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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Lipoprotein(a) Levels in FamilialÂHypercholesterolemia. Journal of the American College of Cardiology, 2014, 63, 1982-1989.	2.8	283
2	Tumor MicroRNA Expression Profiling Identifies Circulating MicroRNAs for Early Breast Cancer Detection. Clinical Chemistry, 2015, 61, 1098-1106.	3.2	183
3	miARma-Seq: a comprehensive tool for miRNA, mRNA and circRNA analysis. Scientific Reports, 2016, 6, 25749.	3.3	114
4	Evaluation of BioCreAtlvE assessment of task 2. BMC Bioinformatics, 2005, 6, S16.	2.6	108
5	Exosomes derived from mesenchymal stem cells enhance radiotherapy-induced cell death in tumor and metastatic tumor foci. Molecular Cancer, 2018, 17, 122.	19.2	100
6	miRGate: a curated database of human, mouse and rat miRNA–mRNA targets. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav035.	3.0	87
7	RNA sequencing and Prediction Tools for Circular RNAs Analysis. Advances in Experimental Medicine and Biology, 2018, 1087, 17-33.	1.6	87
8	Text Mining for Metabolic Pathways, Signaling Cascades, and Protein Networks. Science Signaling, 2005, 2005, pe21-pe21.	3.6	64
9	The Epstein Barr-encoded BART-6-3p microRNA affects regulation of cell growth and immuno response in Burkitt lymphoma. Infectious Agents and Cancer, 2014, 9, 12.	2.6	55
10	Mapping the entire functionally active endometrial microbiota. Human Reproduction, 2021, 36, 1021-1031.	0.9	51
11	Epstein-Barr virus microRNAs repress BCL6 expression in diffuse large B-cell lymphoma. Leukemia, 2012, 26, 180-183.	7.2	50
12	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. Nucleic Acids Research, 2012, 41, D142-D151.	14.5	47
13	The cellular growth rate controls overall mRNA turnover, and modulates either transcription or degradation rates of particular gene regulons. Nucleic Acids Research, 2016, 44, 3643-3658.	14.5	45
14	MicroRNA deregulation in triple negative breast cancer reveals a role of miR-498 in regulating <i>BRCA1</i> expression. Oncotarget, 2016, 7, 20068-20079.	1.8	42
15	Novel miRNA-mRNA interactions conserved in essential cancer pathways. Scientific Reports, 2017, 7, 46101.	3.3	38
16	Impact of DLK1-DIO3 imprinted cluster hypomethylation in smoker patients with lung cancer. Oncotarget, 2018, 9, 4395-4410.	1.8	37
17	Detection of novel fusion-transcripts by RNA-Seq in T-cell lymphoblastic lymphoma. Scientific Reports, 2019, 9, 5179.	3.3	36
18	Intelligent client for integrating bioinformatics services. Bioinformatics, 2006, 22, 106-111.	4.1	34

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19	The RNA Polymerase II Factor RPAP1 Is Critical for Mediator-Driven Transcription and Cell Identity. Cell Reports, 2018, 22, 396-410.	6.4	30
20	EcID. A database for the inference of functional interactions in E. coli. Nucleic Acids Research, 2009, 37, D629-D635.	14.5	28
21	Epigenomics and transcriptomics of systemic sclerosis CD4+ T cells reveal long-range dysregulation of key inflammatory pathways mediated by disease-associated susceptibility loci. Genome Medicine, 2020, 12, 81.	8.2	28
22	The Implications of ncRNAs in the Development of Human Diseases. Non-coding RNA, 2021, 7, 17.	2.6	28
23	Prp40 and early events in splice site definition. Wiley Interdisciplinary Reviews RNA, 2016, 7, 17-32.	6.4	27
24	CD38 promotes pristane-induced chronic inflammation and increases susceptibility to experimental lupus by an apoptosis-driven and TRPM2-dependent mechanism. Scientific Reports, 2018, 8, 3357.	3.3	25
25	SP140 regulates the expression of immune-related genes associated with multiple sclerosis and other autoimmune diseases by NF-κB inhibition. Human Molecular Genetics, 2018, 27, 4012-4023.	2.9	25
26	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. Nature Communications, 2022, 13, 1779.	12.8	25
27	miARma-Seq, a comprehensive pipeline for the simultaneous study and integration of miRNA and mRNA expression data. Methods, 2019, 152, 31-40.	3.8	24
28	MicroRNA-based molecular classification of non-BRCA1/2 hereditary breast tumours. British Journal of Cancer, 2013, 109, 2724-2734.	6.4	23
29	Prediction of Protein Interaction Based on Similarity of Phylogenetic Trees. Methods in Molecular Biology, 2008, 484, 523-535.	0.9	20
30	Prediction of miRNA–mRNA Interactions Using miRGate. Methods in Molecular Biology, 2017, 1580, 225-237.	0.9	17
31	CARGO: a web portal to integrate customized biological information. Nucleic Acids Research, 2007, 35, W16-W20.	14.5	16
32	SUMOylated SNF2PH promotes variant surface glycoprotein expression in bloodstream trypanosomes. EMBO Reports, 2019, 20, e48029.	4.5	15
33	miRNA expression profiling of formalin-fixed paraffin-embedded (FFPE) hereditary breast tumors. Genomics Data, 2015, 3, 75-79.	1.3	12
34	Pluripotency factors regulate the onset of <i>Hox</i> cluster activation in the early embryo. Science Advances, 2022, 8, .	10.3	12
35	Inference of Functional Relations in Predicted Protein Networks with a Machine Learning Approach. PLoS ONE, 2010, 5, e9969.	2.5	11
36	DDRprot: a database of DNA damage response-related proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw123.	3.0	11

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37	Identification of MicroRNAs as Viable Aggressiveness Biomarkers for Prostate Cancer. Biomedicines, 2021, 9, 646.	3.2	11
38	A Parasite Biomarker Set for Evaluating Benznidazole Treatment Efficacy in Patients with Chronic Asymptomatic Trypanosoma cruzi Infection. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	10
39	Selective inhibition of HDAC6 regulates expression of the oncogenic driver EWSR1-FLI1 through the EWSR1 promoter in Ewing sarcoma. Oncogene, 2021, 40, 5843-5853.	5.9	10
40	Selective histone methyltransferase G9a inhibition reduces metastatic development of Ewing sarcoma through the epigenetic regulation of NEU1. Oncogene, 2022, 41, 2638-2650.	5.9	10
41	Cortistatin regulates fibrosis and myofibroblast activation in experimental hepatotoxic―and cholestaticâ€induced liver injury. British Journal of Pharmacology, 2022, 179, 2275-2296.	5.4	7
42	The PARP Inhibitor Olaparib Modulates the Transcriptional Regulatory Networks of Long Non-Coding RNAs during Vasculogenic Mimicry. Cells, 2020, 9, 2690.	4.1	5
43	GWAS loci associated with Chagas cardiomyopathy influences DNA methylation levels. PLoS Neglected Tropical Diseases, 2021, 15, e0009874.	3.0	5
44	RNA-Seq, Bioinformatic Identification of Potential MicroRNA-like Small RNAs in the Edible Mushroom Agaricus bisporus and Experimental Approach for Their Validation. International Journal of Molecular Sciences, 2022, 23, 4923.	4.1	5
45	An inducible ectopic expression system of EWSR1-FLI1 as a tool for understanding Ewing sarcoma oncogenesis. PLoS ONE, 2020, 15, e0234243.	2.5	4
46	Identification of the genetic mechanism that associates <i>L3MBTL3</i> to multiple sclerosis. Human Molecular Genetics, 2022, 31, 2155-2163.	2.9	4
47	NGS Methodologies and Computational Algorithms for the Prediction and Analysis of. Methods in Molecular Biology, 2021, 2362, 119-145.	0.9	2
48	Evidence for a role of phenotypic mutations in virus adaptation. IScience, 2021, 24, 102257.	4.1	2
49	Differently Regulated Gene-Specific Activity of Enhancers Located at the Boundary of Subtopologically Associated Domains: TCRI± Enhancer. Journal of Immunology, 2022, 208, 910-928.	0.8	2
50	Modulation of Cholesterol Pathways in Human Macrophages Infected by Clinical Isolates of Leishmania infantum. Frontiers in Cellular and Infection Microbiology, 2022, 12, 878711.	3.9	2
51	CD38 Deficiency Ameliorates Chronic Graft-Versus-Host Disease Murine Lupus via a B-Cell-Dependent Mechanism. Frontiers in Immunology, 2021, 12, 713697.	4.8	1
52	Transcriptome Analysis of Intracellular Amastigotes of Clinical Leishmania infantum Lines from Therapeutic Failure Patients after Infection of Human Macrophages. Microorganisms, 2022, 10, 1304.	3.6	1
53	Identification of Group II Intron RmInt1 Binding Sites in a Bacterial Genome. Frontiers in Molecular Biosciences, 2022, 9, 834020.	3.5	0