Eduardo AndrÃ©s-LeÃ³n

List of Publications by Year
in descending order

53 papers	1,928 citations	279798 23 h-index	265206 42 g-index
61 all docs	61 docs citations	61 times ranked	3602 citing authors

#	Article	IF	Citations
1	Cortistatin regulates fibrosis and myofibroblast activation in experimental hepatotoxicâ€•and cholestaticâ€•induced liver injury. British Journal of Pharmacology, 2022, 179, 2275-2296.	5.4	7
2	Differently Regulated Gene-Specific Activity of Enhancers Located at the Boundary of Subtopologically Associated Domains: TCRÎ± Enhancer. Journal of Immunology, 2022, 208, 910-928.	0.8	2
3	Identification of the genetic mechanism that associates L3MBTL3 to multiple sclerosis. Human Molecular Genetics, 2022, 31, 2155-2163.	2.9	4
4	Identification of Group II Intron RmInt1 Binding Sites in a Bacterial Genome. Frontiers in Molecular Biosciences, 2022, 9, 834020.	3.5	0
5	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
6	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
7	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
8	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
9	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
10	Pluripotency factors regulate the onset of Hox cluster activation in the early embryo. Science Advances, 2022, 8, .	10.3	12
11	NGS Methodologies and Computational Algorithms for the Prediction and Analysis of. Methods in Molecular Biology, 2021, 2362, 119-145.	0.9	2
12	Mapping the entire functionally active endometrial microbiota. Human Reproduction, 2021, 36, 1021-1031.	0.9	51
13	The Implications of ncRNAs in the Development of Human Diseases. Non-coding RNA, 2021, 7, 17.	2.6	28
14	Evidence for a role of phenotypic mutations in virus adaptation. IScience, 2021, 24, 102257.	4.1	2
15	Identification of MicroRNAs as Viable Aggressiveness Biomarkers for Prostate Cancer. Biomedicines, 2021, 9, 646.	3.2	11
16	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
17	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
18	GWAS loci associated with Chagas cardiomyopathy influences DNA methylation levels. PLoS Neglected Tropical Diseases, 2021, 15, e0009874.	3.0	5

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19	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
20	The PARP Inhibitor Olaparib Modulates the Transcriptional Regulatory Networks of Long Non-Coding RNAs during Vasculogenic Mimicry. Cells, 2020, 9, 2690.	4.1	5
21	An inducible ectopic expression system of EWSR1-FLI1 as a tool for understanding Ewing sarcoma oncogenesis. PLoS ONE, 2020, 15, e0234243.	2.5	4
22	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
23	Detection of novel fusion-transcripts by RNA-Seq in T-cell lymphoblastic lymphoma. Scientific Reports, 2019, 9, 5179.	3.3	36
24	SUMOylated SNF2PH promotes variant surface glycoprotein expression in bloodstream trypanosomes. EMBO Reports, 2019, 20, e48029.	4.5	15
25	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
26	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
27	The RNA Polymerase II Factor RPAP1 Is Critical for Mediator-Driven Transcription and Cell Identity. Cell Reports, 2018, 22, 396-410.	6.4	30
28	RNA sequencing and Prediction Tools for Circular RNAs Analysis. Advances in Experimental Medicine and Biology, 2018, 1087, 17-33.	1.6	87
29	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
30	SP140 regulates the expression of immune-related genes associated with multiple sclerosis and other autoimmune diseases by NF-Î²B inhibition. Human Molecular Genetics, 2018, 27, 4012-4023.	2.9	25
31	Impact of DLK1-DIO3 imprinted cluster hypomethylation in smoker patients with lung cancer. Oncotarget, 2018, 9, 4395-4410.	1.8	37
32	Prediction of miRNAâ€“mRNA Interactions Using miRGate. Methods in Molecular Biology, 2017, 1580, 225-237.	0.9	17
33	Novel miRNA-mRNA interactions conserved in essential cancer pathways. Scientific Reports, 2017, 7, 46101.	3.3	38
34	Prp40 and early events in splice site definition. Wiley Interdisciplinary Reviews RNA, 2016, 7, 17-32.	6.4	27
35	miARma-Seq: a comprehensive tool for miRNA, mRNA and circRNA analysis. Scientific Reports, 2016, 6, 25749.	3.3	114
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	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
38	MicroRNA deregulation in triple negative breast cancer reveals a role of miR-498 in regulating BRCA1 expression. Oncotarget, 2016, 7, 20068-20079.	1.8	42
39	miRGate: a curated database of human, mouse and rat miRNAâ€“mRNA targets. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav035.	3.0	87
40	Tumor MicroRNA Expression Profiling Identifies Circulating MicroRNAs for Early Breast Cancer Detection. Clinical Chemistry, 2015, 61, 1098-1106.	3.2	183
41	miRNA expression profiling of formalin-fixed paraffin-embedded (FFPE) hereditary breast tumors. Genomics Data, 2015, 3, 75-79.	1.3	12
42	Lipoprotein(a) Levels in FamilialÂHypercholesterolemia. Journal of the American College of Cardiology, 2014, 63, 1982-1989.	2.8	283
43	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
44	MicroRNA-based molecular classification of non-BRCA1/2 hereditary breast tumours. British Journal of Cancer, 2013, 109, 2724-2734.	6.4	23
45	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
46	Epstein-Barr virus microRNAs repress BCL6 expression in diffuse large B-cell lymphoma. Leukemia, 2012, 26, 180-183.	7.2	50
47	Inference of Functional Relations in Predicted Protein Networks with a Machine Learning Approach. PLoS ONE, 2010, 5, e9969.	2.5	11
48	EcID. A database for the inference of functional interactions in E. coli. Nucleic Acids Research, 2009, 37, D629-D635.	14.5	28
49	Prediction of Protein Interaction Based on Similarity of Phylogenetic Trees. Methods in Molecular Biology, 2008, 484, 523-535.	0.9	20
50	CARGO: a web portal to integrate customized biological information. Nucleic Acids Research, 2007, 35, W16-W20.	14.5	16
51	Intelligent client for integrating bioinformatics services. Bioinformatics, 2006, 22, 106-111.	4.1	34
52	Evaluation of BioCreAtIvE assessment of task 2. BMC Bioinformatics, 2005, 6, S16.	2.6	108
53	Text Mining for Metabolic Pathways, Signaling Cascades, and Protein Networks. Science Signaling, 2005, 2005, pe21-pe21.	3.6	64