

Eckart Meese

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1230300/publications.pdf>

Version: 2024-02-01

157
papers

8,439
citations

47006

47
h-index

54911

84
g-index

170
all docs

170
docs citations

170
times ranked

13160
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide DNA methylome and transcriptome changes induced by inorganic nanoparticles in human kidney cells after chronic exposure. <i>Cell Biology and Toxicology</i> , 2023, 39, 1939-1956.	5.3	1
2	miRNATissueAtlas2: an update to the human miRNA tissue atlas. <i>Nucleic Acids Research</i> , 2022, 50, D211-D221.	14.5	53
3	The <i>DCCR8</i> E518K mutation found in Wilms tumors leads to a partial miRNA processing defect that alters gene expression patterns and biological processes. <i>Carcinogenesis</i> , 2022, 43, 82-93.	2.8	6
4	Effects of Resistant Starch on Symptoms, Fecal Markers, and Gut Microbiota in Parkinson's Disease "The RESISTA-PD Trial. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 274-287.	6.9	26
5	Unspecific CTL Killing Is Enhanced by High Glucose via TNF-Related Apoptosis-Inducing Ligand. <i>Frontiers in Immunology</i> , 2022, 13, 831680.	4.8	0
6	A Temporary Pause in the Replication Licensing Restriction Leads to Rereplication during Early Human Cell Differentiation. <i>Cells</i> , 2022, 11, 1060.	4.1	1
7	Extracellular vesicles and PD-L1 suppress macrophages, inducing therapy resistance in <i>TP53</i> -deficient B-cell malignancies. <i>Blood</i> , 2022, 139, 3617-3629.	1.4	12
8	Emerging concepts of miRNA therapeutics: from cells to clinic. <i>Trends in Genetics</i> , 2022, 38, 613-626.	6.7	212
9	Altered Regulation of mRNA and miRNA Expression in Epithelial and Stromal Tissue of Keratoconus Corneas. , 2022, 63, 7.		7
10	Validation of human microRNA target pathways enables evaluation of target prediction tools. <i>Nucleic Acids Research</i> , 2021, 49, 127-144.	14.5	36
11	CoolMPS: evaluation of antibody labeling based massively parallel non-coding RNA sequencing. <i>Nucleic Acids Research</i> , 2021, 49, e10-e10.	14.5	10
12	Deep sequencing of sncRNAs reveals hallmarks and regulatory modules of the transcriptome during Parkinson's disease progression. <i>Nature Aging</i> , 2021, 1, 309-322.	11.6	26
13	MicroRNA-targeting in spermatogenesis: Overexpressions of microRNA-23a/b and its affected targeting of the genes <i>ODF2</i> and <i>UBQLN3</i> in spermatozoa of patients with oligoasthenozoospermia. <i>Andrology</i> , 2021, 9, 1137-1144.	3.5	18
14	Integrated microRNA and mRNA Expression Profiling Identifies Novel Targets and Networks Associated with Epstein's Anomaly. <i>Cells</i> , 2021, 10, 1066.	4.1	5
15	miRTargetLink 2.0 "interactive miRNA target gene and target pathway networks. <i>Nucleic Acids Research</i> , 2021, 49, W409-W416.	14.5	74
16	Characterization of micro-RNA in women with different ovarian reserve. <i>Scientific Reports</i> , 2021, 11, 13351.	3.3	9
17	GeneTrail: A Framework for the Analysis of High-Throughput Profiles. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 716544.	3.5	1
18	Chemoradiotherapy-induced increase in Th17 cell frequency in cervical cancer patients is associated with therapy resistance and early relapse. <i>Molecular Oncology</i> , 2021, 15, 3559-3577.	4.6	7

#	ARTICLE	IF	CITATIONS
19	Suppression of endothelial miR-22 mediates non-small cell lung cancer cell-induced angiogenesis. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 849-864.	5.1	7
20	A 10-year prediagnostic follow-up study shows that serum RNA signals are highly dynamic in lung carcinogenesis. <i>Molecular Oncology</i> , 2020, 14, 235-247.	4.6	16
21	miRPathDB 2.0: a novel release of the miRNA Pathway Dictionary Database. <i>Nucleic Acids Research</i> , 2020, 48, D142-D147.	14.5	138
22	What's the target: understanding two decades of <i>in silico</i> microRNA-target prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 1999-2010.	6.5	35
23	MicroRNA signature in spermatozoa and seminal plasma of proven fertile men and in testicular tissue of men with obstructive azoospermia. <i>Andrologia</i> , 2020, 52, e13503.	2.1	18
24	Quantitative and time-resolved miRNA pattern of early human T cell activation. <i>Nucleic Acids Research</i> , 2020, 48, 10164-10183.	14.5	12
25	Common diseases alter the physiological age-related blood microRNA profile. <i>Nature Communications</i> , 2020, 11, 5958.	12.8	46
26	Wrinkle in the plan: miR-34a-5p impacts chemokine signaling by modulating CXCL10/CXCL11/CXCR3-axis in CD4 ⁺ , CD8 ⁺ T cells, and M1 macrophages. , 2020, 8, e001617.		28
27	HumiR: Web Services, Tools and Databases for Exploring Human microRNA Data. <i>Biomolecules</i> , 2020, 10, 1576.	4.0	5
28	A multivariable miRNA signature delineates the systemic hemodynamic impact of arteriovenous shunt placement in a pilot study. <i>Scientific Reports</i> , 2020, 10, 21809.	3.3	5
29	miRSwitch: detecting microRNA arm shift and switch events. <i>Nucleic Acids Research</i> , 2020, 48, W268-W274.	14.5	20
30	Competitive learning suggests circulating miRNA profiles for cancers decades prior to diagnosis. <i>RNA Biology</i> , 2020, 17, 1416-1426.	3.1	10
31	Induction of the Endoplasmic-Reticulum-Stress Response: MicroRNA-34a Targeting of the IRE1 β -Branch. <i>Cells</i> , 2020, 9, 1442.	4.1	13
32	Evaluating the Use of Circulating MicroRNA Profiles for Lung Cancer Detection in Symptomatic Patients. <i>JAMA Oncology</i> , 2020, 6, 714.	7.1	84
33	MicroRNAs in combined spent culture media and sperm are associated with embryo quality and pregnancy outcome. <i>Fertility and Sterility</i> , 2020, 113, 970-980.e2.	1.0	33
34	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. <i>PLoS ONE</i> , 2020, 15, e0231402.	2.5	13
35	GeneTrail 3: advanced high-throughput enrichment analysis. <i>Nucleic Acids Research</i> , 2020, 48, W515-W520.	14.5	67
36	miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems. <i>Nucleic Acids Research</i> , 2020, 48, W521-W528.	14.5	136

#	ARTICLE	IF	CITATIONS
37	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. , 2020, 15, e0231402.		0
38	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. , 2020, 15, e0231402.		0
39	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. , 2020, 15, e0231402.		0
40	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. , 2020, 15, e0231402.		0
41	miR-34a as hub of T cell regulation networks. , 2019, 7, 187.		29
42	Profiling microRNA expression in murine bone healing and non-union formation: Role of miR-140 during the early stage of bone healing. PLoS ONE, 2019, 14, e0218395.	2.5	3
43	A human endogenous retrovirus encoded protease potentially cleaves numerous cellular proteins. Mobile DNA, 2019, 10, 36.	3.6	9
44	Systematic Assessment of Blood-Borne MicroRNAs Highlights Molecular Profiles of Endurance Sport and Carbohydrate Uptake. Cells, 2019, 8, 1045.	4.1	12
45	Low miR-150-5p and miR-320b Expression Predicts Reduced Survival of COPD Patients. Cells, 2019, 8, 1162.	4.1	26
46	MicroRNA profiling from dried blood samples. Critical Reviews in Clinical Laboratory Sciences, 2019, 56, 111-117.	6.1	13
47	Prospect and challenge of detecting dynamic gene copy number increases in stem cells by whole genome sequencing. Journal of Molecular Medicine, 2019, 97, 1099-1111.	3.9	2
48	Integrating Culture-based Antibiotic Resistance Profiles with Whole-genome Sequencing Data for 11,087 Clinical Isolates. Genomics, Proteomics and Bioinformatics, 2019, 17, 169-182.	6.9	8
49	Differential expression of miR-23a/b-3p and its target genes in male patients with subfertility. Fertility and Sterility, 2019, 112, 323-335.e2.	1.0	24
50	Spring is in the air: seasonal profiles indicate vernal change of miRNA activity. RNA Biology, 2019, 16, 1034-1043.	3.1	13
51	An estimate of the total number of true human miRNAs. Nucleic Acids Research, 2019, 47, 3353-3364.	14.5	400
52	The sncRNA Zoo: a repository for circulating small noncoding RNAs in animals. Nucleic Acids Research, 2019, 47, 4431-4441.	14.5	8
53	miR-34a: a new player in the regulation of T cell function by modulation of NF- κ B signaling. Cell Death and Disease, 2019, 10, 46.	6.3	58
54	Micro-RNA signatures in monozygotic twins discordant for congenital heart defects. PLoS ONE, 2019, 14, e0226164.	2.5	16

#	ARTICLE	IF	CITATIONS
55	Machine Learning to Detect Alzheimer's Disease from Circulating Non-coding RNAs. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 430-440.	6.9	67
56	The role of TCF3 as potential master regulator in blastemal Wilms tumors. <i>International Journal of Cancer</i> , 2019, 144, 1432-1443.	5.1	4
57	Large-scale validation of miRNAs by disease association, evolutionary conservation and pathway activity. <i>RNA Biology</i> , 2019, 16, 93-103.	3.1	5
58	MicroRNA-regulated pathways of flow-stimulated angiogenesis and vascular remodeling in vivo. <i>Journal of Translational Medicine</i> , 2019, 17, 22.	4.4	29
59	Acute Myeloid Leukemia Affects Mouse Sperm Parameters, Spontaneous Acrosome Reaction, and Fertility Capacity. <i>International Journal of Molecular Sciences</i> , 2019, 20, 219.	4.1	9
60	Small ncRNA-Seq Results of Human Tissues: Variations Depending on Sample Integrity. <i>Clinical Chemistry</i> , 2018, 64, 1074-1084.	3.2	4
61	A high-resolution map of the human small non-coding transcriptome. <i>Bioinformatics</i> , 2018, 34, 1621-1628.	4.1	24
62	Deregulated microRNA and mRNA expression profiles in the peripheral blood of patients with Marfan syndrome. <i>Journal of Translational Medicine</i> , 2018, 16, 60.	4.4	23
63	Characterization of micro-RNA Profile in the Blood of Patients with Marfan's Syndrome. <i>Thoracic and Cardiovascular Surgeon</i> , 2018, 66, 116-124.	1.0	13
64	miRCarta: a central repository for collecting miRNA candidates. <i>Nucleic Acids Research</i> , 2018, 46, D160-D167.	14.5	86
65	A comprehensive profile of circulating RNAs in human serum. <i>RNA Biology</i> , 2018, 15, 242-250.	3.1	117
66	IMOTA: an interactive multi-omics tissue atlas for the analysis of human miRNA-target interactions. <i>Nucleic Acids Research</i> , 2018, 46, D770-D775.	14.5	19
67	Micro-RNA-Regulated Proangiogenic Signaling in Arteriovenous Loops in Patients with Combined Vascular and Soft-Tissue Reconstructions: Revisiting the Nutrient Flap Concept. <i>Plastic and Reconstructive Surgery</i> , 2018, 142, 489e-502e.	1.4	10
68	Gene amplification in mesenchymal stem cells and during differentiation towards adipocytes or osteoblasts. <i>Oncotarget</i> , 2018, 9, 1803-1812.	1.8	7
69	Circulating small non-coding RNAs associated with age, sex, smoking, body mass and physical activity. <i>Scientific Reports</i> , 2018, 8, 17650.	3.3	31
70	Development of Spermatogenesis In Vitro in Three-Dimensional Culture from Spermatogonial Cells of Busulfan-Treated Immature Mice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3804.	4.1	29
71	Modulation of intracellular calcium signaling by microRNA-34a-5p. <i>Cell Death and Disease</i> , 2018, 9, 1008.	6.3	26
72	Genome-wide analysis of gene expression after one year of venom immunotherapy. <i>Immunology Letters</i> , 2018, 204, 23-28.	2.5	2

#	ARTICLE	IF	CITATIONS
73	Next Generation Sequencing Analysis of Total Small Noncoding RNAs from Low Input RNA from Dried Blood Sampling. <i>Analytical Chemistry</i> , 2018, 90, 11791-11796.	6.5	13
74	The deterministic role of 5-mers in microRNA-gene targeting. <i>RNA Biology</i> , 2018, 15, 1-7.	3.1	13
75	MicroRNA in diagnosis and therapy monitoring of early-stage triple-negative breast cancer. <i>Scientific Reports</i> , 2018, 8, 11584.	3.3	91
76	Transcriptional profiling of HERV-K(HML-2) in amyotrophic lateral sclerosis and potential implications for expression of HML-2 proteins. <i>Molecular Neurodegeneration</i> , 2018, 13, 39.	10.8	47
77	Genome-wide MicroRNA Expression Profiles in COPD: Early Predictors for Cancer Development. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 162-171.	6.9	33
78	REGGAE: a novel approach for the identification of key transcriptional regulators. <i>Bioinformatics</i> , 2018, 34, 3503-3510.	4.1	8
79	Amplified Host Defense by Toll-Like Receptor-Mediated Downregulation of the Glucocorticoid-Induced Leucine Zipper (GILZ) in Macrophages. <i>Frontiers in Immunology</i> , 2018, 9, 3111.	4.8	25
80	miRNAs in ancient tissue specimens of the Tyrolean Iceman. <i>Molecular Biology and Evolution</i> , 2017, 34, msw291.	8.9	17
81	Micro-ribonucleic acids and extracellular vesicles repertoire in the spent culture media is altered in women undergoing In Vitro Fertilization. <i>Scientific Reports</i> , 2017, 7, 13525.	3.3	46
82	Sources to variability in circulating human miRNA signatures. <i>RNA Biology</i> , 2017, 14, 1791-1798.	3.1	38
83	Bias in recent miRBase annotations potentially associated with RNA quality issues. <i>Scientific Reports</i> , 2017, 7, 5162.	3.3	46
84	Web-based NGS data analysis using miRMaster: a large-scale meta-analysis of human miRNAs. <i>Nucleic Acids Research</i> , 2017, 45, 8731-8744.	14.5	63
85	Technical Stability and Biological Variability in MicroRNAs from Dried Blood Spots: A Lung Cancer Therapy-Monitoring Showcase. <i>Clinical Chemistry</i> , 2017, 63, 1476-1488.	3.2	15
86	Differential expression of microRNAs following cardiopulmonary bypass in children with congenital heart diseases. <i>Journal of Translational Medicine</i> , 2017, 15, 117.	4.4	18
87	miRPathDB: a new dictionary on microRNAs and target pathways. <i>Nucleic Acids Research</i> , 2017, 45, D90-D96.	14.5	102
88	The miRNome of Alzheimer's disease: consistent downregulation of the miR-132/212 cluster. <i>Neurobiology of Aging</i> , 2017, 50, 167.e1-167.e10.	3.1	86
89	Analysis of circulating microRNAs in patients with repaired Tetralogy of Fallot with and without heart failure. <i>Journal of Translational Medicine</i> , 2017, 15, 156.	4.4	34
90	About miRNAs, miRNA seeds, target genes and target pathways. <i>Oncotarget</i> , 2017, 8, 107167-107175.	1.8	115

#	ARTICLE	IF	CITATIONS
91	MiR-34a-3p alters proliferation and apoptosis of meningioma cells in vitro and is directly targeting SMAD4, FRAT1 and BCL2. Aging, 2017, 9, 932-954.	3.1	35
92	Specific amplifications and copy number decreases during human neural stem cells differentiation towards astrocytes, neurons and oligodendrocytes. Oncotarget, 2017, 8, 25872-25884.	1.8	8
93	MiR-148a impairs Ras/ERK signaling in B lymphocytes by targeting SOS proteins. Oncotarget, 2017, 8, 56417-56427.	1.8	6
94	miRTargetLink™ miRNAs, Genes and Interaction Networks. International Journal of Molecular Sciences, 2016, 17, 564.	4.1	99
95	Combining miRNA and mRNA Expression Profiles in Wilms Tumor Subtypes. International Journal of Molecular Sciences, 2016, 17, 475.	4.1	61
96	Specific miRNA Disease Biomarkers in Blood, Serum and Plasma: Challenges and Prospects. Molecular Diagnosis and Therapy, 2016, 20, 509-518.	3.8	261
97	Can circulating miRNAs live up to the promise of being minimal invasive biomarkers in clinical settings?. Wiley Interdisciplinary Reviews RNA, 2016, 7, 148-156.	6.4	65
98	DrugTargetInspector: An assistance tool for patient treatment stratification. International Journal of Cancer, 2016, 138, 1765-1776.	5.1	8
99	miEAA: microRNA enrichment analysis and annotation. Nucleic Acids Research, 2016, 44, W110-W116.	14.5	146
100	Syntaxin 8 is required for efficient lytic granule trafficking in cytotoxic T lymphocytes. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 1653-1664.	4.1	20
101	Distribution of microRNA biomarker candidates in solid tissues and body fluids. RNA Biology, 2016, 13, 1084-1088.	3.1	74
102	miRNAs and sports: tracking training status and potentially confounding diagnoses. Journal of Translational Medicine, 2016, 14, 219.	4.4	31
103	Altered micro-ribonucleic acid expression profiles of extracellular microvesicles in the seminal plasma of patients with oligoasthenozoospermia. Fertility and Sterility, 2016, 106, 1061-1069.e3.	1.0	70
104	cPAS-based sequencing on the BGISEQ-500 to explore small non-coding RNAs. Clinical Epigenetics, 2016, 8, 123.	4.1	122
105	Validating Alzheimer's disease micro RNAs using next-generation sequencing. Alzheimer's and Dementia, 2016, 12, 565-576.	0.8	53
106	Multi-omics enrichment analysis using the GeneTrail2 web service. Bioinformatics, 2016, 32, 1502-1508.	4.1	144
107	Bias in High-Throughput Analysis of miRNAs and Implications for Biomarker Studies. Analytical Chemistry, 2016, 88, 2088-2095.	6.5	57
108	Characterization of miR-146a and miR-155 in blood, tissue and cell lines of head and neck squamous cell carcinoma patients and their impact on cell proliferation and migration. Journal of Cancer Research and Clinical Oncology, 2016, 142, 757-766.	2.5	33

#	ARTICLE	IF	CITATIONS
109	EDISON-WMW: Exact Dynamic Programming Solution of the Wilcoxon-Mann-Whitney Test. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 55-61.	6.9	109
110	Deep characterization of blood cell miRNomes by NGS. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 3169-3181.	5.4	15
111	Prioritizing and selecting likely novel miRNAs from NGS data. <i>Nucleic Acids Research</i> , 2016, 44, e53-e53.	14.5	52
112	Differential blood-based diagnosis between benign prostatic hyperplasia and prostate cancer: miRNA as source for biomarkers independent of PSA level, Gleason score, or TNM status. <i>Tumor Biology</i> , 2016, 37, 10177-10185.	1.8	41
113	BALL-SNP from genetic variants toward computational diagnostics. <i>Bioinformatics</i> , 2016, 32, 1888-1890.	4.1	0
114	Distribution of miRNA expression across human tissues. <i>Nucleic Acids Research</i> , 2016, 44, 3865-3877.	14.5	836
115	From Single Variants to Protein Cascades. <i>Journal of Biological Chemistry</i> , 2016, 291, 1582-1590.	3.4	2
116	Cardiac remodeling in $\text{G}\beta\text{q}$ and $\text{G}\beta\text{11}$ knockout mice. <i>International Journal of Cardiology</i> , 2016, 202, 836-845.	1.7	7
117	Human alveolar epithelial cells expressing tight junctions to model the air-blood barrier. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2016, 33, 251-60.	1.5	80
118	Paired proteomics, transcriptomics and miRNomics in non-small cell lung cancers: known and novel signaling cascades. <i>Oncotarget</i> , 2016, 7, 71514-71525.	1.8	8
119	High-throughput qRT-PCR validation of blood microRNAs in non-small cell lung cancer. <i>Oncotarget</i> , 2016, 7, 4611-4623.	1.8	65
120	Gene amplification during myogenic differentiation. <i>Oncotarget</i> , 2016, 7, 6864-6877.	1.8	14
121	Integrated quantitative proteomic and transcriptomic analysis of lung tumor and control tissue: a lung cancer showcase. <i>Oncotarget</i> , 2016, 7, 14857-14870.	1.8	17
122	Identification of miR-34a-target interactions by a combined network based and experimental approach. <i>Oncotarget</i> , 2016, 7, 34288-34299.	1.8	27
123	Next-generation sequencing identifies altered whole blood microRNAs in neuromyelitis optica spectrum disorder which may permit discrimination from multiple sclerosis. <i>Journal of Neuroinflammation</i> , 2015, 12, 196.	7.2	27
124	BALL-SNP: combining genetic and structural information to identify candidate non-synonymous single nucleotide polymorphisms. <i>Genome Medicine</i> , 2015, 7, 65.	8.2	9
125	Combination of Autoantibody Signature with PSA Level Enables a Highly Accurate Blood-Based Differentiation of Prostate Cancer Patients from Patients with Benign Prostatic Hyperplasia. <i>PLoS ONE</i> , 2015, 10, e0128235.	2.5	13
126	miFRame: analysis and visualization of miRNA sequencing data in neurological disorders. <i>Journal of Translational Medicine</i> , 2015, 13, 224.	4.4	10

#	ARTICLE	IF	CITATIONS
127	Differentially regulated miRNAs as prognostic biomarkers in the blood of primary CNS lymphoma patients. <i>European Journal of Cancer</i> , 2015, 51, 382-390.	2.8	31
128	A novel whole-blood miRNA signature for a rapid diagnosis of pulmonary tuberculosis. <i>European Respiratory Journal</i> , 2015, 45, 1173-1176.	6.7	58
129	Mutations in the SIX1/2 Pathway and the DROSHA/DGCR8 miRNA Microprocessor Complex Underlie High-Risk Blastemal Type Wilms Tumors. <i>Cancer Cell</i> , 2015, 27, 298-311.	16.8	248
130	MicroRNA In Vitro Diagnostics Using Immunoassay Analyzers. <i>Clinical Chemistry</i> , 2015, 61, 600-607.	3.2	29
131	Influence of Next-Generation Sequencing and Storage Conditions on miRNA Patterns Generated from PAXgene Blood. <i>Analytical Chemistry</i> , 2015, 87, 8910-8916.	6.5	22
132	Regulatory MicroRNA Networks: Complex Patterns of Target Pathways for Disease-related and Housekeeping MicroRNAs. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 159-168.	6.9	10
133	HERV-K(HML-2) rec and np9 transcripts not restricted to disease but present in many normal human tissues. <i>Mobile DNA</i> , 2015, 6, 4.	3.6	62
134	Circulating serum miRNAs as potential biomarkers for nephroblastoma. <i>Pediatric Blood and Cancer</i> , 2015, 62, 1360-1367.	1.5	56
135	Posttranscriptional deregulation of signaling pathways in meningioma subtypes by differential expression of miRNAs. <i>Neuro-Oncology</i> , 2015, 17, 1250-1260.	1.2	31
136	Towards Clinical Applications of Blood-Borne miRNA Signatures: The Influence of the Anticoagulant EDTA on miRNA Abundance. <i>PLoS ONE</i> , 2015, 10, e0143321.	2.5	23
137	New insights into the genetics of glioblastoma multiforme by familial exome sequencing. <i>Oncotarget</i> , 2015, 6, 5918-5931.	1.8	28
138	Gene amplification during differentiation of mammalian neural stem cells in vitro and in vivo. <i>Oncotarget</i> , 2015, 6, 7023-7039.	1.8	10
139	Longitudinal study on circulating miRNAs in patients after lung cancer resection. <i>Oncotarget</i> , 2015, 6, 16674-16685.	1.8	26
140	miRNAs can be generally associated with human pathologies as exemplified for miR-144*. <i>BMC Medicine</i> , 2014, 12, 224.	5.5	74
141	Secretion and Immunogenicity of the Meningioma-Associated Antigen TXNDC16. <i>Journal of Immunology</i> , 2014, 193, 3146-3154.	0.8	7
142	Panel of five microRNAs as potential biomarkers for the diagnosis and assessment of male infertility. <i>Fertility and Sterility</i> , 2014, 102, 989-997.e1.	1.0	113
143	Influence of the Confounding Factors Age and Sex on MicroRNA Profiles from Peripheral Blood. <i>Clinical Chemistry</i> , 2014, 60, 1200-1208.	3.2	84
144	MicroRNA expression profiles in human testicular tissues of infertile men with different histopathologic patterns. <i>Fertility and Sterility</i> , 2014, 101, 78-86.e2.	1.0	117

#	ARTICLE	IF	CITATIONS
145	Blood Born miRNAs Signatures that Can Serve as Disease Specific Biomarkers Are Not Significantly Affected by Overall Fitness and Exercise. PLoS ONE, 2014, 9, e102183.	2.5	21
146	What makes a blood cell based miRNA expression pattern disease specific? - A miRNome analysis of blood cell subsets in lung cancer patients and healthy controls. Oncotarget, 2014, 5, 9484-9497.	1.8	54
147	Detection of Human <i>c-Myc</i> and <i>EGFR</i> Amplifications in Circulating Extracellular Vesicles in Mouse Tumour Models. Journal of Circulating Biomarkers, 2014, 3, 6.	1.3	1
148	A blood based 12-miRNA signature of Alzheimer disease patients. Genome Biology, 2013, 14, R78.	9.6	438
149	Curcumin Intake Affects miRNA Signature in Murine Melanoma with mmu-miR-205-5p Most Significantly Altered. PLoS ONE, 2013, 8, e81122.	2.5	56
150	Genome-wide miRNA signatures of human longevity. Aging Cell, 2012, 11, 607-616.	6.7	131
151	Toward the blood-borne miRNome of human diseases. Nature Methods, 2011, 8, 841-843.	19.0	339
152	Stable serum miRNA profiles as potential tool for non-invasive lung cancer diagnosis. RNA Biology, 2011, 8, 506-516.	3.1	133
153	A dictionary on microRNAs and their putative target pathways. Nucleic Acids Research, 2010, 38, 4476-4486.	14.5	88
154	Lymphocyte-specific chemokine receptor CXCR3: regulation, chemokine binding and gene localization. European Journal of Immunology, 1998, 28, 3696-3705.	2.9	383
155	Lymphocyte-specific chemokine receptor CXCR3: regulation, chemokine binding and gene localization. , 1998, 28, 3696.		1
156	Enrichment of chromosome specific hncDNAs by magnetic bead coupled Alu sequences. Molecular Biology Reports, 1996, 22, 53-57.	2.3	1
157	Assignment of Alu-repetitive sequences to large restriction fragments from human chromosomes 6 and 22. Molecular Biology Reports, 1995, 21, 81-84.	2.3	0