Ana Maria Aransay

List of Publications by Year
in descending order

102	4,625	101543	110387
papers	citations	36 h-index	64 g-index

112	112	112	9937
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mitochondrial dysfunction governs immunometabolism in leukocytes of patients with acute-on-chronic liver failure. Journal of Hepatology, 2022, 76, 93-106.	3.7	51
2	Absent in Melanoma 2 (AIM2) Regulates the Stability of Regulatory T Cells. International Journal of Molecular Sciences, 2022, 23, 2230.	4.1	10
3	Coding and non-coding co-expression network analysis identifies key modules and driver genes associated with precursor lesions of gastric cancer. Genomics, 2022, 114, 110370.	2.9	2
4	Mitochondrial complex I dysfunction alters the balance of soluble and membrane-bound TNF during chronic experimental colitis. Scientific Reports, 2022, 12, .	3.3	2
5	Borrelia burgdorferi infection induces long-term memory-like responses in macrophages with tissue-wide consequences in the heart. PLoS Biology, 2021, 19, e3001062.	5.6	7
6	The commensal bacterium Lactiplantibacillus plantarum imprints innate memory-like responses in mononuclear phagocytes. Gut Microbes, 2021, 13, 1939598.	9.8	8
7	Peripheral blood mononuclear cells (PBMC) microbiome is not affected by colon microbiota in healthy goats. Animal Microbiome, 2021, 3, 28.	3.8	8
8	Defining a Methylation Signature Associated With Operational Tolerance in Kidney Transplant Recipients. Frontiers in Immunology, 2021, 12, 709164.	4.8	5
9	SALL1 Modulates CBX4 Stability, Nuclear Bodies, and Regulation of Target Genes. Frontiers in Cell and Developmental Biology, 2021, 9, 715868.	3.7	1
10	Identification of proximal SUMO-dependent interactors using SUMO-ID. Nature Communications, 2021, 12, 6671.	12.8	27
11	Variability in Cerebrospinal Fluid MicroRNAs Through Life. Molecular Neurobiology, 2020, 57, 4134-4142.	4.0	5
12	Generation, establishment and characterization of a pluripotent stem cell line (CVTTHi001-A) from primary fibroblasts isolated from a patient with activated PI3 kinase delta syndrome (APDS2). Stem Cell Research, 2020, 49, 102082.	0.7	1
13	Cross-sectional study of human coding- and non-coding RNAs in progressive stages of Helicobacter pylori infection. Scientific Data, 2020, 7, 296.	5.3	1
14	Phosphoinositide 3-Kinaseâ€“Regulated Pericyte Maturation Governs Vascular Remodeling. Circulation, 2020, 142, 688-704.	1.6	29
15	Patients with Cholangiocarcinoma Present Specific RNA Profiles in Serum and Urine Extracellular Vesicles Mirroring the Tumor Expression: Novel Liquid Biopsy Biomarkers for Disease Diagnosis. Cells, 2020, 9, 721.	4.1	63
16	The mitochondrial negative regulator MCJ modulates the interplay between microbiota and the host during ulcerative colitis. Scientific Reports, 2020, 10, 572.	3.3	17
17	Extracellular Vesicles From Liver Progenitor Cells Downregulates Fibroblast Metabolic Activity and Increase the Expression of Immune-Response Related Molecules. Frontiers in Cell and Developmental Biology, 2020, 8, 613583.	3.7	0
18	HuR/ELAVL1 drives malignant peripheral nerve sheath tumor growth and metastasis. Journal of Clinical Investigation, 2020, 130, 3848-3864.	8.2	38

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19	A Comprehensive Study of Vesicular and Non-Vesicular miRNAs from a Volume of Cerebrospinal Fluid Compatible with Clinical Practice. Theranostics, 2019, 9, 4567-4579.	10.0	17
20	Epigenetic loss of RNA-methyltransferase NSUN5 in glioma targets ribosomes to drive a stress adaptive translational program. Acta Neuropathologica, 2019, 138, 1053-1074.	7.7	106
21	Gut microbiome and serum metabolome analyses identify molecular biomarkers and altered glutamate metabolism in fibromyalgia. EBioMedicine, 2019, 46, 499-511.	6.1	128
22	Signal Integration and Transcriptional Regulation of the Inflammatory Response Mediated by the GM-/M-CSF Signaling Axis in Human Monocytes. Cell Reports, 2019, 29, 860-872.e5.	6.4	29
23	Intestinal epithelial deletion of the glucocorticoid receptor NR3C1 alters expression of inflammatory mediators and barrier function. FASEB Journal, 2019, 33, 14067-14082.	0.5	16
24	ANP32E, a Protein Involved in Steroid-Refractoriness in Ulcerative Colitis, Identified by a Systems Biology Approach. Journal of Crohn's and Colitis, 2019, 13, 351-361.	1.3	30
25	A multi-omic analysis reveals the regulatory role of CD180 during the response of macrophages to Borrelia burgdorferi. Emerging Microbes and Infections, 2018, 7, 1-13.	6.5	9
26	Cluster Locator, online analysis and visualization of gene clustering. Bioinformatics, 2018, 34, 3377-3379.	4.1	20
27	Identification of a highly active tannase enzyme from the oral pathogen Fusobacterium nucleatum subsp. polymorphum. Microbial Cell Factories, 2018, 17, 33.	4.0	17
28	PPARÎ´ Elicits Ligand-Independent Repression of Trefoil Factor Family to Limit Prostate Cancer Growth. Cancer Research, 2018, 78, 399-409.	0.9	20
29	Low-dose statin treatment increases prostate cancer aggressiveness. Oncotarget, 2018, 9, 1494-1504.	1.8	15
30	MiR-873-5p acts as an epigenetic regulator in early stages of liver fibrosis and cirrhosis. Cell Death and Disease, 2018, 9, 958.	6.3	38
31	Genetic association study of dyslexia and ADHD candidate genes in a Spanish cohort: Implications of comorbid samples. PLoS ONE, 2018, 13, e0206431.	2.5	15
32	Integrative analysis of transcriptomics and clinical data uncovers the tumor-suppressive activity of MITF in prostate cancer. Cell Death and Disease, 2018, 9, 1041.	6.3	14
33	CANCERTOOL: A Visualization and Representation Interface to Exploit Cancer Datasets. Cancer Research, 2018, 78, 6320-6328.	0.9	76
34	Metabolomic Identification of Subtypes of Nonalcoholic Steatohepatitis. Gastroenterology, 2017, 152, 1449-1461.e7.	1.3	209
35	SOX17 regulates cholangiocyte differentiation and acts as a tumor suppressor in cholangiocarcinoma. Journal of Hepatology, 2017, 67, 72-83.	3.7	81
36	Aramchol reduces established fibrosis in MCD diet animal model. Journal of Hepatology, 2017, 66, S432.	3.7	0

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37	The Expression of mir-19b-3p and HIPK3 is Highly Correlated in Patients with Precancerous Lesions of Gastric Cancer. Gastroenterology, 2017, 152, S664-S665.	1.3	0
38	A synbiotic composed of Lactobacillus fermentum CECT5716 and FOS prevents the development of fatty acid liver and glycemic alterations in rats fed a high fructose diet associated with changes in the microbiota. Molecular Nutrition and Food Research, 2017, 61, 1600622.	3.3	37
39	A fistful of tips for a fruitful high throughput sequencing experiment. BioEssays, 2017, 39, 1700037.	2.5	1
40	Phenotypic characteristics of aged CD4⁺ CD28^{null} T lymphocytes are determined by changes in the whole-genome DNA methylation pattern. Aging Cell, 2017, 16, 293-303.	6.7	39
41	Epigenetic Networks Regulate the Transcriptional Program in Memory and Terminally Differentiated CD8+ T Cells. Journal of Immunology, 2017, 198, 937-949.	0.8	55
42	Role of aramchol in steatohepatitis and fibrosis in mice. Hepatology Communications, 2017, 1, 911-927.	4.3	84
43	The immunosuppressive effect of the tick protein, Salp15, is long-lasting and persists in a murine model of hematopoietic transplant. Scientific Reports, 2017, 7, 10740.	3.3	14
44	Inverse Correlation of Pleckstrin mRNA and miR-200a in the Antrum of Helicobacter Pylori Infected Patients. Gastroenterology, 2017, 152, S665.	1.3	0
45	VerSeDa: vertebrate secretome database. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	19
46	mTORC1-dependent AMD1 regulation sustains polyamine metabolism in prostate cancer. Nature, 2017, 547, 109-113.	27.8	142
47	Stratification and therapeutic potential of PML in metastatic breast cancer. Nature Communications, 2016, 7, 12595.	12.8	45
48	The metabolic co-regulator PGC1Î± suppresses prostate cancer metastasis. Nature Cell Biology, 2016, 18, 645-656.	10.3	176
49	SOX17 Regulates Cholangiocyte Differentiation and Acts as a Tumour Suppressor in Cholangiocarcinoma. Journal of Hepatology, 2016, 64, S569-S570.	3.7	1
50	Transcriptomic profiling of urine extracellular vesicles reveals alterations of CDH3 in prostate cancer. Oncotarget, 2016, 7, 6835-6846.	1.8	55
51	Methodological aspects of the molecular and histological study of prostate cancer: Focus on PTEN. Methods, 2015, 77-78, 25-30.	3.8	16
52	Schwann cell autophagy, myelinophagy, initiates myelin clearance from injured nerves. Journal of Cell Biology, 2015, 210, 153-168.	5.2	322
53	Regulation of the transcriptional program by DNA methylation during human Î±Î² T-cell development. Nucleic Acids Research, 2015, 43, 760-774.	14.5	43
54	PECAS: prokaryotic and eukaryotic classical analysis of secretome. Amino Acids, 2015, 47, 2659-2663.	2.7	7

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55	Loss of Tribbles pseudokinase-3 promotes Akt-driven tumorigenesis via FOXO inactivation. Cell Death and Differentiation, 2015, 22, 131-144.	11.2	70
56	TRIB3 suppresses tumorigenesis by controlling mTORC2/AKT/FOXO signaling. Molecular and Cellular Oncology, 2015, 2, e980134.	0.7	16
57	Single-Cell Genome and Transcriptome Processing Prior to High-Throughput Sequencing. Methods in Molecular Biology, 2015, 1293, 83-114.	0.9	0
58	Global Gene Expression Shift during the Transition from Early Neural Development to Late Neuronal Differentiation in Drosophila melanogaster. PLoS ONE, 2014, 9, e97703.	2.5	7
59	A Pilot Study on the Potential of RNA-Associated to Urinary Vesicles as a Suitable Non-Invasive Source for Diagnostic Purposes in Bladder Cancer. Cancers, 2014, 6, 179-192.	3.7	54
60	seqCNA: an R package for DNA copy number analysis in cancer using high-throughput sequencing. BMC Genomics, 2014, 15, 178.	2.8	11
61	SECRETOOL: integrated secretome analysis tool for fungi. Amino Acids, 2014, 46, 471-473.	2.7	46
62	S-adenosylmethionine Levels Regulate the Schwann Cell DNA Methylome. Neuron, 2014, 81, 1024-1039.	8.1	67
63	Complete Genome Sequence of the Multiresistant Acinetobacter baumannii Strain AbH12O-A2, Isolated during a Large Outbreak in Spain. Genome Announcements, 2014, 2, .	0.8	19
64	Prelamin A accumulation and stress conditions induce impaired Oct-1 activity and autophagy in prematurely aged human mesenchymal stem cell. Aging, 2014, 6, 264-280.	3.1	47
65	Bivariate segmentation of SNP-array data for allele-specific copy number analysis in tumour samples. BMC Bioinformatics, 2013, 14, 84.	2.6	3
66	Genetic study confirms association of HLA-DPA1â^—01:03 subtype with ankylosing spondylitis in HLA-B27-positive populations. Human Immunology, 2013, 74, 764-767.	2.4	11
67	Controlling complexity: the clinical relevance of mouse complex genetics. European Journal of Human Genetics, 2013, 21, 1191-1196.	2.8	29
68	Solute carrier family 2 member 1is involved in the development of nonalcoholic fatty liver disease. Hepatology, 2013, 57, 505-514.	7.3	25
69	Transcriptome of Extracellular Vesicles Released by Hepatocytes. PLoS ONE, 2013, 8, e68693.	2.5	58
70	Whole Transcriptome Analysis of Acinetobacter baumannii Assessed by RNA-Sequencing Reveals Different mRNA Expression Profiles in Biofilm Compared to Planktonic Cells. PLoS ONE, 2013, 8, e72968.	2.5	127
71	A high density SNP genotyping approach within the 19q13 chromosome region identifies an association of a CNOT3 polymorphism with ankylosing spondylitis. Annals of the Rheumatic Diseases, 2012, 71, 714-717.	0.9	14
72	Sp1 Transcription Factor Interaction with Accumulated Prelamin A Impairs Adipose Lineage Differentiation in Human Mesenchymal Stem Cells: Essential Role of Sp1 in the Integrity of Lipid Vesicles. Stem Cells Translational Medicine, 2012, 1, 309-321.	3.3	35

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73	The RNA-Binding Protein Human Antigen R Controls Global Changes in Gene Expression during Schwann Cell Development. Journal of Neuroscience, 2012, 32, 4944-4958.	3.6	12
74	microRNA profiling in duodenal ulcer disease caused by Helicobacter pylori infection in a Western population. Clinical Microbiology and Infection, 2012, 18, E273-E282.	6.0	53
75	Comparison of methods to detect copy number alterations in cancer using simulated and real genotyping data. BMC Bioinformatics, 2012, 13, 192.	2.6	14
76	Whole transcriptome analysis of a reversible neurodegenerative process in Drosophila reveals potential neuroprotective genes. BMC Genomics, 2012, 13, 483.	2.8	10
77	Hepatoma Cells From Mice Deficient in Glycine N-Methyltransferase Have Increased RAS Signaling and Activation of Liver Kinase B1. Gastroenterology, 2012, 143, 787-798.e13.	1.3	40
78	A cytokine gene screen uncovers SOCS1 as genetic risk factor for multiple sclerosis. Genes and Immunity, 2012, 13, 21-28.	4.1	56
79	Distinct Roles for Wnt-4 and Wnt-11 During Retinoic Acid-Induced Neuronal Differentiation. Stem Cells, 2011, 29, 141-153.	3.2	49
80	Fine mapping of a major histocompatibility complex in ankylosing spondylitis: Association of the HLAâ€“DPA1 and HLAâ€“DPB1 regions. Arthritis and Rheumatism, 2011, 63, 3305-3312.	6.7	17
81	miRanalyzer: an update on the detection and analysis of microRNAs in high-throughput sequencing experiments. Nucleic Acids Research, 2011, 39, W132-W138.	14.5	253
82	High-density SNP genotyping detects homogeneity of Spanish and French Basques, and confirms their genomic distinctiveness from other European populations. Human Genetics, 2010, 128, 113-117.	3.8	43
83	SNP-PHAGE: High-Throughput SNP Discovery Pipeline. Methods in Molecular Biology, 2010, 593, 49-65.	0.9	2
84	Genetic Diversity of Toscana Virus. Emerging Infectious Diseases, 2009, 15, 574-577.	4.3	46
85	Association between synapsin III gene promoter SNPs and multiple sclerosis in Basque patients. Multiple Sclerosis Journal, 2009, 15, 124-128.	3.0	11
86	Exploring the diabetogenicity of the HLA-B18-DR3 CEH: independent association with T1D genetic risk close to HLA-DOA. Genes and Immunity, 2009, 10, 596-600.	4.1	16
87	miRanalyzer: a microRNA detection and analysis tool for next-generation sequencing experiments. Nucleic Acids Research, 2009, 37, W68-W76.	14.5	283
88	Loss of the glycine N-methyltransferase gene leads to steatosis and hepatocellular carcinoma in mice. Hepatology, 2008, 47, 1191-1199.	7.3	262
89	The functional R620W variant of the PTPN22 gene is associated with celiac disease. Tissue Antigens, 2008, 71, 247-249.	1.0	20
90	Combined Functional and Positional Gene Information for the Identification of Susceptibility Variants in Celiac Disease. Gastroenterology, 2008, 134, 738-746.	1.3	18

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91	ITGA4 polymorphisms and susceptibility to multiple sclerosis. Journal of Neuroimmunology, 2007, 189, 151-157.	2.3	15
92	Conserved extended haplotypes discriminate HLA-DR3-homozygous Basque patients with type 1 diabetes mellitus and celiac disease. Genes and Immunity, 2006, 7, 550-554.	4.1	48
93	First detection of Leishmania major in peridomestic Phlebotomus papatasi from Isfahan province, Iran: comparison of nested PCR of nuclear ITS ribosomal DNA and semi-nested PCR of minicircle kinetoplast DNA. Acta Tropica, 2005, 93, 75-83.	2.0	66
94	Distribution of sandfly species in relation to canine leishmaniasis from the Ebro Valley to Valencia, northeastern Spain. Parasitology Research, 2004, 94, 416-420.	1.6	46
95	Population differentiation of Phlebotomus perniciosus in Spain following postglacial dispersal. Heredity, 2003, 90, 316-325.	2.6	45
96	Isolation (with enrichment) and characterization of trinucleotide microsatellites from Phlebotomus perniciosus , a vector of Leishmania infantum. Molecular Ecology Notes, 2001, 1, 176-178.	1.7	13
97	Diagnosis of quinolone-resistantCoxiella burnetii strains by PCR-RFLP. Journal of Clinical Laboratory Analysis, 2000, 14, 59-63.	2.1	13
98	Phylogenetic relationships of phlebotomine sandflies inferred from small subunit nuclear ribosomal DNA. Insect Molecular Biology, 2000, 9, 157-168.	2.0	69
99	Detection and Identification of Leishmania DNA within Naturally Infected Sand Flies by Seminested PCR on Minicircle Kinetoplastic DNA. Applied and Environmental Microbiology, 2000, 66, 1933-1938.	3.1	201
100	Diagnosis of quinolone-resistant Coxiella burnetii strains by PCR-RFLP. Journal of Clinical Laboratory Analysis, 2000, 14, 59.	2.1	0
101	Typing of sandflies from Greece and Cyprus by DNA polymorphism of 18S rRNA gene. Insect Molecular Biology, 1999, 8, 179-184.	2.0	45
102	Molecular characterization of the OXA-7 beta-lactamase gene. Antimicrobial Agents and Chemotherapy, 1995, 39, 1379-1382.	3.2	25