Francisco Garcia-Garcia

List of Publications by Year in descending order

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	Overall Survival and Biomarker Analysis of Neoadjuvant Nivolumab Plus Chemotherapy in Operable Stage IIIA Non–Small-Cell Lung Cancer (NADIM phase II trial). Journal of Clinical Oncology, 2022, 40, 2924-2933.	0.8	127
2	Bioenergetic and Autophagic Characterization of Skin Fibroblasts from C9orf72 Patients. Antioxidants, 2022, 11, 1129.	2.2	2
3	CSVS, a crowdsourcing database of the Spanish population genetic variability. Nucleic Acids Research, 2021, 49, D1130-D1137.	6.5	34
4	Hepatic steatosis and steatohepatitis: a functional meta-analysis of sex-based differences in transcriptomic studies. Biology of Sex Differences, 2021, 12, 29.	1.8	18
5	Common pathways and functional profiles reveal underlying patterns in Breast, Kidney and Lung cancers. Biology Direct, 2021, 16, 9.	1.9	7
6	Functional Signatures in Non-Small-Cell Lung Cancer: A Systematic Review and Meta-Analysis of Sex-Based Differences in Transcriptomic Studies. Cancers, 2021, 13, 143.	1.7	19
7	Transcriptomic Analysis of a Diabetic Skin-Humanized Mouse Model Dissects Molecular Pathways Underlying the Delayed Wound Healing Response. Genes, 2021, 12, 47.	1.0	6
8	De novo Transcriptome Assembly and Comprehensive Annotation of Two Tree Tomato Cultivars (Solanum betaceum Cav.) with Different Fruit Color. Horticulturae, 2021, 7, 431.	1.2	5
9	TLR4 Deficiency Affects the Microbiome and Reduces Intestinal Dysfunctions and Inflammation in Chronic Alcohol-Fed Mice. International Journal of Molecular Sciences, 2021, 22, 12830.	1.8	12
10	Rilpivirine attenuates liver fibrosis through selective STAT1-mediated apoptosis in hepatic stellate cells. Gut, 2020, 69, 920-932.	6.1	70
11	Association of a single nucleotide polymorphism in the ubxn6 gene with long-term non-progression phenotype in HIV-positive individuals. Clinical Microbiology and Infection, 2020, 26, 107-114.	2.8	3
12	Exploring sunflower responses to Sclerotinia head rot at early stages of infection using RNA-seq analysis. Scientific Reports, 2020, 10, 13347.	1.6	16
13	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. PLoS ONE, 2020, 15, e0237066.	1.1	12
14	Plasmatic Membrane Expression of Adhesion Molecules in Human Cardiac Progenitor/Stem Cells Might Explain Their Superior Cell Engraftment after Cell Transplantation. Stem Cells International, 2020, 2020, 1-13.	1.2	3
15	Unveiling Sex-Based Differences in the Effects of Alcohol Abuse: A Comprehensive Functional Meta-Analysis of Transcriptomic Studies. Genes, 2020, 11, 1106.	1.0	19
16	Uterine disorders affecting female fertility: what are the molecular functions altered in endometrium?. Fertility and Sterility, 2020, 113, 1261-1274.	0.5	26
17	Transcriptomic Analysis Reveals a Differential Gene Expression Profile Between Two Sunflower Inbred Lines with Different Ability to Tolerate Water Stress. Plant Molecular Biology Reporter, 2020, 38, 222-237.	1.0	5
18	Optimised molecular genetic diagnostics of Fanconi anaemia by whole exome sequencing and functional studies. Journal of Medical Genetics, 2020, 57, 258-268.	1.5	18

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19	Sex is a strong prognostic factor in stage IV non-small-cell lung cancer patients and should be considered in survival rate estimation. Cancer Epidemiology, 2020, 67, 101737.	0.8	15
20	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. , 2020, 15, e0237066.		0
21	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. , 2020, 15, e0237066.		0
22	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. , 2020, 15, e0237066.		0
23	Lack of TLR4 modifies the miRNAs profile and attenuates inflammatory signaling pathways. , 2020, 15, e0237066.		0
24	Fibroblast activation and abnormal extracellular matrix remodelling as common hallmarks in three cancer€prone genodermatoses. British Journal of Dermatology, 2019, 181, 512-522.	1.4	46
25	Differences in gene expression profiling and biomarkers between histological colorectal carcinoma subsets from the serrated pathway. Histopathology, 2019, 75, 496-507.	1.6	6
26	Differential expression of circulating miRNAs as a novel tool to assess BAG3-associated familial dilated cardiomyopathy. Bioscience Reports, 2019, 39, .	1.1	14
27	Characterization of molecular mechanisms underlying the axonal Charcotâ€"Marieâ€"Tooth neuropathy caused by MORC2 mutations. Human Molecular Genetics, 2019, 28, 1629-1644.	1.4	28
28	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.. Journal of Clinical Oncology, 2019, 37, e20580-e20580.	0.8	1
29	Prognostic value of quantitative ctDNA levels in non small cell lung cancer patients. Oncotarget, 2018, 9, 488-494.	0.8	30
30	Extracellular Vesicles Secreted by Hypoxic AC10 Cardiomyocytes Modulate Fibroblast Cell Motility. Frontiers in Cardiovascular Medicine, 2018, 5, 152.	1.1	14
31	Deep sequencing and miRNA profiles in alcohol-induced neuroinflammation and the TLR4 response in mice cerebral cortex. Scientific Reports, 2018, 8, 15913.	1.6	37
32	Integration of transcriptomic and metabolic data reveals hub transcription factors involved in drought stress response in sunflower (Helianthus annuus L.). Plant Molecular Biology, 2017, 94, 549-564.	2.0	51
33	Gender differences in the inflammatory cytokine and chemokine profiles induced by binge ethanol drinking in adolescence. Addiction Biology, 2017, 22, 1829-1841.	1.4	89
34	Mutations in<i>TRAPPC11</i>are associated with a congenital disorder of glycosylation. Human Mutation, 2017, 38, 148-151.	1.1	34
35	Genomic expression differences between cutaneous cells from red hair color individuals and black hair color individuals based on bioinformatic analysis. Oncotarget, 2017, 8, 11589-11599.	0.8	5
36	Serum metabolomic profiling facilitates the non-invasive identification of metabolic biomarkers associated with the onset and progression of non-small cell lung cancer. Oncotarget, 2016, 7, 12904-12916.	0.8	73

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37	The transcriptomics of an experimentally evolved plant-virus interaction. Scientific Reports, 2016, 6, 24901.	1.6	19
38	Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. Plant Biotechnology Journal, 2016, 14, 719-734.	4.1	53
39	Screening of CD96 and ASXL1 in 11 patients with Opitz C or Bohring–Opitz syndromes. American Journal of Medical Genetics, Part A, 2016, 170, 24-31.	0.7	13
40	Integrated gene set analysis for microRNA studies. Bioinformatics, 2016, 32, 2809-2816.	1.8	23
41	Identification of the Photoreceptor Transcriptional Co-Repressor SAMD11 as Novel Cause of Autosomal Recessive Retinitis Pigmentosa. Scientific Reports, 2016, 6, 35370.	1.6	13
42	Dysfunctional mitochondrial fission impairs cell reprogramming. Cell Cycle, 2016, 15, 3240-3250.	1.3	36
43	267 Spanish Exomes Reveal Population-Specific Differences in Disease-Related Genetic Variation. Molecular Biology and Evolution, 2016, 33, 1205-1218.	3.5	78
44	Assessment of Targeted Next-Generation Sequencing as a Tool for the Diagnosis of Charcot-Marie-Tooth Disease and Hereditary Motor Neuropathy. Journal of Molecular Diagnostics, 2016, 18, 225-234.	1.2	36
45	Differential Features between Chronic Skin Inflammatory Diseases Revealed in Skin-Humanized Psoriasis and Atopic Dermatitis Mouse Models. Journal of Investigative Dermatology, 2016, 136, 136-145.	0.3	37
46	Babelomics 5.0: functional interpretation for new generations of genomic data. Nucleic Acids Research, 2015, 43, W117-W121.	6.5	114
47	Deregulation of key signaling pathways involved in oocyte maturation in FMR1 premutation carriers with Fragile X-associated primary ovarian insufficiency. Gene, 2015, 571, 52-57.	1.0	17
48	Whole-exome sequencing reveals ZNF408 as a new gene associated with autosomal recessive retinitis pigmentosa with vitreal alterations. Human Molecular Genetics, 2015, 24, 4037-4048.	1.4	41
49	BRCA1 Alternative splicing landscape in breast tissue samples. BMC Cancer, 2015, 15, 219.	1.1	17
50	Global Transcriptome Analysis of Primary Cerebrocortical Cells: Identification of Genes Regulated by Triiodothyronine in Specific Cell Types. Cerebral Cortex, 2015, 27, bhv273.	1.6	64
51	Capturing the biological impact of CDKN2A and MC1R genes as an early predisposing event in melanoma and non melanoma skin cancer. Oncotarget, 2014, 5, 1439-1451.	0.8	35
52	A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies. Nucleic Acids Research, 2014, 42, W88-W93.	6.5	39
53	The Activation of the Sox2 RR2 Pluripotency Transcriptional Reporter in Human Breast Cancer Cell Lines is Dynamic and Labels Cells with Higher Tumorigenic Potential. Frontiers in Oncology, 2014, 4, 308.	1.3	17
54	A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications. Nucleic Acids Research, 2014, 42, W83-W87.	6.5	6

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55	Programmed cell death activated by Rose Bengal in Arabidopsis thaliana cell suspension cultures requires functional chloroplasts. Journal of Experimental Botany, 2014, 65, 3081-3095.	2.4	41
56	Permanent Cardiac Sarcomere Changes in a Rabbit Model of Intrauterine Growth Restriction. PLoS ONE, 2014, 9, e113067.	1.1	21
57	Expression profiling shows differential molecular pathways and provides potential new diagnostic biomarkers for colorectal serrated adenocarcinoma. International Journal of Cancer, 2013, 132, 297-307.	2.3	43
58	Intrauterine growth restriction is associated with cardiac ultrastructural and gene expression changes related to the energetic metabolism in a rabbit model. American Journal of Physiology - Heart and Circulatory Physiology, 2013, 305, H1752-H1760.	1.5	24
59	Novel genes detected by transcriptional profiling from whole-blood cells in patients with early onset of acute coronary syndrome. Clinica Chimica Acta, 2013, 421, 184-190.	0.5	40
60	Grape antioxidant dietary fiber inhibits intestinal polyposis in Apc Min/+ mice: relation to cell cycle and immune response. Carcinogenesis, 2013, 34, 1881-1888.	1.3	38
61	Mammosphere Formation in Breast Carcinoma Cell Lines Depends upon Expression of E-cadherin. PLoS ONE, 2013, 8, e77281.	1.1	171
62	Role of <i><scp>CPI</scp>â€17</i> in restoring skin homoeostasis in cutaneous field of cancerization: effects of topical application of a filmâ€forming medical device containing photolyase and <scp>UV</scp> filters. Experimental Dermatology, 2013, 22, 494-496.	1.4	19
63	Maslinic Acid-Enriched Diet Decreases Intestinal Tumorigenesis in ApcMin/+ Mice through Transcriptomic and Metabolomic Reprogramming. PLoS ONE, 2013, 8, e59392.	1.1	46
64	IL1Î² Induces Mesenchymal Stem Cells Migration and Leucocyte Chemotaxis Through NF-ÎºB. Stem Cell Reviews and Reports, 2012, 8, 905-916.	5.6	153
65	Development, Characterization and Experimental Validation of a Cultivated Sunflower (Helianthus) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	28
66	Early peroxisome proliferator-activated receptor gamma regulated genes involved in expansion of pancreatic beta cell mass. BMC Medical Genomics, 2011, 4, 86.	0.7	15
67	Early Transcriptional Defense Responses in Arabidopsis Cell Suspension Culture under High-Light Conditions Â Â Â. Plant Physiology, 2011, 156, 1439-1456.	2.3	81
68	Does singlet oxygen activate cell death in Arabidopsis cell suspension cultures?: Analysis of the early transcriptional defense responses to high light stress. Plant Signaling and Behavior, 2011, 6, 1937-1942.	1.2	10
69	Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Nucleic Acids Research, 2010, 38, W210-W213.	6.5	283
70	Functional assessment of time course microarray data. BMC Bioinformatics, 2009, 10, S9.	1.2	19
71	Direct functional assessment of the composite phenotype through multivariate projection strategies. Genomics, 2008, 92, 373-383.	1.3	9
72	GEPAS, a web-based tool for microarray data analysis and interpretation. Nucleic Acids Research, 2008, 36, W308-W314.	6.5	67