

Anna Esteve-Codina

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68 papers	1,795 citations	23 h-index	41 g-index
79 ext. papers	2,450 ext. citations	7 avg, IF	4.66 L-index

#	Paper	IF	Citations
68	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	8.8	0
67	Transcriptome analysis in LRRK2 and idiopathic Parkinson's disease at different glucose levels. <i>Npj Parkinson's Disease</i> , 2021 , 7, 109	9.7	1
66	E3 ubiquitin ligase Atrogin-1 mediates adaptive resistance to KIT-targeted inhibition in gastrointestinal stromal tumor. <i>Oncogene</i> , 2021 , 40, 6614-6626	9.2	0
65	The loss of DHX15 impairs endothelial energy metabolism, lymphatic drainage and tumor metastasis in mice. <i>Communications Biology</i> , 2021 , 4, 1192	6.7	0
64	NADPH oxidase 4 (Nox4) deletion accelerates liver regeneration in mice. <i>Redox Biology</i> , 2021 , 40, 101841	11.3	3
63	Prunus persica plant endogenous peptides PpPep1 and PpPep2 cause PTI-like transcriptome reprogramming in peach and enhance resistance to Xanthomonas arboricola pv. pruni. <i>BMC Genomics</i> , 2021 , 22, 360	4.5	1
62	Impact of DNA methylation on 3D genome structure. <i>Nature Communications</i> , 2021 , 12, 3243	17.4	8
61	RNA sequencing and Immunohistochemistry Reveal as a Stronger Marker of Survival than Molecular Subtypes in G-CIMP-negative Glioblastoma. <i>Clinical Cancer Research</i> , 2021 , 27, 645-655	12.9	3
60	Transcriptomic effects of tributyltin (TBT) in zebrafish eleutheroembryos. A functional benchmark dose analysis. <i>Journal of Hazardous Materials</i> , 2020 , 398, 122881	12.8	11
59	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	10.3	24
58	Functional and molecular heterogeneity of D2R neurons along dorsal ventral axis in the striatum. <i>Nature Communications</i> , 2020 , 11, 1957	17.4	18
57	Identification of tipifarnib sensitivity biomarkers in T-cell acute lymphoblastic leukemia and T-cell lymphoma. <i>Scientific Reports</i> , 2020 , 10, 6721	4.9	3
56	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	9.3	16
55	Linking omics and ecology to dissect interactions between the apple proliferation phytoplasma and its psyllid vector Cacopsylla melanoneura. <i>Insect Biochemistry and Molecular Biology</i> , 2020 , 127, 103474	4.5	0
54	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	12.9	3
53	Analysis of Vibrio harveyi 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	4.9	21
52	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	3.2	3

51	Linking Cell Dynamics With Gene Coexpression Networks to Characterize Key Events in Chronic Virus Infections. <i>Frontiers in Immunology</i> , 2019 , 10, 1002	8.4	4
50	Systems analysis reveals complex biological processes during virus infection fate decisions. <i>Genome Research</i> , 2019 , 29, 907-919	9.7	10
49	PD-1 signaling affects cristae morphology and leads to mitochondrial dysfunction in human CD8 T lymphocytes 2019 , 7, 151		48
48	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	11.5	22
47	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	10.2	23
46	CRISPR editing of sftb-1/SF3B1 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	6	8
45	Glioblastoma gene expression subtypes and correlation with clinical, molecular and immunohistochemical characteristics in a homogenously treated cohort: GLIOCAT project.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 2029-2029	2.2	2
44	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	4.9	14
43	The Genome Sequence of the Eastern Woodchuck () - A Preclinical Animal Model for Chronic Hepatitis B. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 3943-3952	3.2	8
42	Genetic Abnormalities in Large to Giant Congenital Nevi: Beyond NRAS Mutations. <i>Journal of Investigative Dermatology</i> , 2019 , 139, 900-908	4.3	37
41	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	4.3	18
40	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	4.5	6
39	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	6.9	5
38	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	4.9	27
37	CRISPR editing of sftb-1/SF3B1 in <i>Caenorhabditis elegans</i> allows the identification of synthetic interactions with cancer-related mutations and the chemical inhibition of splicing 2019 , 15, e1008464		
36	CRISPR editing of sftb-1/SF3B1 in <i>Caenorhabditis elegans</i> allows the identification of synthetic interactions with cancer-related mutations and the chemical inhibition of splicing 2019 , 15, e1008464		
35	CRISPR editing of sftb-1/SF3B1 in <i>Caenorhabditis elegans</i> allows the identification of synthetic interactions with cancer-related mutations and the chemical inhibition of splicing 2019 , 15, e1008464		
34	CRISPR editing of sftb-1/SF3B1 in <i>Caenorhabditis elegans</i> allows the identification of synthetic interactions with cancer-related mutations and the chemical inhibition of splicing 2019 , 15, e1008464		

33	Transcriptional alterations in skin fibroblasts from Parkinson's disease patients with parkin mutations. <i>Neurobiology of Aging</i> , 2018 , 65, 206-216	5.6	9
32	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	4.3	
31	RNA-Seq Data Analysis, Applications and Challenges. <i>Comprehensive Analytical Chemistry</i> , 2018 , 82, 71-106	10.6	6
30	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	5.8	143
29	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	5.6	15
28	-Oncogenic and -Inactivating Alterations Are Independent Factors That Affect Regulation of PD-L1 Expression in Lung Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 4579-4587	12.9	44
27	Deep analysis of acquired resistance to FGFR1 inhibitor identifies MET and AKT activation and an expansion of mutant cells. <i>Oncotarget</i> , 2018 , 9, 31549-31558	3.3	6
26	Dose-dependent transcriptomic responses of zebrafish eleutheroembryos to Bisphenol A. <i>Environmental Pollution</i> , 2018 , 243, 988-997	9.3	21
25	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	6.1	19
24	Wolf-Hirschhorn Syndrome Candidate 1 Is Necessary for Correct Hematopoietic and B Cell Development. <i>Cell Reports</i> , 2017 , 19, 1586-1601	10.6	17
23	Histone H1 depletion triggers an interferon response in cancer cells via activation of heterochromatic repeats. <i>Nucleic Acids Research</i> , 2017 , 45, 11622-11642	20.1	25
22	Tumor-associated macrophages (TAMs) depend on ZEB1 for their cancer-promoting roles. <i>EMBO Journal</i> , 2017 , 36, 3336-3355	13	69
21	Transcriptional mechanisms underlying life-history responses to climate change in the three-spined stickleback. <i>Evolutionary Applications</i> , 2017 , 10, 718-730	4.8	16
20	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	4.9	23
19	A Comparison of RNA-Seq Results from Paired Formalin-Fixed Paraffin-Embedded and Fresh-Frozen Glioblastoma Tissue Samples. <i>PLoS ONE</i> , 2017 , 12, e0170632	3.7	60
18	Hypoxia-mediated translational activation of ITGB3 in breast cancer cells enhances TGF- β -signaling and malignant features and. <i>Oncotarget</i> , 2017 , 8, 114856-114876	3.3	24
17	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. <i>Scientific Reports</i> , 2016 , 6, 32406	4.9	21
16	Epigenome characterization of CHO cells in response to evolutionary pressures and over time. <i>New Biotechnology</i> , 2016 , 33, S4-S5	6.4	

15	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015 , 47, 746-56	36.3	209
14	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015 , 25, 478-87	9.7	92
13	From SNP co-association to RNA co-expression: novel insights into gene networks for intramuscular fatty acid composition in porcine. <i>BMC Genomics</i> , 2014 , 15, 232	4.5	31
12	HMTI-0197. Whole blood transcriptome analysis in migraine with aura patients: a case control study. <i>Journal of Headache and Pain</i> , 2014 , 15,	8.8	78
11	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. <i>BMC Genomics</i> , 2013 , 14, 148	4.5	40
10	Porcine colonization of the Americas: a 60k SNP story. <i>Heredity</i> , 2013 , 110, 321-30	3.6	42
9	SNP calling by sequencing pooled samples. <i>BMC Bioinformatics</i> , 2012 , 13, 239	3.6	47
8	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , 2012 , 13, 547	4.5	89
7	Nucleotide variability of the porcine SERPINA6 gene and the origin of a putative causal mutation associated with meat quality. <i>Animal Genetics</i> , 2011 , 42, 235-41	2.5	9
6	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. <i>Heredity</i> , 2011 , 107, 256-64	3.6	15
5	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. <i>BMC Genomics</i> , 2011 , 12, 552	4.5	72
4	A natural history of FUT2 polymorphism in humans. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1993-2003	3.3	169
3	"GenderPlex" a PCR multiplex for reliable gender determination of degraded human DNA samples and complex gender constellations. <i>International Journal of Legal Medicine</i> , 2009 , 123, 459-64	3.1	31
2	Comparative analysis of neutrophil and monocyte epigenomes		2
1	Time-resolved systems analysis reveals a critical role of XCR1+ dendritic cells in the maintenance of effector T cells during chronic viral infection		1