Anna Gonzalez-Neira

List of Publications by Year
in descending order

177 papers	17,268 citations	23500 58 h-index	15683 125 g-index
188 all docs	188 docs citations	188 times ranked	20768 citing authors

#	Article	IF	Citations
1	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
2	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
3	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
4	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
5	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	3.0	45
6	Regulatory CDH4 Genetic Variants Associate With Risk to Develop Capecitabineâ€Induced Handâ€Foot Syndrome. Clinical Pharmacology and Therapeutics, 2021, 109, 462-470.	2.3	6
7	CSVS, a crowdsourcing database of the Spanish population genetic variability. Nucleic Acids Research, 2021, 49, D1130-D1137.	6.5	34
8	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	2.9	5
9	Pharmacogenetics and personalized medicine. , 2021, , 193-219.		0
10	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
11	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
12	Whole exome sequencing characterization of individuals presenting extreme phenotypes of high and low risk of developing tobacco-induced lung adenocarcinoma. Translational Lung Cancer Research, 2021, 10, 1327-1337.	1.3	3
13	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	1.7	4
14	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6
15	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
16	POLRMT as a Novel Susceptibility Gene for Cardiotoxicity in Epirubicin Treatment of Breast Cancer Patients. Pharmaceutics, 2021, 13, 1942.	2.0	7
17	Hsaâ€miRâ€139â€5p is a prognostic thyroid cancer marker involved in HNRNPFâ€mediated alternative splicing. International Journal of Cancer, 2020, 146, 521-530.	2.3	29
18	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120

#	Article	IF	Citations
19	BRAF V600E Detection in Liquid Biopsies from Pediatric Central Nervous System Tumors. Cancers, 2020, 12, 66.	1.7	35
20	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	1.1	82
21	Association Between ABCB1 Genetic Variants and Persistent Chemotherapy-Induced Alopecia in Women With Breast Cancer. JAMA Dermatology, 2020, 156, 987.	2.0	8
22	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
23	Low-frequency variation near common germline susceptibility loci are associated with risk of Ewing sarcoma. PLoS ONE, 2020, 15, e0237792.	1.1	6
24	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
25	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
26	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
27	Title is missing!. , 2020, 15, e0237792.		0
28	Title is missing!. , 2020, 15, e0237792.		0
29	Title is missing!. , 2020, 15, e0237792.		0
30	Title is missing!. , 2020, 15, e0237792.		0
31	The functional ALDH2 polymorphism is associated with breast cancer risk: A pooled analysis from the Breast Cancer Association Consortium. Molecular Genetics & Genomic Medicine, 2019, 7, e707.	0.6	9
32	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
33	Polyethylene glycol improves current methods for circulating extracellular vesicle-derived DNA isolation. Journal of Translational Medicine, 2019, 17, 75.	1.8	55
34	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
35	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
36	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	0.9	81

#	Article	IF	Citations
37	Whole exome sequencing of germline DNA of individuals presenting extreme phenotypes of high and low risk to develop tobacco-induced lung adenocarcinoma (LUAD) according to KRAS status.. Journal of Clinical Oncology, 2019, 37, 1540-1540.	0.8	1
38	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19
39	Exome array analysis identifies ETFB as a novel susceptibility gene for anthracycline-induced cardiotoxicity in cancer patients. Breast Cancer Research and Treatment, 2018, 167, 249-256.	1.1	23
40	Pharmacogenetic variants and response to neoadjuvant single-agent doxorubicin or docetaxel. Pharmacogenetics and Genomics, 2018, 28, 245-250.	0.7	3
41	Genomic characterization of individuals presenting extreme phenotypes of high and low risk to develop tobacco-induced lung cancer. Cancer Medicine, 2018, 7, 3474-3483.	1.3	11
42	Genome-wide association study identifies multiple new loci associated with Ewing sarcoma susceptibility. Nature Communications, 2018, 9, 3184.	5.8	50
43	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
44	The application of cognitive computing technology in genomics in precision oncological medicine: The Sistemas Genomicos Experience.. Journal of Clinical Oncology, 2018, 36, e18544-e18544.	0.8	1
45	Abstract 2970: Multiple new susceptibility loci identified in genome-wide association study of Ewing sarcoma. , 2018, , .		0
46	Abstract A13: Genome-wide association study identifies multiple new loci associated with Ewing sarcoma susceptibility. , 2018, , .		0
47	Genetic alterations of <scp>IDH</scp>1 and Vegf in brain tumors. Brain and Behavior, 2017, 7, e00718.	1.0	5
48	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
49	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
50	Exome array analysis identifies GPR35 as a novel susceptibility gene for anthracycline-induced cardiotoxicity in childhood cancer. Pharmacogenetics and Genomics, 2017, 27, 445-453.	0.7	22
51	Pharmacogenetics of Chemotherapy Response in Osteosarcoma: A Genetic Variant in SLC7A8 is Associated with Progressive Disease. Clinical Therapeutics, 2017, 39, e10.	1.1	2
52	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	2.2	43
53	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
54	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	0.8	31

#	Article	IF	Citations
55	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
56	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
57	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	2.2	31
58	Inflammatory-Related Genetic Variants in Nonâ€“Muscle-Invasive Bladder Cancer Prognosis: A Multimarker Bayesian Assessment. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1144-1150.	1.1	8
59	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
60	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
61	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
62	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	1.6	2
63	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
64	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
65	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
66	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	1.6	19
67	Identification of genetic variants in pharmacokinetic genes associated with Ewing Sarcoma treatment outcome. Annals of Oncology, 2016, 27, 1788-1793.	0.6	10
68	DNMT1 Inhibition Reprograms Pancreatic Cancer Stem Cells via Upregulation of the miR-17-92 Cluster. Cancer Research, 2016, 76, 4546-4558.	0.4	94
69	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
70	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
71	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. Human Genetics, 2016, 135, 137-154.	1.8	8
72	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77

#	Article	IF	Citations
73	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
74	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	2.3	34
75	Genome wide association study identifies a novel putative mammographic density locus at 1q12â€q21. International Journal of Cancer, 2015, 136, 2427-2436.	2.3	18
76	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.2	0
77	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
78	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
79	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	2.6	76
80	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	1.3	14
81	Genome-wide linkage analysis and tumoral characterization reveal heterogeneity in familial colorectal cancer type X. Journal of Gastroenterology, 2015, 50, 657-666.	2.3	28
82	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
83	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	2.6	37
84	Multi-stage genome-wide association study identifies new susceptibility locus for testicular germ cell tumour on chromosome 3q25. Human Molecular Genetics, 2015, 24, 1169-1176.	1.4	31
85	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
86	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
87	Standard Versus Continuous Administration of Capecitabine in Metastatic Breast Cancer (GEICAM/2009-05): A Randomized, Noninferiority Phase II Trial With a Pharmacogenetic Analysis. Oncologist, 2015, 20, 111-112.	1.9	20
88	A candidate gene study of capecitabine-related toxicity in colorectal cancer identifies new toxicity variants atDPYDand a putative role forENOSF1rather thanTYMS. Gut, 2015, 64, 111-120.	6.1	93
89	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38
90	Genetic Variation in the TP53 Pathway and Bladder Cancer Risk. A Comprehensive Analysis. PLoS ONE, 2014, 9, e89952.	1.1	18

#	Article	IF	Citations
91	Oxidative stress in susceptibility to breast cancer: study in Spanish population. BMC Cancer, 2014, 14, 861.	1.1	34
92	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
93	Exome sequencing of three cases of familial exceptional longevity. Aging Cell, 2014, 13, 1087-1090.	3.0	16
94	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
95	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	2.2	97
96	Identification of genetic variants associated with capecitabine-induced handâ€“foot syndrome through integration of patient and cell line genomic analyses. Pharmacogenetics and Genomics, 2014, 24, 231-237.	0.7	10
97	Tu1938 Identification of New Genetic Variants Related to Thiopurine-Induced Myelotoxicity in Inflammatory Bowel Disease (IBD) Patients With Normal Thiopurines-Methyltransferase (TPMT): A Genome-Wide Association Study. Gastroenterology, 2014, 146, S-877.	0.6	0
98	P651 Identification of new genetic variants related to thiopurine-induced myelotoxicity in inflammatory bowel disease (IBD) patients with normal thiopurines-methyltransferase (TPMT): a genome-wide association study. Journal of Crohn's and Colitis, 2014, 8, S342.	0.6	0
99	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	1.4	32
100	Genetic Markers of Toxicity From Capecitabine and Other Fluorouracil-Based Regimens: Investigation in the QUASAR2 Study, Systematic Review, and Meta-Analysis. Journal of Clinical Oncology, 2014, 32, 1031-1039.	0.8	216
101	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	2.9	21
102	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
103	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
104	Genome Wide Association Study (Gwas) for Identification of Single Nucleotide Polymorphisms (Snps) Associated with Individuals Presenting Extreme Phenotypes of Tobacco Induced Non-Small Cell Lung Cancer (Nsclc) Risk. Annals of Oncology, 2014, 25, iv548.	0.6	0
105	Identification through genome-wide association study (GWAS) of single nucleotide polymorphisms (SNPs) associated with extreme phenotypes of tobacco-induced non-small cell lung cancer (NSCLC) risk.. Journal of Clinical Oncology, 2014, 32, 11046-11046.	0.8	1
106	Influence of Genetic Variants in TPMT and COMT Associated with Cisplatin Induced Hearing Loss in Patients with Cancer: Two New Cohorts and a Meta-Analysis Reveal Significant Heterogeneity between Cohorts. PLoS ONE, 2014, 9, e115869.	1.1	47
107	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	9.4	493
108	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	2.6	201

#	Article	IF	Citations
109	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
110	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
111	Association analysis between breast cancer genetic variants and mammographic density in a large population-based study (Determinants of Density in Mammographies in Spain) identifies susceptibility loci in TOX3 gene. European Journal of Cancer, 2013, 49, 474-481.	1.3	24
112	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genomeâ€“wide interaction study. Endocrine-Related Cancer, 2013, 20, 875-887.	1.6	26
113	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
114	Genome-wide association study identifies ephrin type A receptors implicated in paclitaxel induced peripheral sensory neuropathy. Journal of Medical Genetics, 2013, 50, 599-605.	1.5	67
115	Whole Exome Sequencing Suggests Much of Non-BRCA1/BRCA2 Familial Breast Cancer Is Due to Moderate and Low Penetrance Susceptibility Alleles. PLoS ONE, 2013, 8, e55681.	1.1	95
116	Application of Multi-SNP Approaches Bayesian LASSO and AUC-RF to Detect Main Effects of Inflammatory-Gene Variants Associated with Bladder Cancer Risk. PLoS ONE, 2013, 8, e83745.	1.1	21
117	The GoldenGate Genotyping Assay: Custom Design, Processing, and Data Analysis. Methods in Molecular Biology, 2013, 1015, 147-153.	0.4	3
118	Common Breast Cancer Susceptibility Variants in LSP1 and RAD51L1 Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1156-1166.	1.1	101
119	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
120	Pharmacogenetics of chemotherapy efficacy in breast cancer. Pharmacogenomics, 2012, 13, 677-690.	0.6	20
121	Common variants near TARDBP and EGR2 are associated with susceptibility to Ewing sarcoma. Nature Genetics, 2012, 44, 323-327.	9.4	160
122	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	1.1	51
123	Exome sequencing identifies MAX mutations as a cause of hereditary pheochromocytoma. Nature Genetics, 2011, 43, 663-667.	9.4	478
124	Single nucleotide polymorphisms of matrix metalloproteinase 9 (MMP9) and tumor protein 73 (TP73) interact with Epstein-Barr virus in chronic lymphocytic leukemia: results from the European case-control study EpiLymph. Haematologica, 2011, 96, 323-327.	1.7	15
125	Rationale for an international consortium to study inherited genetic susceptibility to childhood acute lymphoblastic leukemia. Haematologica, 2011, 96, 1049-1054.	1.7	36
126	Genetic polymorphisms among C57BL/6 mouse inbred strains. Transgenic Research, 2011, 20, 481-489.	1.3	160

#	Article	IF	Citations
127	Constitutional mosaic genome-wide uniparental disomy due to diploidisation: an unusual cancer-predisposing mechanism. Journal of Medical Genetics, 2011, 48, 212-216.	1.5	32
128	A Polymorphism in the Cytidine Deaminase Promoter Predicts Severe Capecitabine-Induced Hand-Foot Syndrome. Clinical Cancer Research, 2011, 17, 2006-2013.	3.2	75
129	Multiple Genetic Loci Modulate Lung Adenocarcinoma Clinical Staging. Clinical Cancer Research, 2011, 17, 2410-2416.	3.2	11
130	Evaluation of variation in the phosphoinositide-3-kinase catalytic subunit alpha oncogene and breast cancer risk. British Journal of Cancer, 2011, 105, 1934-1939.	2.9	4
131	Effect of ABCB1 and ABCC3 Polymorphisms on Osteosarcoma Survival after Chemotherapy: A Pharmacogenetic Study. PLoS ONE, 2011, 6, e26091.	1.1	72
132	Variation in CDKN2A at 9p21.3 influences childhood acute lymphoblastic leukemia risk. Nature Genetics, 2010, 42, 492-494.	9.4	248
133	Genome-wide association study in discordant sibships identifies multiple inherited susceptibility alleles linked to lung cancer. Carcinogenesis, 2010, 31, 462-465.	1.3	15
134	Common variations in ERCC2 are associated with response to cisplatin chemotherapy and clinical outcome in osteosarcoma patients. Pharmacogenomics Journal, 2009, 9, 347-353.	0.9	112
135	Genetics of Pheochromocytoma and Paraganglioma in Spanish Patients. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 1701-1705.	1.8	120
136	Risk of Estrogen Receptorâ€"Positive and â€"Negative Breast Cancer and Singleâ€"Nucleotide Polymorphism 2q35-rs13387042. Journal of the National Cancer Institute, 2009, 101, 1012-1018.	3.0	99
137	Mouse Genome-Wide Association Mapping Needs Linkage Analysis to Avoid False-Positive Loci. PLoS Genetics, 2009, 5, e1000331.	1.5	54
138	The Variant rs1867277 in FOXE1 Gene Confers Thyroid Cancer Susceptibility through the Recruitment of USF1/USF2 Transcription Factors. PLoS Genetics, 2009, 5, e1000637.	1.5	140
139	The SRY-HMG box gene, SOX4, is a target of gene amplification at chromosome 6p in lung cancerâ€. Human Molecular Genetics, 2009, 18, 1343-1352.	1.4	99
140	A 7 Mb region within 11q13 may contain a high penetrance gene for breast cancer. Breast Cancer Research and Treatment, 2009, 118, 151-159.	1.1	23
141	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. European Journal of Human Genetics, 2009, 17, 1490-1494.	1.4	17
142	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434
143	Genome-wide Linkage Scan Reveals Three Putative Breast-Cancer-Susceptibility Loci. American Journal of Human Genetics, 2009, 84, 115-122.	2.6	30
144	Early-Onset Familial Lewy Body Dementia With Extensive Tauopathy: A Clinical, Genetic, and Neuropathological Study. Journal of Neuropathology and Experimental Neurology, 2009, 68, 73-82.	0.9	33

#	Article	IF	Citations
145	A polygenic model with common variants may predict lung adenocarcinoma risk in humans. International Journal of Cancer, 2008, 123, 2327-2330.	2.3	13
146	Genetic control of resistance to hepatocarcinogenesis by the mouseHpcr3locus. Hepatology, 2008, 48, 617-623.	3.6	16
147	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
148	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
149	Neurofibromatosis 1, and Not TP53, Seems to Be the Main Target of Chromosome 17 Deletions in De Novo Acute Myeloid Leukemia. Journal of Clinical Oncology, 2007, 25, 1151-1152.	0.8	8
150	Association Study of 69 Genes in the Ret Pathway Identifies Low-penetrance Loci in Sporadic Medullary Thyroid Carcinoma. Cancer Research, 2007, 67, 9561-9567.	0.4	36
151	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	9.4	591
152	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
153	Genomewide high-density SNP linkage analysis of non-BRCA1/2 breast cancer families identifies various candidate regions and has greater power than microsatellite studies. BMC Genomics, 2007, 8, 299.	1.2	26
154	Variation in estimated recombination rates across human populations. Human Genetics, 2007, 122, 301-310.	1.8	40
155	Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. Annals of Human Genetics, 2006, 70, 459-487.	0.3	97
156	Extreme population differences across Neuregulin 1 gene, with implications for association studies. Molecular Psychiatry, 2006, 11, 66-75.	4.1	83
157	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
158	The portability of tagSNPs across populations: A worldwide survey. Genome Research, 2006, 16, 323-330.	2.4	82
159	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
160	High prevalence of theW24X mutation in the gene encoding connexin-26 (GJB2) in Spanish Romani (gypsies) with autosomal recessive non-syndromic hearing loss. American Journal of Medical Genetics, Part A, 2005, 137A, 255-258.	0.7	68
161	Micro-geographical differentiation in Northern Iberia revealed by Y-chromosomal DNA analysis. Gene, 2004, 329, 17-25.	1.0	38
162	Geographic stratification of linkage disequilibrium: a worldwide population study in a region of chromosome 22. Human Genomics, 2004, 1, 399.	1.4	13

#	Article	IF	Citations
163	Extending STR markers in Y chromosome haplotypes. International Journal of Legal Medicine, 2003, 117, 27-33.	1.2	60
164	Insights into Iberian population origins through the construction of highly informative Y-chromosome haplotypes using biallelic markers, STRs, and the MSY1 minisatellite. American Journal of Physical Anthropology, 2003, 122, 147-161.	2.1	30
165	Optimisation of Y-STR multiplexing combining established and newly described loci. International Congress Series, 2003, 1239, 415-418.	0.2	0
166	Y-chromosome short tandem repeat polymorphisms: a comparison between humans and chimpanzees. International Congress Series, 2003, 1239, 287-290.	0.2	0
167	Microgeographic patterns of highly informative Y-chromosome haplotypes (using biallelic markers) Tj ETQq1 1 0.784314 rgBT /Overlock Series, 2003, 1239, 61-66.	0.2	0
168	Sequence structure of 12 novel Y chromosome microsatellites and PCR amplification strategies. International Congress Series, 2003, 1239, 425-429.	0.2	0
169	Structure of Linkage Disequilibrium in Humans: Genome Factors and Population Stratification. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 79-88.	2.0	12
170	Genetic diversity of Y-specific STRs in chimpanzees (Pan troglodytes). American Journal of Primatology, 2002, 57, 21-29.	0.8	11
171	Point mutations in the flanking regions of the Y-chromosome specific STRs DYS391, DYS437 and DYS438. International Journal of Legal Medicine, 2002, 116, 322-326.	1.2	14
172	Chimpanzee homologous of human Y specific STRs. Forensic Science International, 2002, 126, 129-136.	1.3	50
173	Sequence structure of 12 novel Y chromosome microsatellites and PCR amplification strategies. Forensic Science International, 2001, 122, 19-26.	1.3	33
174	Alternative primers for DYS391 typing: advantages of their application to forensic genetics. Forensic Science International, 2000, 112, 49-57.	1.3	30
175	Distribution of Y-chromosome STR defined haplotypes in Iberia. Forensic Science International, 2000, 110, 117-126.	1.3	43
176	Y chromosome specific polymorphisms in forensic analysis. Legal Medicine, 1999, 1, 55-60.	0.6	17
177	Robustness of the Y STRs DYS19, DYS389 I and II, DYS390 and DYS393: optimization of a PCR pentaplex. Forensic Science International, 1999, 106, 163-172.	1.3	70