Eckart Meese

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1230300/publications.pdf Version: 2024-02-01



FCKADT MEESE

#	Article	IF	CITATIONS
1	Distribution of miRNA expression across human tissues. Nucleic Acids Research, 2016, 44, 3865-3877.	14.5	836
2	A blood based 12-miRNA signature of Alzheimer disease patients. Genome Biology, 2013, 14, R78.	9.6	438
3	An estimate of the total number of true human miRNAs. Nucleic Acids Research, 2019, 47, 3353-3364.	14.5	400
4	Lymphocyte-specific chemokine receptor CXCR3: regulation, chemokine binding and gene localization. European Journal of Immunology, 1998, 28, 3696-3705.	2.9	383
5	Toward the blood-borne miRNome of human diseases. Nature Methods, 2011, 8, 841-843.	19.0	339
6	Specific miRNA Disease Biomarkers in Blood, Serum and Plasma: Challenges and Prospects. Molecular Diagnosis and Therapy, 2016, 20, 509-518.	3.8	261
7	Mutations in the SIX1/2 Pathway and the DROSHA/DGCR8 miRNA Microprocessor Complex Underlie High-Risk Blastemal Type Wilms Tumors. Cancer Cell, 2015, 27, 298-311.	16.8	248
8	Emerging concepts of miRNA therapeutics: from cells to clinic. Trends in Genetics, 2022, 38, 613-626.	6.7	212
9	miEAA: microRNA enrichment analysis and annotation. Nucleic Acids Research, 2016, 44, W110-W116.	14.5	146
10	Multi-omics enrichment analysis using the GeneTrail2 web service. Bioinformatics, 2016, 32, 1502-1508.	4.1	144
11	miRPathDB 2.0: a novel release of the miRNA Pathway Dictionary Database. Nucleic Acids Research, 2020, 48, D142-D147.	14.5	138
12	miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems. Nucleic Acids Research, 2020, 48, W521-W528.	14.5	136
13	Stable serum miRNA profiles as potential tool for non-invasive lung cancer diagnosis. RNA Biology, 2011, 8, 506-516.	3.1	133
14	Genomeâ€wide miRNA signatures of human longevity. Aging Cell, 2012, 11, 607-616.	6.7	131
15	cPAS-based sequencing on the BGISEQ-500 to explore small non-coding RNAs. Clinical Epigenetics, 2016, 8, 123.	4.1	122
16	MicroRNA expression profiles in human testicular tissues of infertile men with different histopathologic patterns. Fertility and Sterility, 2014, 101, 78-86.e2.	1.0	117
17	A comprehensive profile of circulating RNAs in human serum. RNA Biology, 2018, 15, 242-250.	3.1	117
18	About miRNAs, miRNA seeds, target genes and target pathways. Oncotarget, 2017, 8, 107167-107175.	1.8	115

#	Article	IF	CITATIONS
19	Panel of five microRNAs as potentialÂbiomarkers for the diagnosis and assessment of male infertility. Fertility and Sterility, 2014, 102, 989-997.e1.	1.0	113
20	EDISON-WMW: Exact Dynamic Programing Solution of the Wilcoxon–Mann–Whitney Test. Genomics, Proteomics and Bioinformatics, 2016, 14, 55-61.	6.9	109
21	miRPathDB: a new dictionary on microRNAs and target pathways. Nucleic Acids Research, 2017, 45, D90-D96.	14.5	102
22	miRTargetLink—miRNAs, Genes and Interaction Networks. International Journal of Molecular Sciences, 2016, 17, 564.	4.1	99
23	MicroRNA in diagnosis and therapy monitoring of early-stage triple-negative breast cancer. Scientific Reports, 2018, 8, 11584.	3.3	91
24	A dictionary on microRNAs and their putative target pathways. Nucleic Acids Research, 2010, 38, 4476-4486.	14.5	88
25	The miRNome of Alzheimer's disease: consistent downregulation of the miR-132/212 cluster. Neurobiology of Aging, 2017, 50, 167.e1-167.e10.	3.1	86
26	miRCarta: a central repository for collecting miRNA candidates. Nucleic Acids Research, 2018, 46, D160-D167.	14.5	86
27	Influence of the Confounding Factors Age and Sex on MicroRNA Profiles from Peripheral Blood. Clinical Chemistry, 2014, 60, 1200-1208.	3.2	84
28	Evaluating the Use of Circulating MicroRNA Profiles for Lung Cancer Detection in Symptomatic Patients. JAMA Oncology, 2020, 6, 714.	7.1	84
29	Human alveolar epithelial cells expressing tight junctions to model the air-blood barrier. ALTEX: Alternatives To Animal Experimentation, 2016, 33, 251-60.	1.5	80
30	miRNAs can be generally associated with human pathologies as exemplified for miR-144*. BMC Medicine, 2014, 12, 224.	5.5	74
31	Distribution of microRNA biomarker candidates in solid tissues and body fluids. RNA Biology, 2016, 13, 1084-1088.	3.1	74
32	miRTargetLink 2.0—interactive miRNA target gene and target pathway networks. Nucleic Acids Research, 2021, 49, W409-W416.	14.5	74
33	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
34	Machine Learning to Detect Alzheimer's Disease from Circulating Non-coding RNAs. Genomics, Proteomics and Bioinformatics, 2019, 17, 430-440.	6.9	67
35	GeneTrail 3: advanced high-throughput enrichment analysis. Nucleic Acids Research, 2020, 48, W515-W520.	14.5	67
36	Can circulating <scp>miRNAs</scp> live up to the promise of being minimal invasive biomarkers in clinical settings?. Wiley Interdisciplinary Reviews RNA, 2016, 7, 148-156.	6.4	65

#	Article	IF	CITATIONS
37	High-throughput qRT-PCR validation of blood microRNAs in non-small cell lung cancer. Oncotarget, 2016, 7, 4611-4623.	1.8	65
38	Web-based NGS data analysis using miRMaster: a large-scale meta-analysis of human miRNAs. Nucleic Acids Research, 2017, 45, 8731-8744.	14.5	63
39	HERV-K(HML-2) rec and np9 transcripts not restricted to disease but present in many normal human tissues. Mobile DNA, 2015, 6, 4.	3.6	62
40	Combining miRNA and mRNA Expression Profiles in Wilms Tumor Subtypes. International Journal of Molecular Sciences, 2016, 17, 475.	4.1	61
41	A novel whole-blood miRNA signature for a rapid diagnosis of pulmonary tuberculosis. European Respiratory Journal, 2015, 45, 1173-1176.	6.7	58
42	miR-34a: a new player in the regulation of T cell function by modulation of NF-κB signaling. Cell Death and Disease, 2019, 10, 46.	6.3	58
43	Bias in High-Throughput Analysis of miRNAs and Implications for Biomarker Studies. Analytical Chemistry, 2016, 88, 2088-2095.	6.5	57
44	Curcumin Intake Affects miRNA Signature in Murine Melanoma with mmu-miR-205-5p Most Significantly Altered. PLoS ONE, 2013, 8, e81122.	2.5	56
45	Circulating serum miRNAs as potential biomarkers for nephroblastoma. Pediatric Blood and Cancer, 2015, 62, 1360-1367.	1.5	56
46	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
47	Validating Alzheimer's disease micro RNAs using nextâ€generation sequencing. Alzheimer's and Dementia, 2016, 12, 565-576.	0.8	53
48	miRNATissueAtlas2: an update to the human miRNA tissue atlas. Nucleic Acids Research, 2022, 50, D211-D221.	14.5	53
49	Prioritizing and selecting likely novel miRNAs from NGS data. Nucleic Acids Research, 2016, 44, e53-e53.	14.5	52
50	Transcriptional profiling of HERV-K(HML-2) in amyotrophic lateral sclerosis and potential implications for expression of HML-2 proteins. Molecular Neurodegeneration, 2018, 13, 39.	10.8	47
51	Micro-ribonucleic acids and extracellular vesicles repertoire in the spent culture media is altered in women undergoing In Vitro Fertilization. Scientific Reports, 2017, 7, 13525.	3.3	46
52	Bias in recent miRBase annotations potentially associated with RNA quality issues. Scientific Reports, 2017, 7, 5162.	3.3	46
53	Common diseases alter the physiological age-related blood microRNA profile. Nature Communications, 2020, 11, 5958.	12.8	46
54	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. Tumor Biology, 2016, 37, 10177-10185.	1.8	41

#	Article	IF	CITATIONS
55	Sources to variability in circulating human miRNA signatures. RNA Biology, 2017, 14, 1791-1798.	3.1	38
56	Validation of human microRNA target pathways enables evaluation of target prediction tools. Nucleic Acids Research, 2021, 49, 127-144.	14.5	36
57	What's the target: understanding two decades of <i>in silico</i> microRNA-target prediction. Briefings in Bioinformatics, 2020, 21, 1999-2010.	6.5	35
58	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
59	Analysis of circulating microRNAs in patients with repaired Tetralogy of Fallot with and without heart failure. Journal of Translational Medicine, 2017, 15, 156.	4.4	34
60	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
61	Genome-wide MicroRNA Expression Profiles in COPD: Early Predictors for Cancer Development. Genomics, Proteomics and Bioinformatics, 2018, 16, 162-171.	6.9	33
62	MicroRNAs in combined spent culture media and sperm are associated with embryo quality and pregnancy outcome. Fertility and Sterility, 2020, 113, 970-980.e2.	1.0	33
63	Differentially regulated miRNAs as prognostic biomarkers in the blood of primary CNS lymphoma patients. European Journal of Cancer, 2015, 51, 382-390.	2.8	31
64	Posttranscriptional deregulation of signaling pathways in meningioma subtypes by differential expression of miRNAs. Neuro-Oncology, 2015, 17, 1250-1260.	1.2	31
65	miRNAs and sports: tracking training status and potentially confounding diagnoses. Journal of Translational Medicine, 2016, 14, 219.	4.4	31
66	Circulating small non-coding RNAs associated with age, sex, smoking, body mass and physical activity. Scientific Reports, 2018, 8, 17650.	3.3	31
67	MicroRNA In Vitro Diagnostics Using Immunoassay Analyzers. Clinical Chemistry, 2015, 61, 600-607.	3.2	29
68	Development of Spermatogenesis In Vitro in Three-Dimensional Culture from Spermatogonial Cells of Busulfan-Treated Immature Mice. International Journal of Molecular Sciences, 2018, 19, 3804.	4.1	29
69	miR-34a as hub of T cell regulation networks. , 2019, 7, 187.		29
70	MicroRNA-regulated pathways of flow-stimulated angiogenesis and vascular remodeling in vivo. Journal of Translational Medicine, 2019, 17, 22.	4.4	29
71	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
72	New insights into the genetics of glioblastoma multiforme by familial exome sequencing. Oncotarget, 2015, 6, 5918-5931.	1.8	28

#	Article	IF	CITATIONS
73	Next-generation sequencing identifies altered whole blood microRNAs in neuromyelitis optica spectrum disorder which may permit discrimination from multiple sclerosis. Journal of Neuroinflammation, 2015, 12, 196.	7.2	27
74	Identification of miR-34a-target interactions by a combined network based and experimental approach. Oncotarget, 2016, 7, 34288-34299.	1.8	27
75	Modulation of intracellular calcium signaling by microRNA-34a-5p. Cell Death and Disease, 2018, 9, 1008.	6.3	26
76	Low miR-150-5p and miR-320b Expression Predicts Reduced Survival of COPD Patients. Cells, 2019, 8, 1162.	4.1	26
77	Deep sequencing of sncRNAs reveals hallmarks and regulatory modules of the transcriptome during Parkinson's disease progression. Nature Aging, 2021, 1, 309-322.	11.6	26
78	Longitudinal study on circulating miRNAs in patients after lung cancer resection. Oncotarget, 2015, 6, 16674-16685.	1.8	26
79	Effects of Resistant Starch on Symptoms, Fecal Markers, and Gut Microbiota in Parkinson's Disease — The RESISTA-PD Trial. Genomics, Proteomics and Bioinformatics, 2022, 20, 274-287.	6.9	26
80	Amplified Host Defense by Toll-Like Receptor-Mediated Downregulation of the Glucocorticoid-Induced Leucine Zipper (GILZ) in Macrophages. Frontiers in Immunology, 2018, 9, 3111.	4.8	25
81	A high-resolution map of the human small non-coding transcriptome. Bioinformatics, 2018, 34, 1621-1628.	4.1	24
82	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
83	Deregulated microRNA and mRNA expression profiles in the peripheral blood of patients with Marfan syndrome. Journal of Translational Medicine, 2018, 16, 60.	4.4	23
84	Towards Clinical Applications of Blood-Borne miRNA Signatures: The Influence of the Anticoagulant EDTA on miRNA Abundance. PLoS ONE, 2015, 10, e0143321.	2.5	23
85	Influence of Next-Generation Sequencing and Storage Conditions on miRNA Patterns Generated from PAXgene Blood. Analytical Chemistry, 2015, 87, 8910-8916.	6.5	22
86	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
87	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
88	miRSwitch: detecting microRNA arm shift and switch events. Nucleic Acids Research, 2020, 48, W268-W274.	14.5	20
89	IMOTA: an interactive multi-omics tissue atlas for the analysis of human miRNA–target interactions. Nucleic Acids Research, 2018, 46, D770-D775.	14.5	19
90	Differential expression of microRNAs following cardiopulmonary bypass in children with congenital heart diseases. Journal of Translational Medicine, 2017, 15, 117.	4.4	18

#	Article	IF	CITATIONS
91	MicroRNA signature in spermatozoa and seminal plasma of proven fertile men and in testicular tissue of men with obstructive azoospermia. Andrologia, 2020, 52, e13503.	2.1	18
92	MicroRNAâ€ŧargeting in spermatogenesis: Overâ€expressions of microRNAâ€23a/bâ€3p and its affected targeting of the genes <i>ODF2</i> and <i>UBQLN3</i> in spermatozoa of patients with oligoasthenozoospermia. Andrology, 2021, 9, 1137-1144.	3.5	18
93	miRNAs in ancient tissue specimens of the Tyrolean Iceman. Molecular Biology and Evolution, 2017, 34, msw291.	8.9	17
94	Integrated quantitative proteomic and transcriptomic analysis of lung tumor and control tissue: a lung cancer showcase. Oncotarget, 2016, 7, 14857-14870.	1.8	17
95	Micro-RNA signatures in monozygotic twins discordant for congenital heart defects. PLoS ONE, 2019, 14, e0226164.	2.5	16
96	A 10â€year prediagnostic followâ€up study shows that serum RNA signals are highly dynamic in lung carcinogenesis. Molecular Oncology, 2020, 14, 235-247.	4.6	16
97	Deep characterization of blood cell miRNomes by NGS. Cellular and Molecular Life Sciences, 2016, 73, 3169-3181.	5.4	15
98	Technical Stability and Biological Variability in MicroRNAs from Dried Blood Spots: A Lung Cancer Therapy-Monitoring Showcase. Clinical Chemistry, 2017, 63, 1476-1488.	3.2	15
99	Gene amplification during myogenic differentiation. Oncotarget, 2016, 7, 6864-6877.	1.8	14
100	Combination of Autoantibody Signature with PSA Level Enables a Highly Accurate Blood-Based Differentiation of Prostate Cancer Patients from Patients with Benign Prostatic Hyperplasia. PLoS ONE, 2015, 10, e0128235.	2.5	13
101	Characterization of micro-RNA Profile in the Blood of Patients with Marfan's Syndrome. Thoracic and Cardiovascular Surgeon, 2018, 66, 116-124.	1.0	13
102	Next Generation Sequencing Analysis of Total Small Noncoding RNAs from Low Input RNA from Dried Blood Sampling. Analytical Chemistry, 2018, 90, 11791-11796.	6.5	13
103	The deterministic role of 5-mers in microRNA-gene targeting. RNA Biology, 2018, 15, 1-7.	3.1	13
104	MicroRNA profiling from dried blood samples. Critical Reviews in Clinical Laboratory Sciences, 2019, 56, 111-117.	6.1	13
105	Spring is in the air: seasonal profiles indicate vernal change of miRNA activity. RNA Biology, 2019, 16, 1034-1043.	3.1	13
106	Induction of the Endoplasmic-Reticulum-Stress Response: MicroRNA-34a Targeting of the IRE1α-Branch. Cells, 2020, 9, 1442.	4.1	13
107	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. PLoS ONE, 2020, 15, e0231402.	2.5	13
108	Systematic Assessment of Blood-Borne MicroRNAs Highlights Molecular Profiles of Endurance Sport and Carbohydrate Uptake. Cells, 2019, 8, 1045.	4.1	12

#	Article	IF	CITATIONS
109	Quantitative and time-resolved miRNA pattern of early human T cell activation. Nucleic Acids Research, 2020, 48, 10164-10183.	14.5	12
110	Extracellular vesicles and PD-L1 suppress macrophages, inducing therapy resistance in <i>TP53</i> -deficient B-cell malignancies. Blood, 2022, 139, 3617-3629.	1.4	12
111	miFRame: analysis and visualization of miRNA sequencing data in neurological disorders. Journal of Translational Medicine, 2015, 13, 224.	4.4	10
112	Regulatory MicroRNA Networks: Complex Patterns of Target Pathways for Disease-related and Housekeeping MicroRNAs. Genomics, Proteomics and Bioinformatics, 2015, 13, 159-168.	6.9	10
113	Micro-RNA–Regulated Proangiogenic Signaling in Arteriovenous Loops in Patients with Combined Vascular and Soft-Tissue Reconstructions: Revisiting the Nutrient Flap Concept. Plastic and Reconstructive Surgery, 2018, 142, 489e-502e.	1.4	10
114	Competitive learning suggests circulating miRNA profiles for cancers decades prior to diagnosis. RNA Biology, 2020, 17, 1416-1426.	3.1	10
115	CoolMPS: evaluation of antibody labeling based massively parallel non-coding RNA sequencing. Nucleic Acids Research, 2021, 49, e10-e10.	14.5	10
116	Gene amplification during differentiation of mammalian neural stem cellsin vitroandin vivo. Oncotarget, 2015, 6, 7023-7039.	1.8	10
117	BALL-SNP: combining genetic and structural information to identify candidate non-synonymous single nucleotide polymorphisms. Genome Medicine, 2015, 7, 65.	8.2	9
118	A human endogenous retrovirus encoded protease potentially cleaves numerous cellular proteins. Mobile DNA, 2019, 10, 36.	3.6	9
119	Acute Myeloid Leukemia Affects Mouse Sperm Parameters, Spontaneous Acrosome Reaction, and Fertility Capacity. International Journal of Molecular Sciences, 2019, 20, 219.	4.1	9
120	Characterization of micro-RNA in women with different ovarian reserve. Scientific Reports, 2021, 11, 13351.	3.3	9
121	Drug <scp>T</scp> arget <scp>I</scp> nspector: An assistance tool for patient treatment stratification. International Journal of Cancer, 2016, 138, 1765-1776.	5.1	8
122	REGGAE: a novel approach for the identification of key transcriptional regulators. Bioinformatics, 2018, 34, 3503-3510.	4.1	8
123	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
124	The sncRNA Zoo: a repository for circulating small noncoding RNAs in animals. Nucleic Acids Research, 2019, 47, 4431-4441.	14.5	8
125	Paired proteomics, transcriptomics and miRNomics in non-small cell lung cancers: known and novel signaling cascades. Oncotarget, 2016, 7, 71514-71525.	1.8	8
126	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

#	Article	IF	CITATIONS
127	Secretion and Immunogenicity of the Meningioma-Associated Antigen TXNDC16. Journal of Immunology, 2014, 193, 3146-3154.	0.8	7
128	Cardiac remodeling in Gαq and Gα11 knockout mice. International Journal of Cardiology, 2016, 202, 836-845.	1.7	7
129	Gene amplification in mesenchymal stem cells and during differentiation towards adipocytes or osteoblasts. Oncotarget, 2018, 9, 1803-1812.	1.8	7
130	Chemoradiotherapyâ€induced increase in Th17 cell frequency in cervical cancer patients is associated with therapy resistance and early relapse. Molecular Oncology, 2021, 15, 3559-3577.	4.6	7
131	Suppression of endothelial miR-22 mediates non-small cell lung cancer cell-induced angiogenesis. Molecular Therapy - Nucleic Acids, 2021, 26, 849-864.	5.1	7
132	Altered Regulation of mRNA and miRNA Expression in Epithelial and Stromal Tissue of Keratoconus Corneas. , 2022, 63, 7.		7
133	MiR-148a impairs Ras/ERK signaling in B lymphocytes by targeting SOS proteins. Oncotarget, 2017, 8, 56417-56427.	1.8	6
134	The <i>DGCR8</i> E518K mutation found in Wilms tumors leads to a partial miRNA processing defect that alters gene expression patterns and biological processes. Carcinogenesis, 2022, 43, 82-93.	2.8	6
135	Large-scale validation of miRNAs by disease association, evolutionary conservation and pathway activity. RNA Biology, 2019, 16, 93-103.	3.1	5
136	HumiR: Web Services, Tools and Databases for Exploring Human microRNA Data. Biomolecules, 2020, 10, 1576.	4.0	5
137	A multivariable miRNA signature delineates the systemic hemodynamic impact of arteriovenous shunt placement in a pilot study. Scientific Reports, 2020, 10, 21809.	3.3	5
138	Integrated microRNA and mRNA Expression Profiling Identifies Novel Targets and Networks Associated with Ebstein's Anomaly. Cells, 2021, 10, 1066.	4.1	5
139	Small ncRNA-Seq Results of Human Tissues: Variations Depending on Sample Integrity. Clinical Chemistry, 2018, 64, 1074-1084.	3.2	4
140	The role of TCF3 as potential master regulator in blastemal Wilms tumors. International Journal of Cancer, 2019, 144, 1432-1443.	5.1	4
141	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
142	From Single Variants to Protein Cascades. Journal of Biological Chemistry, 2016, 291, 1582-1590.	3.4	2
143	Genome-wide analysis of gene expression after one year of venom immunotherapy. Immunology Letters, 2018, 204, 23-28.	2.5	2
144	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

#	Article	IF	CITATIONS
145	Enrichment of chromosome specific hncDNAs by magnetic bead coupled Alu sequences. Molecular Biology Reports, 1996, 22, 53-57.	2.3	1
146	GeneTrail: A Framework for the Analysis of High-Throughput Profiles. Frontiers in Molecular Biosciences, 2021, 8, 716544.	3.5	1
147	Lymphocyte-specific chemokine receptor CXCR3: regulation, chemokine binding and gene localization. , 1998, 28, 3696.		1
148	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
149	Genome-wide DNA methylome and transcriptome changes induced by inorganic nanoparticles in human kidney cells after chronic exposure. Cell Biology and Toxicology, 2023, 39, 1939-1956.	5.3	1
150	A Temporary Pause in the Replication Licensing Restriction Leads to Rereplication during Early Human Cell Differentiation. Cells, 2022, 11, 1060.	4.1	1
151	Assignment of Alu-repetitive sequences to large restriction fragments from human chromosomes 6 and 22. Molecular Biology Reports, 1995, 21, 81-84.	2.3	Ο
152	BALL-SNPgp—from genetic variants toward computational diagnostics. Bioinformatics, 2016, 32, 1888-1890.	4.1	0
153	Unspecific CTL Killing Is Enhanced by High Glucose via TNF-Related Apoptosis-Inducing Ligand. Frontiers in Immunology, 2022, 13, 831680.	4.8	0
154	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. , 2020, 15, e0231402.		0
155	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. , 2020, 15, e0231402.		0
156	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. , 2020, 15, e0231402.		0
157	Insights from circulating microRNAs in cardiovascular entities in turner syndrome patients. , 2020, 15, e0231402.		0