2015 , 13, 337-49	10.6	24
162	Getting up to speed with transcription elongation by RNA polymerase II. <i>Nature Reviews Molecular Cell Biology</i> , 2015 , 16, 167-77	48.7	485
161	A Unified Model Describing The Architecture And Creation Of Promoters And Enhancers. <i>FASEB Journal</i> , 2015 , 29, 497.3	0.9	
160	High-throughput binding characterization of RNA aptamer selections using a microplate-based multiplex microcolumn device. <i>Analytical and Bioanalytical Chemistry</i> , 2014 , 406, 2727-32	4.4	14
159	The metazoan-specific mediator subunit 26 (Med26) is essential for viability and is found at both active genes and pericentric heterochromatin in <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Biology</i> , 2014 , 34, 2710-20	4.8	13
158	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. <i>Nature Genetics</i> , 2014 , 46, 1311-20	36.3	399
157	Comprehensive analysis of RNA-protein interactions by high-throughput sequencing-RNA affinity profiling. <i>Nature Methods</i> , 2014 , 11, 683-8	21.6	92
156	Pol II docking and pausing at growth and stress genes in <i>C. elegans</i> . <i>Cell Reports</i> , 2014 , 6, 455-66	10.6	39
155	RNA-DNA differences are generated in human cells within seconds after RNA exits polymerase II. <i>Cell Reports</i> , 2014 , 6, 906-15	10.6	44
154	Imaging RNA Polymerase II transcription sites in living cells. <i>Current Opinion in Genetics and Development</i> , 2014 , 25, 126-30	4.9	31
153	Discovering aptamers by cell-SELEX against human soluble growth factors ectopically expressed on yeast cell surface. <i>PLoS ONE</i> , 2014 , 9, e93052	3.7	2
152	Inhibiting heat shock factor 1 in human cancer cells with a potent RNA aptamer. <i>PLoS ONE</i> , 2014 , 9, e96339	3.9	27
151	New Technologies Provide Quantum Changes in the Scale, Speed, and Success of SELEX Methods and Aptamer Characterization. <i>Molecular Therapy - Nucleic Acids</i> , 2014 , 3, e183	10.7	111

150	Defining NELF-E RNA binding in HIV-1 and promoter-proximal pause regions. <i>PLoS Genetics</i> , 2014 , 10, e1004090	6	48
149	Targeted H3R26 deimination specifically facilitates estrogen receptor binding by modifying nucleosome structure. <i>PLoS Genetics</i> , 2014 , 10, e1004613	6	31
148	Kinetics of promoter Pol II on Hsp70 reveal stable pausing and key insights into its regulation. <i>Genes and Development</i> , 2014 , 28, 14-9	12.6	38
147	Genome-wide dynamics of Pol II elongation and its interplay with promoter proximal pausing, chromatin, and exons. <i>ELife</i> , 2014 , 3, e02407	8.9	337
146	Coordinated effects of sequence variation on DNA binding, chromatin structure, and transcription. <i>Science</i> , 2013 , 342, 744-7	33.3	278
145	A universal DNA-based protein detection system. <i>Journal of the American Chemical Society</i> , 2013 , 135, 14008-11	16.4	32
144	Mechanisms by which transcription factors gain access to target sequence elements in chromatin. <i>Current Opinion in Genetics and Development</i> , 2013 , 23, 116-23	4.9	61
143	Control of transcriptional elongation. <i>Annual Review of Genetics</i> , 2013 , 47, 483-508	14.5	285
142	Extensive polymerase pausing during <i>Drosophila</i> axis patterning enables high-level and pliable transcription. <i>Genes and Development</i> , 2013 , 27, 1146-58	12.6	61
141	Development of temperature-sensitive mutants of the <i>Drosophila melanogaster</i> P-TEFb (Cyclin T/CDK9) heterodimer using yeast two-hybrid screening. <i>Biochemical and Biophysical Research Communications</i> , 2013 , 433, 243-8	3.4	
140	Precise maps of RNA polymerase reveal how promoters direct initiation and pausing. <i>Science</i> , 2013 , 339, 950-3	33.3	466
139	Signaling pathways differentially affect RNA polymerase II initiation, pausing, and elongation rate in cells. <i>Molecular Cell</i> , 2013 , 50, 212-22	17.6	231
138	Multiplexed microcolumn-based process for efficient selection of RNA aptamers. <i>Analytical Chemistry</i> , 2013 , 85, 3417-24	7.8	24
137	A new player in Pol II pausing. <i>EMBO Journal</i> , 2013 , 32, 1796-8	13	3
136	Genome-wide control of RNA polymerase II activity by cohesin. <i>PLoS Genetics</i> , 2013 , 9, e1003382	6	83
135	A systematic study of the features critical for designing a high avidity multivalent aptamer. <i>Nucleic Acid Therapeutics</i> , 2013 , 23, 238-42	4.8	24
134	Density-dependent cooperative non-specific binding in solid-phase SELEX affinity selection. <i>Nucleic Acids Research</i> , 2013 , 41, 7167-75	20.1	22
133	RAPID-SELEX for RNA aptamers. <i>PLoS ONE</i> , 2013 , 8, e82667	3.7	48

132	Condensin controls recruitment of RNA polymerase II to achieve nematode X-chromosome dosage compensation. <i>ELife</i> , 2013 , 2, e00808	8.9	123
131	Overcoming the nucleosome barrier during transcript elongation. <i>Trends in Genetics</i> , 2012 , 28, 285-94	8.5	112
130	The Drosophila 7SK snRNP and the essential role of dHEXIM in development. <i>Nucleic Acids Research</i> , 2012 , 40, 5283-97	20.1	30
129	Promoter-proximal pausing of RNA polymerase II: emerging roles in metazoans. <i>Nature Reviews Genetics</i> , 2012 , 13, 720-31	30.1	775
128	Defining the status of RNA polymerase at promoters. <i>Cell Reports</i> , 2012 , 2, 1025-35	10.6	163
127	Activator-induced spread of poly(ADP-ribose) polymerase promotes nucleosome loss at Hsp70. <i>Molecular Cell</i> , 2012 , 45, 64-74	17.6	87
126	Accurate prediction of inducible transcription factor binding intensities in vivo. <i>PLoS Genetics</i> , 2012 , 8, e1002610	6	43
125	Peptidylarginine deiminase 2-catalyzed histone H3 arginine 26 citrullination facilitates estrogen receptor β target gene activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 13331-6	11.5	140
124	RNA aptamers that functionally interact with green fluorescent protein and its derivatives. <i>Nucleic Acids Research</i> , 2012 , 40, e39	20.1	38
123	Fcp1 dephosphorylation of the RNA polymerase II C-terminal domain is required for efficient transcription of heat shock genes. <i>Molecular and Cellular Biology</i> , 2012 , 32, 3428-37	4.8	24
122	A rapid, extensive, and transient transcriptional response to estrogen signaling in breast cancer cells. <i>Cell</i> , 2011 , 145, 622-34	56.2	377
121	The polycomb group mutant <i>esc</i> leads to augmented levels of paused Pol II in the Drosophila embryo. <i>Molecular Cell</i> , 2011 , 42, 837-44	17.6	39
120	X chromosome dosage compensation via enhanced transcriptional elongation in Drosophila. <i>Nature</i> , 2011 , 471, 115-8	50.4	149
119	Drosophila <i>Set1</i> is the major histone H3 lysine 4 trimethyltransferase with role in transcription. <i>EMBO Journal</i> , 2011 , 30, 2817-28	13	133
118	Regulating RNA polymerase pausing and transcription elongation in embryonic stem cells. <i>Genes and Development</i> , 2011 , 25, 742-54	12.6	243
117	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, 17702-7	11.5	63
116	An RNA aptamer perturbs heat shock transcription factor activity in Drosophila melanogaster. <i>Nucleic Acids Research</i> , 2011 , 39, 6729-40	20.1	16
115	CDK12 is a transcription elongation-associated CTD kinase, the metazoan ortholog of yeast Ctk1. <i>Genes and Development</i> , 2010 , 24, 2303-16	12.6	267

114	Knocking down gene function with an RNA aptamer expressed as part of an intron. <i>Nucleic Acids Research</i> , 2010 , 38, e154	20.1	11
113	Chromatin landscape dictates HSF binding to target DNA elements. <i>PLoS Genetics</i> , 2010 , 6, e1001114	6	163
112	Recruitment timing and dynamics of transcription factors at the Hsp70 loci in living cells. <i>Molecular Cell</i> , 2010 , 40, 965-75	17.6	99
111	Spt6 enhances the elongation rate of RNA polymerase II in vivo. <i>EMBO Journal</i> , 2009 , 28, 1067-77	13	108
110	Defining mechanisms that regulate RNA polymerase II transcription in vivo. <i>Nature</i> , 2009 , 461, 186-92	50.4	399
109	High-resolution dynamic mapping of histone-DNA interactions in a nucleosome. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 124-9	17.6	290
108	Paused Pol II captures enhancer activity and acts as a potent insulator. <i>Genes and Development</i> , 2009 , 23, 1606-12	12.6	18
107	Selection and elution of aptamers using nanoporous sol-gel arrays with integrated microheaters. <i>Lab on A Chip</i> , 2009 , 9, 1206-12	7.2	77
106	Phosphorylation of the RNA polymerase II C-terminal domain by TFIIH 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, 14276-80	11.5	41
105	Divergent transcription: a new feature of active promoters. <i>Cell Cycle</i> , 2009 , 8, 2557-64	4.7	140
104	Massively-Parallel Sequencing Of Nascent RNA Sequencing Reveals Widespread Pausing And Divergent Initiation From Mammalian Promoters. <i>FASEB Journal</i> , 2009 , 23, 316.1	0.9	
103	Imaging transcription dynamics at endogenous genes in living <i>Drosophila</i> tissues. <i>Methods</i> , 2008 , 45, 233-41	4.6	22
102	Rapid, transcription-independent loss of nucleosomes over a large chromatin domain at Hsp70 loci. <i>Cell</i> , 2008 , 134, 74-84	56.2	263
101	Transcription regulation through promoter-proximal pausing of RNA polymerase II. <i>Science</i> , 2008 , 319, 1791-2	33.3	310
100	P-TEFb is critical for the maturation of RNA polymerase II into productive elongation in vivo. <i>Molecular and Cellular Biology</i> , 2008 , 28, 1161-70	4.8	101
99	TFIIB aptamers inhibit transcription by perturbing PIC formation at distinct stages. <i>Nucleic Acids Research</i> , 2008 , 36, 3118-27	20.1	18
98	Nascent RNA sequencing reveals widespread pausing and divergent initiation at human promoters. <i>Science</i> , 2008 , 322, 1845-8	33.3	1441
97	Imaging <i>Drosophila</i> gene activation and polymerase pausing in vivo. <i>Nature</i> , 2007 , 450, 198-202	50.4	60

96	Comparison of femtosecond laser and continuous wave UV sources for protein-nucleic acid crosslinking. <i>Photochemistry and Photobiology</i> , 2007 , 83, 1394-404	3.6	21
95	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, 3742-6	11.5	47
94	Intranuclear distribution and local dynamics of RNA polymerase II during transcription activation. <i>Molecular Cell</i> , 2007 , 28, 978-90	17.6	92
93	An RNA aptamer that interferes with the DNA binding of the HSF transcription activator. <i>Nucleic Acids Research</i> , 2006 , 34, 3755-61	20.1	38
92	Drosophila Paf1 modulates chromatin structure at actively transcribed genes. <i>Molecular and Cellular Biology</i> , 2006 , 26, 250-60	4.8	98
91	Promoter cleavage: a topolbeta and PARP-1 collaboration. <i>Cell</i> , 2006 , 125, 1225-7	56.2	21
90	Breaking barriers to transcription elongation. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 557-67	48.7	399
89	Probing SWI/SNF remodeling of the nucleosome by unzipping single DNA molecules. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 549-54	17.6	83
88	Dynamics of heat shock factor association with native gene loci in living cells. <i>Nature</i> , 2006 , 442, 1050-3	50.4	169
87	Specific contributions of histone tails and their acetylation to the mechanical stability of nucleosomes. <i>Journal of Molecular Biology</i> , 2005 , 346, 135-46	6.5	152
86	Efficient release from promoter-proximal stall sites requires transcript cleavage factor TFIIIS. <i>Molecular Cell</i> , 2005 , 17, 103-12	17.6	132
85	Improving slide-based assays by stirring: application of liquid-on-liquid mixing to immunofluorescence staining of polytene chromosomes. <i>Journal of Proteomics</i> , 2005 , 64, 59-68		1
84	Interactions between subunits of Drosophila Mediator and activator proteins. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 245-9	10.3	35
83	Distinct transcriptional responses of RNA polymerases I, II and III to aptamers that bind TBP. <i>Nucleic Acids Research</i> , 2005 , 33, 838-45	20.1	15
82	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, 6934-9	11.5	34
81	Indirect immunofluorescent labeling of Drosophila polytene chromosomes: visualizing protein interactions with chromatin in vivo. <i>Methods in Enzymology</i> , 2004 , 376, 393-404	1.7	24
80	NAD ⁺ -dependent modulation of chromatin structure and transcription by nucleosome binding properties of PARP-1. <i>Cell</i> , 2004 , 119, 803-14	56.2	437
79	A unified nomenclature for protein subunits of mediator complexes linking transcriptional regulators to RNA polymerase II. <i>Molecular Cell</i> , 2004 , 14, 553-7	17.6	209

78	Molecular mechanism of transcription inhibition by peptide antibiotic Microcin J25. <i>Molecular Cell</i> , 2004 , 14, 753-62	17.6	140
77	Coordination of transcription, RNA processing, and surveillance by P-TEFb kinase on heat shock genes. <i>Molecular Cell</i> , 2004 , 13, 55-65	17.6	199
76	Tracking FACT and the RNA polymerase II elongation complex through chromatin in vivo. <i>Science</i> , 2003 , 301, 1094-6	33.3	233
75	PARP goes transcription. <i>Cell</i> , 2003 , 113, 677-83	56.2	435
74	Specific SR protein-dependent splicing substrates identified through genomic SELEX. <i>Nucleic Acids Research</i> , 2003 , 31, 1955-61	20.1	54
73	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, 7628-37	4.8	192
72	Cdk7 is required for full activation of Drosophila heat shock genes and RNA polymerase II phosphorylation in vivo. <i>Molecular and Cellular Biology</i> , 2003 , 23, 6876-86	4.8	58
71	The RNA processing exosome is linked to elongating RNA polymerase II in Drosophila. <i>Nature</i> , 2002 , 420, 837-41	50.4	208
70	The Drosophila BRM complex facilitates global transcription by RNA polymerase II. <i>EMBO Journal</i> , 2002 , 21, 5245-54	13	140
69	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, 13538-43	11.5	145
68	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, 1960-5	11.5	368
67	Evolutionary dynamics and population control during in vitro selection and amplification with multiple targets. <i>Rna</i> , 2002 , 8, 1461-70	5.8	16
66	How does Pol II overcome the nucleosome barrier?. <i>Molecular Cell</i> , 2002 , 9, 451-2	17.6	12
65	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, 1201-13	17.6	462
64	Mediator, not holoenzyme, is directly recruited to the heat shock promoter by HSF upon heat shock. <i>Molecular Cell</i> , 2001 , 8, 9-19	17.6	122
63	Pre-mRNA splicing by the essential Drosophila protein B52: tissue and target specificity. <i>Molecular and Cellular Biology</i> , 2000 , 20, 181-6	4.8	30
62	High-resolution localization of Drosophila Spt5 and Spt6 at heat shock genes in vivo: roles in promoter proximal pausing and transcription elongation. <i>Genes and Development</i> , 2000 , 14, 2635-49	12.6	221
61	A TRF1:BRF complex directs Drosophila RNA polymerase III transcription. <i>Cell</i> , 2000 , 101, 459-69	56.2	88

60	P-TEFb kinase recruitment and function at heat shock loci. <i>Genes and Development</i> , 2000 , 14, 792-803	12.6	229
59	P-TEFb kinase recruitment and function at heat shock loci. <i>Genes and Development</i> , 2000 , 14, 792-803	12.6	184
58	Nuclear run-on assays: assessing transcription by measuring density of engaged RNA polymerases. <i>Methods in Enzymology</i> , 1999 , 304, 351-62	1.7	49
57	DNA distortion and multimerization: novel functions of the glutamine-rich domain of GAGA factor. <i>Journal of Molecular Biology</i> , 1999 , 285, 515-25	6.5	48
56	Glycogen synthase phosphatase interacts with heat shock factor to activate CUP1 gene transcription in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999 , 19, 3237-45	4.8	25
55	Transcription factor TFIIH is required for promoter melting in vivo. <i>Molecular and Cellular Biology</i> , 1999 , 19, 5652-8	4.8	34
54	Transcriptional activation independent of TFIIH kinase and the RNA polymerase II mediator in vivo. <i>Nature</i> , 1998 , 393, 389-92	50.4	88
53	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, 919-24	20.1	28
52	Cooperative and competitive protein interactions at the hsp70 promoter. <i>Journal of Biological Chemistry</i> , 1997 , 272, 33227-33	5.4	78
51	Dynamics of potentiation and activation: GAGA factor and its role in heat shock gene regulation. <i>Nucleic Acids Research</i> , 1997 , 25, 3963-8	20.1	86
50	Transcription properties of a cell type-specific TATA-binding protein, TRF. <i>Cell</i> , 1997 , 91, 71-83	56.2	145
49	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, 158-71	2.8	43
48	HSF recruitment and loss at most <i>Drosophila</i> heat shock loci is coordinated and depends on proximal promoter sequences 1996 , 105, 158		2
47	Sodium salicylate and yeast heat shock gene transcription. <i>Journal of Biological Chemistry</i> , 1995 , 270, 10369-72	5.4	35
46	Binding of heat shock factor to and transcriptional activation of heat shock genes in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 1995 , 23, 4799-804	20.1	37
45	Short transcripts of the ternary complex provide insight into RNA polymerase II elongational pausing. <i>Journal of Molecular Biology</i> , 1995 , 252, 522-35	6.5	69
44	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, 167-73	20.1	161
43	Phosphorylation of RNA polymerase II C-terminal domain and transcriptional elongation. <i>Nature</i> , 1994 , 370, 75-7	50.4	301

42	The upstream activator CTF/NF1 and RNA polymerase II share a common element involved in transcriptional activation. <i>Nucleic Acids Research</i> , 1994 , 22, 1966-73	20.1	55
41	Protein traffic on the heat shock promoter: parking, stalling, and trucking along. <i>Cell</i> , 1993 , 74, 1-4	56.2	438
40	Promoter sequence containing (CT)n.(GA)n repeats is critical for the formation of the DNase I hypersensitive sites in the Drosophila hsp26 gene. <i>Journal of Molecular Biology</i> , 1992 , 225, 985-98	6.5	79
39	Protein-DNA cross-linking as a means to determine the distribution of proteins on DNA in vivo. <i>Methods in Cell Biology</i> , 1991 , 35, 369-81	1.8	23
38	Cooperative binding of Drosophila heat shock factor to arrays of a conserved 5 bp unit. <i>Cell</i> , 1991 , 64, 585-93	56.2	231
37	Optimal heat-induced expression of the Drosophila hsp26 gene requires a promoter sequence containing (CT)n.(GA)n repeats. <i>Journal of Molecular Biology</i> , 1990 , 211, 751-61	6.5	84
36	Stable binding of Drosophila 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	56.2	423
35	Localized heat-shock induction in Drosophila melanogaster. <i>The Journal of Experimental Zoology</i> , 1988 , 247, 279-84		27
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30	Localization and expression of transformed DNA sequences within heat shock puffs of Drosophila melanogaster. <i>Chromosoma</i> , 1985 , 93, 26-30	2.8	20
29	Determinants of heat shock-induced chromosome puffing. <i>Cell</i> , 1985 , 40, 805-17	56.2	294
28	Update for users of the Cornell sequence analysis package. <i>Nucleic Acids Research</i> , 1984 , 12, 619-25	20.1	18
27	New heat shock puffs and beta-galactosidase activity resulting from transformation of Drosophila with an hsp70-lacZ hybrid gene. <i>Cell</i> , 1983 , 35, 403-10	56.2	339
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25	Portable microcomputer software for nucleotide sequence analysis. <i>Nucleic Acids Research</i> , 1982 , 10, 6451-63	20.1	100

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10	Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation		1
9	Natural Selection has Shaped Coding and Non-coding Transcription in Primate CD4+ T-cells		1
8	A Cdk9-PP1 kinase-phosphatase switch regulates the elongation-termination transition of RNA polymerase II		2
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6	A rapid, sensitive, scalable method for Precision Run-On sequencing (PRO-seq)	9
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