

Francisco Garcia-Garcia

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

2,618
citations

185998

28
h-index

205818

48
g-index

81
all docs

81
docs citations

81
times ranked

5871
citing authors

#	ARTICLE	IF	CITATIONS
1	Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. <i>Nucleic Acids Research</i> , 2010, 38, W210-W213.	6.5	283
2	Mammosphere Formation in Breast Carcinoma Cell Lines Depends upon Expression of E-cadherin. <i>PLoS ONE</i> , 2013, 8, e77281.	1.1	171
3	IL1 β Induces Mesenchymal Stem Cells Migration and Leucocyte Chemotaxis Through NF- κ B. <i>Stem Cell Reviews and Reports</i> , 2012, 8, 905-916.	5.6	153
4	Overall Survival and Biomarker Analysis of Neoadjuvant Nivolumab Plus Chemotherapy in Operable Stage IIIA Non-Small-Cell Lung Cancer (NADIM phase II trial). <i>Journal of Clinical Oncology</i> , 2022, 40, 2924-2933.	0.8	127
5	Babelomics 5.0: functional interpretation for new generations of genomic data. <i>Nucleic Acids Research</i> , 2015, 43, W117-W121.	6.5	114
6	Gender differences in the inflammatory cytokine and chemokine profiles induced by binge ethanol drinking in adolescence. <i>Addiction Biology</i> , 2017, 22, 1829-1841.	1.4	89
7	Early Transcriptional Defense Responses in Arabidopsis Cell Suspension Culture under High-Light Conditions. <i>Plant Physiology</i> , 2011, 156, 1439-1456.	2.3	81
8	267 Spanish Exomes Reveal Population-Specific Differences in Disease-Related Genetic Variation. <i>Molecular Biology and Evolution</i> , 2016, 33, 1205-1218.	3.5	78
9	Serum metabolomic profiling facilitates the non-invasive identification of metabolic biomarkers associated with the onset and progression of non-small cell lung cancer. <i>Oncotarget</i> , 2016, 7, 12904-12916.	0.8	73
10	Rilpivirine attenuates liver fibrosis through selective STAT1-mediated apoptosis in hepatic stellate cells. <i>Gut</i> , 2020, 69, 920-932.	6.1	70
11	GEPAS, a web-based tool for microarray data analysis and interpretation. <i>Nucleic Acids Research</i> , 2008, 36, W308-W314.	6.5	67
12	Global Transcriptome Analysis of Primary Cerebrocortical Cells: Identification of Genes Regulated by Triiodothyronine in Specific Cell Types. <i>Cerebral Cortex</i> , 2015, 27, bhv273.	1.6	64
13	Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. <i>Plant Biotechnology Journal</i> , 2016, 14, 719-734.	4.1	53
14	Integration of transcriptomic and metabolic data reveals hub transcription factors involved in drought stress response in sunflower (<i>Helianthus annuus</i> L.). <i>Plant Molecular Biology</i> , 2017, 94, 549-564.	2.0	51
15	Fibroblast activation and abnormal extracellular matrix remodelling as common hallmarks in three cancer-prone genodermatoses. <i>British Journal of Dermatology</i> , 2019, 181, 512-522.	1.4	46
16	Maslinic Acid-Enriched Diet Decreases Intestinal Tumorigenesis in ApcMin/+ Mice through Transcriptomic and Metabolomic Reprogramming. <i>PLoS ONE</i> , 2013, 8, e59392.	1.1	46
17	Expression profiling shows differential molecular pathways and provides potential new diagnostic biomarkers for colorectal serrated adenocarcinoma. <i>International Journal of Cancer</i> , 2013, 132, 297-307.	2.3	43
18	Programmed cell death activated by Rose Bengal in Arabidopsis thaliana cell suspension cultures requires functional chloroplasts. <i>Journal of Experimental Botany</i> , 2014, 65, 3081-3095.	2.4	41

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19	Whole-exome sequencing reveals ZNF408 as a new gene associated with autosomal recessive retinitis pigmentosa with vitreal alterations. <i>Human Molecular Genetics</i> , 2015, 24, 4037-4048.	1.4	41
20	Novel genes detected by transcriptional profiling from whole-blood cells in patients with early onset of acute coronary syndrome. <i>Clinica Chimica Acta</i> , 2013, 421, 184-190.	0.5	40
21	A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies. <i>Nucleic Acids Research</i> , 2014, 42, W88-W93.	6.5	39
22	Grape antioxidant dietary fiber inhibits intestinal polyposis in Apc Min/+ mice: relation to cell cycle and immune response. <i>Carcinogenesis</i> , 2013, 34, 1881-1888.	1.3	38
23	Differential Features between Chronic Skin Inflammatory Diseases Revealed in Skin-Humanized Psoriasis and Atopic Dermatitis Mouse Models. <i>Journal of Investigative Dermatology</i> , 2016, 136, 136-145.	0.3	37
24	Deep sequencing and miRNA profiles in alcohol-induced neuroinflammation and the TLR4 response in mice cerebral cortex. <i>Scientific Reports</i> , 2018, 8, 15913.	1.6	37
25	Dysfunctional mitochondrial fission impairs cell reprogramming. <i>Cell Cycle</i> , 2016, 15, 3240-3250.	1.3	36
26	Assessment of Targeted Next-Generation Sequencing as a Tool for the Diagnosis of Charcot-Marie-Tooth Disease and Hereditary Motor Neuropathy. <i>Journal of Molecular Diagnostics</i> , 2016, 18, 225-234.	1.2	36
27	Capturing the biological impact of CDKN2A and MC1R genes as an early predisposing event in melanoma and non melanoma skin cancer. <i>Oncotarget</i> , 2014, 5, 1439-1451.	0.8	35
28	Mutations in <i>TRAPPC11</i> are associated with a congenital disorder of glycosylation. <i>Human Mutation</i> , 2017, 38, 148-151.	1.1	34
29	CSVS, a crowdsourcing database of the Spanish population genetic variability. <i>Nucleic Acids Research</i> , 2021, 49, D1130-D1137.	6.5	34
30	Prognostic value of quantitative ctDNA levels in non small cell lung cancer patients. <i>Oncotarget</i> , 2018, 9, 488-494.	0.8	30
31	Characterization of molecular mechanisms underlying the axonal Charcot-Marie-Tooth neuropathy caused by MORC2 mutations. <i>Human Molecular Genetics</i> , 2019, 28, 1629-1644.	1.4	28
32	Development, Characterization and Experimental Validation of a Cultivated Sunflower (<i>Helianthus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	28
33	Uterine disorders affecting female fertility: what are the molecular functions altered in endometrium?. <i>Fertility and Sterility</i> , 2020, 113, 1261-1274.	0.5	26
34	Intrauterine growth restriction is associated with cardiac ultrastructural and gene expression changes related to the energetic metabolism in a rabbit model. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2013, 305, H1752-H1760.	1.5	24
35	Integrated gene set analysis for microRNA studies. <i>Bioinformatics</i> , 2016, 32, 2809-2816.	1.8	23
36	Permanent Cardiac Sarcomere Changes in a Rabbit Model of Intrauterine Growth Restriction. <i>PLoS ONE</i> , 2014, 9, e113067.	1.1	21

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37	Functional assessment of time course microarray data. <i>BMC Bioinformatics</i> , 2009, 10, S9.	1.2	19
38	Role of <i>CPI</i> in restoring skin homeostasis in cutaneous field of cancerization: effects of topical application of a film-forming medical device containing photolyase and <i>UV</i> filters. <i>Experimental Dermatology</i> , 2013, 22, 494-496.	1.4	19
39	The transcriptomics of an experimentally evolved plant-virus interaction. <i>Scientific Reports</i> , 2016, 6, 24901.	1.6	19
40	Unveiling Sex-Based Differences in the Effects of Alcohol Abuse: A Comprehensive Functional Meta-Analysis of Transcriptomic Studies. <i>Genes</i> , 2020, 11, 1106.	1.0	19
41	Functional Signatures in Non-Small-Cell Lung Cancer: A Systematic Review and Meta-Analysis of Sex-Based Differences in Transcriptomic Studies. <i>Cancers</i> , 2021, 13, 143.	1.7	19
42	Optimised molecular genetic diagnostics of Fanconi anaemia by whole exome sequencing and functional studies. <i>Journal of Medical Genetics</i> , 2020, 57, 258-268.	1.5	18
43	Hepatic steatosis and steatohepatitis: a functional meta-analysis of sex-based differences in transcriptomic studies. <i>Biology of Sex Differences</i> , 2021, 12, 29.	1.8	18
44	The Activation of the Sox2 RR2 Pluripotency Transcriptional Reporter in Human Breast Cancer Cell Lines is Dynamic and Labels Cells with Higher Tumorigenic Potential. <i>Frontiers in Oncology</i> , 2014, 4, 308.	1.3	17
45	Deregulation of key signaling pathways involved in oocyte maturation in FMR1 premutation carriers with Fragile X-associated primary ovarian insufficiency. <i>Gene</i> , 2015, 571, 52-57.	1.0	17
46	BRCA1 Alternative splicing landscape in breast tissue samples. <i>BMC Cancer</i> , 2015, 15, 219.	1.1	17
47	Exploring sunflower responses to Sclerotinia head rot at early stages of infection using RNA-seq analysis. <i>Scientific Reports</i> , 2020, 10, 13347.	1.6	16
48	Early peroxisome proliferator-activated receptor gamma regulated genes involved in expansion of pancreatic beta cell mass. <i>BMC Medical Genomics</i> , 2011, 4, 86.	0.7	15
49	Sex is a strong prognostic factor in stage IV non-small-cell lung cancer patients and should be considered in survival rate estimation. <i>Cancer Epidemiology</i> , 2020, 67, 101737.	0.8	15
50	Extracellular Vesicles Secreted by Hypoxic AC10 Cardiomyocytes Modulate Fibroblast Cell Motility. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 152.	1.1	14
51	Differential expression of circulating miRNAs as a novel tool to assess BAG3-associated familial dilated cardiomyopathy. <i>Bioscience Reports</i> , 2019, 39, .	1.1	14
52	Screening of CD96 and ASXL1 in 11 patients with Opitz C or Bohring-Opitz syndromes. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 24-31.	0.7	13
53	Identification of the Photoreceptor Transcriptional Co-Repressor SAMD11 as Novel Cause of Autosomal Recessive Retinitis Pigmentosa. <i>Scientific Reports</i> , 2016, 6, 35370.	1.6	13
54	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. <i>PLoS ONE</i> , 2020, 15, e0237066.	1.1	12

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55	TLR4 Deficiency Affects the Microbiome and Reduces Intestinal Dysfunctions and Inflammation in Chronic Alcohol-Fed Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12830.	1.8	12
56	Does singlet oxygen activate cell death in Arabidopsis cell suspension cultures?: Analysis of the early transcriptional defense responses to high light stress. <i>Plant Signaling and Behavior</i> , 2011, 6, 1937-1942.	1.2	10
57	Direct functional assessment of the composite phenotype through multivariate projection strategies. <i>Genomics</i> , 2008, 92, 373-383.	1.3	9
58	Common pathways and functional profiles reveal underlying patterns in Breast, Kidney and Lung cancers. <i>Biology Direct</i> , 2021, 16, 9.	1.9	7
59	A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications. <i>Nucleic Acids Research</i> , 2014, 42, W83-W87.	6.5	6
60	Differences in gene expression profiling and biomarkers between histological colorectal carcinoma subsets from the serrated pathway. <i>Histopathology</i> , 2019, 75, 496-507.	1.6	6
61	Transcriptomic Analysis of a Diabetic Skin-Humanized Mouse Model Dissects Molecular Pathways Underlying the Delayed Wound Healing Response. <i>Genes</i> , 2021, 12, 47.	1.0	6
62	Transcriptomic Analysis Reveals a Differential Gene Expression Profile Between Two Sunflower Inbred Lines with Different Ability to Tolerate Water Stress. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 222-237.	1.0	5
63	Genomic expression differences between cutaneous cells from red hair color individuals and black hair color individuals based on bioinformatic analysis. <i>Oncotarget</i> , 2017, 8, 11589-11599.	0.8	5
64	De novo Transcriptome Assembly and Comprehensive Annotation of Two Tree Tomato Cultivars (<i>Solanum betaceum</i> Cav.) with Different Fruit Color. <i>Horticulturae</i> , 2021, 7, 431.	1.2	5
65	Association of a single nucleotide polymorphism in the ubxn6 gene with long-term non-progression phenotype in HIV-positive individuals. <i>Clinical Microbiology and Infection</i> , 2020, 26, 107-114.	2.8	3
66	Plasmatic Membrane Expression of Adhesion Molecules in Human Cardiac Progenitor/Stem Cells Might Explain Their Superior Cell Engraftment after Cell Transplantation. <i>Stem Cells International</i> , 2020, 2020, 1-13.	1.2	3
67	Bioenergetic and Autophagic Characterization of Skin Fibroblasts from C9orf72 Patients. <i>Antioxidants</i> , 2022, 11, 1129.	2.2	2
68	Sex is a strong prognostic factor for overall survival in advanced non small cell lung cancer patients and should be considered for survival rates estimations.. <i>Journal of Clinical Oncology</i> , 2019, 37, e20580-e20580.	0.8	1
69	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. , 2020, 15, e0237066.		0
70	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. , 2020, 15, e0237066.		0
71	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. , 2020, 15, e0237066.		0
72	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. , 2020, 15, e0237066.		0