

Karen Adelman

List of Publications by Year in descending order

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76
papers

9,234
citations

71102

41
h-index

71685

76
g-index

94
all docs

94
docs citations

94
times ranked

9020
citing authors

#	ARTICLE	IF	CITATIONS
1	Promoter-proximal pausing of RNA polymerase II: emerging roles in metazoans. <i>Nature Reviews Genetics</i> , 2012, 13, 720-731.	16.3	1,003
2	RNA polymerase stalling at developmental control genes in the <i>Drosophila melanogaster</i> embryo. <i>Nature Genetics</i> , 2007, 39, 1512-1516.	21.4	671
3	RNA polymerase is poised for activation across the genome. <i>Nature Genetics</i> , 2007, 39, 1507-1511.	21.4	661
4	Global Analysis of Short RNAs Reveals Widespread Promoter-Proximal Stalling and Arrest of Pol II in <i>Drosophila</i> . <i>Science</i> , 2010, 327, 335-338.	12.6	373
5	Promoter-proximal pausing of RNA polymerase II: a nexus of gene regulation. <i>Genes and Development</i> , 2019, 33, 960-982.	5.9	373
6	Pausing of RNA Polymerase II Disrupts DNA-Specified Nucleosome Organization to Enable Precise Gene Regulation. <i>Cell</i> , 2010, 143, 540-551.	28.9	369
7	Mll3 and Mll4 Facilitate Enhancer RNA Synthesis and Transcription from Promoters Independently of H3K4 Monomethylation. <i>Molecular Cell</i> , 2017, 66, 568-576.e4.	9.7	322
8	CDK12 is a transcription elongation-associated CTD kinase, the metazoan ortholog of yeast Ctk1. <i>Genes and Development</i> , 2010, 24, 2303-2316.	5.9	320
9	Widespread transcriptional pausing and elongation control at enhancers. <i>Genes and Development</i> , 2018, 32, 26-41.	5.9	269
10	NELF-mediated stalling of Pol II can enhance gene expression by blocking promoter-proximal nucleosome assembly. <i>Genes and Development</i> , 2008, 22, 1921-1933.	5.9	256
11	Defining the Status of RNA Polymerase at Promoters. <i>Cell Reports</i> , 2012, 2, 1025-1035.	6.4	222
12	Pol II waiting in the starting gates: Regulating the transition from transcription initiation into productive elongation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 34-45.	1.9	217
13	Bidirectional Transcription Arises from Two Distinct Hubs of Transcription Factor Binding and Active Chromatin. <i>Molecular Cell</i> , 2015, 58, 1101-1112.	9.7	204
14	Stable Pausing by RNA Polymerase II Provides an Opportunity to Target and Integrate Regulatory Signals. <i>Molecular Cell</i> , 2013, 52, 517-528.	9.7	203
15	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.	7.1	182
16	PCIF1 Catalyzes m6Am mRNA Methylation to Regulate Gene Expression. <i>Molecular Cell</i> , 2019, 75, 620-630.e9.	9.7	178
17	Mapping information-rich genotype-phenotype landscapes with genome-scale Perturb-seq. <i>Cell</i> , 2022, 185, 2559-2575.e28.	28.9	169
18	Molecular Mechanism of Transcription Inhibition by Peptide Antibiotic Microcin J25. <i>Molecular Cell</i> , 2004, 14, 753-762.	9.7	165

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19	Pausing of RNA Polymerase II Regulates Mammalian Developmental Potential through Control of Signaling Networks. <i>Molecular Cell</i> , 2015, 58, 311-322.	9.7	155
20	Rapid activity-induced transcription of Arc and other IEGs relies on poised RNA polymerase II. <i>Nature Neuroscience</i> , 2011, 14, 848-856.	14.8	153
21	The Integrator Complex Attenuates Promoter-Proximal Transcription at Protein-Coding Genes. <i>Molecular Cell</i> , 2019, 76, 738-752.e7.	9.7	150
22	Efficient Release from Promoter-Proximal Stall Sites Requires Transcript Cleavage Factor TFIIIS. <i>Molecular Cell</i> , 2005, 17, 103-112.	9.7	145
23	Immediate mediators of the inflammatory response are poised for gene activation through RNA polymerase II stalling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18207-18212.	7.1	132
24	Spt6 enhances the elongation rate of RNA polymerase II in vivo. <i>EMBO Journal</i> , 2009, 28, 1067-1077.	7.8	131
25	Evaluating Enhancer Function and Transcription. <i>Annual Review of Biochemistry</i> , 2020, 89, 213-234.	11.1	123
26	Emerging Roles of Non-Coding RNA Transcription. <i>Trends in Biochemical Sciences</i> , 2018, 43, 654-667.	7.5	116
27	Regulating the regulators: the pervasive effects of Pol II pausing on stimulus-responsive gene networks. <i>Genes and Development</i> , 2012, 26, 933-944.	5.9	111
28	Drosophila Paf1 Modulates Chromatin Structure at Actively Transcribed Genes. <i>Molecular and Cellular Biology</i> , 2006, 26, 250-260.	2.3	110
29	Integrator Recruits Protein Phosphatase 2A to Prevent Pause Release and Facilitate Transcription Termination. <i>Molecular Cell</i> , 2020, 80, 345-358.e9.	9.7	109
30	Acetylation of RNA Polymerase II Regulates Growth-Factor-Induced Gene Transcription in Mammalian Cells. <i>Molecular Cell</i> , 2013, 52, 314-324.	9.7	103
31	Co-transcriptional splicing regulates 3' end cleavage during mammalian erythropoiesis. <i>Molecular Cell</i> , 2021, 81, 998-1012.e7.	9.7	102
32	Herpes simplex virus DNA packaging sequences adopt novel structures that are specifically recognized by a component of the cleavage and packaging machinery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 3086-3091.	7.1	96
33	Intragenic Enhancers Attenuate Host Gene Expression. <i>Molecular Cell</i> , 2017, 68, 104-117.e6.	9.7	85
34	Bacteriophage T4 MotA and AsiA proteins suffice to direct Escherichia coli RNA polymerase to initiate transcription at T4 middle promoters.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 1451-1455.	7.1	78
35	Promoter-proximal Pol II: When stalling speeds things up. <i>Cell Cycle</i> , 2008, 7, 1539-1544.	2.6	74
36	Dynamic control of chromatin-associated m6A methylation regulates nascent RNA synthesis. <i>Molecular Cell</i> , 2022, 82, 1156-1168.e7.	9.7	69

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37	More uses for genomic junk. <i>Nature</i> , 2017, 543, 183-185.	27.8	60
38	The kinetics of pre-mRNA splicing in the <i>Drosophila</i> genome and the influence of gene architecture. <i>ELife</i> , 2017, 6, .	6.0	57
39	Glucocorticoid receptor represses proinflammatory genes at distinct steps of the transcription cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14616-14621.	7.1	55
40	The Interaction between the AsiA Protein of Bacteriophage T4 and the β 70 Subunit of <i>Escherichia coli</i> RNA Polymerase. <i>Journal of Biological Chemistry</i> , 1997, 272, 27435-27443.	3.4	53
41	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. <i>Nature Communications</i> , 2019, 10, 3072.	12.8	53
42	The Histone Deacetylase SIRT6 Restrains Transcription Elongation via Promoter-Proximal Pausing. <i>Molecular Cell</i> , 2019, 75, 683-699.e7.	9.7	50
43	Using ChIP-chip and ChIP-seq to study the regulation of gene expression: Genome-wide localization studies reveal widespread regulation of transcription elongation. <i>Methods</i> , 2009, 48, 398-408.	3.8	49
44	Histone gene replacement reveals a post-transcriptional role for H3K36 in maintaining metazoan transcriptome fidelity. <i>ELife</i> , 2017, 6, .	6.0	42
45	Preparing the First Responders: Building the Inflammatory Transcriptome from the Ground Up. <i>Molecular Cell</i> , 2014, 54, 245-254.	9.7	39
46	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.	7.1	37
47	RNA helicase DDX21 mediates nucleotide stress responses in neural crest and melanoma cells. <i>Nature Cell Biology</i> , 2020, 22, 372-379.	10.3	37
48	Solution structure and stability of the anti-sigma factor AsiA: Implications for novel functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1831-1835.	7.1	36
49	Stimulation of bacteriophage T4 middle transcription by the T4 proteins MotA and AsiA occurs at two distinct steps in the transcription cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 15247-15252.	7.1	34
50	Transcription start site profiling uncovers divergent transcription and enhancer-associated RNAs in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2018, 19, 157.	2.8	34
51	A ubiquitous disordered protein interaction module orchestrates transcription elongation. <i>Science</i> , 2021, 374, 1113-1121.	12.6	34
52	Conserved Regions 4.1 and 4.2 of β 70 Constitute the Recognition Sites for the Anti- β 70 Factor AsiA, and AsiA Is a Dimer Free in Solution. <i>Journal of Biological Chemistry</i> , 2001, 276, 41128-41132.	3.4	32
53	Enhanced chromatin accessibility of the dosage compensated <i>Drosophila</i> male X-chromosome requires the CLAMP zinc finger protein. <i>PLoS ONE</i> , 2017, 12, e0186855.	2.5	29
54	Characterization of the Interactions between the Bacteriophage T4 AsiA Protein and RNA Polymerase β . <i>Biochemistry</i> , 2003, 42, 7717-7726.	2.5	26

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55	Coupling polymerase pausing and chromatin landscapes for precise regulation of transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 700-706.	1.9	25
56	Interaction of T4 AsiA with its Target Sites in the RNA Polymerase β 70 Subunit Leads to Distinct and Opposite Effects on Transcription. <i>Journal of Molecular Biology</i> , 2003, 326, 679-690.	4.2	24
57	Screening thousands of transcribed coding and non-coding regions reveals sequence determinants of RNA polymerase II elongation potential. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 613-620.	8.2	19
58	Numerous recursive sites contribute to accuracy of splicing in long introns in flies. <i>PLoS Genetics</i> , 2018, 14, e1007588.	3.5	18
59	Negative elongation factor regulates muscle progenitor expansion for efficient myofiber repair and stem cell pool repopulation. <i>Developmental Cell</i> , 2021, 56, 1014-1029.e7.	7.0	18
60	Rixosomal RNA degradation contributes to silencing of Polycomb target genes. <i>Nature</i> , 2022, 604, 167-174.	27.8	18
61	Temporal resolution of gene derepression and proteome changes upon PROTAC-mediated degradation of BCL11A protein in erythroid cells. <i>Cell Chemical Biology</i> , 2022, 29, 1273-1287.e8.	5.2	14
62	How Does Pol II Overcome the Nucleosome Barrier?. <i>Molecular Cell</i> , 2002, 9, 451-452.	9.7	12
63	ORIO (Online Resource for Integrative Omics): a web-based platform for rapid integration of next generation sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, 5678-5690.	14.5	11
64	ecDNA party bus: Bringing the enhancer to you. <i>Molecular Cell</i> , 2021, 81, 1866-1867.	9.7	9
65	Overcoming IMiD resistance in T-cell lymphomas through potent degradation of ZFP91 and IKZF1. <i>Blood</i> , 2022, 139, 2024-2037.	1.4	9
66	Negative elongation factor is essential for endometrial function. <i>FASEB Journal</i> , 2019, 33, 3010-3023.	0.5	8
67	SnapShot: Transcription Regulation: Pausing. <i>Cell</i> , 2013, 153, 930-930.e1.	28.9	7
68	Transcriptional speed bumps revealed in high resolution. <i>Nature</i> , 2018, 560, 560-561.	27.8	7
69	RNA polymerase II stalling mediates cytokine gene expression. <i>Cell Cycle</i> , 2010, 9, 630-631.	2.6	6
70	The Importance of Controlling Transcription Elongation at Coding and Noncoding RNA Loci. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015, 80, 33-44.	1.1	6
71	Main-chain NMR assignments for AsiA. <i>Journal of Biomolecular NMR</i> , 1997, 10, 205-206.	2.8	5
72	MAML1-Dependent Notch-Responsive Genes Exhibit Differing Cofactor Requirements for Transcriptional Activation. <i>Molecular and Cellular Biology</i> , 2020, 40, .	2.3	5

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73	Taking MLL through the MudPIT: Identification of Novel Complexes that Bring Together MLL-Fusion Proteins and Transcription Elongation Factors. <i>Molecular Cell</i> , 2010, 37, 449-450.	9.7	4
74	Catching the Waves: Following the Leading Edge of Elongating RNA Polymerase II. <i>Molecular Cell</i> , 2013, 50, 159-160.	9.7	3
75	moonshine Illuminates a Developmental Role for Regulated Transcription Elongation. <i>Developmental Cell</i> , 2010, 19, 9-10.	7.0	2
76	Nascent transcription as a predictor and driver of histone modifications. <i>Nature Genetics</i> , 2022, 54, 223-224.	21.4	2