

Pieter Mestdagh

List of Publications by Year in descending order

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Version: 2024-02-01

140
papers

13,620
citations

36303

51
h-index

23533

111
g-index

166
all docs

166
docs citations

166
times ranked

24312
citing authors

#	ARTICLE	IF	CITATIONS
1	miR-9, a MYC/MYCN-activated microRNA, regulates E-cadherin and cancer metastasis. <i>Nature Cell Biology</i> , 2010, 12, 247-256.	10.3	1,216
2	EV-TRACK: transparent reporting and centralizing knowledge in extracellular vesicle research. <i>Nature Methods</i> , 2017, 14, 228-232.	19.0	886
3	A novel and universal method for microRNA RT-qPCR data normalization. <i>Genome Biology</i> , 2009, 10, R64.	9.6	849
4	The impact of disparate isolation methods for extracellular vesicles on downstream RNA profiling. <i>Journal of Extracellular Vesicles</i> , 2014, 3, .	12.2	725
5	Evaluation of quantitative miRNA expression platforms in the microRNA quality control (miRQC) study. <i>Nature Methods</i> , 2014, 11, 809-815.	19.0	564
6	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. <i>Nucleic Acids Research</i> , 2013, 41, D246-D251.	14.5	488
7	Melanoma addiction to the long non-coding RNA SAMMSON. <i>Nature</i> , 2016, 531, 518-522.	27.8	488
8	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	16.8	478
9	LNCipedia 5: towards a reference set of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, D135-D139.	14.5	403
10	LIN28B induces neuroblastoma and enhances MYCN levels via let-7 suppression. <i>Nature Genetics</i> , 2012, 44, 1199-1206.	21.4	336
11	An update on LNCipedia: a database for annotated human lncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D174-D180.	14.5	298
12	The miR-17-92 MicroRNA Cluster Regulates Multiple Components of the TGF- β Pathway in Neuroblastoma. <i>Molecular Cell</i> , 2010, 40, 762-773.	9.7	279
13	High-throughput stem-loop RT-qPCR miRNA expression profiling using minute amounts of input RNA. <i>Nucleic Acids Research</i> , 2008, 36, e143-e143.	14.5	261
14	Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. <i>Scientific Reports</i> , 2017, 7, 1559.	3.3	247
15	MicroRNA Expression in Induced Sputum of Smokers and Patients with Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 183, 898-906.	5.6	209
16	Benchmarking of cell type deconvolution pipelines for transcriptomics data. <i>Nature Communications</i> , 2020, 11, 5650.	12.8	207
17	MicroRNA expression profiling to identify and validate reference genes for relative quantification in colorectal cancer. <i>BMC Cancer</i> , 2010, 10, 173.	2.6	193
18	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. <i>Nucleic Acids Research</i> , 2010, 38, 5919-5928.	14.5	183

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19	Computational deconvolution of transcriptomics data from mixed cell populations. <i>Bioinformatics</i> , 2018, 34, 1969-1979.	4.1	181
20	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	14.5	174
21	Asthma inflammatory phenotypes show differential microRNA expression in sputum. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1433-1446.	2.9	168
22	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	14.5	160
23	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. <i>Science Translational Medicine</i> , 2012, 4, 141ra91.	12.4	147
24	miRNA Expression Profiling: From Reference Genes to Global Mean Normalization. <i>Methods in Molecular Biology</i> , 2012, 822, 261-272.	0.9	143
25	Cross-Cohort Analysis Identifies a TEAD4-MYCN Positive Feedback Loop as the Core Regulatory Element of High-Risk Neuroblastoma. <i>Cancer Discovery</i> , 2018, 8, 582-599.	9.4	119
26	Alternative Routes to Induce Naïve Pluripotency in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2015, 33, 2686-2698.	3.2	118
27	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 191-199.	2.8	117
28	Widespread Dysregulation of MiRNAs by MYCN Amplification and Chromosomal Imbalances in Neuroblastoma: Association of miRNA Expression with Survival. <i>PLoS ONE</i> , 2009, 4, e7850.	2.5	112
29	The cancer-associated microprotein CASIMO1 controls cell proliferation and interacts with squalene epoxidase modulating lipid droplet formation. <i>Oncogene</i> , 2018, 37, 4750-4768.	5.9	111
30	MicroRNA Profiling Reveals a Role for MicroRNA-218-5p in the Pathogenesis of Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 43-56.	5.6	108
31	Cancer-Associated Adipose Tissue Promotes Breast Cancer Progression by Paracrine Oncostatin M and Jak/STAT3 Signaling. <i>Cancer Research</i> , 2014, 74, 6806-6819.	0.9	105
32	Identification of miR-145 as a Key Regulator of the Pigmentary Process. <i>Journal of Investigative Dermatology</i> , 2013, 133, 201-209.	0.7	99
33	Renal microRNA and miRNA profiles in progressive chronic kidney disease. <i>European Journal of Clinical Investigation</i> , 2016, 46, 213-226.	3.4	96
34	The generation and use of recombinant extracellular vesicles as biological reference material. <i>Nature Communications</i> , 2019, 10, 3288.	12.8	96
35	miRNA Expression Profiling Enables Risk Stratification in Archived and Fresh Neuroblastoma Tumor Samples. <i>Clinical Cancer Research</i> , 2011, 17, 7684-7692.	7.0	92
36	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. <i>Scientific Reports</i> , 2017, 7, 40127.	3.3	92

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37	Mir-137 functions as a tumor suppressor in neuroblastoma by downregulating KDM1A. International Journal of Cancer, 2013, 133, 1064-1073.	5.1	91
38	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXO1 reactivation of DREAM targets. Nature Communications, 2018, 9, 4866.	12.8	91
39	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. International Journal of Cancer, 2010, 127, 2374-2385.	5.1	88
40	SAMSON fosters cancer cell fitness by concertedly enhancing mitochondrial and cytosolic translation. Nature Structural and Molecular Biology, 2018, 25, 1035-1046.	8.2	84
41	Synthetic lethality between Rb, p53 and Dicer or miR-17-92 in retinal progenitors suppresses retinoblastoma formation. Nature Cell Biology, 2012, 14, 958-965.	10.3	79
42	miR-542c-3p exerts tumor suppressive functions in neuroblastoma by downregulating survivin. International Journal of Cancer, 2015, 136, 1308-1320.	5.1	78
43	The RNA Atlas expands the catalog of human non-coding RNAs. Nature Biotechnology, 2021, 39, 1453-1465.	17.5	75
44	miRBase Tracker: keeping track of microRNA annotation changes. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	3.0	73
45	The microRNA body map: dissecting microRNA function through integrative genomics. Nucleic Acids Research, 2011, 39, e136-e136.	14.5	72
46	Non-coding RNAs in the pathogenesis of COPD. Thorax, 2015, 70, 782-791.	5.6	71
47	Chromosomal and MicroRNA Expression Patterns Reveal Biologically Distinct Subgroups of 11q ²³ Neuroblastoma. Clinical Cancer Research, 2010, 16, 2971-2978.	7.0	70
48	A Genome-Wide Search for Promoters That Respond to Increased MYCN Reveals Both New Oncogenic and Tumor Suppressor MicroRNAs Associated with Aggressive Neuroblastoma. Cancer Research, 2011, 71, 3841-3851.	0.9	70
49	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. Nature Communications, 2019, 10, 5026.	12.8	67
50	Comparison of miRNA profiles of microdissected Hodgkin/Reed-Sternberg cells and Hodgkin cell lines versus CD77 ⁺ B cells reveals a distinct subset of differentially expressed miRNAs. British Journal of Haematology, 2009, 147, 686-690.	2.5	55
51	MicroRNA-128-3p is a novel oncomiR targeting PHF6 in T-cell acute lymphoblastic leukemia. Haematologica, 2014, 99, 1326-1333.	3.5	55
52	MicroRNA-184 is a downstream effector of albuminuria driving renal fibrosis in rats with diabetic nephropathy. Diabetologia, 2017, 60, 1114-1125.	6.3	54
53	Comparative analysis of naive, primed and ground state pluripotency in mouse embryonic stem cells originating from the same genetic background. Scientific Reports, 2018, 8, 5884.	3.3	54
54	A microRNA-21-mediated SATB1/S100A9/NF- κ B axis promotes chronic obstructive pulmonary disease pathogenesis. Science Translational Medicine, 2021, 13, eaav7223.	12.4	54

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55	Accurate RT-qPCR gene expression analysis on cell culture lysates. <i>Scientific Reports</i> , 2012, 2, 222.	3.3	52
56	The Notch driven long non-coding RNA repertoire in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2014, 99, 1808-1816.	3.5	50
57	The transcriptome of lung tumor-infiltrating dendritic cells reveals a tumor-supporting phenotype and a microRNA signature with negative impact on clinical outcome. <i>Oncolmmunology</i> , 2017, 6, e1253655.	4.6	50
58	Charting Extracellular Transcriptomes in The Human Biofluid RNA Atlas. <i>Cell Reports</i> , 2020, 33, 108552.	6.4	50
59	Performance assessment of total RNA sequencing of human biofluids and extracellular vesicles. <i>Scientific Reports</i> , 2019, 9, 17574.	3.3	46
60	Regulatory microRNA Network Identification in Bovine Blastocyst Development. <i>Stem Cells and Development</i> , 2013, 22, 1907-1920.	2.1	45
61	Vapor nanobubble is the more reliable photothermal mechanism for inducing endosomal escape of siRNA without disturbing cell homeostasis. <i>Journal of Controlled Release</i> , 2020, 319, 262-275.	9.9	45
62	Noncoding after All: Biases in Proteomics Data Do Not Explain Observed Absence of lncRNA Translation Products. <i>Journal of Proteome Research</i> , 2017, 16, 2508-2515.	3.7	44
63	microRNA profiling in lung tissue and bronchoalveolar lavage of cigarette smoke-exposed mice and in COPD patients: a translational approach. <i>Scientific Reports</i> , 2017, 7, 12871.	3.3	44
64	<i>Dickkopfâ€³</i> is regulated by the MYCNâ€­induced miRâ€­17â€­92 cluster in neuroblastoma. <i>International Journal of Cancer</i> , 2012, 130, 2591-2598.	5.1	43
65	Differential gene expression analysis tools exhibit substandard performance for long non-coding RNA-sequencing data. <i>Genome Biology</i> , 2018, 19, 96.	8.8	43
66	<scp>M</scp><scp>R</scp>â€­34a deficiency accelerates medulloblastoma formation <i>in vivo</i>. <i>International Journal of Cancer</i> , 2015, 136, 2293-2303.	5.1	40
67	How long noncoding RNAs enforce their will on mitochondrial activity: regulation of mitochondrial respiration, reactive oxygen species production, apoptosis, and metabolic reprogramming in cancer. <i>Current Genetics</i> , 2018, 64, 163-172.	1.7	40
68	SMARTer single cell total RNA sequencing. <i>Nucleic Acids Research</i> , 2019, 47, e93-e93.	14.5	38
69	Ectopic MicroRNA-150-5p Transcription Sensitizes Glucocorticoid Therapy Response in MM1S Multiple Myeloma Cells but Fails to Overcome Hormone Therapy Resistance in MM1R Cells. <i>PLoS ONE</i> , 2014, 9, e113842.	2.5	38
70	MYCN-targeting miRNAs are predominantly downregulated during MYCN-driven neuroblastoma tumor formation. <i>Oncotarget</i> , 2015, 6, 5204-5216.	1.8	38
71	MISpheroid: a knowledgebase and transparency tool for minimum information in spheroid identity. <i>Nature Methods</i> , 2021, 18, 1294-1303.	19.0	38
72	Robust sequential biophysical fractionation of blood plasma to study variations in the biomolecular landscape of systemically circulating extracellular vesicles across clinical conditions. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12122.	12.2	37

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73	Focal DNA Copy Number Changes in Neuroblastoma Target MYCN Regulated Genes. PLoS ONE, 2013, 8, e52321.	2.5	37
74	Long Noncoding RNA Expression Profiling in Normal B-Cell Subsets and Hodgkin Lymphoma Reveals Hodgkin and Reed-Sternberg Cell-Specific Long Noncoding RNAs. American Journal of Pathology, 2016, 186, 2462-2472.	3.8	36
75	miR-135a Inhibits Cancer Stem Cell-Driven Medulloblastoma Development by Directly Repressing Arhgef6 Expression. Stem Cells, 2015, 33, 1377-1389.	3.2	35
76	Long non-coding RNAs in cutaneous melanoma: clinical perspectives. Oncotarget, 2017, 8, 43470-43480.	1.8	35
77	Distinct Notch1 and BCL11B requirements mediate human $\gamma\delta$ T cell development. EMBO Reports, 2020, 21, e49006.	4.5	31
78	CLL Cells Respond to B-Cell Receptor Stimulation with a MicroRNA/mRNA Signature Associated with MYC Activation and Cell Cycle Progression. PLoS ONE, 2013, 8, e60275.	2.5	31
79	microRNAs in colon cancer: A roadmap for discovery. FEBS Letters, 2012, 586, 3000-3007.	2.8	30
80	Dynamic Activity of miR-125b and miR-93 during Murine Neural Stem Cell Differentiation In Vitro and in the Subventricular Zone Neurogenic Niche. PLoS ONE, 2013, 8, e67411.	2.5	30
81	Straightforward and sensitive RT-qPCR based gene expression analysis of FFPE samples. Scientific Reports, 2016, 6, 21418.	3.3	30
82	Early Targets of miR-34a in Neuroblastoma. Molecular and Cellular Proteomics, 2014, 13, 2114-2131.	3.8	29
83	Genome wide expression profiling of p53 regulated miRNAs in neuroblastoma. Scientific Reports, 2015, 5, 9027.	3.3	29
84	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. Scientific Reports, 2016, 6, 36111.	3.3	28
85	Circulating microRNA biomarkers for metastatic disease in neuroblastoma patients. JCI Insight, 2018, 3, .	5.0	28
86	IL-1 β potently stabilizes IL-6 mRNA in human astrocytes. Biochemical Pharmacology, 2011, 81, 1004-1015.	4.4	27
87	Lung tumours reprogram pulmonary dendritic cell immunogenicity at the microRNA level. International Journal of Cancer, 2014, 135, 2868-2877.	5.1	27
88	Candidate RNA biomarkers in biofluids for early diagnosis of ovarian cancer: A systematic review. Gynecologic Oncology, 2021, 160, 633-642.	1.4	27
89	External oligonucleotide standards enable cross laboratory comparison and exchange of real-time quantitative PCR data. Nucleic Acids Research, 2009, 37, e138-e138.	14.5	25
90	Identification of miRNAs contributing to neuroblastoma chemoresistance. Computational and Structural Biotechnology Journal, 2015, 13, 307-319.	4.1	23

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91	Non-coding RNAs and respiratory disease. <i>Thorax</i> , 2015, 70, 388-390.	5.6	22
92	Genome-wide study of the effect of blood collection tubes on the cell-free DNA methylome. <i>Epigenetics</i> , 2021, 16, 797-807.	2.7	21
93	EV11 mediated down regulation of <i>MIR449A</i> is essential for the survival of EV11 positive leukaemic cells. <i>British Journal of Haematology</i> , 2011, 154, 337-348.	2.5	20
94	Targeted Therapy of <i>TERT</i> -Rearranged Neuroblastoma with BET Bromodomain Inhibitor and Proteasome Inhibitor Combination Therapy. <i>Clinical Cancer Research</i> , 2021, 27, 1438-1451.	7.0	20
95	Expression Profiling Identifies the Noncoding Processed Transcript of HNRNPU with Proliferative Properties in Pancreatic Ductal Adenocarcinoma. <i>Non-coding RNA</i> , 2017, 3, 24.	2.6	19
96	Unlocking the secrets of long non-coding RNAs in asthma. <i>Thorax</i> , 2022, 77, 514-522.	5.6	18
97	Depletion of tRNA-halves enables effective small RNA sequencing of low-input murine serum samples. <i>Scientific Reports</i> , 2016, 6, 37876.	3.3	17
98	When DNA gets in the way: A cautionary note for DNA contamination in extracellular RNA-seq studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18934-18936.	7.1	17
99	decodeRNA™ predicting non-coding RNA functions using guilt-by-association. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	16
100	Discovering cancer vulnerabilities using high-throughput micro-RNA screening. <i>Nucleic Acids Research</i> , 2017, 45, 12657-12670.	14.5	15
101	A high-throughput 3' UTR reporter screening identifies microRNA interactomes of cancer genes. <i>PLoS ONE</i> , 2018, 13, e0194017.	2.5	15
102	The long non-coding RNA SAMMSON is essential for uveal melanoma cell survival. <i>Oncogene</i> , 2022, 41, 15-25.	5.9	15
103	Predicting outcomes for children with neuroblastoma. <i>Discovery Medicine</i> , 2010, 10, 29-36.	0.5	15
104	Integrative analysis identifies lincRNAs up- and downstream of neuroblastoma driver genes. <i>Scientific Reports</i> , 2019, 9, 5685.	3.3	14
105	RT-qPCR-Based Quantification of Small Non-Coding RNAs. <i>Methods in Molecular Biology</i> , 2015, 1296, 85-102.	0.9	14
106	Effective Alu Repeat Based RT-Qpcr Normalization in Cancer Cell Perturbation Experiments. <i>PLoS ONE</i> , 2013, 8, e71776.	2.5	13
107	In silico discovery of a FOXM1 driven embryonal signaling pathway in therapy resistant neuroblastoma tumors. <i>Scientific Reports</i> , 2018, 8, 17468.	3.3	11
108	Next generation sequencing of microRNAs from isogenic neuroblastoma cell lines isolated before and after treatment. <i>Cancer Letters</i> , 2016, 372, 128-136.	7.2	10

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109	Checkpoint inhibition in combination with an immunoboost of external beam radiotherapy in solid tumors (CHEERS): study protocol for a phase 2, open-label, randomized controlled trial. <i>BMC Cancer</i> , 2021, 21, 514.	2.6	10
110	SPECS: a non-parametric method to identify tissue-specific molecular features for unbalanced sample groups. <i>BMC Bioinformatics</i> , 2020, 21, 58.	2.6	9
111	Some cautionary notes on the petite "Holy Grail" of molecular diagnostics. <i>Haematologica</i> , 2014, 99, 401-402.	3.5	8
112	Messenger RNA capture sequencing of extracellular RNA from human biofluids using a comprehensive set of spike-in controls. <i>STAR Protocols</i> , 2021, 2, 100475.	1.2	8
113	Evaluating Diagnostic Accuracy of Saliva Sampling Methods for Severe Acute Respiratory Syndrome Coronavirus 2 Reveals Differential Sensitivity and Association with Viral Load. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 1249-1258.	2.8	7
114	Determining differentially expressed miRNAs and validating miRNA-target relationships using the SPRET/Ei mouse strain. <i>Mammalian Genome</i> , 2015, 26, 94-107.	2.2	6
115	MicroRNAs as future therapeutic targets in COPD?. <i>European Respiratory Journal</i> , 2017, 49, 1700431.	6.7	6
116	Robust Selection of Cancer Survival Signatures from High-Throughput Genomic Data Using Two-Fold Subsampling. <i>PLoS ONE</i> , 2014, 9, e108818.	2.5	6
117	The mutational landscape of <i>MYCN</i> , <i>Lin28b</i> and <i>ALK</i> driven murine neuroblastoma mimics human disease. <i>Oncotarget</i> , 2018, 9, 8334-8349.	1.8	6
118	Zipper plot: visualizing transcriptional activity of genomic regions. <i>BMC Bioinformatics</i> , 2017, 18, 231.	2.6	5
119	Targeted Genomic Screen Reveals Focal Long Non-Coding RNA Copy Number Alterations in Cancer Cell Lines. <i>Non-coding RNA</i> , 2018, 4, 21.	2.6	5
120	Long non-coding RNA expression profiling in the NCI60 cancer cell line panel using high-throughput RT-qPCR. <i>Scientific Data</i> , 2016, 3, 160052.	5.3	5
121	miR-99b-5p, miR-380-3p, and miR-485-3p are novel chemosensitizing miRNAs in high-risk neuroblastoma. <i>Molecular Therapy</i> , 2022, 30, 1119-1134.	8.2	5
122	The MicroRNA Landscape of Acute Beta Cell Destruction in Type 1 Diabetic Recipients of Intraportal Islet Grafts. <i>Cells</i> , 2021, 10, 1693.	4.1	4
123	Custom long non-coding RNA capture enhances detection sensitivity in different human sample types. <i>RNA Biology</i> , 2021, 18, 215-222.	3.1	4
124	RNA biomarkers from proximal liquid biopsy for diagnosis of ovarian cancer. <i>Neoplasia</i> , 2022, 24, 155-164.	5.3	4
125	Whole-Genome RT-qPCR MicroRNA Expression Profiling. <i>Methods in Molecular Biology</i> , 2012, 815, 121-130.	0.9	3
126	Recurrent chromosomal imbalances provide selective advantage to human embryonic stem cells under enhanced replicative stress conditions. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 272-281.	2.8	3

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127	Transient nuclear lamin A/C accretion aids in recovery from vapor nanobubble-induced permeabilisation of the plasma membrane. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 23.	5.4	3
128	Orthogonal proteomics methods to unravel the HOTAIR interactome. <i>Scientific Reports</i> , 2022, 12, 1513.	3.3	3
129	Open Problems in Extracellular RNA Data Analysis: Insights From an ERCC Online Workshop. <i>Frontiers in Genetics</i> , 2021, 12, 778416.	2.3	2
130	MicroRNA Expression Analysis Using Small RNA Sequencing Discovery and RT-qPCR-Based Validation. <i>Methods in Molecular Biology</i> , 2017, 1654, 197-208.	0.9	1
131	CiLiQuant: Quantification of RNA Junction Reads Based on Their Circular or Linear Transcript Origin. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	1
132	A 3â€²â€¢end capture sequencing method for highâ€¢throughput targeted gene expression profiling. <i>Biotechnology Journal</i> , 2022, 17, e2100660.	3.5	1
133	1.6 BCR Stimulation in CLL, Regardless of Mutation Status, Increases Expression of miR-132 and miR-212. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2011, 11, S144-S145.	0.4	0
134	Reply: Direct Detection of Circulating MicroRNAs Unveiled the Absence of MicroRNA-218-5p in Smoker Subjects. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 533-533.	5.6	0
135	MicroRNA Profiling of EVI1 Deregulated Myeloid Leukemia.. <i>Blood</i> , 2007, 110, 4146-4146.	1.4	0
136	MicroRNA Profiling of EVI1 Deregulated Myeloid Leukemia. <i>Blood</i> , 2008, 112, 5322-5322.	1.4	0
137	Comparison of miRNA Profiles of Microdissected Hodgkin/Reed-Sternberg Cells and Hodgkin Cell Lines Versus CD77+ B-Cells Reveals a Distinct Subset of Differentially Expressed miRNAs. <i>Blood</i> , 2008, 112, 4488-4488.	1.4	0
138	Downregulation of MiR-449a Is Essential for the Survival of EVI1 Positive Leukemic Cells through Modulation of NOTCH1 and BCL2.. <i>Blood</i> , 2009, 114, 361-361.	1.4	0
139	Regulatory Networks Governed by MicroRNAs in T-ALL Oncogenesis and Normal T-Cell Development. <i>Blood</i> , 2011, 118, 1366-1366.	1.4	0
140	Expanding The TLX1-Regulome In T Cell Acute Lymphoblastic Leukemia Towards Long Non-Coding RNAs. <i>Blood</i> , 2013, 122, 813-813.	1.4	0