

# Nikolaus Rajewsky

## 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.

127 papers	43,879 citations	68 h-index	143 g-index
143 ext. papers	52,130 ext. citations	18.4 avg, IF	7.39 L-index

#	Paper	IF	Citations
127	Expression of Circ_Satb1 Is Decreased in Mesial Temporal Lobe Epilepsy and Regulates Dendritic Spine Morphology.. <i>Frontiers in Molecular Neuroscience</i> , <b>2022</b> , 15, 832133	6.1	0
126	Defective metabolic programming impairs early neuronal morphogenesis in neural cultures and an organoid model of Leigh syndrome. <i>Nature Communications</i> , <b>2021</b> , 12, 1929	17.4	17
125	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. <i>IScience</i> , <b>2021</b> , 24, 102151	6.1	72
124	Parallel genetics of regulatory sequences using scalable genome editing in vivo. <i>Cell Reports</i> , <b>2021</b> , 35, 108988	10.6	0
123	Kidney Single-cell Transcriptomes Predict Spatial Corticomedullary Gene Expression and Tissue Osmolality Gradients. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2021</b> , 32, 291-306	12.7	5
122	NovoSpaRc: flexible spatial reconstruction of single-cell gene expression with optimal transport. <i>Nature Protocols</i> , <b>2021</b> , 16, 4177-4200	18.8	2
121	A Highly Conserved Circular RNA Is Required to Keep Neural Cells in a Progenitor State in the Mammalian Brain. <i>Cell Reports</i> , <b>2020</b> , 30, 2170-2179.e5	10.6	27
120	Tracing tumorigenesis in a solid tumor model at single-cell resolution. <i>Nature Communications</i> , <b>2020</b> , 11, 991	17.4	24
119	The transcriptome dynamics of single cells during the cell cycle. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9946	12.2	9
118	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. <i>Life Science Alliance</i> , <b>2020</b> , 3,	5.8	11
117	Gene Expression Signatures of a Preclinical Mouse Model during Colorectal Cancer Progression under Low-Dose Metronomic Chemotherapy. <i>Cancers</i> , <b>2020</b> , 13,	6.6	2
116	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , <b>2020</b> , 587, 377-386	50.4	56
115	Comprehensive analysis of translation from overexpressed circular RNAs reveals pervasive translation from linear transcripts. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 10368-10382	20.1	29
114	Identification of proteins and miRNAs that specifically bind an mRNA in vivo. <i>Nature Communications</i> , <b>2019</b> , 10, 4205	17.4	10
113	The Translational Landscape of the Human Heart. <i>Cell</i> , <b>2019</b> , 178, 242-260.e29	56.2	210
112	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. <i>Genome Biology</i> , <b>2019</b> , 20, 59	18.3	369
111	Roles of Long Noncoding RNAs and Circular RNAs in Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2019</b> , 11,	10.2	20

110	FLAM-seq: full-length mRNA sequencing reveals principles of poly(A) tail length control. <i>Nature Methods</i> , <b>2019</b> , 16, 879-886	21.6	53
109	Single-cell RNA-sequencing of herpes simplex virus 1-infected cells connects NRF2 activation to an antiviral program. <i>Nature Communications</i> , <b>2019</b> , 10, 4878	17.4	51
108	Context-specific regulation of cell survival by a miRNA-controlled BIM rheostat. <i>Genes and Development</i> , <b>2019</b> , 33, 1673-1687	12.6	7
107	Human muscle-derived CLEC14A-positive cells regenerate muscle independent of PAX7. <i>Nature Communications</i> , <b>2019</b> , 10, 5776	17.4	21
106	Gene expression cartography. <i>Nature</i> , <b>2019</b> , 576, 132-137	50.4	109
105	Cell type atlas and lineage tree of a whole complex animal by single-cell transcriptomics. <i>Science</i> , <b>2018</b> , 360,	33.3	233
104	Single-Molecule Fluorescence In Situ Hybridization (FISH) of Circular RNA CDR1as. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1724, 77-96	1.4	18
103	Post-transcriptional Regulation by 3'UTRs Can Be Masked by Regulatory Elements in 5'UTRs. <i>Cell Reports</i> , <b>2018</b> , 22, 3217-3226	10.6	13
102	Characterization of Transcription Termination-Associated RNAs: New Insights into their Biogenesis, Tailing, and Expression in Primary Tumors. <i>International Journal of Genomics</i> , <b>2018</b> , 2018, 1243858	2.5	3
101	Selective targeting of pro-inflammatory Th1 cells by microRNA-148a-specific antagomirs in vivo. <i>Journal of Autoimmunity</i> , <b>2018</b> , 89, 41-52	15.5	15
100	Spatiotemporal m(i)RNA Architecture and 3'UTR Regulation in the C. elegans Germline. <i>Developmental Cell</i> , <b>2018</b> , 47, 785-800.e8	10.2	16
99	Single-Cell Transcriptomics Characterizes Cell Types in the Subventricular Zone and Uncovers Molecular Defects Impairing Adult Neurogenesis. <i>Cell Reports</i> , <b>2018</b> , 25, 2457-2469.e8	10.6	82
98	A Single-Cell Transcriptome Atlas of the Mouse Glomerulus. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2018</b> , 29, 2060-2068	12.7	87
97	RCAS: an RNA centric annotation system for transcriptome-wide regions of interest. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e91	20.1	13
96	RNA-bioinformatics: Tools, services and databases for the analysis of RNA-based regulation. <i>Journal of Biotechnology</i> , <b>2017</b> , 261, 76-84	3.7	17
95	Circ-ZNF609 Is a Circular RNA that Can Be Translated and Functions in Myogenesis. <i>Molecular Cell</i> , <b>2017</b> , 66, 22-37.e9	17.6	1146
94	Translation of CircRNAs. <i>Molecular Cell</i> , <b>2017</b> , 66, 9-21.e7	17.6	945
93	Widespread activation of antisense transcription of the host genome during herpes simplex virus 1 infection. <i>Genome Biology</i> , <b>2017</b> , 18, 209	18.3	24

92	The oncogenic role of circPVT1 in head and neck squamous cell carcinoma is mediated through the mutant p53/YAP/TEAD transcription-competent complex. <i>Genome Biology</i> , <b>2017</b> , 18, 237	18.3	129
91	A map of human circular RNAs in clinically relevant tissues. <i>Journal of Molecular Medicine</i> , <b>2017</b> , 95, 1179-1189	15.189	195
90	The embryo at single-cell transcriptome resolution. <i>Science</i> , <b>2017</b> , 358, 194-199	33.3	243
89	RNA localization is a key determinant of neurite-enriched proteome. <i>Nature Communications</i> , <b>2017</b> , 8, 583	17.4	118
88	Loss of a mammalian circular RNA locus causes miRNA deregulation and affects brain function. <i>Science</i> , <b>2017</b> , 357,	33.3	649
87	Cell fixation and preservation for droplet-based single-cell transcriptomics. <i>BMC Biology</i> , <b>2017</b> , 15, 44	7.3	135
86	Essentials of miRNA-dependent Control of mRNA Translation and decay, miRNA Targeting Principles, and Methods for Target Identification <b>2017</b> , 19-38		0
85	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , <b>2016</b> , 9, 33	5.8	54
84	Epigenomic Profiling of Human CD4 T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. <i>Immunity</i> , <b>2016</b> , 45, 1148-1161	32.3	118
83	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
82	The Lupus Autoantigen La Prevents Mis-channeling of tRNA Fragments into the Human MicroRNA Pathway. <i>Molecular Cell</i> , <b>2016</b> , 63, 110-24	17.6	73
81	Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. <i>ELife</i> , <b>2016</b> , 5,	8.9	39
80	microRNAs regulate cell-to-cell variability of endogenous target gene expression in developing mouse thymocytes. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005020	6	16
79	Insm1 cooperates with Neurod1 and Foxa2 to maintain mature pancreatic B-cell function. <i>EMBO Journal</i> , <b>2015</b> , 34, 1417-33	13	50
78	Circular RNAs in the Mammalian Brain Are Highly Abundant, Conserved, and Dynamically Expressed. <i>Molecular Cell</i> , <b>2015</b> , 58, 870-85	17.6	1376
77	Extensive identification and analysis of conserved small ORFs in animals. <i>Genome Biology</i> , <b>2015</b> , 16, 179	18.3	117
76	Competition between target sites of regulators shapes post-transcriptional gene regulation. <i>Nature Reviews Genetics</i> , <b>2015</b> , 16, 113-26	30.1	182
75	miR-148a is upregulated by Twist1 and T-bet and promotes Th1-cell survival by regulating the proapoptotic gene Bim. <i>European Journal of Immunology</i> , <b>2015</b> , 45, 1192-205	6.1	34

74	Identification and Characterization of Circular RNAs As a New Class of Putative Biomarkers in Human Blood. <i>PLoS ONE</i> , <b>2015</b> , 10, e0141214	3.7	423
73	Analysis of intron sequences reveals hallmarks of circular RNA biogenesis in animals. <i>Cell Reports</i> , <b>2015</b> , 10, 170-7	10.6	643
72	DoRiNA 2.0--upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D160-7	20.1	97
71	Identification of small ORFs in vertebrates using ribosome footprinting and evolutionary conservation. <i>EMBO Journal</i> , <b>2014</b> , 33, 981-93	13	418
70	Unambiguous identification of miRNA:target site interactions by different types of ligation reactions. <i>Molecular Cell</i> , <b>2014</b> , 54, 1042-1054	17.6	209
69	A variety of dicer substrates in human and <i>C. elegans</i> . <i>Cell</i> , <b>2014</b> , 159, 1153-1167	56.2	80
68	Mixed messages: Re-initiation factors regulate translation of animal mRNAs. <i>Cell Research</i> , <b>2014</b> , 24, 1383-4	24.7	1
67	Global characterization of the oocyte-to-embryo transition in <i>Caenorhabditis elegans</i> uncovers a novel mRNA clearance mechanism. <i>EMBO Journal</i> , <b>2014</b> , 33, 1751-66	13	52
66	circBase: a database for circular RNAs. <i>Rna</i> , <b>2014</b> , 20, 1666-70	5.8	944
65	circRNA biogenesis competes with pre-mRNA splicing. <i>Molecular Cell</i> , <b>2014</b> , 56, 55-66	17.6	1753
64	Paternal RNA contributions in the <i>Caenorhabditis elegans</i> zygote. <i>EMBO Journal</i> , <b>2014</b> , 33, 1740-50	13	47
63	Conservation of mRNA and protein expression during development of <i>C. elegans</i> . <i>Cell Reports</i> , <b>2014</b> , 6, 565-77	10.6	64
62	Paternal diet defines offspring chromatin state and intergenerational obesity. <i>Cell</i> , <b>2014</b> , 159, 1352-64	56.2	253
61	Binding site discovery from nucleic acid sequences by discriminative learning of hidden Markov models. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 12995-3011	20.1	19
60	RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. <i>Journal of Clinical Investigation</i> , <b>2014</b> , 124, 3419-30	15.9	129
59	Circular RNAs are a large class of animal RNAs with regulatory potency. <i>Nature</i> , <b>2013</b> , 495, 333-8	50.4	4603
58	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. <i>RNA Biology</i> , <b>2013</b> , 10, 1146-59	4.8	47
57	The CCR4-NOT complex mediates deadenylation and degradation of stem cell mRNAs and promotes planarian stem cell differentiation. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1004003	6	21

56	Select microRNAs are essential for early development in the sea urchin. <i>Developmental Biology</i> , <b>2012</b> , 362, 104-13	3.1	42
55	Gene expression of pluripotency determinants is conserved between mammalian and planarian stem cells. <i>EMBO Journal</i> , <b>2012</b> , 31, 2755-69	13	113
54	doRiNA: a database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D180-6	20.1	151
53	miRDeep2 accurately identifies known and hundreds of novel microRNA genes in seven animal clades. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 37-52	20.1	1631
52	The SNF2-like helicase HELLS mediates E2F3-dependent transcription and cellular transformation. <i>EMBO Journal</i> , <b>2012</b> , 31, 972-85	13	60
51	Transcriptome-wide analysis of regulatory interactions of the RNA-binding protein HuR. <i>Molecular Cell</i> , <b>2011</b> , 43, 340-52	17.6	513
50	MicroRNAs and the Operon paper. <i>Journal of Molecular Biology</i> , <b>2011</b> , 409, 70-5	6.5	12
49	In vivo and transcriptome-wide identification of RNA binding protein target sites. <i>Molecular Cell</i> , <b>2011</b> , 44, 828-40	17.6	124
48	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. <i>Genome Research</i> , <b>2011</b> , 21, 1193-200	9.7	90
47	The impact of miRNA target sites in coding sequences and in 3ΨTRs. <i>PLoS ONE</i> , <b>2011</b> , 6, e18067	3.7	216
46	The microRNA miR-182 is induced by IL-2 and promotes clonal expansion of activated helper T lymphocytes. <i>Nature Immunology</i> , <b>2010</b> , 11, 1057-62	19.1	269
45	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , <b>2010</b> , 330, 1775-87	33.3	744
44	The landscape of <i>C. elegans</i> 3ΨTRs. <i>Science</i> , <b>2010</b> , 329, 432-5	33.3	222
43	Correlating gene expression variation with cis-regulatory polymorphism in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology and Evolution</i> , <b>2010</b> , 2, 697-707	3.9	28
42	Deciphering the porcine intestinal microRNA transcriptome. <i>BMC Genomics</i> , <b>2010</b> , 11, 275	4.5	65
41	High-resolution profiling and discovery of planarian small RNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 11546-51	11.5	114
40	Large-scale sorting of <i>C. elegans</i> embryos reveals the dynamics of small RNA expression. <i>Nature Methods</i> , <b>2009</b> , 6, 745-51	21.6	72
39	Reexamining microRNA site accessibility in <i>Drosophila</i> : a population genomics study. <i>PLoS ONE</i> , <b>2009</b> , 4, e5681	3.7	13

38	Widespread changes in protein synthesis induced by microRNAs. <i>Nature</i> , <b>2008</b> , 455, 58-63	50.4	2766
37	Discovering microRNAs from deep sequencing data using miRDeep. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 407-415	44.5	936
36	Dicer ablation affects antibody diversity and cell survival in the B lymphocyte lineage. <i>Cell</i> , <b>2008</b> , 132, 860-74	56.2	486
35	A human snoRNA with microRNA-like functions. <i>Molecular Cell</i> , <b>2008</b> , 32, 519-28	17.6	624
34	The evolution of gene regulation by transcription factors and microRNAs. <i>Nature Reviews Genetics</i> , <b>2007</b> , 8, 93-103	30.1	1155
33	MiR-150 controls B cell differentiation by targeting the transcription factor c-Myb. <i>Cell</i> , <b>2007</b> , 131, 146-59	56.2	848
32	Regulation of the germinal center response by microRNA-155. <i>Science</i> , <b>2007</b> , 316, 604-8	33.3	1256
31	A genome-wide map of conserved microRNA targets in <i>C. elegans</i> . <i>Current Biology</i> , <b>2006</b> , 16, 460-71	6.3	353
30	Cell-type-specific signatures of microRNAs on target mRNA expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 2746-51	11.5	528
29	microRNA target predictions in animals. <i>Nature Genetics</i> , <b>2006</b> , 38 Suppl, S8-13	36.3	890
28	Natural selection on human microRNA binding sites inferred from SNP data. <i>Nature Genetics</i> , <b>2006</b> , 38, 1452-6	36.3	391
27	MicroRNA profiling of the murine hematopoietic system. <i>Genome Biology</i> , <b>2005</b> , 6, R71	18.3	356
26	Combinatorial microRNA target predictions. <i>Nature Genetics</i> , <b>2005</b> , 37, 495-500	36.3	3846
25	Silencing of microRNAs in vivo with 'antagomirs'. <i>Nature</i> , <b>2005</b> , 438, 685-9	50.4	3298
24	microRNA target predictions across seven <i>Drosophila</i> species and comparison to mammalian targets. <i>PLoS Computational Biology</i> , <b>2005</b> , 1, e13	5	349
23	A cis element in the recombination activating gene locus regulates gene expression by counteracting a distant silencer. <i>Nature Immunology</i> , <b>2004</b> , 5, 443-50	19.1	53
22	A pancreatic islet-specific microRNA regulates insulin secretion. <i>Nature</i> , <b>2004</b> , 432, 226-30	50.4	1714
21	Transcriptional control in the segmentation gene network of <i>Drosophila</i> . <i>PLoS Biology</i> , <b>2004</b> , 2, E271	9.7	193

20	Survival of resting mature B lymphocytes depends on BCR signaling via the Igalphabeta heterodimer. <i>Cell</i> , <b>2004</b> , 117, 787-800	56.2	449
19	Computational identification of microRNA targets. <i>Developmental Biology</i> , <b>2004</b> , 267, 529-35	3.1	258
18	Conservation of regulatory elements between two species of Drosophila. <i>BMC Bioinformatics</i> , <b>2003</b> , 4, 57	3.6	76
17	Decay rates of human mRNAs: correlation with functional characteristics and sequence attributes. <i>Genome Research</i> , <b>2003</b> , 13, 1863-72	9.7	351
16	Computational detection of genomic cis-regulatory modules applied to body patterning in the early Drosophila embryo. <i>BMC Bioinformatics</i> , <b>2002</b> , 3, 30	3.6	168
15	The evolution of DNA regulatory regions for proteo-gamma bacteria by interspecies comparisons. <i>Genome Research</i> , <b>2002</b> , 12, 298-308	9.7	58
14	Probabilistic clustering of sequences: inferring new bacterial regulons by comparative genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 7323-8	11.5	55
13	Circadian regulation of gene expression systems in the Drosophila head. <i>Neuron</i> , <b>2001</b> , 32, 657-71	13.9	383
12	A Probabilistic Cellular Automaton for Evolution. <i>Journal De Physique, I</i> , <b>1995</b> , 5, 1129-1134		2
11	Timing, genetic requirements and functional consequences of somatic hypermutation during B-cell development. <i>Immunological Reviews</i> , <b>1987</b> , 96, 5-22	11.3	204
10	Computational prediction of microRNA targets in vertebrates, fruitflies and nematodes172-186		
9	Spacemake: processing and analysis of large-scale spatial transcriptomics data		2
8	Rapid nuclear deadenylation of mammalian messenger RNA		1
7	Regulation of spatial and temporal gene expression in an animal germline		1
6	Predicting cellular position in the Drosophila embryo from Single-Cell Transcriptomics data		3
5	Cell fixation and preservation for droplet-based single-cell transcriptomics		4
4	Graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells		23
3	Charting a tissue from single-cell transcriptomes		7



2	Optogenetic perturbations of RNA expression in tissue space	2
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1	Best practice standards for circular RNA research. <i>Nature Methods</i> ,	21.6	1
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