

# Bastian Fromm

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

2,738  
citations

236925

25  
h-index

197818

49  
g-index

71  
all docs

71  
docs citations

71  
times ranked

4090  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Uniform System for the Annotation of Vertebrate microRNA Genes and the Evolution of the Human microRNAome. <i>Annual Review of Genetics</i> , 2015, 49, 213-242.	7.6	467
2	MirGeneDB 2.0: the metazoan microRNA complement. <i>Nucleic Acids Research</i> , 2020, 48, D132-D141.	14.5	194
3	Identification of non-invasive miRNAs biomarkers for prostate cancer by deep sequencing analysis of urinary exosomes. <i>Molecular Cancer</i> , 2017, 16, 156.	19.2	188
4	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	14.5	160
5	sRNAbench and sRNAtoolbox 2019: intuitive fast small RNA profiling and differential expression. <i>Nucleic Acids Research</i> , 2019, 47, W530-W535.	14.5	136
6	A comprehensive profile of circulating RNAs in human serum. <i>RNA Biology</i> , 2018, 15, 242-250.	3.1	117
7	Exploration of extracellular vesicles from <i>Ascaris suum</i> provides evidence of parasite-host cross talk. <i>Journal of Extracellular Vesicles</i> , 2019, 8, 1578116.	12.2	103
8	Substantial Loss of Conserved and Gain of Novel MicroRNA Families in Flatworms. <i>Molecular Biology and Evolution</i> , 2013, 30, 2619-2628.	8.9	84
9	The Long Noncoding RNA CCAT2 Induces Chromosomal Instability Through BOP1-AURKB Signaling. <i>Gastroenterology</i> , 2020, 159, 2146-2162.e33.	1.3	75
10	Comparative Genomics of Flatworms (Platyhelminthes) Reveals Shared Genomic Features of Ecto- and Endoparasitic Neodermata. <i>Genome Biology and Evolution</i> , 2014, 6, 1105-1117.	2.5	73
11	The revised microRNA complement of <i>Fasciola hepatica</i> reveals a plethora of overlooked microRNAs and evidence for enrichment of immuno-regulatory microRNAs in extracellular vesicles. <i>International Journal for Parasitology</i> , 2015, 45, 697-702.	3.1	64
12	MirGeneDB 2.1: toward a complete sampling of all major animal phyla. <i>Nucleic Acids Research</i> , 2022, 50, D204-D210.	14.5	63
13	On the presence and immunoregulatory functions of extracellular microRNAs in the trematode <i>Fasciola hepatica</i> . <i>Parasite Immunology</i> , 2017, 39, e12399.	1.5	59
14	Subtype-specific microRNA expression signatures in breast cancer progression. <i>International Journal of Cancer</i> , 2016, 139, 1117-1128.	5.1	53
15	Common diseases alter the physiological age-related blood microRNA profile. <i>Nature Communications</i> , 2020, 11, 5958.	12.8	46
16	miRTrace reveals the organismal origins of microRNA sequencing data. <i>Genome Biology</i> , 2018, 19, 213.	8.8	44
17	Unicellular Origin of the Animal MicroRNA Machinery. <i>Current Biology</i> , 2018, 28, 3288-3295.e5.	3.9	42
18	Base-pair conformational switch modulates miR-34a targeting of Sirt1 mRNA. <i>Nature</i> , 2020, 583, 139-144.	27.8	42

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19	Well-Annotated microRNAs Do Not Evidence Pervasive miRNA Loss. <i>Genome Biology and Evolution</i> , 2018, 10, 1457-1470.	2.5	41
20	A proteomic approach for studying insect phylogeny: CAPA peptides of ancient insect taxa (Dictyoptera, Blattoptera) as a test case. <i>BMC Evolutionary Biology</i> , 2009, 9, 50.	3.2	40
21	The microRNA toolkit of insects. <i>Scientific Reports</i> , 2016, 6, 37736.	3.3	40
22	Atp8 is in the ground pattern of flatworm mitochondrial genomes. <i>BMC Genomics</i> , 2017, 18, 414.	2.8	35
23	Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. <i>Cell Reports</i> , 2020, 33, 108448.	6.4	35
24	Unification of miRNA and isomiR research: the mirGFF3 format and the mirtop API. <i>Bioinformatics</i> , 2020, 36, 698-703.	4.1	33
25	Big Strides in Cellular MicroRNA Expression. <i>Trends in Genetics</i> , 2018, 34, 165-167.	6.7	32
26	Large scale changes in the transcriptome of <i>Eisenia fetida</i> during regeneration. <i>PLoS ONE</i> , 2018, 13, e0204234.	2.5	31
27	Human and Cow Have Identical miR-21-5p and miR-30a-5p Sequences, Which Are Likely Unsuitable to Study Dietary Uptake from Cow Milk. <i>Journal of Nutrition</i> , 2018, 148, 1506-1507.	2.9	26
28	Extended FMRFamides in dipteran insects: Conservative expression in the neuroendocrine system is accompanied by rapid sequence evolution. <i>General and Comparative Endocrinology</i> , 2009, 162, 52-58.	1.8	24
29	Quo vadis microRNAs?. <i>Trends in Genetics</i> , 2020, 36, 461-463.	6.7	24
30	sRNAbench and sRNAtoolbox 2022 update: accurate miRNA and sncRNA profiling for model and non-model organisms. <i>Nucleic Acids Research</i> , 2022, 50, W710-W717.	14.5	24
31	GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. <i>GigaScience</i> , 2017, 6, 1-12.	6.4	22
32	MicroRNA loci support conspecificity of <i>Gyrodactylus salaris</i> and <i>Gyrodactylus thymalli</i> (Platyhelminthes: Monogenea). <i>International Journal for Parasitology</i> , 2014, 44, 787-793.	3.1	20
33	Deciphering the function of non-coding RNAs in prostate cancer. <i>Cancer and Metastasis Reviews</i> , 2016, 35, 235-262.	5.9	20
34	EV-transported microRNAs of <i>Schistosoma mansoni</i> and <i>Fasciola hepatica</i> : Potential targets in definitive hosts. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104528.	2.3	20
35	The mitochondrial genome of the egg-laying flatworm <i>Aglaiogyrodactylus forficulatus</i> (Platyhelminthes: Monogenea). <i>Parasites and Vectors</i> , 2016, 9, 285.	2.5	18
36	MapToCleave: High-throughput profiling of microRNA biogenesis in living cells. <i>Cell Reports</i> , 2021, 37, 110015.	6.4	18

#	ARTICLE	IF	CITATIONS
37	The limits of human microRNA annotation have been met. <i>Rna</i> , 2022, 28, 781-785.	3.5	18
38	Pathway-based classification of breast cancer subtypes. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 1697-1712.	3.0	17
39	Plant microRNAs in human sera are likely contaminants. <i>Journal of Nutritional Biochemistry</i> , 2019, 65, 139-140.	4.2	17
40	MicroRNAs as Indicators into the Causes and Consequences of Whole-Genome Duplication Events. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	17
41	microRNAs as cancer biomarkers. <i>Scandinavian Journal of Clinical and Laboratory Investigation</i> , 2016, 76, S80-S83.	1.2	16
42	Digging into bivalve miRNAomes: between conservation and innovation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200165.	4.0	16
43	Differential expression of microRNAs and tRNA fragments mediate the adaptation of the liver fluke <i>Fasciola gigantica</i> to its intermediate snail and definitive mammalian hosts. <i>International Journal for Parasitology</i> , 2021, 51, 405-414.	3.1	15
44	MicroRNA preparations from individual monogenean <i>Gyrodactylus salaris</i> -a comparison of six commercially available totalRNA extraction kits. <i>BMC Research Notes</i> , 2011, 4, 217.	1.4	13
45	Extreme conservation of miRNA complements in opisthorchiids. <i>Parasitology International</i> , 2017, 66, 773-776.	1.3	8
46	Ancient microRNA profiles of 14,300-yr-old canid samples confirm taxonomic origin and provide glimpses into tissue-specific gene regulation from the Pleistocene. <i>Rna</i> , 2021, 27, 324-334.	3.5	7
47	Integrative genomic analysis of peritoneal malignant mesothelioma: understanding a case with extraordinary chemotherapy response. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003566.	1.2	6
48	Evolutionary Implications of the microRNA- and piRNA Complement of <i>Lepidodermella squamata</i> (Gastrotricha). <i>Non-coding RNA</i> , 2019, 5, 19.	2.6	5
49	A comprehensive framework for analysis of microRNA sequencing data in metastatic colorectal cancer. <i>NAR Cancer</i> , 2022, 4, zcab051.	3.1	5
50	microRNA Discovery and Expression Analysis in Animals. , 2016, , 121-142.		4
51	Encyclopedia of tools for the analysis of miRNA isoforms. <i>Briefings in Bioinformatics</i> , 2020, 22, .	6.5	2
52	A comparative analysis of heart microRNAs in vertebrates brings novel insights into the evolution of genetic regulatory networks. <i>BMC Genomics</i> , 2021, 22, 153.	2.8	2
53	In Silico Analysis of Micro-RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2284, 231-251.	0.9	0