

Anna Esteve-Codina

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

2,751
citations

186265

28
h-index

197818

49
g-index

79
all docs

79
docs citations

79
times ranked

6419
citing authors

#	ARTICLE	IF	CITATIONS
1	PLC β 1/PKC δ Downstream Signaling Controls Cutaneous T-Cell Lymphoma Development and Progression. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1391-1400.e15.	0.7	5
2	Epigenetic landscape in the kick-and-kill therapeutic vaccine BCN02 clinical trial is associated with antiretroviral treatment interruption (ATI) outcome. <i>EBioMedicine</i> , 2022, 78, 103956.	6.1	5
3	RNA sequencing and Immunohistochemistry Reveal ZFN7 as a Stronger Marker of Survival than Molecular Subtypes in G-CIMP ⁺ negative Glioblastoma. <i>Clinical Cancer Research</i> , 2021, 27, 645-655.	7.0	5
4	NADPH oxidase 4 (Nox4) deletion accelerates liver regeneration in mice. <i>Redox Biology</i> , 2021, 40, 101841.	9.0	13
5	<i>Prunus persica</i> plant endogenous peptides PpPep1 and PpPep2 cause PTI-like transcriptome reprogramming in peach and enhance resistance to <i>Xanthomonas arboricola</i> pv. <i>pruni</i> . <i>BMC Genomics</i> , 2021, 22, 360.	2.8	8
6	Impact of DNA methylation on 3D genome structure. <i>Nature Communications</i> , 2021, 12, 3243.	12.8	61
7	Dual Role of Integrin Alpha-6 in Glioblastoma: Supporting Stemness in Proneural Stem-Like Cells While Inducing Radioresistance in Mesenchymal Stem-Like Cells. <i>Cancers</i> , 2021, 13, 3055.	3.7	6
8	E3 ubiquitin ligase Atrogin-1 mediates adaptive resistance to KIT-targeted inhibition in gastrointestinal stromal tumor. <i>Oncogene</i> , 2021, 40, 6614-6626.	5.9	7
9	The loss of DHX15 impairs endothelial energy metabolism, lymphatic drainage and tumor metastasis in mice. <i>Communications Biology</i> , 2021, 4, 1192.	4.4	5
10	Transcriptome analysis in LRRK2 and idiopathic Parkinson's disease at different glucose levels. <i>Npj Parkinson's Disease</i> , 2021, 7, 109.	5.3	1
11	Blood eosinophil count and airway epithelial transcriptome relationships in COPD versus asthma. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 370-380.	5.7	37
12	Linking omics and ecology to dissect interactions between the apple proliferation phytoplasma and its psyllid vector <i>Cacopsylla melanoneura</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 127, 103474.	2.7	5
13	Glioblastoma TCGA Mesenchymal and IGS 23 Tumors are Identifiable by IHC and have an Immune-phenotype Indicating a Potential Benefit from Immunotherapy. <i>Clinical Cancer Research</i> , 2020, 26, 6600-6609.	7.0	10
14	Transcriptomic effects of tributyltin (TBT) in zebrafish eleutheroembryos. A functional benchmark dose analysis. <i>Journal of Hazardous Materials</i> , 2020, 398, 122881.	12.4	30
15	Genome-wide profiling of non-smoking-related lung cancer cells reveals common RB1 rearrangements associated with histopathologic transformation in EGFR-mutant tumors. <i>Annals of Oncology</i> , 2020, 31, 274-282.	1.2	36
16	Functional and molecular heterogeneity of D2R neurons along dorsal ventral axis in the striatum. <i>Nature Communications</i> , 2020, 11, 1957.	12.8	41
17	Identification of tipifarnib sensitivity biomarkers in T-cell acute lymphoblastic leukemia and T-cell lymphoma. <i>Scientific Reports</i> , 2020, 10, 6721.	3.3	5
18	CRISPR editing of <i>sftb-1/SF3B1</i> in <i>Caenorhabditis elegans</i> allows the identification of synthetic interactions with cancer-related mutations and the chemical inhibition of splicing. <i>PLoS Genetics</i> , 2019, 15, e1008464.	3.5	16

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19	Analysis of <i>Vibrio harveyi</i> adaptation in sea water microcosms at elevated temperature provides insights into the putative mechanisms of its persistence and spread in the time of global warming. <i>Scientific Reports</i> , 2019, 9, 289.	3.3	47
20	<i>De Novo</i> Assembly and Annotation of the Larval Transcriptome of Two Spadefoot Toads Widely Divergent in Developmental Rate. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2647-2655.	1.8	5
21	Linking Cell Dynamics With Gene Coexpression Networks to Characterize Key Events in Chronic Virus Infections. <i>Frontiers in Immunology</i> , 2019, 10, 1002.	4.8	7
22	Systems analysis reveals complex biological processes during virus infection fate decisions. <i>Genome Research</i> , 2019, 29, 907-919.	5.5	21
23	PD-1 signaling affects cristae morphology and leads to mitochondrial dysfunction in human CD8+ T lymphocytes. , 2019, 7, 151.		83
24	Intergenerational transmission of the positive effects of physical exercise on brain and cognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10103-10112.	7.1	36
25	Unravelling the mechanisms of PFOS toxicity by combining morphological and transcriptomic analyses in zebrafish embryos. <i>Science of the Total Environment</i> , 2019, 674, 462-471.	8.0	51
26	Integrated single-base resolution maps of transcriptome, sRNAome and methylome of Tomato yellow leaf curl virus (TYLCV) in tomato. <i>Scientific Reports</i> , 2019, 9, 2863.	3.3	26
27	The Genome Sequence of the Eastern Woodchuck (<i>Marmota monax</i>) – A Preclinical Animal Model for Chronic Hepatitis B. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3943-3952.	1.8	13
28	P1.03-26 Genetic and Molecular Profiling of Non-Smoking Related Lung Adenocarcinomas. <i>Journal of Thoracic Oncology</i> , 2019, 14, S428.	1.1	0
29	Genetic Abnormalities in Large to Giant Congenital Nevi: Beyond NRAS Mutations. <i>Journal of Investigative Dermatology</i> , 2019, 139, 900-908.	0.7	67
30	European sea bass brain DLB-1 cell line is susceptible to nodavirus: A transcriptomic study. <i>Fish and Shellfish Immunology</i> , 2019, 86, 14-24.	3.6	35
31	Differential expression of long non-coding RNAs are related to proliferation and histological diversity in follicular lymphomas. <i>British Journal of Haematology</i> , 2019, 184, 373-383.	2.5	12
32	A FBN1 3'UTR mutation variant is associated with endoplasmic reticulum stress in aortic aneurysm in Marfan syndrome. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 107-114.	3.8	18
33	Epigenetic regulation of gene expression in Chinese Hamster Ovary cells in response to the changing environment of a batch culture. <i>Biotechnology and Bioengineering</i> , 2019, 116, 677-692.	3.3	37
34	Glioblastoma gene expression subtypes and correlation with clinical, molecular and immunohistochemical characteristics in a homogeneously treated cohort: GLIOCAT project.. <i>Journal of Clinical Oncology</i> , 2019, 37, 2029-2029.	1.6	4
35	<i>Prevotella</i> genera abundance in bronchial brush samples differentiates COPD from health and is associated with gene expression. , 2019, , .		0
36	Title is missing!. , 2019, 15, e1008464.		0

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37	Title is missing!. , 2019, 15, e1008464.		0
38	Title is missing!. , 2019, 15, e1008464.		0
39	Title is missing!. , 2019, 15, e1008464.		0
40	Transcriptional alterations in skin fibroblasts from Parkinson's disease patients with parkin mutations. <i>Neurobiology of Aging</i> , 2018, 65, 206-216.	3.1	13
41	Genetically defined variants of toll-like receptors 3, 7 and 9 as phenotype and risk modifier factors for psoriasis. <i>Journal of Dermatological Science</i> , 2018, 89, 301-304.	1.9	0
42	Dose-dependent transcriptomic responses of zebrafish eleutheroembryos to Bisphenol A. <i>Environmental Pollution</i> , 2018, 243, 988-997.	7.5	30
43	RNA-Seq Data Analysis, Applications and Challenges. <i>Comprehensive Analytical Chemistry</i> , 2018, 82, 71-106.	1.3	9
44	Consistent inverse correlation between DNA methylation of the first intron and gene expression across tissues and species. <i>Epigenetics and Chromatin</i> , 2018, 11, 37.	3.9	277
45	SP140 regulates the expression of immune-related genes associated with multiple sclerosis and other autoimmune diseases by NF- κ B inhibition. <i>Human Molecular Genetics</i> , 2018, 27, 4012-4023.	2.9	25
46	<i>MET</i> -Oncogenic and <i>JAK2</i> -Inactivating Alterations Are Independent Factors That Affect Regulation of PD-L1 Expression in Lung Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 4579-4587.	7.0	71
47	Deep analysis of acquired resistance to FGFR1 inhibitor identifies MET and AKT activation and an expansion of AKT1 mutant cells. <i>Oncotarget</i> , 2018, 9, 31549-31558.	1.8	8
48	Relationship between blood eosinophil count and bronchial epithelial gene expression in COPD versus Asthma. , 2018, , .		1
49	Genomic and Molecular Screenings Identify Different Mechanisms for Acquired Resistance to MET Inhibitors in Lung Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 1366-1376.	4.1	23
50	Wolf-Hirschhorn Syndrome Candidate 1 Is Necessary for Correct Hematopoietic and B Cell Development. <i>Cell Reports</i> , 2017, 19, 1586-1601.	6.4	28
51	Histone H1 depletion triggers an interferon response in cancer cells via activation of heterochromatic repeats. <i>Nucleic Acids Research</i> , 2017, 45, 11622-11642.	14.5	46
52	Tumor-associated macrophages (TAMs) depend on ZEB1 for their cancer-promoting roles. <i>EMBO Journal</i> , 2017, 36, 3336-3355.	7.8	112
53	Transcriptional mechanisms underlying life-history responses to climate change in the three-spined stickleback. <i>Evolutionary Applications</i> , 2017, 10, 718-730.	3.1	24
54	Innate Cell-Mediated Cytotoxic Activity of European Sea Bass Leucocytes Against Nodavirus-Infected Cells: A Functional and RNA-seq Study. <i>Scientific Reports</i> , 2017, 7, 15396.	3.3	33

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55	A Comparison of RNA-Seq Results from Paired Formalin-Fixed Paraffin-Embedded and Fresh-Frozen Glioblastoma Tissue Samples. PLoS ONE, 2017, 12, e0170632.	2.5	100
56	Hypoxia-mediated translational activation of ITGB3 in breast cancer cells enhances TGF- β 2 signaling and malignant features <i>in vitro</i> and <i>in vivo</i> . Oncotarget, 2017, 8, 114856-114876.	1.8	35
57	Epigenome characterization of CHO cells in response to evolutionary pressures and over time. New Biotechnology, 2016, 33, S4-S5.	4.4	0
58	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	3.3	28
59	Differential bronchial epithelial gene expression in COPD versus controls. , 2016, , .		0
60	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	21.4	278
61	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	5.5	118
62	HMTI-0197. Whole blood transcriptome analysis in migraine with aura patients: a case control study. Journal of Headache and Pain, 2014, 15, .	6.0	0
63	From SNP co-association to RNA co-expression: Novel insights into gene networks for intramuscular fatty acid composition in porcine. BMC Genomics, 2014, 15, 232.	2.8	44
64	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. BMC Genomics, 2013, 14, 148.	2.8	45
65	Porcine colonization of the Americas: a 60k SNP story. Heredity, 2013, 110, 321-330.	2.6	58
66	SNP calling by sequencing pooled samples. BMC Bioinformatics, 2012, 13, 239.	2.6	63
67	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. BMC Genomics, 2012, 13, 547.	2.8	118
68	Nucleotide variability of the porcine <i>SERPINA6</i> gene and the origin of a putative causal mutation associated with meat quality. Animal Genetics, 2011, 42, 235-241.	1.7	9
69	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. Heredity, 2011, 107, 256-264.	2.6	16
70	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. BMC Genomics, 2011, 12, 552.	2.8	127
71	A Natural History of FUT2 Polymorphism in Humans. Molecular Biology and Evolution, 2009, 26, 1993-2003.	8.9	209
72	â€œGenderPlexâ€ a PCR multiplex for reliable gender determination of degraded human DNA samples and complex gender constellations. International Journal of Legal Medicine, 2009, 123, 459-464.	2.2	35