

Nikolaus Rajewsky

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4686655/publications.pdf>

Version: 2024-02-01

122
papers

56,980
citations

10389

72
h-index

17592

121
g-index

143
all docs

143
docs citations

143
times ranked

55159
citing authors

#	ARTICLE	IF	CITATIONS
1	Circular RNAs are a large class of animal RNAs with regulatory potency. <i>Nature</i> , 2013, 495, 333-338.	27.8	6,474
2	Combinatorial microRNA target predictions. <i>Nature Genetics</i> , 2005, 37, 495-500.	21.4	4,258
3	Silencing of microRNAs in vivo with "antagomirs"™. <i>Nature</i> , 2005, 438, 685-689.	27.8	3,706
4	Widespread changes in protein synthesis induced by microRNAs. <i>Nature</i> , 2008, 455, 58-63.	27.8	3,120
5	miRDeep2 accurately identifies known and hundreds of novel microRNA genes in seven animal clades. <i>Nucleic Acids Research</i> , 2012, 40, 37-52.	14.5	2,624
6	circRNA Biogenesis Competes with Pre-mRNA Splicing. <i>Molecular Cell</i> , 2014, 56, 55-66.	9.7	2,490
7	Circular RNAs in the Mammalian Brain Are Highly Abundant, Conserved, and Dynamically Expressed. <i>Molecular Cell</i> , 2015, 58, 870-885.	9.7	1,974
8	A pancreatic islet-specific microRNA regulates insulin secretion. <i>Nature</i> , 2004, 432, 226-230.	27.8	1,932
9	Circ-ZNF609 Is a Circular RNA that Can Be Translated and Functions in Myogenesis. <i>Molecular Cell</i> , 2017, 66, 22-37.e9.	9.7	1,672
10	Translation of CircRNAs. <i>Molecular Cell</i> , 2017, 66, 9-21.e7.	9.7	1,431
11	circBase: a database for circular RNAs. <i>Rna</i> , 2014, 20, 1666-1670.	3.5	1,417
12	Regulation of the Germinal Center Response by MicroRNA-155. <i>Science</i> , 2007, 316, 604-608.	12.6	1,393
13	The evolution of gene regulation by transcription factors and microRNAs. <i>Nature Reviews Genetics</i> , 2007, 8, 93-103.	16.3	1,371
14	Discovering microRNAs from deep sequencing data using miRDeep. <i>Nature Biotechnology</i> , 2008, 26, 407-415.	17.5	1,102
15	microRNA target predictions in animals. <i>Nature Genetics</i> , 2006, 38, S8-S13.	21.4	987
16	Loss of a mammalian circular RNA locus causes miRNA deregulation and affects brain function. <i>Science</i> , 2017, 357, .	12.6	978
17	MiR-150 Controls B Cell Differentiation by Targeting the Transcription Factor c-Myb. <i>Cell</i> , 2007, 131, 146-159.	28.9	965
18	Analysis of Intron Sequences Reveals Hallmarks of Circular RNA Biogenesis in Animals. <i>Cell Reports</i> , 2015, 10, 170-177.	6.4	918

#	ARTICLE	IF	CITATIONS
19	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	12.6	912
20	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. <i>Genome Biology</i> , 2019, 20, 59.	8.8	911
21	A Human snoRNA with MicroRNA-Like Functions. <i>Molecular Cell</i> , 2008, 32, 519-528.	9.7	738
22	Transcriptome-wide Analysis of Regulatory Interactions of the RNA-Binding Protein HuR. <i>Molecular Cell</i> , 2011, 43, 340-352.	9.7	640
23	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, 2746-2751.	7.1	602
24	Identification of small ORFs in vertebrates using ribosome footprinting and evolutionary conservation. <i>EMBO Journal</i> , 2014, 33, 981-993.	7.8	587
25	Dicer Ablation Affects Antibody Diversity and Cell Survival in the B Lymphocyte Lineage. <i>Cell</i> , 2008, 132, 860-874.	28.9	547
26	Identification and Characterization of Circular RNAs As a New Class of Putative Biomarkers in Human Blood. <i>PLoS ONE</i> , 2015, 10, e0141214.	2.5	542
27	Survival of Resting Mature B Lymphocytes Depends on BCR Signaling via the I κ B β Heterodimer. <i>Cell</i> , 2004, 117, 787-800.	28.9	517
28	Decay Rates of Human mRNAs: Correlation With Functional Characteristics and Sequence Attributes. <i>Genome Research</i> , 2003, 13, 1863-1872.	5.5	467
29	Circadian Regulation of Gene Expression Systems in the <i>Drosophila</i> Head. <i>Neuron</i> , 2001, 32, 657-671.	8.1	442
30	Natural selection on human microRNA binding sites inferred from SNP data. <i>Nature Genetics</i> , 2006, 38, 1452-1456.	21.4	431
31	The Translational Landscape of the Human Heart. <i>Cell</i> , 2019, 178, 242-260.e29.	28.9	407
32	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
33	microRNA Target Predictions across Seven <i>Drosophila</i> Species and Comparison to Mammalian Targets. <i>PLoS Computational Biology</i> , 2005, 1, e13.	3.2	393
34	MicroRNA profiling of the murine hematopoietic system. <i>Genome Biology</i> , 2005, 6, R71.	9.6	388
35	Cell type atlas and lineage tree of a whole complex animal by single-cell transcriptomics. <i>Science</i> , 2018, 360, .	12.6	381
36	A Genome-Wide Map of Conserved MicroRNA Targets in <i>C. elegans</i> . <i>Current Biology</i> , 2006, 16, 460-471.	3.9	380

#	ARTICLE	IF	CITATIONS
37	The <i>Drosophila</i> embryo at single-cell transcriptome resolution. <i>Science</i> , 2017, 358, 194-199.	12.6	352
38	Paternal Diet Defines Offspring Chromatin State and Intergenerational Obesity. <i>Cell</i> , 2014, 159, 1352-1364.	28.9	345
39	The microRNA miR-182 is induced by IL-2 and promotes clonal expansion of activated helper T lymphocytes. <i>Nature Immunology</i> , 2010, 11, 1057-1062.	14.5	304
40	A map of human circular RNAs in clinically relevant tissues. <i>Journal of Molecular Medicine</i> , 2017, 95, 1179-1189.	3.9	286
41	Computational identification of microRNA targets. <i>Developmental Biology</i> , 2004, 267, 529-535.	2.0	278
42	Unambiguous Identification of miRNA:Target Site Interactions by Different Types of Ligation Reactions. <i>Molecular Cell</i> , 2014, 54, 1042-1054.	9.7	258
43	The Landscape of <i>C. elegans</i> 3' UTRs. <i>Science</i> , 2010, 329, 432-435.	12.6	248
44	The Impact of miRNA Target Sites in Coding Sequences and in 3' UTRs. <i>PLoS ONE</i> , 2011, 6, e18067.	2.5	244
45	Timing, Genetic Requirements and Functional Consequences of Somatic Hypermutation during B-Cell Development. <i>Immunological Reviews</i> , 1987, 96, 5-22.	6.0	228
46	Competition between target sites of regulators shapes post-transcriptional gene regulation. <i>Nature Reviews Genetics</i> , 2015, 16, 113-126.	16.3	220
47	Transcriptional Control in the Segmentation Gene Network of <i>Drosophila</i> . <i>PLoS Biology</i> , 2004, 2, e271.	5.6	216
48	Gene expression cartography. <i>Nature</i> , 2019, 576, 132-137.	27.8	216
49	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. <i>Science</i> , 2021, 24, 102151.	4.1	202
50	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.	2.6	194
51	Cell fixation and preservation for droplet-based single-cell transcriptomics. <i>BMC Biology</i> , 2017, 15, 44.	3.8	186
52	Extensive identification and analysis of conserved small ORFs in animals. <i>Genome Biology</i> , 2015, 16, 179.	8.8	180
53	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.	8.8	179
54	doRiNA: a database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , 2012, 40, D180-D186.	14.5	177

#	ARTICLE	IF	CITATIONS
55	RNA localization is a key determinant of neurite-enriched proteome. <i>Nature Communications</i> , 2017, 8, 583.	12.8	176
56	RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. <i>Journal of Clinical Investigation</i> , 2014, 124, 3419-3430.	8.2	176
57	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.	14.3	174
58	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.	6.4	162
59	In Vivo and Transcriptome-wide Identification of RNA Binding Protein Target Sites. <i>Molecular Cell</i> , 2011, 44, 828-840.	9.7	146
60	A Single-Cell Transcriptome Atlas of the Mouse Glomerulus. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 2060-2068.	6.1	137
61	Gene expression of pluripotency determinants is conserved between mammalian and planarian stem cells. <i>EMBO Journal</i> , 2012, 31, 2755-2769.	7.8	136
62	DoRiNA 2.0—upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. <i>Nucleic Acids Research</i> , 2015, 43, D160-D167.	14.5	136
63	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, 11546-11551.	7.1	128
64	FLAM-seq: full-length mRNA sequencing reveals principles of poly(A) tail length control. <i>Nature Methods</i> , 2019, 16, 879-886.	19.0	119
65	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	27.8	108
66	The Lupus Autoantigen La Prevents Mis-channeling of tRNA Fragments into the Human MicroRNA Pathway. <i>Molecular Cell</i> , 2016, 63, 110-124.	9.7	107
67	A Variety of Dicer Substrates in Human and <i>C. elegans</i> . <i>Cell</i> , 2014, 159, 1153-1167.	28.9	106
68	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. <i>Genome Research</i> , 2011, 21, 1193-1200.	5.5	100
69	Conservation of mRNA and Protein Expression during Development of <i>C. elegans</i> . <i>Cell Reports</i> , 2014, 6, 565-577.	6.4	98
70	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.	12.8	96
71	Large-scale sorting of <i>C. elegans</i> embryos reveals the dynamics of small RNA expression. <i>Nature Methods</i> , 2009, 6, 745-751.	19.0	91
72	The Evolution of DNA Regulatory Regions for Proteo-Gamma Bacteria by Interspecies Comparisons. <i>Genome Research</i> , 2002, 12, 298-308.	5.5	86

#	ARTICLE	IF	CITATIONS
73	Conservation of regulatory elements between two species of <i>Drosophila</i> . <i>BMC Bioinformatics</i> , 2003, 4, 57.	2.6	84
74	<i>Insm1</i> cooperates with <i>N</i> and <i>Foxo1</i> to maintain mature pancreatic β -cell function. <i>EMBO Journal</i> , 2015, 34, 1417-1433.	7.8	77
75	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. <i>RNA Biology</i> , 2013, 10, 1146-1159.	3.1	76
76	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016, 9, 33.	3.9	73
77	Deciphering the porcine intestinal microRNA transcriptome. <i>BMC Genomics</i> , 2010, 11, 275.	2.8	71
78	A cis element in the recombination activating gene locus regulates gene expression by counteracting a distant silencer. <i>Nature Immunology</i> , 2004, 5, 443-450.	14.5	69
79	The SNF2-like helicase HELLS mediates E2F3-dependent transcription and cellular transformation. <i>EMBO Journal</i> , 2012, 31, 972-985.	7.8	68
80	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, 1751-1766.	7.8	68
81	Paternal RNA contributions in the <i>Caenorhabditis elegans</i> zygote. <i>EMBO Journal</i> , 2014, 33, 1740-1750.	7.8	67
82	Best practice standards for circular RNA research. <i>Nature Methods</i> , 2022, 19, 1208-1220.	19.0	58
83	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, 7323-7328.	7.1	57
84	Comprehensive analysis of translation from overexpressed circular RNAs reveals pervasive translation from linear transcripts. <i>Nucleic Acids Research</i> , 2020, 48, 10368-10382.	14.5	57
85	miR-148a is upregulated by Twist1 and β and promotes Th1 cell survival by regulating the proapoptotic gene Bim. <i>European Journal of Immunology</i> , 2015, 45, 1192-1205.	2.9	56
86	Select microRNAs are essential for early development in the sea urchin. <i>Developmental Biology</i> , 2012, 362, 104-113.	2.0	55
87	Defective metabolic programming impairs early neuronal morphogenesis in neural cultures and an organoid model of Leigh syndrome. <i>Nature Communications</i> , 2021, 12, 1929.	12.8	55
88	NovoSpaRc: flexible spatial reconstruction of single-cell gene expression with optimal transport. <i>Nature Protocols</i> , 2021, 16, 4177-4200.	12.0	55
89	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.	6.4	53
90	Widespread activation of antisense transcription of the host genome during herpes simplex virus 1 infection. <i>Genome Biology</i> , 2017, 18, 209.	8.8	49

#	ARTICLE	IF	CITATIONS
91	Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. <i>ELife</i> , 2016, 5, .	6.0	48
92	Tracing tumorigenesis in a solid tumor model at single-cell resolution. <i>Nature Communications</i> , 2020, 11, 991.	12.8	44
93	Roles of Long Noncoding RNAs and Circular RNAs in Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032680.	5.5	38
94	The transcriptome dynamics of single cells during the cell cycle. <i>Molecular Systems Biology</i> , 2020, 16, e9946.	7.2	35
95	Correlating Gene Expression Variation with cis-Regulatory Polymorphism in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 697-707.	2.5	31
96	Selective targeting of pro-inflammatory Th1 cells by microRNA-148a-specific antagomirs in vivo. <i>Journal of Autoimmunity</i> , 2018, 89, 41-52.	6.5	30
97	Human muscle-derived CLEC14A-positive cells regenerate muscle independent of PAX7. <i>Nature Communications</i> , 2019, 10, 5776.	12.8	30
98	L(ou)sy miRNA targets?. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 754-755.	8.2	29
99	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.	3.5	29
100	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.	7.0	27
101	Single-Molecule Fluorescence In Situ Hybridization (FISH) of Circular RNA CDR1as. <i>Methods in Molecular Biology</i> , 2018, 1724, 77-96.	0.9	26
102	Identification of proteins and miRNAs that specifically bind an mRNA in vivo. <i>Nature Communications</i> , 2019, 10, 4205.	12.8	26
103	Binding site discovery from nucleic acid sequences by discriminative learning of hidden Markov models. <i>Nucleic Acids Research</i> , 2014, 42, 12995-13011.	14.5	24
104	Post-transcriptional Regulation by 3' UTRs Can Be Masked by Regulatory Elements in 5' UTRs. <i>Cell Reports</i> , 2018, 22, 3217-3226.	6.4	24
105	RCAS: an RNA centric annotation system for transcriptome-wide regions of interest. <i>Nucleic Acids Research</i> , 2017, 45, e91-e91.	14.5	23
106	microRNAs Regulate Cell-to-Cell Variability of Endogenous Target Gene Expression in Developing Mouse Thymocytes. <i>PLoS Genetics</i> , 2015, 11, e1005020.	3.5	22
107	RNA-bioinformatics: Tools, services and databases for the analysis of RNA-based regulation. <i>Journal of Biotechnology</i> , 2017, 261, 76-84.	3.8	21
108	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. <i>Life Science Alliance</i> , 2020, 3, e202000867.	2.8	20

#	ARTICLE	IF	CITATIONS
109	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.	6.1	18
110	microRNAs and the Operon Paper. <i>Journal of Molecular Biology</i> , 2011, 409, 70-75.	4.2	14
111	Reexamining microRNA Site Accessibility in <i>Drosophila</i> : A Population Genomics Study. <i>PLoS ONE</i> , 2009, 4, e5681.	2.5	14
112	Context-specific regulation of cell survival by a miRNA-controlled BIM rheostat. <i>Genes and Development</i> , 2019, 33, 1673-1687.	5.9	13
113	Parallel genetics of regulatory sequences using scalable genome editing in <i>Â</i> vivo. <i>Cell Reports</i> , 2021, 35, 108988.	6.4	9
114	Gene Expression Signatures of a Preclinical Mouse Model during Colorectal Cancer Progression under Low-Dose Metronomic Chemotherapy. <i>Cancers</i> , 2021, 13, 49.	3.7	7
115	Expression of <i>Circ_Satb1</i> Is Decreased in Mesial Temporal Lobe Epilepsy and Regulates Dendritic Spine Morphology. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 832133.	2.9	6
116	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, 1-11.	1.6	5
117	Mixed messages: Re-initiation factors regulate translation of animal mRNAs. <i>Cell Research</i> , 2014, 24, 1383-1384.	12.0	2
118	A Probabilistic Cellular Automaton for Evolution. <i>Journal De Physique, I</i> , 1995, 5, 1129-1134.	1.2	2
119	Essentials of miRNA-dependent Control of mRNA Translation and decay, miRNA Targeting Principles, and Methods for Target Identification. , 2017, , 19-38.		1
120	Estimation of cell- and tissue volumes. <i>MicroPublication Biology</i> , 2021, 2021, .	0.1	1
121	Optocoder: computational decoding of spatially indexed bead arrays. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	3.2	1
122	Computational prediction of microRNA targets in vertebrates, fruitflies and nematodes. , 0, , 172-186.		0