

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 | MirGeneDB 2.1: toward a complete sampling of all major animal phyla. <i>Nucleic Acids Research</i> , 2022, 50, D204-D210. | 14.5 | 63 |
| 2 | A comprehensive framework for analysis of microRNA sequencing data in metastatic colorectal cancer. <i>NAR Cancer</i> , 2022, 4, zcab051. | 3.1 | 5 |
| 3 | The limits of human microRNA annotation have been met. <i>Rna</i> , 2022, 28, 781-785. | 3.5 | 18 |
| 4 | MicroRNAs as Indicators into the Causes and Consequences of Whole-Genome Duplication Events. <i>Molecular Biology and Evolution</i> , 2022, 39, . | 8.9 | 17 |
| 5 | 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 |
| 6 | RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220. | 14.5 | 160 |
| 7 | 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 |
| 8 | In Silico Analysis of Micro-RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2284, 231-251. | 0.9 | 0 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | MapToCleave: High-throughput profiling of microRNA biogenesis in living cells. <i>Cell Reports</i> , 2021, 37, 110015. | 6.4 | 18 |
| 13 | Unification of miRNA and isomiR research: the mirGFF3 format and the mirtop API. <i>Bioinformatics</i> , 2020, 36, 698-703. | 4.1 | 33 |
| 14 | MirGeneDB 2.0: the metazoan microRNA complement. <i>Nucleic Acids Research</i> , 2020, 48, D132-D141. | 14.5 | 194 |
| 15 | Common diseases alter the physiological age-related blood microRNA profile. <i>Nature Communications</i> , 2020, 11, 5958. | 12.8 | 46 |
| 16 | Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. <i>Cell Reports</i> , 2020, 33, 108448. | 6.4 | 35 |
| 17 | The Long Noncoding RNA CCAT2 Induces Chromosomal Instability Through BOP1-AURKB Signaling. <i>Gastroenterology</i> , 2020, 159, 2146-2162.e33. | 1.3 | 75 |
| 18 | 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 |

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|----|--|------|-----------|
| 19 | Encyclopedia of tools for the analysis of miRNA isoforms. <i>Briefings in Bioinformatics</i> , 2020, 22, . | 6.5 | 2 |
| 20 | Base-pair conformational switch modulates miR-34a targeting of Sirt1 mRNA. <i>Nature</i> , 2020, 583, 139-144. | 27.8 | 42 |
| 21 | Quo vadis microRNAs?. <i>Trends in Genetics</i> , 2020, 36, 461-463. | 6.7 | 24 |
| 22 | sRNAbench and sRNAtoolbox 2019: intuitive fast small RNA profiling and differential expression. <i>Nucleic Acids Research</i> , 2019, 47, W530-W535. | 14.5 | 136 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | Plant microRNAs in human sera are likely contaminants. <i>Journal of Nutritional Biochemistry</i> , 2019, 65, 139-140. | 4.2 | 17 |
| 27 | Big Strides in Cellular MicroRNA Expression. <i>Trends in Genetics</i> , 2018, 34, 165-167. | 6.7 | 32 |
| 28 | A comprehensive profile of circulating RNAs in human serum. <i>RNA Biology</i> , 2018, 15, 242-250. | 3.1 | 117 |
| 29 | miRTrace reveals the organismal origins of microRNA sequencing data. <i>Genome Biology</i> , 2018, 19, 213. | 8.8 | 44 |
| 30 | Large scale changes in the transcriptome of <i>Eisenia fetida</i> during regeneration. <i>PLoS ONE</i> , 2018, 13, e0204234. | 2.5 | 31 |
| 31 | Unicellular Origin of the Animal MicroRNA Machinery. <i>Current Biology</i> , 2018, 28, 3288-3295.e5. | 3.9 | 42 |
| 32 | 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 |
| 33 | Well-Annotated microRNAs Do Not Evidence Pervasive miRNA Loss. <i>Genome Biology and Evolution</i> , 2018, 10, 1457-1470. | 2.5 | 41 |
| 34 | GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. <i>GigaScience</i> , 2017, 6, 1-12. | 6.4 | 22 |
| 35 | Extreme conservation of miRNA complements in opisthorchiids. <i>Parasitology International</i> , 2017, 66, 773-776. | 1.3 | 8 |
| 36 | Atp8 is in the ground pattern of flatworm mitochondrial genomes. <i>BMC Genomics</i> , 2017, 18, 414. | 2.8 | 35 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | On the presence and immunoregulatory functions of extracellular microRNA in the trematode <i>Fasciola hepatica</i> . <i>Parasite Immunology</i> , 2017, 39, e12399. | 1.5 | 59 |
| 38 | 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 |
| 39 | Pathway-based classification of breast cancer subtypes. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 1697-1712. | 3.0 | 17 |
| 40 | 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 |
| 41 | Subtype-specific microRNA expression signatures in breast cancer progression. <i>International Journal of Cancer</i> , 2016, 139, 1117-1128. | 5.1 | 53 |
| 42 | Deciphering the function of non-coding RNAs in prostate cancer. <i>Cancer and Metastasis Reviews</i> , 2016, 35, 235-262. | 5.9 | 20 |
| 43 | microRNAs as cancer biomarkers. <i>Scandinavian Journal of Clinical and Laboratory Investigation</i> , 2016, 76, S80-S83. | 1.2 | 16 |
| 44 | The microRNA toolkit of insects. <i>Scientific Reports</i> , 2016, 6, 37736. | 3.3 | 40 |
| 45 | microRNA Discovery and Expression Analysis in Animals. , 2016, , 121-142. | | 4 |
| 46 | 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 |
| 47 | 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 |
| 48 | 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 |
| 49 | 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 |
| 50 | 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 |
| 51 | 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 |
| 52 | A proteomic approach for studying insect phylogeny: CAPA peptides of ancient insect taxa (Diptera, Blattodea) as a test case. <i>BMC Evolutionary Biology</i> , 2009, 9, 50. | 3.2 | 40 |
| 53 | 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 |