

Artemis G Hatzigeorgiou

List of Publications by Year in descending order

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Version: 2024-02-01

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-miTED: a microRNA tissue expression database. <i>Nucleic Acids Research</i> , 2022, 50, D1055-D1061.	14.5	40
2	AGAMEMNON: an Accurate metaGenomics And MEtatranscriptoMics quaNtificatiON analysis suite. <i>Genome Biology</i> , 2022, 23, 39.	8.8	3
3	A stromal Integrated Stress Response activates perivascular cancer-associated fibroblasts to drive angiogenesis and tumour progression. <i>Nature Cell Biology</i> , 2022, 24, 940-953.	10.3	52
4	Transcriptional Profiling of <i>Leishmania infantum</i> Infected Dendritic Cells: Insights into the Role of Immunometabolism in Host-Parasite Interaction. <i>Microorganisms</i> , 2022, 10, 1271.	3.6	6
5	Peryton: a manual collection of experimentally supported microbe-disease associations. <i>Nucleic Acids Research</i> , 2021, 49, D1328-D1333.	14.5	23
6	Characterizing miRNA-lncRNA Interplay. <i>Methods in Molecular Biology</i> , 2021, 2372, 243-262.	0.9	32
7	PlasmiR: A Manual Collection of Circulating microRNAs of Prognostic and Diagnostic Value. <i>Cancers</i> , 2021, 13, 3680.	3.7	9
8	FLASH Proton Radiotherapy Spares Normal Epithelial and Mesenchymal Tissues While Preserving Sarcoma Response. <i>Cancer Research</i> , 2021, 81, 4808-4821.	0.9	77
9	DIANA-miRGen v4: indexing promoters and regulators for more than 1500 microRNAs. <i>Nucleic Acids Research</i> , 2021, 49, D151-D159.	14.5	18
10	DIANA-mAP: Analyzing miRNA from Raw NGS Data to Quantification. <i>Genes</i> , 2021, 12, 46.	2.4	9
11	DIANA-LncBase v3: indexing experimentally supported miRNA targets on non-coding transcripts. <i>Nucleic Acids Research</i> , 2020, 48, D101-D110.	14.5	137
12	Manatee: detection and quantification of small non-coding RNAs from next-generation sequencing data. <i>Scientific Reports</i> , 2020, 10, 705.	3.3	18
13	Solving the transcription start site identification problem with ADAPT-CAGE: a Machine Learning algorithm for the analysis of CAGE data. <i>Scientific Reports</i> , 2020, 10, 877.	3.3	17
14	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. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 590106.	3.7	2
15	MicroRNA-934 is a novel primate-specific small non-coding RNA with neurogenic function during early development. <i>ELife</i> , 2020, 9, .	6.0	13
16	Transcriptome Analysis Identifies Immune Markers Related to Visceral Leishmaniasis Establishment in the Experimental Model of BALB/c Mice. <i>Frontiers in Immunology</i> , 2019, 10, 2749.	4.8	13
17	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	14.5	153
18	DIANA-TarBase v8: a decade-long collection of experimentally supported miRNA-gene interactions. <i>Nucleic Acids Research</i> , 2018, 46, D239-D245.	14.5	852

#	ARTICLE	IF	CITATIONS
19	ECCB 2018: The 17th European Conference on Computational Biology. <i>Bioinformatics</i> , 2018, 34, i595-i598.	4.1	1
20	microCLIP super learning framework uncovers functional transcriptome-wide miRNA interactions. <i>Nature Communications</i> , 2018, 9, 3601.	12.8	30
21	Identifying Pri-miRNA Transcription Start Sites. <i>Methods in Molecular Biology</i> , 2018, 1823, 11-31.	0.9	4
22	Functional Analysis of miRNAs Using the DIANA Tools Online Suite. <i>Methods in Molecular Biology</i> , 2017, 1517, 25-50.	0.9	66
23	Computational Challenges and -omics Approaches for the Identification of microRNAs and Targets. , 2017, , 39-59.		1
24	DIANA-mirExTra v2.0: Uncovering microRNAs and transcription factors with crucial roles in NGS expression data. <i>Nucleic Acids Research</i> , 2016, 44, W128-W134.	14.5	43
25	DIANA TarBase and DIANA Suite Tools: Studying Experimentally Supported microRNA Targets. <i>Current Protocols in Bioinformatics</i> , 2016, 55, 12.14.1-12.14.18.	25.8	43
26	The whole genome sequence of the Mediterranean fruit fly, <i>Ceratitis capitata</i> (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. <i>Genome Biology</i> , 2016, 17, 192.	8.8	130
27	A Positive Regulatory Loop between a Wnt-Regulated Non-coding RNA and ASCL2 Controls Intestinal Stem Cell Fate. <i>Cell Reports</i> , 2016, 15, 2588-2596.	6.4	47
28	Analyzing MiRNA LncRNA Interactions. <i>Methods in Molecular Biology</i> , 2016, 1402, 271-286.	0.9	690
29	DIANA-LncBase v2: indexing microRNA targets on non-coding transcripts. <i>Nucleic Acids Research</i> , 2016, 44, D231-D238.	14.5	628
30	DIANA-miRGen v3.0: accurate characterization of microRNA promoters and their regulators. <i>Nucleic Acids Research</i> , 2016, 44, D190-D195.	14.5	53
31	DIANA-miRPath v3.0: deciphering microRNA function with experimental support. <i>Nucleic Acids Research</i> , 2015, 43, W460-W466.	14.5	1,494
32	DIANA-TarBase v7.0: indexing more than half a million experimentally supported miRNA:mRNA interactions. <i>Nucleic Acids Research</i> , 2015, 43, D153-D159.	14.5	683
33	mirPub: a database for searching microRNA publications. <i>Bioinformatics</i> , 2015, 31, 1502-1504.	4.1	20
34	microTSS: accurate microRNA transcription start site identification reveals a significant number of divergent pri-miRNAs. <i>Nature Communications</i> , 2014, 5, 5700.	12.8	58
35	Integrated analysis of microRNA and mRNA expression and association with HIF binding reveals the complexity of microRNA expression regulation under hypoxia. <i>Molecular Cancer</i> , 2014, 13, 28.	19.2	135
36	Online resources for miRNA analysis. <i>Clinical Biochemistry</i> , 2013, 46, 879-900.	1.9	64

#	ARTICLE	IF	CITATIONS
37	DIANA-LncBase: experimentally verified and computationally predicted microRNA targets on long non-coding RNAs. <i>Nucleic Acids Research</i> , 2013, 41, D239-D245.	14.5	327
38	DIANA miRPath v.2.0: investigating the combinatorial effect of microRNAs in pathways. <i>Nucleic Acids Research</i> , 2012, 40, W498-W504.	14.5	486
39	The DIANA-mirExTra Web Server: From Gene Expression Data to MicroRNA Function. <i>PLoS ONE</i> , 2010, 5, e9171.	2.5	74
40	The database of experimentally supported targets: a functional update of TarBase. <i>Nucleic Acids Research</i> , 2009, 37, D155-D158.	14.5	364
41	A combined computational-experimental approach predicts human microRNA targets. <i>Genes and Development</i> , 2004, 18, 1165-1178.	5.9	680