

# Christina Backes

## List of Publications by Year in descending order

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Version: 2024-02-01

75  
papers

5,958  
citations

87723

38  
h-index

76769

74  
g-index

83  
all docs

83  
docs citations

83  
times ranked

10110  
citing authors

#	ARTICLE	IF	CITATIONS
1	Validation of human microRNA target pathways enables evaluation of target prediction tools. <i>Nucleic Acids Research</i> , 2021, 49, 127-144.	6.5	36
2	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.	5.3	26
3	miRMaster 2.0: multi-species non-coding RNA sequencing analyses at scale. <i>Nucleic Acids Research</i> , 2021, 49, W397-W408.	6.5	12
4	miRPathDB 2.0: a novel release of the miRNA Pathway Dictionary Database. <i>Nucleic Acids Research</i> , 2020, 48, D142-D147.	6.5	138
5	What's the target: understanding two decades of <i>in silico</i> microRNA-target prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 1999-2010.	3.2	35
6	Common diseases alter the physiological age-related blood microRNA profile. <i>Nature Communications</i> , 2020, 11, 5958.	5.8	46
7	miRSwitch: detecting microRNA arm shift and switch events. <i>Nucleic Acids Research</i> , 2020, 48, W268-W274.	6.5	20
8	Competitive learning suggests circulating miRNA profiles for cancers decades prior to diagnosis. <i>RNA Biology</i> , 2020, 17, 1416-1426.	1.5	10
9	Cigarette smoke and electronic cigarettes differentially activate bronchial epithelial cells. <i>Respiratory Research</i> , 2020, 21, 67.	1.4	33
10	Evaluating the Use of Circulating MicroRNA Profiles for Lung Cancer Detection in Symptomatic Patients. <i>JAMA Oncology</i> , 2020, 6, 714.	3.4	84
11	miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems. <i>Nucleic Acids Research</i> , 2020, 48, W521-W528.	6.5	136
12	Systematic Assessment of Blood-Borne MicroRNAs Highlights Molecular Profiles of Endurance Sport and Carbohydrate Uptake. <i>Cells</i> , 2019, 8, 1045.	1.8	12
13	Integrating Culture-based Antibiotic Resistance Profiles with Whole-genome Sequencing Data for 11,087 Clinical Isolates. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 169-182.	3.0	8
14	Spring is in the air: seasonal profiles indicate vernal change of miRNA activity. <i>RNA Biology</i> , 2019, 16, 1034-1043.	1.5	13
15	ClinOmicsTrailbc: a visual analytics tool for breast cancer treatment stratification. <i>Bioinformatics</i> , 2019, 35, 5171-5181.	1.8	11
16	An estimate of the total number of true human miRNAs. <i>Nucleic Acids Research</i> , 2019, 47, 3353-3364.	6.5	400
17	The sncRNA Zoo: a repository for circulating small noncoding RNAs in animals. <i>Nucleic Acids Research</i> , 2019, 47, 4431-4441.	6.5	8
18	DynaVenn: web-based computation of the most significant overlap between ordered sets. <i>BMC Bioinformatics</i> , 2019, 20, 743.	1.2	18

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19	Machine Learning to Detect Alzheimer's Disease from Circulating Non-coding RNAs. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 430-440.	3.0	67
20	Large-scale validation of miRNAs by disease association, evolutionary conservation and pathway activity. <i>RNA Biology</i> , 2019, 16, 93-103.	1.5	5
21	Comparing genome versus proteome-based identification of clinical bacterial isolates. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw122.	3.2	7
22	Small ncRNA-Seq Results of Human Tissues: Variations Depending on Sample Integrity. <i>Clinical Chemistry</i> , 2018, 64, 1074-1084.	1.5	4
23	A high-resolution map of the human small non-coding transcriptome. <i>Bioinformatics</i> , 2018, 34, 1621-1628.	1.8	24
24	miRCarta: a central repository for collecting miRNA candidates. <i>Nucleic Acids Research</i> , 2018, 46, D160-D167.	6.5	86
25	The deterministic role of 5-mers in microRNA-gene targeting. <i>RNA Biology</i> , 2018, 15, 1-7.	1.5	13
26	Genome-wide MicroRNA Expression Profiles in COPD: Early Predictors for Cancer Development. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 162-171.	3.0	33
27	miRNAs in ancient tissue specimens of the Tyrolean Iceman. <i>Molecular Biology and Evolution</i> , 2017, 34, msw291.	3.5	17
28	BusyBee Web: metagenomic data analysis by bootstrapped supervised binning and annotation. <i>Nucleic Acids Research</i> , 2017, 45, W171-W179.	6.5	84
29	Sources to variability in circulating human miRNA signatures. <i>RNA Biology</i> , 2017, 14, 1791-1798.	1.5	38
30	Web-based NGS data analysis using miRMaster: a large-scale meta-analysis of human miRNAs. <i>Nucleic Acids Research</i> , 2017, 45, 8731-8744.	6.5	63
31	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.	1.5	15
32	miRPathDB: a new dictionary on microRNAs and target pathways. <i>Nucleic Acids Research</i> , 2017, 45, D90-D96.	6.5	102
33	About miRNAs, miRNA seeds, target genes and target pathways. <i>Oncotarget</i> , 2017, 8, 107167-107175.	0.8	115
34	miRTargetLink's miRNAs, Genes and Interaction Networks. <i>International Journal of Molecular Sciences</i> , 2016, 17, 564.	1.8	99
35	Combining miRNA and mRNA Expression Profiles in Wilms Tumor Subtypes. <i>International Journal of Molecular Sciences</i> , 2016, 17, 475.	1.8	61
36	Specific miRNA Disease Biomarkers in Blood, Serum and Plasma: Challenges and Prospects. <i>Molecular Diagnosis and Therapy</i> , 2016, 20, 509-518.	1.6	261

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37	miEAA: microRNA enrichment analysis and annotation. <i>Nucleic Acids Research</i> , 2016, 44, W110-W116.	6.5	146
38	Distribution of microRNA biomarker candidates in solid tissues and body fluids. <i>RNA Biology</i> , 2016, 13, 1084-1088.	1.5	74
39	miRNAs and sports: tracking training status and potentially confounding diagnoses. <i>Journal of Translational Medicine</i> , 2016, 14, 219.	1.8	31
40	cPAS-based sequencing on the BGISEQ-500 to explore small non-coding RNAs. <i>Clinical Epigenetics</i> , 2016, 8, 123.	1.8	122
41	Validating Alzheimer's disease micro RNAs using next-generation sequencing. <i>Alzheimer's and Dementia</i> , 2016, 12, 565-576.	0.4	53
42	Multi-omics enrichment analysis using the GeneTrail2 web service. <i>Bioinformatics</i> , 2016, 32, 1502-1508.	1.8	144
43	Bias in High-Throughput Analysis of miRNAs and Implications for Biomarker Studies. <i>Analytical Chemistry</i> , 2016, 88, 2088-2095.	3.2	57
44	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. <i>Journal of Cancer Research and Clinical Oncology</i> , 2016, 142, 757-766.	1.2	33
45	EDISON-WMW: Exact Dynamic Programming Solution of the Wilcoxon-Mann-Whitney Test. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 55-61.	3.0	109
46	Deep characterization of blood cell miRNomes by NGS. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 3169-3181.	2.4	15
47	Prioritizing and selecting likely novel miRNAs from NGS data. <i>Nucleic Acids Research</i> , 2016, 44, e53-e53.	6.5	52
48	Distribution of miRNA expression across human tissues. <i>Nucleic Acids Research</i> , 2016, 44, 3865-3877.	6.5	836
49	Cardiac remodeling in $G\beta q$ and $G\beta 11$ knockout mice. <i>International Journal of Cardiology</i> , 2016, 202, 836-845.	0.8	7
50	High-throughput qRT-PCR validation of blood microRNAs in non-small cell lung cancer. <i>Oncotarget</i> , 2016, 7, 4611-4623.	0.8	65
51	Identification of miR-34a-target interactions by a combined network based and experimental approach. <i>Oncotarget</i> , 2016, 7, 34288-34299.	0.8	27
52	Differentially regulated miRNAs as prognostic biomarkers in the blood of primary CNS lymphoma patients. <i>European Journal of Cancer</i> , 2015, 51, 382-390.	1.3	31
53	MicroRNA In Vitro Diagnostics Using Immunoassay Analyzers. <i>Clinical Chemistry</i> , 2015, 61, 600-607.	1.5	29
54	Influence of Next-Generation Sequencing and Storage Conditions on miRNA Patterns Generated from PAXgene Blood. <i>Analytical Chemistry</i> , 2015, 87, 8910-8916.	3.2	22

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55	Regulatory MicroRNA Networks: Complex Patterns of Target Pathways for Disease-related and Housekeeping MicroRNAs. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 159-168.	3.0	10
56	Circulating serum miRNAs as potential biomarkers for nephroblastoma. <i>Pediatric Blood and Cancer</i> , 2015, 62, 1360-1367.	0.8	56
57	RNA splicing regulated by RBFOX1 is essential for cardiac function in zebrafish. <i>Journal of Cell Science</i> , 2015, 128, 3030-40.	1.2	16
58	Posttranscriptional deregulation of signaling pathways in meningioma subtypes by differential expression of miRNAs. <i>Neuro-Oncology</i> , 2015, 17, 1250-1260.	0.6	31
59	Towards Clinical Applications of Blood-Borne miRNA Signatures: The Influence of the Anticoagulant EDTA on miRNA Abundance. <i>PLoS ONE</i> , 2015, 10, e0143321.	1.1	23
60	Gene amplification during differentiation of mammalian neural stem cells in vitro and in vivo. <i>Oncotarget</i> , 2015, 6, 7023-7039.	0.8	10
61	miRNAs can be generally associated with human pathologies as exemplified for miR-144*. <i>BMC Medicine</i> , 2014, 12, 224.	2.3	74
62	Secretion and Immunogenicity of the Meningioma-Associated Antigen TXNDC16. <i>Journal of Immunology</i> , 2014, 193, 3146-3154.	0.4	7
63	Comprehensive analysis of microRNA profiles in multiple sclerosis including next-generation sequencing. <i>Multiple Sclerosis Journal</i> , 2014, 20, 295-303.	1.4	115
64	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.	0.5	113
65	Influence of the Confounding Factors Age and Sex on MicroRNA Profiles from Peripheral Blood. <i>Clinical Chemistry</i> , 2014, 60, 1200-1208.	1.5	84
66	MicroRNA expression profiles in human testicular tissues of infertile men with different histopathologic patterns. <i>Fertility and Sterility</i> , 2014, 101, 78-86.e2.	0.5	117
67	Blood Born miRNAs Signatures that Can Serve as Disease Specific Biomarkers Are Not Significantly Affected by Overall Fitness and Exercise. <i>PLoS ONE</i> , 2014, 9, e102183.	1.1	21
68	A blood based 12-miRNA signature of Alzheimer disease patients. <i>Genome Biology</i> , 2013, 14, R78.	13.9	438
69	Curcumin Intake Affects miRNA Signature in Murine Melanoma with mmu-miR-205-5p Most Significantly Altered. <i>PLoS ONE</i> , 2013, 8, e81122.	1.1	56
70	An integer linear programming approach for finding deregulated subgraphs in regulatory networks. <i>Nucleic Acids Research</i> , 2012, 40, e43-e43.	6.5	84
71	Genome-wide miRNA signatures of human longevity. <i>Aging Cell</i> , 2012, 11, 607-616.	3.0	131
72	Toward the blood-borne miRNome of human diseases. <i>Nature Methods</i> , 2011, 8, 841-843.	9.0	339

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73	A dictionary on microRNAs and their putative target pathways. <i>Nucleic Acids Research</i> , 2010, 38, 4476-4486.	6.5	88
74	Computation of significance scores of unweighted Gene Set Enrichment Analyses. <i>BMC Bioinformatics</i> , 2007, 8, 290.	1.2	46
75	GraBCas: a bioinformatics tool for score-based prediction of Caspase- and Granzyme B-cleavage sites in protein sequences. <i>Nucleic Acids Research</i> , 2005, 33, W208-W213.	6.5	95