# Artemis G Hatzigeorgiou

List of Publications by Year
in descending order

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|---|---|---|---|
| 41 papers | 7,667 citations | 218677 26 h-index | 254184 43 g-index |
| 46 all docs | 46 docs citations | 46 times ranked | 13041 citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | DIANA-miRPath v3.0: deciphering microRNA function with experimental support. Nucleic Acids Research, 2015, 43, W460-W466. | 14.5 | 1,494 |
| 2 | DIANA-TarBase v8: a decade-long collection of experimentally supported miRNA–gene interactions. Nucleic Acids Research, 2018, 46, D239-D245. | 14.5 | 852 |
| 3 | Analyzing MiRNA–LncRNA Interactions. Methods in Molecular Biology, 2016, 1402, 271-286. | 0.9 | 690 |
| 4 | DIANA-TarBase v7.0: indexing more than half a million experimentally supported miRNA:mRNA interactions. Nucleic Acids Research, 2015, 43, D153-D159. | 14.5 | 683 |
| 5 | A combined computational-experimental approach predicts human microRNA targets. Genes and Development, 2004, 18, 1165-1178. | 5.9 | 680 |
| 6 | DIANA-LncBase v2: indexing microRNA targets on non-coding transcripts. Nucleic Acids Research, 2016, 44, D231-D238. | 14.5 | 628 |
| 7 | DIANA miRPath v.2.0: investigating the combinatorial effect of microRNAs in pathways. Nucleic Acids Research, 2012, 40, W498-W504. | 14.5 | 486 |
| 8 | The database of experimentally supported targets: a functional update of TarBase. Nucleic Acids Research, 2009, 37, D155-D158. | 14.5 | 364 |
| 9 | DIANA-LncBase: experimentally verified and computationally predicted microRNA targets on long non-coding RNAs. Nucleic Acids Research, 2013, 41, D239-D245. | 14.5 | 327 |
| 10 | RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229. | 14.5 | 153 |
| 11 | DIANA-LncBase v3: indexing experimentally supported miRNA targets on non-coding transcripts. Nucleic Acids Research, 2020, 48, D101-D110. | 14.5 | 137 |
| 12 | Integrated analysis of microRNA and mRNA expression and association with HIF binding reveals the complexity of microRNA expression regulation under hypoxia. Molecular Cancer, 2014, 13, 28. | 19.2 | 135 |
| 13 | The whole genome sequence of the Mediterranean fruit fly, Ceratitis capitata (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. Genome Biology, 2016, 17, 192. | 8.8 | 130 |
| 14 | FLASH Proton Radiotherapy Spares Normal Epithelial and Mesenchymal Tissues While Preserving Sarcoma Response. Cancer Research, 2021, 81, 4808-4821. | 0.9 | 77 |
| 15 | The DIANA-mirExTra Web Server: From Gene Expression Data to MicroRNA Function. PLoS ONE, 2010, 5, e9171. | 2.5 | 74 |
| 16 | Functional Analysis of miRNAs Using the DIANA Tools Online Suite. Methods in Molecular Biology, 2017, 1517, 25-50. | 0.9 | 66 |
| 17 | Online resources for miRNA analysis. Clinical Biochemistry, 2013, 46, 879-900. | 1.9 | 64 |
| 18 | microTSS: accurate microRNA transcription start site identification reveals a significant number of divergent pri-miRNAs. Nature Communications, 2014, 5, 5700. | 12.8 | 58 |

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|---|---------|-----|-----------|
| 19 | DIANA-miRGen v3.0: accurate characterization of microRNA promoters and their regulators. Nucleic Acids Research, 2016, 44, D190-D195. | 14.5 | 53 |
| 20 | A stromal Integrated Stress Response activates perivascular cancer-associated fibroblasts to drive angiogenesis and tumour progression. Nature Cell Biology, 2022, 24, 940-953. | 10.3 | 52 |
| 21 | A Positive Regulatory Loop between a Wnt-Regulated Non-coding RNA and ASCL2 Controls Intestinal Stem Cell Fate. Cell Reports, 2016, 15, 2588-2596. | 6.4 | 47 |
| 22 | DIANA-mirExTra v2.0: Uncovering microRNAs and transcription factors with crucial roles in NGS expression data. Nucleic Acids Research, 2016, 44, W128-W134. | 14.5 | 43 |
| 23 | DIANAâ€‹TarBase and DIANA Suite Tools: Studying Experimentally Supported microRNA Targets. Current Protocols in Bioinformatics, 2016, 55, 12.14.1-12.14.18. | 25.8 | 43 |
| 24 | DIANA-miTED: a microRNA tissue expression database. Nucleic Acids Research, 2022, 50, D1055-D1061. | 14.5 | 40 |
| 25 | Characterizing miRNAâ€‹lncRNA Interplay. Methods in Molecular Biology, 2021, 2372, 243-262. | 0.9 | 32 |
| 26 | microCLIP super learning framework uncovers functional transcriptome-wide miRNA interactions. Nature Communications, 2018, 9, 3601. | 12.8 | 30 |
| 27 | Peryton: a manual collection of experimentally supported microbe-disease associations. Nucleic Acids Research, 2021, 49, D1328-D1333. | 14.5 | 23 |
| 28 | mirPub: a database for searching microRNA publications. Bioinformatics, 2015, 31, 1502-1504. | 4.1 | 20 |
| 29 | Manatee: detection and quantification of small non-coding RNAs from next-generation sequencing data. Scientific Reports, 2020, 10, 705. | 3.3 | 18 |
| 30 | DIANA-miRGen v4: indexing promoters and regulators for more than 1500 microRNAs. Nucleic Acids Research, 2021, 49, D151-D159. | 14.5 | 18 |
| 31 | Solving the transcription start site identification problem with ADAPT-CAGE: a Machine Learning algorithm for the analysis of CAGE data. Scientific Reports, 2020, 10, 877. | 3.3 | 17 |
| 32 | Transcriptome Analysis Identifies Immune Markers Related to Visceral Leishmaniasis Establishment in the Experimental Model of BALB/c Mice. Frontiers in Immunology, 2019, 10, 2749. | 4.8 | 13 |
| 33 | MicroRNA-934 is a novel primate-specific small non-coding RNA with neurogenic function during early development. ELife, 2020, 9, . | 6.0 | 13 |
| 34 | PlasmiR: A Manual Collection of Circulating microRNAs of Prognostic and Diagnostic Value. Cancers, 2021, 13, 3680. | 3.7 | 9 |
| 35 | DIANA-mAP: Analyzing miRNA from Raw NGS Data to Quantification. Genes, 2021, 12, 46. | 2.4 | 9 |
| 36 | Transcriptional Profiling of Leishmania infantum Infected Dendritic Cells: Insights into the Role of Immunometabolism in Host-Parasite Interaction. Microorganisms, 2022, 10, 1271. | 3.6 | 6 |

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|---|---------|----|-----------| 
| 37 | Identifying Pri-miRNA Transcription Start Sites. Methods in Molecular Biology, 2018, 1823, 11-31. | 0.9 | 4 |
| 38 | AGAMEMNON: an Accurate metaGenomics And MEtatranscriptoMics quaNtificatiON analysis suite. Genome Biology, 2022, 23, 39. | 8.8 | 3 |
| 39 | Reporting on the Role of miRNAs and Affected Pathways on the Molecular Backbone of Ovarian Insufficiency: A Systematic Review and Critical Analysis Mapping of Future Research. Frontiers in Cell and Developmental Biology, 2020, 8, 590106. | 3.7 | 2 |
| 40 | Computational Challenges and -omics Approaches for the Identification of microRNAs and Targets. , 2017, , 39-59. | | 1 |
| 41 | ECCB 2018: The 17th European Conference on Computational Biology. Bioinformatics, 2018, 34, i595-i598. | 4.1 | 1 |