

Nikolaus Rajewsky

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|--------------------|--------------------------|-----------------|-----------------|
| 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 | Circular RNAs are a large class of animal RNAs with regulatory potency. <i>Nature</i> , 2013 , 495, 333-8 | 50.4 | 4603 |
| 126 | Combinatorial microRNA target predictions. <i>Nature Genetics</i> , 2005 , 37, 495-500 | 36.3 | 3846 |
| 125 | Silencing of microRNAs in vivo with Antagomirs. <i>Nature</i> , 2005 , 438, 685-9 | 50.4 | 3298 |
| 124 | Widespread changes in protein synthesis induced by microRNAs. <i>Nature</i> , 2008 , 455, 58-63 | 50.4 | 2766 |
| 123 | circRNA biogenesis competes with pre-mRNA splicing. <i>Molecular Cell</i> , 2014 , 56, 55-66 | 17.6 | 1753 |
| 122 | A pancreatic islet-specific microRNA regulates insulin secretion. <i>Nature</i> , 2004 , 432, 226-30 | 50.4 | 1714 |
| 121 | miRDeep2 accurately identifies known and hundreds of novel microRNA genes in seven animal clades. <i>Nucleic Acids Research</i> , 2012 , 40, 37-52 | 20.1 | 1631 |
| 120 | Circular RNAs in the Mammalian Brain Are Highly Abundant, Conserved, and Dynamically Expressed. <i>Molecular Cell</i> , 2015 , 58, 870-85 | 17.6 | 1376 |
| 119 | Regulation of the germinal center response by microRNA-155. <i>Science</i> , 2007 , 316, 604-8 | 33.3 | 1256 |
| 118 | The evolution of gene regulation by transcription factors and microRNAs. <i>Nature Reviews Genetics</i> , 2007 , 8, 93-103 | 30.1 | 1155 |
| 117 | Circ-ZNF609 Is a Circular RNA that Can Be Translated and Functions in Myogenesis. <i>Molecular Cell</i> , 2017 , 66, 22-37.e9 | 17.6 | 1146 |
| 116 | Translation of CircRNAs. <i>Molecular Cell</i> , 2017 , 66, 9-21.e7 | 17.6 | 945 |
| 115 | circBase: a database for circular RNAs. <i>Rna</i> , 2014 , 20, 1666-70 | 5.8 | 944 |
| 114 | Discovering microRNAs from deep sequencing data using miRDeep. <i>Nature Biotechnology</i> , 2008 , 26, 407-415 | 41.5 | 936 |
| 113 | microRNA target predictions in animals. <i>Nature Genetics</i> , 2006 , 38 Suppl, S8-13 | 36.3 | 890 |
| 112 | MIR-150 controls B cell differentiation by targeting the transcription factor c-Myb. <i>Cell</i> , 2007 , 131, 146-59 | 36.2 | 848 |
| 111 | Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87 | 33.3 | 744 |

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|-----|---|------|-----|
| 110 | Loss of a mammalian circular RNA locus causes miRNA deregulation and affects brain function. <i>Science</i> , 2017 , 357, | 33.3 | 649 |
| 109 | Analysis of intron sequences reveals hallmarks of circular RNA biogenesis in animals. <i>Cell Reports</i> , 2015 , 10, 170-7 | 10.6 | 643 |
| 108 | A human snoRNA with microRNA-like functions. <i>Molecular Cell</i> , 2008 , 32, 519-28 | 17.6 | 624 |
| 107 | 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> , 2006 , 103, 2746-51 | 11.5 | 528 |
| 106 | Transcriptome-wide analysis of regulatory interactions of the RNA-binding protein HuR. <i>Molecular Cell</i> , 2011 , 43, 340-52 | 17.6 | 513 |
| 105 | Dicer ablation affects antibody diversity and cell survival in the B lymphocyte lineage. <i>Cell</i> , 2008 , 132, 860-74 | 56.2 | 486 |
| 104 | Survival of resting mature B lymphocytes depends on BCR signaling via the Igalpha/beta heterodimer. <i>Cell</i> , 2004 , 117, 787-800 | 56.2 | 449 |
| 103 | Identification and Characterization of Circular RNAs As a New Class of Putative Biomarkers in Human Blood. <i>PLoS ONE</i> , 2015 , 10, e0141214 | 3.7 | 423 |
| 102 | Identification of small ORFs in vertebrates using ribosome footprinting and evolutionary conservation. <i>EMBO Journal</i> , 2014 , 33, 981-93 | 13 | 418 |
| 101 | Natural selection on human microRNA binding sites inferred from SNP data. <i>Nature Genetics</i> , 2006 , 38, 1452-6 | 36.3 | 391 |
| 100 | Circadian regulation of gene expression systems in the Drosophila head. <i>Neuron</i> , 2001 , 32, 657-71 | 13.9 | 383 |
| 99 | PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. <i>Genome Biology</i> , 2019 , 20, 59 | 18.3 | 369 |
| 98 | MicroRNA profiling of the murine hematopoietic system. <i>Genome Biology</i> , 2005 , 6, R71 | 18.3 | 356 |
| 97 | A genome-wide map of conserved microRNA targets in <i>C. elegans</i> . <i>Current Biology</i> , 2006 , 16, 460-71 | 6.3 | 353 |
| 96 | Decay rates of human mRNAs: correlation with functional characteristics and sequence attributes. <i>Genome Research</i> , 2003 , 13, 1863-72 | 9.7 | 351 |
| 95 | microRNA target predictions across seven Drosophila species and comparison to mammalian targets. <i>PLoS Computational Biology</i> , 2005 , 1, e13 | 5 | 349 |
| 94 | The microRNA miR-182 is induced by IL-2 and promotes clonal expansion of activated helper T lymphocytes. <i>Nature Immunology</i> , 2010 , 11, 1057-62 | 19.1 | 269 |
| 93 | Computational identification of microRNA targets. <i>Developmental Biology</i> , 2004 , 267, 529-35 | 3.1 | 258 |

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| 92 | Paternal diet defines offspring chromatin state and intergenerational obesity. <i>Cell</i> , 2014 , 159, 1352-64 | 56.2 | 253 |
| 91 | The embryo at single-cell transcriptome resolution. <i>Science</i> , 2017 , 358, 194-199 | 33.3 | 243 |
| 90 | Cell type atlas and lineage tree of a whole complex animal by single-cell transcriptomics. <i>Science</i> , 2018 , 360, | 33.3 | 233 |
| 89 | The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149 | 56.2 | 232 |
| 88 | The landscape of <i>C. elegans</i> 3ΨTRs. <i>Science</i> , 2010 , 329, 432-5 | 33.3 | 222 |
| 87 | The impact of miRNA target sites in coding sequences and in 3ΨTRs. <i>PLoS ONE</i> , 2011 , 6, e18067 | 3.7 | 216 |
| 86 | The Translational Landscape of the Human Heart. <i>Cell</i> , 2019 , 178, 242-260.e29 | 56.2 | 210 |
| 85 | Unambiguous identification of miRNA:target site interactions by different types of ligation reactions. <i>Molecular Cell</i> , 2014 , 54, 1042-1054 | 17.6 | 209 |
| 84 | Timing, genetic requirements and functional consequences of somatic hypermutation during B-cell development. <i>Immunological Reviews</i> , 1987 , 96, 5-22 | 11.3 | 204 |
| 83 | A map of human circular RNAs in clinically relevant tissues. <i>Journal of Molecular Medicine</i> , 2017 , 95, 1179-1189 | 55.1 | 195 |
| 82 | Transcriptional control in the segmentation gene network of <i>Drosophila</i> . <i>PLoS Biology</i> , 2004 , 2, E271 | 9.7 | 193 |
| 81 | Competition between target sites of regulators shapes post-transcriptional gene regulation. <i>Nature Reviews Genetics</i> , 2015 , 16, 113-26 | 30.1 | 182 |
| 80 | Computational detection of genomic cis-regulatory modules applied to body patterning in the early <i>Drosophila</i> embryo. <i>BMC Bioinformatics</i> , 2002 , 3, 30 | 3.6 | 168 |
| 79 | doRiNA: a database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , 2012 , 40, D180-6 | 20.1 | 151 |
| 78 | Cell fixation and preservation for droplet-based single-cell transcriptomics. <i>BMC Biology</i> , 2017 , 15, 44 | 7.3 | 135 |
| 77 | 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> , 2017 , 18, 237 | 18.3 | 129 |
| 76 | RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. <i>Journal of Clinical Investigation</i> , 2014 , 124, 3419-30 | 15.9 | 129 |
| 75 | In vivo and transcriptome-wide identification of RNA binding protein target sites. <i>Molecular Cell</i> , 2011 , 44, 828-40 | 17.6 | 124 |

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| 74 | Epigenomic Profiling of Human CD4 T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. <i>Immunity</i> , 2016 , 45, 1148-1161 | 32.3 | 118 |
| 73 | RNA localization is a key determinant of neurite-enriched proteome. <i>Nature Communications</i> , 2017 , 8, 583 | 17.4 | 118 |
| 72 | Extensive identification and analysis of conserved small ORFs in animals. <i>Genome Biology</i> , 2015 , 16, 179 | 18.3 | 117 |
| 71 | High-resolution profiling and discovery of planarian small RNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 11546-51 | 11.5 | 114 |
| 70 | Gene expression of pluripotency determinants is conserved between mammalian and planarian stem cells. <i>EMBO Journal</i> , 2012 , 31, 2755-69 | 13 | 113 |
| 69 | Gene expression cartography. <i>Nature</i> , 2019 , 576, 132-137 | 50.4 | 109 |
| 68 | DoRiNA 2.0--upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , 2015 , 43, D160-7 | 20.1 | 97 |
| 67 | De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. <i>Genome Research</i> , 2011 , 21, 1193-200 | 9.7 | 90 |
| 66 | A Single-Cell Transcriptome Atlas of the Mouse Glomerulus. <i>Journal of the American Society of Nephrology: JASN</i> , 2018 , 29, 2060-2068 | 12.7 | 87 |
| 65 | Single-Cell Transcriptomics Characterizes Cell Types in the Subventricular Zone and Uncovers Molecular Defects Impairing Adult Neurogenesis. <i>Cell Reports</i> , 2018 , 25, 2457-2469.e8 | 10.6 | 82 |
| 64 | A variety of dicer substrates in human and <i>C. elegans</i> . <i>Cell</i> , 2014 , 159, 1153-1167 | 56.2 | 80 |
| 63 | Conservation of regulatory elements between two species of <i>Drosophila</i> . <i>BMC Bioinformatics</i> , 2003 , 4, 57 | 3.6 | 76 |
| 62 | The Lupus Autoantigen La Prevents Mis-channeling of tRNA Fragments into the Human MicroRNA Pathway. <i>Molecular Cell</i> , 2016 , 63, 110-24 | 17.6 | 73 |
| 61 | Large-scale sorting of <i>C. elegans</i> embryos reveals the dynamics of small RNA expression. <i>Nature Methods</i> , 2009 , 6, 745-51 | 21.6 | 72 |
| 60 | Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. <i>iScience</i> , 2021 , 24, 102151 | 6.1 | 72 |
| 59 | Deciphering the porcine intestinal microRNA transcriptome. <i>BMC Genomics</i> , 2010 , 11, 275 | 4.5 | 65 |
| 58 | Conservation of mRNA and protein expression during development of <i>C. elegans</i> . <i>Cell Reports</i> , 2014 , 6, 565-77 | 10.6 | 64 |
| 57 | The SNF2-like helicase HELLS mediates E2F3-dependent transcription and cellular transformation. <i>EMBO Journal</i> , 2012 , 31, 972-85 | 13 | 60 |

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| 56 | The evolution of DNA regulatory regions for proteo-gamma bacteria by interspecies comparisons. <i>Genome Research</i> , 2002 , 12, 298-308 | 9.7 | 58 |
| 55 | LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020 , 587, 377-386 | 50.4 | 56 |
| 54 | 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> , 2002 , 99, 7323-8 | 11.5 | 55 |
| 53 | Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016 , 9, 33 | 5.8 | 54 |
| 52 | FLAM-seq: full-length mRNA sequencing reveals principles of poly(A) tail length control. <i>Nature Methods</i> , 2019 , 16, 879-886 | 21.6 | 53 |
| 51 | A cis element in the recombination activating gene locus regulates gene expression by counteracting a distant silencer. <i>Nature Immunology</i> , 2004 , 5, 443-50 | 19.1 | 53 |
| 50 | Global characterization of the oocyte-to-embryo transition in <i>Caenorhabditis elegans</i> uncovers a novel mRNA clearance mechanism. <i>EMBO Journal</i> , 2014 , 33, 1751-66 | 13 | 52 |
| 49 | Single-cell RNA-sequencing of herpes simplex virus 1-infected cells connects NRF2 activation to an antiviral program. <i>Nature Communications</i> , 2019 , 10, 4878 | 17.4 | 51 |
| 48 | Insm1 cooperates with Neurod1 and Foxa2 to maintain mature pancreatic β -cell function. <i>EMBO Journal</i> , 2015 , 34, 1417-33 | 13 | 50 |
| 47 | Paternal RNA contributions in the <i>Caenorhabditis elegans</i> zygote. <i>EMBO Journal</i> , 2014 , 33, 1740-50 | 13 | 47 |
| 46 | Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. <i>RNA Biology</i> , 2013 , 10, 1146-59 | 4.8 | 47 |
| 45 | Select microRNAs are essential for early development in the sea urchin. <i>Developmental Biology</i> , 2012 , 362, 104-13 | 3.1 | 42 |
| 44 | Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. <i>ELife</i> , 2016 , 5, | 8.9 | 39 |
| 43 | 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> , 2015 , 45, 1192-205 | 6.1 | 34 |
| 42 | Comprehensive analysis of translation from overexpressed circular RNAs reveals pervasive translation from linear transcripts. <i>Nucleic Acids Research</i> , 2020 , 48, 10368-10382 | 20.1 | 29 |
| 41 | Correlating gene expression variation with cis-regulatory polymorphism in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology and Evolution</i> , 2010 , 2, 697-707 | 3.9 | 28 |
| 40 | A Highly Conserved Circular RNA Is Required to Keep Neural Cells in a Progenitor State in the Mammalian Brain. <i>Cell Reports</i> , 2020 , 30, 2170-2179.e5 | 10.6 | 27 |
| 39 | Tracing tumorigenesis in a solid tumor model at single-cell resolution. <i>Nature Communications</i> , 2020 , 11, 991 | 17.4 | 24 |

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|----|--|------|----|
| 38 | Widespread activation of antisense transcription of the host genome during herpes simplex virus 1 infection. <i>Genome Biology</i> , 2017 , 18, 209 | 18.3 | 24 |
| 37 | Graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells | | 23 |
| 36 | The CCR4-NOT complex mediates deadenylation and degradation of stem cell mRNAs and promotes planarian stem cell differentiation. <i>PLoS Genetics</i> , 2013 , 9, e1004003 | 6 | 21 |
| 35 | Human muscle-derived CLEC14A-positive cells regenerate muscle independent of PAX7. <i>Nature Communications</i> , 2019 , 10, 5776 | 17.4 | 21 |
| 34 | Roles of Long Noncoding RNAs and Circular RNAs in Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019 , 11, | 10.2 | 20 |
| 33 | Binding site discovery from nucleic acid sequences by discriminative learning of hidden Markov models. <i>Nucleic Acids Research</i> , 2014 , 42, 12995-3011 | 20.1 | 19 |
| 32 | Single-Molecule Fluorescence In Situ Hybridization (FISH) of Circular RNA CDR1as. <i>Methods in Molecular Biology</i> , 2018 , 1724, 77-96 | 1.4 | 18 |
| 31 | RNA-bioinformatics: Tools, services and databases for the analysis of RNA-based regulation. <i>Journal of Biotechnology</i> , 2017 , 261, 76-84 | 3.7 | 17 |
| 30 | Defective metabolic programming impairs early neuronal morphogenesis in neural cultures and an organoid model of Leigh syndrome. <i>Nature Communications</i> , 2021 , 12, 1929 | 17.4 | 17 |
| 29 | microRNAs regulate cell-to-cell variability of endogenous target gene expression in developing mouse thymocytes. <i>PLoS Genetics</i> , 2015 , 11, e1005020 | 6 | 16 |
| 28 | Spatiotemporal m(i)RNA Architecture and 3'UTR Regulation in the <i>C. elegans</i> Germline. <i>Developmental Cell</i> , 2018 , 47, 785-800.e8 | 10.2 | 16 |
| 27 | Selective targeting of pro-inflammatory Th1 cells by microRNA-148a-specific antagomirs in vivo. <i>Journal of Autoimmunity</i> , 2018 , 89, 41-52 | 15.5 | 15 |
| 26 | RCAS: an RNA centric annotation system for transcriptome-wide regions of interest. <i>Nucleic Acids Research</i> , 2017 , 45, e91 | 20.1 | 13 |
| 25 | Post-transcriptional Regulation by 3'UTRs Can Be Masked by Regulatory Elements in 5'UTRs. <i>Cell Reports</i> , 2018 , 22, 3217-3226 | 10.6 | 13 |
| 24 | Reexamining microRNA site accessibility in Drosophila: a population genomics study. <i>PLoS ONE</i> , 2009 , 4, e5681 | 3.7 | 13 |
| 23 | MicroRNAs and the Operon paper. <i>Journal of Molecular Biology</i> , 2011 , 409, 70-5 | 6.5 | 12 |
| 22 | Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. <i>Life Science Alliance</i> , 2020 , 3, | 5.8 | 11 |
| 21 | Identification of proteins and miRNAs that specifically bind an mRNA in vivo. <i>Nature Communications</i> , 2019 , 10, 4205 | 17.4 | 10 |

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| 20 | The transcriptome dynamics of single cells during the cell cycle. <i>Molecular Systems Biology</i> , 2020 , 16, e9946 | 12.2 | 9 |
| 19 | Context-specific regulation of cell survival by a miRNA-controlled BIM rheostat. <i>Genes and Development</i> , 2019 , 33, 1673-1687 | 12.6 | 7 |
| 18 | Charting a tissue from single-cell transcriptomes | | 7 |
| 17 | Kidney Single-cell Transcriptomes Predict Spatial Corticomedullary Gene Expression and Tissue Osmolality Gradients. <i>Journal of the American Society of Nephrology: JASN</i> , 2021 , 32, 291-306 | 12.7 | 5 |
| 16 | Cell fixation and preservation for droplet-based single-cell transcriptomics | | 4 |
| 15 | Characterization of Transcription Termination-Associated RNAs: New Insights into their Biogenesis, Tailing, and Expression in Primary Tumors. <i>International Journal of Genomics</i> , 2018 , 2018, 1243858 | 2.5 | 3 |
| 14 | Predicting cellular position in the Drosophila embryo from Single-Cell Transcriptomics data | | 3 |
| 13 | Spacemake: processing and analysis of large-scale spatial transcriptomics data | | 2 |
| 12 | Gene Expression Signatures of a Preclinical Mouse Model during Colorectal Cancer Progression under Low-Dose Metronomic Chemotherapy. <i>Cancers</i> , 2020 , 13, | 6.6 | 2 |
| 11 | A Probabilistic Cellular Automaton for Evolution. <i>Journal De Physique, I</i> , 1995 , 5, 1129-1134 | | 2 |
| 10 | NovoSpaRc: flexible spatial reconstruction of single-cell gene expression with optimal transport. <i>Nature Protocols</i> , 2021 , 16, 4177-4200 | 18.8 | 2 |
| 9 | Optogenetic perturbations of RNA expression in tissue space | | 2 |
| 8 | Mixed messages: Re-initiation factors regulate translation of animal mRNAs. <i>Cell Research</i> , 2014 , 24, 1383-4 | 24.7 | 1 |
| 7 | Rapid nuclear deadenylation of mammalian messenger RNA | | 1 |
| 6 | Regulation of spatial and temporal gene expression in an animal germline | | 1 |
| 5 | Best practice standards for circular RNA research. <i>Nature Methods</i> , | 21.6 | 1 |
| 4 | Essentials of miRNA-dependent Control of mRNA Translation and decay, miRNA Targeting Principles, and Methods for Target Identification 2017 , 19-38 | | 0 |
| 3 | Parallel genetics of regulatory sequences using scalable genome editing in vivo. <i>Cell Reports</i> , 2021 , 35, 108988 | 10.6 | 0 |

- 2 Expression of Circ_Satb1 Is Decreased in Mesial Temporal Lobe Epilepsy and Regulates Dendritic Spine Morphology.. *Frontiers in Molecular Neuroscience*, **2022**, 15, 832133 6.1 o
- 1 Computational prediction of microRNA targets in vertebrates, fruitflies and nematodes172-186