Gloria Ribas Despuig

List of Publications by Year
in descending order

84 papers	7,479 citations	136740 32 h-index	56606 83 g-index
86 all docs	86 docs citations	86 times ranked	10286 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
2	Complete sequence and gene map of a human major histocompatibility complex. Nature, 1999, 401, 921-923.	13.7	1,011
3	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	9.4	591
4	Localization of type 1 diabetes susceptibility to the MHC class I genes HLA-B and HLA-A. Nature, 2007, 450, 887-892.	13.7	493
5	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434
6	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
7	Mutation in myosin heavy chain 6 causes atrial septal defect. Nature Genetics, 2005, 37, 423-428.	9.4	243
8	Herbicide-induced DNA damage in human lymphocytes evaluated by the single-cell gel electrophoresis (SCGE) assay. Mutation Research - Genetic Toxicology Testing and Biomonitoring of Environmental Or Occupational Exposure, 1995, 344, 41-54.	1.2	121
9	SLC45A2: a novel malignant melanoma-associated gene. Human Mutation, 2008, 29, 1161-1167.	1.1	98
10	Evaluating HapMap SNP data transferability in a large-scale genotyping project involving 175 cancer-associated genes. Human Genetics, 2006, 118, 669-679.	1.8	92
11	MC1R variants increased the risk of sporadic cutaneous melanoma in darkerâ€pigmented <scp>C</scp>aucasians: A pooledâ€analysis from the Mâ€SKIP project. International Journal of Cancer, 2015, 136, 618-631.	2.3	92
12	High stability of microRNAs in tissue samples of compromised quality. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2013, 463, 765-774.	1.4	78
13	Phenotypic Characterization of Nevus and Tumor Patterns in MITF E318K Mutation Carrier Melanoma Patients. Journal of Investigative Dermatology, 2014, 134, 141-149.	0.3	68
14	Genotoxicity of the herbicides alachlor and maleic hydrazide in cultured human lymphocytes. Mutagenesis, 1996, 11, 221-227.	1.0	64
15	Pigmentationâ€related genes and their implication in malignant melanoma susceptibility. Experimental Dermatology, 2009, 18, 634-642.	1.4	64
16	MC1R: three novel variants identified in a malignant melanoma association study in the Spanish population. Carcinogenesis, 2007, 28, 1659-1664.	1.3	60
17	ERCC4 Associated with Breast Cancer Risk: A Two-Stage Case-Control Study Using High-throughput Genotyping. Cancer Research, 2006, 66, 9420-9427.	0.4	58
18	Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1610-1616.	1.1	57

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19	MicroRNA profile in very young women with breast cancer. BMC Cancer, 2014, 14, 529.	1.1	56
20	Identification and functional analysis of novel variants of the human melanocortin 1 receptor found in melanoma patients. Human Mutation, 2009, 30, 811-822.	1.1	54
21	Genetic analysis of the vitamin D receptor gene in two epithelial cancers: melanoma and breast cancer case-control studies. BMC Cancer, 2008, 8, 385.	1.1	50
22	Genetic polymorphisms in DNA repair and oxidative stress pathways associated with malignant melanoma susceptibility. European Journal of Cancer, 2011, 47, 2618-2625.	1.3	46
23	Effects in the comet assay of storage conditions on human blood. Teratogenesis, Carcinogenesis, and Mutagenesis, 1997, 17, 115-125.	0.8	43
24	MC1R gene variants and non-melanoma skin cancer: a pooled-analysis from the M-SKIP project. British Journal of Cancer, 2015, 113, 354-363.	2.9	43
25	FANCD2 associated with sporadic breast cancer risk. Carcinogenesis, 2006, 27, 1930-1937.	1.3	40
26	MC1R, SLC45A2 and TYR genetic variants involved in melanoma susceptibility in Southern European populations: Results from a Meta-analysis. European Journal of Cancer, 2012, 48, 2183-2191.	1.3	40
27	Role of glutathione S-transferases in melanoma susceptibility: association with GSTP1 rs1695 polymorphism. British Journal of Dermatology, 2012, 166, 1176-1183.	1.4	40
28	Methylation deregulation of miRNA promoters identifies miR124-2 as a survival biomarker in Breast Cancer in very young women. Scientific Reports, 2018, 8, 14373.	1.6	38
29	Long telomere length and a TERT-CLPTM1 locus polymorphism association with melanoma risk. European Journal of Cancer, 2014, 50, 3168-3177.	1.3	35
30	Deregulation ofARID1A,CDH1,cMETandPIK3CAand target-related microRNA expression in gastric cancer. Oncotarget, 2015, 6, 26935-26945.	0.8	35
31	Assessing molecular subtypes of gastric cancer: microsatellite unstable and Epstein-Barr virus subtypes. Methods for detection and clinical and pathological implications. ESMO Open, 2019, 4, e000470.	2.0	35
32	Lack of genotoxicity of the herbicide atrazine in cultured human lymphocytes. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 1998, 416, 93-99.	0.9	33
33	Gender is a major factor explaining discrepancies in eye colour prediction based on HERC2/OCA2 genotype and the IrisPlex model. Forensic Science International: Genetics, 2013, 7, 453-460.	1.6	33
34	Genotoxicity of four herbicides in the Drosophila wing spot test. Mutation Research - Genetic Toxicology Testing and Biomonitoring of Environmental Or Occupational Exposure, 1992, 280, 291-295.	1.2	32
35	The Fanconi anemia family of genes and its correlation with breast cancer susceptibility and breast cancer features. Breast Cancer Research and Treatment, 2009, 118, 655-660.	1.1	32
36	Estrogen and progesterone receptor gene polymorphisms and sporadic breast cancer risk: A Spanish case-control study. International Journal of Cancer, 2006, 119, 467-471.	2.3	31

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37	Genetic variants in PARP1 (rs3219090) and IRF4(rs12203592) genes associated with melanoma susceptibility in a Spanish population. BMC Cancer, 2013, 13, 160.	1.1	31
38	MicroRNA Profile in Response to Doxorubicin Treatment in Breast Cancer. Journal of Cellular Biochemistry, 2015, 116, 2061-2073.	1.2	31
39	Low miR200c expression in tumor budding of invasive front predicts worse survival in patients with localized colon cancer and is related to PD-L1 overexpression. Modern Pathology, 2019, 32, 306-313.	2.9	31
40	Simultaneous Purifying Selection on the Ancestral MC1R Allele and Positive Selection on the Melanoma-Risk Allele V60L in South Europeans. Molecular Biology and Evolution, 2013, 30, 2654-2665.	3.5	30
41	Sex-specific genetic effects associated with pigmentation, sensitivity to sunlight, and melanoma in a population of Spanish origin. Biology of Sex Differences, 2016, 7, 17.	1.8	30
42	Genetic analysis of three important genes in pigmentation and melanoma susceptibility: CDKN2A, MC1R and HERC2/OCA2. Experimental Dermatology, 2010, 19, 836-844.	1.4	28
43	Genes involved in the <scp>WNT</scp> and vesicular trafficking pathways are associated with melanoma predisposition. International Journal of Cancer, 2015, 136, 2109-2119.	2.3	27
44	The variant E233G of theRAD51Dgene could be a low-penetrance allele in high-risk breast cancer families withoutBRCA1/2mutations. International Journal of Cancer, 2004, 110, 845-849.	2.3	26
45	Complex haplotypic structure of the central MHC region flanking TNF in a West African population. Genes and Immunity, 2003, 4, 476-486.	2.2	24
46	rs12512631 on the Group Specific Complement (Vitamin D-Binding Protein GC) Implicated in Melanoma Susceptibility. PLoS ONE, 2013, 8, e59607.	1.1	21
47	Involvement of Different networks in mammary gland involution after the pregnancy/lactation cycle: Implications in breast cancer. IUBMB Life, 2015, 67, 227-238.	1.5	21
48	Genotoxic evaluation of the herbicide trifluralin on human lymphocytes exposed in vitro. Mutation Research - Genetic Toxicology Testing and Biomonitoring of Environmental Or Occupational Exposure, 1996, 371, 15-21.	1.2	20
49	Single-nucleotide polymorphism detection by denaturing high-performance liquid chromatography and direct sequencing in genes in the MHC classÂIII region encoding novel cell surface molecules. Immunogenetics, 2001, 53, 369-381.	1.2	20
50	Clinical implications of routine genomic mutation sequencing in PIK3CA/AKT1 and KRAS/NRAS/BRAF in metastatic breast cancer. Breast Cancer Research and Treatment, 2016, 160, 69-77.	1.1	20
51	Sister-chromatid exchanges (SCE) induction by inhibitors of DNA topoisomerases in cultured human lymphocytes. Mutation Research - Genetic Toxicology Testing and Biomonitoring of Environmental Or Occupational Exposure, 1996, 368, 205-211.	1.2	18
52	A Customized Pigmentation SNP Array Identifies a Novel SNP Associated with Melanoma Predisposition in the SLC45A2 Gene. PLoS ONE, 2011, 6, e19271.	1.1	18
53	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: AÂPooled Analysis from the M-Skip Project. Journal of Investigative Dermatology, 2016, 136, 1914-1917.	0.3	16
54	Acceleration in the DNA methylation age in breast cancer tumours from very young women. Scientific Reports, 2019, 9, 14991.	1.6	16

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55	MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. The Lancet Child and Adolescent Health, 2019, 3, 332-342.	2.7	16
56	HDAC5 Inhibitors as a Potential Treatment in Breast Cancer Affecting Very Young Women. Cancers, 2020, 12, 412.	1.7	16
57	Evaluating new candidate SNPs as low penetrance risk factors in sporadic breast cancer: A two-stage Spanish caseâ€“control study. Gynecologic Oncology, 2009, 112, 210-214.	0.6	13
58	MassARRAY determination of somatic oncogenic mutations in solid tumors: Moving forward to personalized medicine. Cancer Treatment Reviews, 2016, 49, 57-64.	3.4	13
59	A novel gene encoding a coiled-coil mitochondrial protein located at the telomeric end of the human MHC Class III region. Gene, 2003, 314, 41-54.	1.0	12
60	Melanocortin-1 receptor, skin cancer and phenotypic characteristics (M-SKIP) project: study design and methods for pooling results of genetic epidemiological studies. BMC Medical Research Methodology, 2012, 12, 116.	1.4	12
61	Epigenetic changes in localized gastric cancer: the role of RUNX3 in tumor progression and the immune microenvironment. Oncotarget, 2016, 7, 63424-63436.	0.8	12
62	Involvement of ANXA5 and ILKAP in Susceptibility to Malignant Melanoma. PLoS ONE, 2014, 9, e95522.	1.1	11
63	Determination of somatic oncogenic mutations linked to target-based therapies using MassARRAY technology. Oncotarget, 2016, 7, 22543-22555.	0.8	11
64	Genetic Variability of Immunomodulatory Genes in Ectromelia Virus Isolates Detected by Denaturing High-Performance Liquid Chromatography. Journal of Virology, 2003, 77, 10139-10146.	1.5	10
65	Sex and MC1R variants in human pigmentation: Differences in tanning ability and sensitivity to sunlight between sexes. Journal of Dermatological Science, 2016, 84, 346-348.	1.0	10
66	Breast Cancer in Very Young Patients in a Spanish Cohort: Age as an Independent Bad Prognostic Indicator. Breast Cancer: Basic and Clinical Research, 2019, 13, 117822341982876.	0.6	10
67	Genetic 3â€²<scp>UTR</scp> variation is associated with human pigmentation characteristics and sensitivity to sunlight. Experimental Dermatology, 2017, 26, 896-903.	1.4	9
68	Allelic expression and quantitative RT-PCR study of TAp73 and Î”Np73 in non-Hodgkin's lymphomas. Leukemia Research, 2006, 30, 170-177.	0.4	8
69	A novel adenine-based diruthenium(III) complex: Synthesis, crystal structure, electrochemical properties and evaluation of the anticancer activity. Journal of Inorganic Biochemistry, 2022, 232, 111812.	1.5	8
70	Haplotype patterns in cancer-related genes with long-range linkage disequilibrium: no evidence of association with breast cancer or positive selection. European Journal of Human Genetics, 2008, 16, 252-260.	1.4	7
71	Gender and eye colour prediction discrepancies: A reply to criticisms. Forensic Science International: Genetics, 2014, 9, e7-e9.	1.6	6
72	Modeling MC1R Rare Variants: A Structural Evaluation of Variants Detected in a Mediterranean Caseâ€“Control Study. Journal of Investigative Dermatology, 2014, 134, 1146-1149.	0.3	6

#	Article	IF	Citations
73	MC1R variants and cutaneous melanoma risk according to histological type, body site, and Breslow thickness: a pooled analysis from the M-SKIP project. Melanoma Research, 2020, 30, 500-510.	0.6	6
74	Niveles de 25-hidroxivitamina D en pacientes con melanoma y factores asociados con su insuficiencia. Actas Dermo-sifiliogrÃ¡ficas, 2016, 107, 758-764.	0.2	5
75	Genotoxicity of tritiated water in human lymphocytes. Toxicology Letters, 1994, 70, 63-69.	0.4	4
76	Conceptual schema of miRNA's expression: Using efficient information systems practices to manage and analyse data about miRNA expression studies in breast cancer. , 2016, , .		4
77	Germinal and somatic mutation induction in Drosophila after treatment of larvae with tritiated water. Mutation Research - Genetic Toxicology Testing and Biomonitoring of Environmental Or Occupational Exposure, 1992, 278, 43-46.	1.2	3
78	Human Î²-defensins (HBD1 and HBD3) and malignant melanoma susceptibility. Melanoma Research, 2009, 19, 340-341.	0.6	3
79	Phenotypic and Histologic Characteristics of Cutaneous Melanoma in Patients With Melanocortin-1 Receptor Polymorphisms. Actas Dermo-sifiliogrÃ¡ficas, 2012, 103, 44-50.	0.2	3
80	First Nationwide Molecular Screening Program in Spain for Patients With Advanced Breast Cancer: Results From the AGATA SOLTI-1301 Study. Frontiers in Oncology, 2021, 11, 744112.	1.3	3
81	Molecular profile in Paraguayan colorectal cancer patients, towards to a precision medicine strategy. Cancer Medicine, 2019, 8, 3120-3130.	1.3	2
82	Sun exposure and PDZK1 genotype modulate PDZK1 gene expression in normal skin. Photodermatology Photoimmunology and Photomedicine, 2020, 36, 70-72.	0.7	1
83	Younger age as a prognostic indicator in breast cancer: Correlation between clinical-pathologic factors and miRNAs and long-term follow-up. Annals of Oncology, 2016, 27, vi55.	0.6	0
84	miRNA Expression Analysis: Cell Lines HCC1500 and HCC1937 as Models for Breast Cancer in Young Women and the miR-23a as a Poor Prognostic Biomarker. Breast Cancer: Basic and Clinical Research, 2020, 14, 117822342097784.	0.6	0