

John T Lis

List of Publications by Year in descending order

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196
papers

28,646
citations

5126

86
h-index

7234

158
g-index

215
all docs

215
docs citations

215
times ranked

24966
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Prediction of histone post-translational modification patterns based on nascent transcription data. <i>Nature Genetics</i> , 2022, 54, 295-305.	9.4	53
3	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
4	EmPC-seq: Accurate RNA-sequencing and Bioinformatics Platform to Map RNA Polymerases and Remove Background Error. <i>Bio-protocol</i> , 2021, 11, e3921.	0.2	1
5	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021, 34, 108783.	2.9	53
6	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
7	RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	11
8	An improved 4-aminomethyltrioxsalen-based nucleic acid crosslinker for biotinylation of double-stranded DNA or RNA. <i>RSC Advances</i> , 2020, 10, 39870-39874.	1.7	2
9	Transcription imparts architecture, function and logic to enhancer units. <i>Nature Genetics</i> , 2020, 52, 1067-1075.	9.4	60
10	Chemical roadblocking of DNA transcription for nascent RNA display. <i>Journal of Biological Chemistry</i> , 2020, 295, 6401-6412.	1.6	16
11	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.	7.1	12
12	RNA aptamer capture of macromolecular complexes for mass spectrometry analysis. <i>Nucleic Acids Research</i> , 2020, 48, e90-e90.	6.5	2
13	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.	2.0	2
14	Nascent RNA analyses: tracking transcription and its regulation. <i>Nature Reviews Genetics</i> , 2019, 20, 705-723.	7.7	177
15	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
16	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
17	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
18	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

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19	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
20	Dynamic evolution of regulatory element ensembles in primate CD4+ T cells. <i>Nature Ecology and Evolution</i> , 2018, 2, 537-548.	3.4	65
21	Enhancer transcription: what, where, when, and why?. <i>Genes and Development</i> , 2018, 32, 1-3.	2.7	96
22	Molecular mechanisms driving transcriptional stress responses. <i>Nature Reviews Genetics</i> , 2018, 19, 385-397.	7.7	206
23	Single-molecule nascent RNA sequencing identifies regulatory domain architecture at promoters and enhancers. <i>Nature Genetics</i> , 2018, 50, 1533-1541.	9.4	89
24	Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. <i>Nature Genetics</i> , 2018, 50, 1553-1564.	9.4	108
25	A Cdk9-PP1 switch regulates the elongation-termination transition of RNA polymerase II. <i>Nature</i> , 2018, 558, 460-464.	13.7	105
26	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
27	CBP Regulates Recruitment and Release of Promoter-Proximal RNA Polymerase II. <i>Molecular Cell</i> , 2017, 68, 491-503.e5.	4.5	59
28	The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.	13.7	579
29	Transcriptional response to stress is pre-wired by promoter and enhancer architecture. <i>Nature Communications</i> , 2017, 8, 255.	5.8	136
30	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.	1.2	20
31	Highly Multiplexed RNA Aptamer Selection using a Microplate-based Microcolumn Device. <i>Scientific Reports</i> , 2016, 6, 29771.	1.6	13
32	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
33	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
34	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
35	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
36	Cotranscriptional folding of a riboswitch at nucleotide resolution. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1124-1131.	3.6	163

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37	Mammalian Heat Shock Response and Mechanisms Underlying Its Genome-wide Transcriptional Regulation. <i>Molecular Cell</i> , 2016, 62, 63-78.	4.5	322
38	Chromatin Architecture of the Pitx2 Locus Requires CTCF- and Pitx2-Dependent Asymmetry that Mirrors Embryonic Gut Laterality. <i>Cell Reports</i> , 2015, 13, 337-349.	2.9	30
39	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
40	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
41	Quantitative assessment of RNA-protein interactions with high-throughput sequencing—RNA affinity profiling. <i>Nature Protocols</i> , 2015, 10, 1212-1233.	5.5	19
42	Identification of active transcriptional regulatory elements from GRO-seq data. <i>Nature Methods</i> , 2015, 12, 433-438.	9.0	198
43	Human Gene Promoters Are Intrinsically Bidirectional. <i>Molecular Cell</i> , 2015, 60, 346-347.	4.5	55
44	A Unified Model Describing The Architecture And Creation Of Promoters And Enhancers. <i>FASEB Journal</i> , 2015, 29, 497.3.	0.2	0
45	Discovering Aptamers by Cell-SELEX against Human Soluble Growth Factors Ectopically Expressed on Yeast Cell Surface. <i>PLoS ONE</i> , 2014, 9, e93052.	1.1	2
46	Inhibiting Heat Shock Factor 1 in Human Cancer Cells with a Potent RNA Aptamer. <i>PLoS ONE</i> , 2014, 9, e96330.	1.1	32
47	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.	2.3	140
48	Defining NELF-E RNA Binding in HIV-1 and Promoter-Proximal Pause Regions. <i>PLoS Genetics</i> , 2014, 10, e1004090.	1.5	55
49	Targeted H3R26 Deimination Specifically Facilitates Estrogen Receptor Binding by Modifying Nucleosome Structure. <i>PLoS Genetics</i> , 2014, 10, e1004613.	1.5	43
50	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
51	High-throughput binding characterization of RNA aptamer selections using a microplate-based multiplex microcolumn device. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 2727-2732.	1.9	15
52	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, 2710-2720.	1.1	15
53	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
54	Comprehensive analysis of RNA-protein interactions by high-throughput sequencing—RNA affinity profiling. <i>Nature Methods</i> , 2014, 11, 683-688.	9.0	124

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55	Pol II Docking and Pausing at Growth and Stress Genes in <i>C.Âelegans</i> . <i>Cell Reports</i> , 2014, 6, 455-466.	2.9	61
56	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
57	Imaging RNA Polymerase II transcription sites in living cells. <i>Current Opinion in Genetics and Development</i> , 2014, 25, 126-130.	1.5	40
58	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
59	Coordinated Effects of Sequence Variation on DNA Binding, Chromatin Structure, and Transcription. <i>Science</i> , 2013, 342, 744-747.	6.0	364
60	A Universal DNA-Based Protein Detection System. <i>Journal of the American Chemical Society</i> , 2013, 135, 14008-14011.	6.6	35
61	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
62	Control of Transcriptional Elongation. <i>Annual Review of Genetics</i> , 2013, 47, 483-508.	3.2	359
63	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
64	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, 243-248.	1.0	0
65	Precise Maps of RNA Polymerase Reveal How Promoters Direct Initiation and Pausing. <i>Science</i> , 2013, 339, 950-953.	6.0	683
66	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
67	Multiplexed Microcolumn-Based Process for Efficient Selection of RNA Aptamers. <i>Analytical Chemistry</i> , 2013, 85, 3417-3424.	3.2	29
68	A new player in Pol II pausing. <i>EMBO Journal</i> , 2013, 32, 1796-1798.	3.5	3
69	Genome-Wide Control of RNA Polymerase II Activity by Cohesin. <i>PLoS Genetics</i> , 2013, 9, e1003382.	1.5	97
70	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
71	Density-dependent cooperative non-specific binding in solid-phase SELEX affinity selection. <i>Nucleic Acids Research</i> , 2013, 41, 7167-7175.	6.5	26
72	RAPID-SELEX for RNA Aptamers. <i>PLoS ONE</i> , 2013, 8, e82667.	1.1	58

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73	Condensin controls recruitment of RNA polymerase II to achieve nematode X-chromosome dosage compensation. <i>ELife</i> , 2013, 2, e00808.	2.8	165
74	Accurate Prediction of Inducible Transcription Factor Binding Intensities In Vivo. <i>PLoS Genetics</i> , 2012, 8, e1002610.	1.5	56
75	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, 13331-13336.	3.3	173
76	RNA aptamers that functionally interact with green fluorescent protein and its derivatives. <i>Nucleic Acids Research</i> , 2012, 40, e39-e39.	6.5	47
77	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, 3428-3437.	1.1	26
78	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
79	Promoter-proximal pausing of RNA polymerase II: emerging roles in metazoans. <i>Nature Reviews Genetics</i> , 2012, 13, 720-731.	7.7	1,003
80	Defining the Status of RNA Polymerase at Promoters. <i>Cell Reports</i> , 2012, 2, 1025-1035.	2.9	222
81	Activator-Induced Spread of Poly(ADP-Ribose) Polymerase Promotes Nucleosome Loss at Hsp70. <i>Molecular Cell</i> , 2012, 45, 64-74.	4.5	101
82	Overcoming the nucleosome barrier during transcript elongation. <i>Trends in Genetics</i> , 2012, 28, 285-294.	2.9	150
83	<i>Drosophila</i> Set1 is the major histone H3 lysine 4 trimethyltransferase with role in transcription. <i>EMBO Journal</i> , 2011, 30, 2817-2828.	3.5	168
84	A Rapid, Extensive, and Transient Transcriptional Response to Estrogen Signaling in Breast Cancer Cells. <i>Cell</i> , 2011, 145, 622-634.	13.5	458
85	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
86	X chromosome dosage compensation via enhanced transcriptional elongation in <i>Drosophila</i> . <i>Nature</i> , 2011, 471, 115-118.	13.7	169
87	Regulating RNA polymerase pausing and transcription elongation in embryonic stem cells. <i>Genes and Development</i> , 2011, 25, 742-754.	2.7	281
88	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
89	An RNA aptamer perturbs heat shock transcription factor activity in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2011, 39, 6729-6740.	6.5	17
90	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

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91	Knocking down gene function with an RNA aptamer expressed as part of an intron. <i>Nucleic Acids Research</i> , 2010, 38, e154-e154.	6.5	12
92	Chromatin Landscape Dictates HSF Binding to Target DNA Elements. <i>PLoS Genetics</i> , 2010, 6, e1001114.	1.5	194
93	Recruitment Timing and Dynamics of Transcription Factors at the Hsp70 Loci in Living Cells. <i>Molecular Cell</i> , 2010, 40, 965-975.	4.5	125
94	Spt6 enhances the elongation rate of RNA polymerase II in vivo. <i>EMBO Journal</i> , 2009, 28, 1067-1077.	3.5	131
95	Defining mechanisms that regulate RNA polymerase II transcription in vivo. <i>Nature</i> , 2009, 461, 186-192.	13.7	476
96	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
97	Tracking rates of transcription and splicing in vivo. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1123-1124.	3.6	111
98	Paused Pol II captures enhancer activity and acts as a potent insulator. <i>Genes and Development</i> , 2009, 23, 1606-1612.	2.7	20
99	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
100	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
101	Divergent transcription: A new feature of active promoters. <i>Cell Cycle</i> , 2009, 8, 2557-2564.	1.3	172
102	Massively Parallel Sequencing Of Nascent RNA Sequencing Reveals Widespread Pausing And Divergent Initiation From Mammalian Promoters. <i>FASEB Journal</i> , 2009, 23, 316.1.	0.2	0
103	Nascent RNA Sequencing Reveals Widespread Pausing and Divergent Initiation at Human Promoters. <i>Science</i> , 2008, 322, 1845-1848.	6.0	1,758
104	Imaging transcription dynamics at endogenous genes in living <i>Drosophila</i> tissues. <i>Methods</i> , 2008, 45, 233-241.	1.9	25
105	Rapid, Transcription-Independent Loss of Nucleosomes over a Large Chromatin Domain at Hsp70 Loci. <i>Cell</i> , 2008, 134, 74-84.	13.5	290
106	Transcription Regulation Through Promoter-Proximal Pausing of RNA Polymerase II. <i>Science</i> , 2008, 319, 1791-1792.	6.0	347
107	P-TEFb Is Critical for the Maturation of RNA Polymerase II into Productive Elongation In Vivo. <i>Molecular and Cellular Biology</i> , 2008, 28, 1161-1170.	1.1	128
108	TFIIB aptamers inhibit transcription by perturbing PIC formation at distinct stages. <i>Nucleic Acids Research</i> , 2008, 36, 3118-3127.	6.5	19

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109	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, 3742-3746.	3.3	52
110	Intranuclear Distribution and Local Dynamics of RNA Polymerase II during Transcription Activation. Molecular Cell, 2007, 28, 978-990.	4.5	110
111	Imaging Drosophila gene activation and polymerase pausing in vivo. Nature, 2007, 450, 198-202.	13.7	65
112	Comparison of Femtosecond Laser and Continuous Wave UV Sources for Protein-Nucleic Acid Crosslinking. Photochemistry and Photobiology, 2007, 83, 1394-1404.	1.3	27
113	Promoter Cleavage: A TopoII ² and PARP-1 Collaboration. Cell, 2006, 125, 1225-1227.	13.5	22
114	Breaking barriers to transcription elongation. Nature Reviews Molecular Cell Biology, 2006, 7, 557-567.	16.1	434
115	Probing SWI/SNF remodeling of the nucleosome by unzipping single DNA molecules. Nature Structural and Molecular Biology, 2006, 13, 549-554.	3.6	89
116	Dynamics of heat shock factor association with native gene loci in living cells. Nature, 2006, 442, 1050-1053.	13.7	186
117	An RNA aptamer that interferes with the DNA binding of the HSF transcription activator. Nucleic Acids Research, 2006, 34, 3755-3761.	6.5	39
118	Drosophila Paf1 Modulates Chromatin Structure at Actively Transcribed Genes. Molecular and Cellular Biology, 2006, 26, 250-260.	1.1	110
119	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.	2.4	1
120	Interactions between subunits of Drosophila Mediator and activator proteins. Trends in Biochemical Sciences, 2005, 30, 245-249.	3.7	46
121	Distinct transcriptional responses of RNA polymerases I, II and III to aptamers that bind TBP. Nucleic Acids Research, 2005, 33, 838-845.	6.5	18
122	Specific Contributions of Histone Tails and their Acetylation to the Mechanical Stability of Nucleosomes. Journal of Molecular Biology, 2005, 346, 135-146.	2.0	177
123	Efficient Release from Promoter-Proximal Stall Sites Requires Transcript Cleavage Factor TFIIIS. Molecular Cell, 2005, 17, 103-112.	4.5	145
124	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, 6934-6939.	3.3	37
125	NAD ⁺ -Dependent Modulation of Chromatin Structure and Transcription by Nucleosome Binding Properties of PARP-1. Cell, 2004, 119, 803-814.	13.5	487
126	A Unified Nomenclature for Protein Subunits of Mediator Complexes Linking Transcriptional Regulators to RNA Polymerase II. Molecular Cell, 2004, 14, 553-557.	4.5	230

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127	Molecular Mechanism of Transcription Inhibition by Peptide Antibiotic Microcin J25. <i>Molecular Cell</i> , 2004, 14, 753-762.	4.5	165
128	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
129	Indirect Immunofluorescent Labeling of Drosophila Polytene Chromosomes: Visualizing Protein Interactions with Chromatin In Vivo. <i>Methods in Enzymology</i> , 2003, 376, 393-404.	0.4	25
130	Tracking FACT and the RNA Polymerase II Elongation Complex Through Chromatin in Vivo. <i>Science</i> , 2003, 301, 1094-1096.	6.0	261
131	PARP Goes Transcription. <i>Cell</i> , 2003, 113, 677-683.	13.5	478
132	Specific SR protein-dependent splicing substrates identified through genomic SELEX. <i>Nucleic Acids Research</i> , 2003, 31, 1955-1961.	6.5	59
133	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
134	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, 6876-6886.	1.1	61
135	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
136	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
137	Evolutionary dynamics and population control during in vitro selection and amplification with multiple targets. <i>Rna</i> , 2002, 8, 1461-1470.	1.6	18
138	How Does Pol II Overcome the Nucleosome Barrier?. <i>Molecular Cell</i> , 2002, 9, 451-452.	4.5	12
139	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
140	The RNA processing exosome is linked to elongating RNA polymerase II in Drosophila. <i>Nature</i> , 2002, 420, 837-841.	13.7	228
141	The Drosophila BRM complex facilitates global transcription by RNA polymerase II. <i>EMBO Journal</i> , 2002, 21, 5245-5254.	3.5	147
142	Mediator, Not Holoenzyme, Is Directly Recruited to the Heat Shock Promoter by HSF upon Heat Shock. <i>Molecular Cell</i> , 2001, 8, 9-19.	4.5	132
143	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
144	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, 2635-2649.	2.7	248

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145	A TRF1:BRF Complex Directs Drosophila RNA Polymerase III Transcription. <i>Cell</i> , 2000, 101, 459-469.	13.5	93
146	P-TEFb kinase recruitment and function at heat shock loci. <i>Genes and Development</i> , 2000, 14, 792-803.	2.7	265
147	P-TEFb kinase recruitment and function at heat shock loci. <i>Genes and Development</i> , 2000, 14, 792-803.	2.7	244
148	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
149	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
150	Glycogen Synthase Phosphatase Interacts with Heat Shock Factor To Activate <i>CLIP1</i> Gene Transcription in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 3237-3245.	1.1	25
151	Transcription Factor TFIIH Is Required for Promoter Melting In Vivo. <i>Molecular and Cellular Biology</i> , 1999, 19, 5652-5658.	1.1	34
152	Transcriptional activation independent of TFIIH kinase and the RNA polymerase II mediator in vivo. <i>Nature</i> , 1998, 393, 389-392.	13.7	91
153	Direct cloning of DNA that interacts in vivo with a specific protein: application to RNA polymerase II and sites of pausing in Drosophila. <i>Nucleic Acids Research</i> , 1998, 26, 919-924.	6.5	33
154	Cooperative and Competitive Protein Interactions at the Hsp70 Promoter. <i>Journal of Biological Chemistry</i> , 1997, 272, 33227-33233.	1.6	84
155	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
156	Transcription Properties of a Cell Type-Specific TATA-Binding Protein, TRF. <i>Cell</i> , 1997, 91, 71-83.	13.5	159
157	HSF recruitment and loss at most Drosophila heat shock loci is coordinated and depends on proximal promoter sequences. <i>Chromosoma</i> , 1996, 105, 158-171.	1.0	43
158	HSF recruitment and loss at most Drosophila heat shock loci is coordinated and depends on proximal promoter sequences. <i>Chromosoma</i> , 1996, 105, 158-171.	1.0	4
159	Sodium Salicylate and Yeast Heat Shock Gene Transcription. <i>Journal of Biological Chemistry</i> , 1995, 270, 10369-10372.	1.6	43
160	Binding of heat shock factor to and transcriptional activation of heat shock genes in Drosophila. <i>Nucleic Acids Research</i> , 1995, 23, 4799-4804.	6.5	41
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