

Karla M Neugebauer

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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.

90 papers	6,211 citations	43 h-index	78 g-index
160 ext. papers	7,379 ext. citations	11.9 avg, IF	6.2 L-index

#	Paper	IF	Citations
90	N-cadherin and integrins: two receptor systems that mediate neuronal process outgrowth on astrocyte surfaces. <i>Neuron</i> , 1988 , 1, 33-43	13.9	340
89	An endoribonuclease-prepared siRNA screen in human cells identifies genes essential for cell division. <i>Nature</i> , 2004 , 432, 1036-40	50.4	339
88	How cells get the message: dynamic assembly and function of mRNA-protein complexes. <i>Nature Reviews Genetics</i> , 2013 , 14, 275-87	30.1	266
87	Cotranscriptional coupling of splicing factor recruitment and precursor messenger RNA splicing in mammalian cells. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 815-22	17.6	248
86	On the importance of being co-transcriptional. <i>Journal of Cell Science</i> , 2002 , 115, 3865-71	5.3	241
85	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. <i>Cell</i> , 2020 , 181, 990-996.e5	56.2	235
84	Cotranscriptional spliceosome assembly occurs in a stepwise fashion and requires the cap binding complex. <i>Molecular Cell</i> , 2005 , 19, 53-63	17.6	213
83	Droplet organelles?. <i>EMBO Journal</i> , 2016 , 35, 1603-12	13	205
82	Global analysis of nascent RNA reveals transcriptional pausing in terminal exons. <i>Molecular Cell</i> , 2010 , 40, 571-81	17.6	192
81	The RNA-binding landscapes of two SR proteins reveal unique functions and binding to diverse RNA classes. <i>Genome Biology</i> , 2012 , 13, R17	18.3	181
80	SR proteins are NXF1 adaptors that link alternative RNA processing to mRNA export. <i>Genes and Development</i> , 2016 , 30, 553-66	12.6	173
79	Splicing and transcription touch base: co-transcriptional spliceosome assembly and function. <i>Nature Reviews Molecular Cell Biology</i> , 2017 , 18, 637-650	48.7	173
78	Regulation of alternative polyadenylation by U1 snRNPs and SRp20. <i>Molecular and Cellular Biology</i> , 1998 , 18, 4977-85	4.8	156
77	In vivo kinetics of Cajal body components. <i>Journal of Cell Biology</i> , 2004 , 164, 831-42	7.3	153
76	The in vivo kinetics of RNA polymerase II elongation during co-transcriptional splicing. <i>PLoS Biology</i> , 2011 , 9, e1000573	9.7	150
75	Structural basis for dimethylarginine recognition by the Tudor domains of human SMN and SPF30 proteins. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1414-20	17.6	132
74	Splicing of Nascent RNA Coincides with Intron Exit from RNA Polymerase II. <i>Cell</i> , 2016 , 165, 372-381	56.2	124

73	The earliest transcribed zygotic genes are short, newly evolved, and different across species. <i>Cell Reports</i> , 2014 , 6, 285-92	10.6	121
72	The histone 3 lysine 36 methyltransferase, SET2, is involved in transcriptional elongation. <i>Nucleic Acids Research</i> , 2003 , 31, 2475-82	20.1	121
71	First exon length controls active chromatin signatures and transcription. <i>Cell Reports</i> , 2012 , 2, 62-8	10.6	119
70	Cajal bodies: where form meets function. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013 , 4, 17-34	9.3	117
69	Coilin-dependent snRNP assembly is essential for zebrafish embryogenesis. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 403-9	17.6	114
68	The Cajal body: a meeting place for spliceosomal snRNPs in the nuclear maze. <i>Chromosoma</i> , 2006 , 115, 343-54	2.8	114
67	SR protein family members display diverse activities in the formation of nascent and mature mRNPs in vivo. <i>Molecular Cell</i> , 2009 , 34, 179-90	17.6	110
66	Pause locally, splice globally. <i>Trends in Cell Biology</i> , 2011 , 21, 328-35	18.3	101
65	Cotranscriptional recruitment of the U1 snRNP to intron-containing genes in yeast. <i>Molecular and Cellular Biology</i> , 2003 , 23, 5768-79	4.8	95
64	Detection of snRNP assembly intermediates in Cajal bodies by fluorescence resonance energy transfer. <i>Journal of Cell Biology</i> , 2004 , 166, 1015-25	7.3	84
63	Targeting of U4/U6 small nuclear RNP assembly factor SART3/p110 to Cajal bodies. <i>Journal of Cell Biology</i> , 2003 , 160, 505-16	7.3	84
62	Counting on co-transcriptional splicing. <i>F1000prime Reports</i> , 2013 , 5, 9		79
61	The differential interaction of snRNPs with pre-mRNA reveals splicing kinetics in living cells. <i>Journal of Cell Biology</i> , 2010 , 191, 75-86	7.3	79
60	Enhancement of U4/U6 small nuclear ribonucleoprotein particle association in Cajal bodies predicted by mathematical modeling. <i>Molecular Biology of the Cell</i> , 2006 , 17, 4972-81	3.5	68
59	The coilin interactome identifies hundreds of small noncoding RNAs that traffic through Cajal bodies. <i>Molecular Cell</i> , 2014 , 56, 389-399	17.6	67
58	Integrins and cell adhesion molecules: neuronal receptors that regulate axon growth on extracellular matrices and cell surfaces. <i>Developmental Neuroscience</i> , 1989 , 11, 332-47	2.2	64
57	RNA-protein interactions in vivo: global gets specific. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 255-62	10.3	63
56	Spliceosomal small nuclear ribonucleoprotein particles repeatedly cycle through Cajal bodies. <i>Molecular Biology of the Cell</i> , 2008 , 19, 2534-43	3.5	63

55	A systematic RNAi synthetic interaction screen reveals a link between p53 and snoRNP assembly. <i>Nature Cell Biology</i> , 2011 , 13, 809-18	23.4	59
54	Introns and gene expression: cellular constraints, transcriptional regulation, and evolutionary consequences. <i>BioEssays</i> , 2015 , 37, 148-54	4.1	55
53	Extragenic accumulation of RNA polymerase II enhances transcription by RNA polymerase III. <i>PLoS Genetics</i> , 2007 , 3, e212	6	50
52	Global analysis reveals SRp20- and SRp75-specific mRNPs in cycling and neural cells. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 962-70	17.6	46
51	Long-read sequencing of nascent RNA reveals coupling among RNA processing events. <i>Genome Research</i> , 2018 , 28, 1008-1019	9.7	45
50	Dynamic control of Cajal body number during zebrafish embryogenesis. <i>Nucleus</i> , 2010 , 1, 96-108	3.9	45
49	Perfect timing: splicing and transcription rates in living cells. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017 , 8, e1401	9.3	43
48	Maternal respiratory SARS-CoV-2 infection in pregnancy is associated with a robust inflammatory response at the maternal-fetal interface. <i>Med</i> , 2021 , 2, 591-610.e10	31.7	43
47	The nuclear cap-binding complex interacts with the U4/U6/U5 tri-snRNP and promotes spliceosome assembly in mammalian cells. <i>Rna</i> , 2013 , 19, 1054-63	5.8	42
46	Cellular differentiation state modulates the mRNA export activity of SR proteins. <i>Journal of Cell Biology</i> , 2017 , 216, 1993-2009	7.3	40
45	Coilin: The first 25 years. <i>RNA Biology</i> , 2015 , 12, 590-6	4.8	40
44	Long noncoding RNAs add another layer to pre-mRNA splicing regulation. <i>Molecular Cell</i> , 2010 , 39, 833-47.6	47.6	36
43	Dynamic RNA-protein interactions underlie the zebrafish maternal-to-zygotic transition. <i>Genome Research</i> , 2017 , 27, 1184-1194	9.7	34
42	Nascent RNA and the Coordination of Splicing with Transcription. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019 , 11,	10.2	32
41	Heat Oscillations Driven by the Embryonic Cell Cycle Reveal the Energetic Costs of Signaling. <i>Developmental Cell</i> , 2019 , 48, 646-658.e6	10.2	30
40	Fractionation iCLIP detects persistent SR protein binding to conserved, retained introns in chromatin, nucleoplasm and cytoplasm. <i>Nucleic Acids Research</i> , 2017 , 45, 10452-10465	20.1	28
39	Activation of transcription enforces the formation of distinct nuclear bodies in zebrafish embryos. <i>RNA Biology</i> , 2017 , 14, 752-760	4.8	25
38	Differential responses of L5 and rat primary muscle cells to factors in rat brain extract. <i>Brain Research</i> , 1985 , 346, 58-69	3.7	25

37	Uncoupling of nucleo-cytoplasmic RNA export and localization during stress. <i>Nucleic Acids Research</i> , 2019 , 47, 4778-4797	20.1	24
36	Co-transcriptional splicing regulates 3' end cleavage during mammalian erythropoiesis. <i>Molecular Cell</i> , 2021 , 81, 998-1012.e7	17.6	24
35	Cotranscriptional spliceosome assembly and splicing are independent of the Prp40p WW domain. <i>Rna</i> , 2011 , 17, 2119-29	5.8	23
34	Good cap/bad cap: how the cap-binding complex determines RNA fate. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 9-12	17.6	21
33	Quantification of co-transcriptional splicing from RNA-Seq data. <i>Methods</i> , 2015 , 85, 36-43	4.6	19
32	RNA tales - how embryos read and discard messages from mom. <i>Journal of Cell Science</i> , 2018 , 131,	5.3	16
31	Dynamics and Function of Nuclear Bodies during Embryogenesis. <i>Biochemistry</i> , 2018 , 57, 2462-2469	3.2	15
30	Binding properties and dynamic localization of an alternative isoform of the cap-binding complex subunit CBP20. <i>Nucleus</i> , 2010 , 1, 412-21	3.9	14
29	Keeping tabs on the women: life scientists in Europe. <i>PLoS Biology</i> , 2006 , 4, e97	9.7	14
28	Identification of four functional NR3B isoforms in developing white matter reveals unexpected diversity among glutamate receptors. <i>Journal of Neurochemistry</i> , 2011 , 117, 449-60	6	13
27	Transcription Regulation Through Nascent RNA Folding. <i>Journal of Molecular Biology</i> , 2021 , 433, 1669756.5		11
26	Pre-mRNA Splicing in the Nuclear Landscape. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019 , 84, 11-20	3.9	10
25	SARS-CoV-2 infection in pregnancy is associated with robust inflammatory response at the maternal-fetal interface 2021 ,		10
24	DNA-tudor interaction modules control the specificity of in vivo condensates. <i>Cell</i> , 2021 , 184, 3612-3625.e17	5.17	9
23	3D Multicolor Nanoscopy at 10,000 Cells a Day		8
22	Nuclear mechanisms of gene expression control: pre-mRNA splicing as a life or death decision. <i>Current Opinion in Genetics and Development</i> , 2021 , 67, 67-76	4.9	8
21	Paraspeckles: paragons of functional aggregation. <i>Journal of Cell Biology</i> , 2015 , 210, 527-8	7.3	7
20	2001 interactions? An extracellular space odyssey. <i>Current Opinion in Neurobiology</i> , 1991 , 1, 364-9	7.6	7

19	Contribution of increasing plasma membrane to the energetic cost of early zebrafish embryogenesis. <i>Molecular Biology of the Cell</i> , 2020 , 31, 520-526	3.5	6
18	Widespread Transcriptional Readthrough Caused by Nab2 Depletion Leads to Chimeric Transcripts with Retained Introns. <i>Cell Reports</i> , 2020 , 33, 108324	10.6	6
17	Blood Relatives: Splicing Mechanisms underlying Erythropoiesis in Health and Disease. <i>F1000Research</i> , 2018 , 7,	3.6	4
16	Co-transcriptional splicing regulates 3' end cleavage during mammalian erythropoiesis		4
15	Purification of Zygotically Transcribed RNA through Metabolic Labeling of Early Zebrafish Embryos. <i>Methods in Molecular Biology</i> , 2017 , 1605, 121-131	1.4	3
14	Preparation of Mammalian Nascent RNA for Long Read Sequencing. <i>Current Protocols in Molecular Biology</i> , 2020 , 133, e128	2.9	3
13	RNA: master or servant?. <i>Rna</i> , 2015 , 21, 701-2	5.8	2
12	Analysis of RNA-protein interactions in vertebrate embryos using UV crosslinking approaches. <i>Methods</i> , 2017 , 126, 44-53	4.6	1
11	Splicing Factor ChIP and ChRIP: Detection of Splicing and Splicing Factors at Genes by Chromatin Immunoprecipitation 2012 , 416-427		1
10	Precision analysis of mutant U2AF1 activity reveals deployment of stress granules in myeloid malignancies.. <i>Molecular Cell</i> , 2022 , 82, 1107-1122.e7	17.6	1
9	Identification of Alternative Polyadenylation in Through Long-Read Sequencing of mRNA.. <i>Frontiers in Genetics</i> , 2021 , 12, 818697	4.5	0
8	Generation of scalable cancer models by combining AAV-intron-trap, CRISPR/Cas9, and inducible Cre-recombinase. <i>Communications Biology</i> , 2021 , 4, 1184	6.7	0
7	Integrative genome-wide analysis reveals EIF3A as a key downstream regulator of translational repressor protein Musashi 2 (MSI2).. <i>NAR Cancer</i> , 2022 , 4, zcac015	5.2	0
6	Transcriptome-wide mapping reveals a diverse dihydrouridine landscape including mRNA. <i>PLoS Biology</i> , 2022 , 20, e3001622	9.7	0
5	Integration of Splicing with Nuclear and Cellular Events 2012 , 109-117		
4	High-Resolution Binding Atlas of U2AF1 Mutants Uncovers New Complexity in Splicing Alterations and Kinetics in Myeloid Malignancies. <i>Blood</i> , 2020 , 136, 3-4	2.2	
3	U2AF1 Mutations Enhance Stress Granule Response in Myeloid Malignancies. <i>Blood</i> , 2021 , 138, 321-321	2.2	
2	U2AF1 Driver Mutations in Hematopoietic Disorders Alter but Do Not Abrogate RNA Binding and Enlighten Structural Dependencies of the U2AF-RNA Complex. <i>Blood</i> , 2019 , 134, 1230-1230	2.2	

- 1 Calorimetric Heat Dissipation Measurements of Developing Zebrafish Embryos. *Methods in Molecular Biology*, **2021**, 2329, 311-321 1.4