

# 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  
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94  
docs citations

94  
times ranked

9020  
citing authors

#	ARTICLE	IF	CITATIONS
1	Overcoming IMiD resistance in T-cell lymphomas through potent degradation of ZFP91 and IKZF1. <i>Blood</i> , 2022, 139, 2024-2037.	1.4	9
2	Rixosomal RNA degradation contributes to silencing of Polycomb target genes. <i>Nature</i> , 2022, 604, 167-174.	27.8	18
3	Nascent transcription as a predictor and driver of histone modifications. <i>Nature Genetics</i> , 2022, 54, 223-224.	21.4	2
4	Dynamic control of chromatin-associated m6A methylation regulates nascent RNA synthesis. <i>Molecular Cell</i> , 2022, 82, 1156-1168.e7.	9.7	69
5	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
6	Mapping information-rich genotype-phenotype landscapes with genome-scale Perturb-seq. <i>Cell</i> , 2022, 185, 2559-2575.e28.	28.9	169
7	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
8	Co-transcriptional splicing regulates 3' end cleavage during mammalian erythropoiesis. <i>Molecular Cell</i> , 2021, 81, 998-1012.e7.	9.7	102
9	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
10	ecDNA party bus: Bringing the enhancer to you. <i>Molecular Cell</i> , 2021, 81, 1866-1867.	9.7	9
11	A ubiquitous disordered protein interaction module orchestrates transcription elongation. <i>Science</i> , 2021, 374, 1113-1121.	12.6	34
12	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
13	Evaluating Enhancer Function and Transcription. <i>Annual Review of Biochemistry</i> , 2020, 89, 213-234.	11.1	123
14	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
15	MAML1-Dependent Notch-Responsive Genes Exhibit Differing Cofactor Requirements for Transcriptional Activation. <i>Molecular and Cellular Biology</i> , 2020, 40, .	2.3	5
16	The Histone Deacetylase SIRT6 Restrains Transcription Elongation via Promoter-Proximal Pausing. <i>Molecular Cell</i> , 2019, 75, 683-699.e7.	9.7	50
17	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
18	PCIF1 Catalyzes m6Am mRNA Methylation to Regulate Gene Expression. <i>Molecular Cell</i> , 2019, 75, 620-630.e9.	9.7	178

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19	Promoter-proximal pausing of RNA polymerase II: a nexus of gene regulation. <i>Genes and Development</i> , 2019, 33, 960-982.	5.9	373
20	The Integrator Complex Attenuates Promoter-Proximal Transcription at Protein-Coding Genes. <i>Molecular Cell</i> , 2019, 76, 738-752.e7.	9.7	150
21	Negative elongation factor is essential for endometrial function. <i>FASEB Journal</i> , 2019, 33, 3010-3023.	0.5	8
22	Widespread transcriptional pausing and elongation control at enhancers. <i>Genes and Development</i> , 2018, 32, 26-41.	5.9	269
23	Numerous recursive sites contribute to accuracy of splicing in long introns in flies. <i>PLoS Genetics</i> , 2018, 14, e1007588.	3.5	18
24	Emerging Roles of Non-Coding RNA Transcription. <i>Trends in Biochemical Sciences</i> , 2018, 43, 654-667.	7.5	116
25	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
26	Transcriptional speed bumps revealed in high resolution. <i>Nature</i> , 2018, 560, 560-561.	27.8	7
27	More uses for genomic junk. <i>Nature</i> , 2017, 543, 183-185.	27.8	60
28	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
29	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
30	Intragenic Enhancers Attenuate Host Gene Expression. <i>Molecular Cell</i> , 2017, 68, 104-117.e6.	9.7	85
31	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
32	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
33	Histone gene replacement reveals a post-transcriptional role for H3K36 in maintaining metazoan transcriptome fidelity. <i>ELife</i> , 2017, 6, .	6.0	42
34	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
35	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
36	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

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37	Preparing the First Responders: Building the Inflammatory Transcriptome from the Ground Up. <i>Molecular Cell</i> , 2014, 54, 245-254.	9.7	39
38	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
39	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
40	Catching the Waves: Following the Leading Edge of Elongating RNA Polymerase II. <i>Molecular Cell</i> , 2013, 50, 159-160.	9.7	3
41	SnapShot: Transcription Regulation: Pausing. <i>Cell</i> , 2013, 153, 930-930.e1.	28.9	7
42	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
43	Promoter-proximal pausing of RNA polymerase II: emerging roles in metazoans. <i>Nature Reviews Genetics</i> , 2012, 13, 720-731.	16.3	1,003
44	Defining the Status of RNA Polymerase at Promoters. <i>Cell Reports</i> , 2012, 2, 1025-1035.	6.4	222
45	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
46	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
47	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
48	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
49	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
50	RNA polymerase II stalling mediates cytokine gene expression. <i>Cell Cycle</i> , 2010, 9, 630-631.	2.6	6
51	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
52	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
53	moonshine Illuminates a Developmental Role for Regulated Transcription Elongation. <i>Developmental Cell</i> , 2010, 19, 9-10.	7.0	2
54	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

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55	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
56	Spt6 enhances the elongation rate of RNA polymerase II in vivo. <i>EMBO Journal</i> , 2009, 28, 1067-1077.	7.8	131
57	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
58	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
59	Promoter-proximal Pol II: When stalling speeds things up. <i>Cell Cycle</i> , 2008, 7, 1539-1544.	2.6	74
60	RNA polymerase is poised for activation across the genome. <i>Nature Genetics</i> , 2007, 39, 1507-1511.	21.4	661
61	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
62	<i>Drosophila</i> Paf1 Modulates Chromatin Structure at Actively Transcribed Genes. <i>Molecular and Cellular Biology</i> , 2006, 26, 250-260.	2.3	110
63	Efficient Release from Promoter-Proximal Stall Sites Requires Transcript Cleavage Factor TFIIIS. <i>Molecular Cell</i> , 2005, 17, 103-112.	9.7	145
64	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
65	Molecular Mechanism of Transcription Inhibition by Peptide Antibiotic Microcin J25. <i>Molecular Cell</i> , 2004, 14, 753-762.	9.7	165
66	Characterization of the Interactions between the Bacteriophage T4 AsiA Protein and RNA Polymerase. <i>Biochemistry</i> , 2003, 42, 7717-7726.	2.5	26
67	Interaction of T4 AsiA with its Target Sites in the RNA Polymerase $\beta$ 70 Subunit Leads to Distinct and Opposite Effects on Transcription. <i>Journal of Molecular Biology</i> , 2003, 326, 679-690.	4.2	24
68	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
69	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
70	How Does Pol II Overcome the Nucleosome Barrier?. <i>Molecular Cell</i> , 2002, 9, 451-452.	9.7	12
71	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
72	Conserved Regions 4.1 and 4.2 of $\beta$ 70 Constitute the Recognition Sites for the Anti- $\beta$ Factor AsiA, and AsiA Is a Dimer Free in Solution. <i>Journal of Biological Chemistry</i> , 2001, 276, 41128-41132.	3.4	32

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73	Stimulation of bacteriophage T4 middle transcription by the T4 proteins MotA and AsiA occurs at two distinct steps in the transcription cycle. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 15247-15252.	7.1	34
74	The Interaction between the AsiA Protein of Bacteriophage T4 and the $\beta$ ,70 Subunit of Escherichia coli RNA Polymerase. Journal of Biological Chemistry, 1997, 272, 27435-27443.	3.4	53
75	Main-chain NMR assignments for AsiA. Journal of Biomolecular NMR, 1997, 10, 205-206.	2.8	5
76	Bacteriophage T4 MotA and AsiA proteins suffice to direct Escherichia coli RNA polymerase to initiate transcription at T4 middle promoters.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 1451-1455.	7.1	78