Angela R Brooks-Wilson

List of Publications by Year
in descending order

187 papers	17,712 citations	31976 53 h-index	14759 127 g-index
194 all docs	194 docs citations	194 times ranked	24092 citing authors

#	Article	IF	Citations
1	The Genome Sequence of the SARS-Associated Coronavirus. Science, 2003, 300, 1399-1404.	12.6	1,842
2	Mutations in ABC1 in Tangier disease and familial high-density lipoprotein deficiency. Nature Genetics, 1999, 22, 336-345.	21.4	1,609
3	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
4	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
5	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
6	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.	21.4	493
7	Gender and telomere length: Systematic review and meta-analysis. Experimental Gerontology, 2014, 51, 15-27.	2.8	394
8	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
9	Mutations in the ABC 1 gene in familial HDL deficiency with defective cholesterol efflux. Lancet, The, 1999, 354, 1341-1346.	13.7	345
10	Genetic variation in TNF and IL10 and risk of non-Hodgkin lymphoma: a report from the InterLymph Consortium. Lancet Oncology, The, 2006, 7, 27-38.	10.7	345
11	Germline E-cadherin mutations in hereditary diffuse gastric cancer: assessment of 42 new families and review of genetic screening criteria. Journal of Medical Genetics, 2004, 41, 508-517.	3.2	327
12	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
13	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
14	Two Genes That Map to the STSL Locus Cause Sitosterolemia: Genomic Structure and Spectrum of Mutations Involving Sterolin-1 and Sterolin-2, Encoded by ABCG5 and ABCG8, Respectively. American Journal of Human Genetics, 2001, 69, 278-290.	6.2	318
15	Age and residual cholesterol efflux affect HDL cholesterol levels and coronary artery disease in ABCA1 heterozygotes. Journal of Clinical Investigation, 2000, 106, 1263-1270.	8.2	295
16	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
17	Common Genetic Variation inABCA1Is Associated With Altered Lipoprotein Levels and a Modified Risk for Coronary Artery Disease. Circulation, 2001, 103, 1198-1205.	1.6	280
18	Genetics of healthy aging and longevity. Human Genetics, 2013, 132, 1323-1338.	3.8	274

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19	Etiologic Heterogeneity Among Non-Hodgkin Lymphoma Subtypes: The InterLymph Non-Hodgkin Lymphoma Subtypes Project. Journal of the National Cancer Institute Monographs, 2014, 2014, 130-144.	2.1	265
20	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
21	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
22	Analysis of long-lived C. elegans daf-2 mutants using serial analysis of gene expression. Genome Research, 2005, 15, 603-615.	5.5	180
23	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	21.4	179
24	Human ABCA1 BAC Transgenic Mice Show Increased High Density Lipoprotein Cholesterol and ApoAI-dependent Efflux Stimulated by an Internal Promoter Containing Liver X Receptor Response Elements in Intron 1. Journal of Biological Chemistry, 2001, 276, 33969-33979.	3.4	176
25	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
26	Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. Nature Genetics, 2010, 42, 661-664.	21.4	152
27	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	6.3	152
28	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	21.4	147
29	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
30	Genetic variants at 6p21.33 are associated with susceptibility to follicular lymphoma. Nature Genetics, 2009, 41, 873-875.	21.4	142
31	BCL2 mutations in diffuse large B-cell lymphoma. Leukemia, 2012, 26, 1383-1390.	7.2	135
32	Diffuse large B-cell lymphoma: reduced CD20 expression is associated with an inferior survival. Blood, 2009, 113, 3773-3780.	1.4	133
33	Tumor Necrosis Factor (TNF) and Lymphotoxin-Â (LTA) Polymorphisms and Risk of Non-Hodgkin Lymphoma in the InterLymph Consortium. American Journal of Epidemiology, 2010, 171, 267-276.	3.4	128
34	Organochlorines and risk of nonâ€Hodgkin lymphoma. International Journal of Cancer, 2007, 121, 2767-2775.	5.1	121
35	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
36	Cholesterol efflux regulatory protein, Tangier disease and familial high-density lipoprotein deficiency. Current Opinion in Lipidology, 2000, 11, 117-122.	2.7	111

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37	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	1.9	111
38	High-resolution whole genome tiling path array CGH analysis of CD34+ cells from patients with low-risk myelodysplastic syndromes reveals cryptic copy number alterations and predicts overall and leukemia-free survival. Blood, 2008, 112, 3412-3424.	1.4	108
39	Differential expression of a novel ankyrin containing E3 ubiquitin-protein ligase, Hace1, in sporadic Wilms' tumor versus normal kidney. Human Molecular Genetics, 2004, 13, 2061-2074.	2.9	100
40	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
41	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	6.2	96
42	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	12.8	94
43	GWAS of Follicular Lymphoma Reveals Allelic Heterogeneity at 6p21.32 and Suggests Shared Genetic Susceptibility with Diffuse Large B-cell Lymphoma. PLoS Genetics, 2011, 7, e1001378.	3.5	93
44	Progeria of Stem Cells: Stem Cell Exhaustion in Hutchinson-Gilford Progeria Syndrome. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2007, 62, 3-8.	3.6	81
45	The Relationship between Telomere Length and Mortality in Chronic Obstructive Pulmonary Disease (COPD). PLoS ONE, 2012, 7, e35567.	2.5	80
46	Genome-wide significant risk associations for mucinous ovarian carcinoma. Nature Genetics, 2015, 47, 888-897.	21.4	78
47	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	12.8	75
48	Rapid cloning and characterization of new chromosome 10 DNA markers by Alu element-mediated PCR. Genomics, 1990, 7, 614-620.	2.9	74
49	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	1.9	71
50	Genetic variations of NAT2 and CYP2E1 and isoniazid hepatotoxicity in a diverse population. Pharmacogenomics, 2009, 10, 1433-1445.	1.3	69
51	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
52	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
53	Reduced telomere length variation in healthy oldest old. Mechanisms of Ageing and Development, 2008, 129, 638-641.	4.6	59
54	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	12.8	58

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55	Associations of Non-Hodgkin Lymphoma (NHL) Risk With Autoimmune Conditions According to Putative NHL Loci. American Journal of Epidemiology, 2015, 181, 406-421.	3.4	54
56	CD20 mutations involving the rituximab epitope are rare in diffuse large B-cell lymphomas and are not a significant cause of R-CHOP failure. Haematologica, 2009, 94, 423-427.	3.5	53
57	Shift work, circadian gene variants and risk of breast cancer. Cancer Epidemiology, 2013, 37, 606-612.	1.9	52
58	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	2.9	52
59	GBVâ€C/hepatitis G virus infection and nonâ€Hodgkin lymphoma: a case control study. International Journal of Cancer, 2010, 126, 2885-2892.	5.1	51
60	Identification and functional analysis of a naturally occurring E89K mutation in the ABCA1 gene of the WHAM chicken. Journal of Lipid Research, 2002, 43, 1610-1617.	4.2	49
61	Genetic variation in carboxylesterase genes and susceptibility to isoniazid-induced hepatotoxicity. Pharmacogenomics Journal, 2010, 10, 524-536.	2.0	49
62	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. PLoS ONE, 2011, 6, e24987.	2.5	48
63	Risk of Ovarian Cancer and the NF-ÎºB Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.9	48
64	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	7.0	47
65	Ovarian Carcinoma Histotype: Strengths and Limitations of Integrating Morphology With Immunohistochemical Predictions. International Journal of Gynecological Pathology, 2019, 38, 353-362.	1.4	45
66	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
67	Genetic Variation in Healthy Oldest-Old. PLoS ONE, 2009, 4, e6641.	2.5	42
68	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
69	Genetic Variation in H2AFX Contributes to Risk of Nonâ€“Hodgkin Lymphoma. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1098-1106.	2.5	37
70	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	1.0	37
71	Initial association of NR2E1 with bipolar disorder and identification of candidate mutations in bipolar disorder, schizophrenia, and aggression through resequencing. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 880-889.	1.7	36
72	Interaction between organochlorines and the AHR gene, and risk of non-Hodgkin lymphoma. Cancer Causes and Control, 2010, 21, 11-22.	1.8	36

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73	Prevalence and type distribution of human papillomavirus in 5,000 British Columbia womenâ€"implications for vaccination. Cancer Causes and Control, 2009, 20, 1387-1396.	1.8	35
74	Clinical and pathological associations of PTEN expression in ovarian cancer: a multicentre study from the Ovarian Tumour Tissue Analysis Consortium. British Journal of Cancer, 2020, 123, 793-802.	6.4	35
75	PRRC2A and BCL2L11 gene variants influence risk of non-Hodgkin lymphoma: results from the InterLymph consortium. Blood, 2012, 120, 4645-4648.	1.4	34
76	HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. Cancer Research, 2018, 78, 4086-4096.	0.9	34
77	Racial/ethnic differences in the epidemiology of ovarian cancer: a pooled analysis of 12 case-control studies. International Journal of Epidemiology, 2018, 47, 460-472.	1.9	33
78	Medical History, Lifestyle, Family History, and Occupational Risk Factors for Lymphoplasmacytic Lymphoma/Waldenstrom's Macroglobulinemia: The InterLymph Non-Hodgkin Lymphoma Subtypes Project. Journal of the National Cancer Institute Monographs, 2014, 2014, 87-97.	2.1	32
79	Incidence and Survival for Gastric and Esophageal Cancer Diagnosed in British Columbia, 1990 to 1999. Canadian Journal of Gastroenterology & Hepatology, 2008, 22, 143-148.	1.7	29
80	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	2.5	28
81	Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863.	1.3	28
82	CGMIM: automated text-mining of Online Mendelian Inheritance in Man (OMIM) to identify genetically-associated cancers and candidate genes. BMC Bioinformatics, 2005, 6, 78.	2.6	27
83	Hepatitis C virus and risk of nonâ€Hodgkin lymphoma in British Columbia, Canada. International Journal of Cancer, 2008, 122, 630-633.	5.1	27
84	Genetic variation in the NBS1, MRE11, RAD50 and BLM genes and susceptibility to non-Hodgkin lymphoma. BMC Medical Genetics, 2009, 10, 117.	2.1	27
85	Effect of age on chronic inflammation and responsiveness to bacterial and viral challenges. PLoS ONE, 2017, 12, e0188881.	2.5	26
86	Lipid and Alzheimerâ€™s disease genes associated with healthy aging and longevity in healthy oldest-old. Oncotarget, 2017, 8, 20612-20621.	1.8	26
87	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
88	A Survey of Genomic Properties for the Detection of Regulatory Polymorphisms. PLoS Computational Biology, 2007, 3, e106.	3.2	24
89	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
90	Genetic Polymorphisms at TIMP3 Are Associated with Survival of Adenocarcinoma of the Gastroesophageal Junction. PLoS ONE, 2013, 8, e59157.	2.5	23

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91	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23
92	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
93	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
94	The prognostic effect of ethnicity for gastric and esophageal cancer: the population-based experience in British Columbia, Canada. BMC Cancer, 2011, 11, 164.	2.6	21
95	Catenin Family Genes Are Not Commonly Mutated in Hereditary Diffuse Gastric Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 2272-2274.	2.5	21
96	Association of polygenic risk score with the risk of chronic lymphocytic leukemia and monoclonal B-cell lymphocytosis. Blood, 2018, 131, 2541-2551.	1.4	21
97	Assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk, in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2020, 49, 216-232.	1.9	21
98	Genetic Variation in Cell Death Genes and Risk of Non-Hodgkin Lymphoma. PLoS ONE, 2012, 7, e31560.	2.5	21
99	Tea, coffee, and caffeinated beverage consumption and risk of epithelial ovarian cancers. Cancer Epidemiology, 2016, 45, 119-125.	1.9	20
100	Adult lifetime alcohol consumption and invasive epithelial ovarian cancer risk in a population-based caseâ€“control study. Gynecologic Oncology, 2016, 140, 277-284.	1.4	20
101	Dietary patterns in the healthy oldest old in the healthy aging study and the Canadian longitudinal study of aging: a cohort study. BMC Geriatrics, 2020, 20, 106.	2.7	20
102	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
103	Estimates of array and pool-construction variance for planning efficient DNA-pooling genome wide association studies. BMC Medical Genomics, 2011, 4, 81.	1.5	18
104	A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1609-1618.	2.5	18
105	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
106	Cohort Profile: The British Columbia Generations Project (BCGP). International Journal of Epidemiology, 2019, 48, 377-378k.	1.9	18
107	Elevated circulating t(14;18) translocation levels prior to diagnosis of follicular lymphoma. Blood, 2010, 116, 6146-6147.	1.4	17
108	Occupational exposure and ovarian cancer risk. Cancer Causes and Control, 2014, 25, 829-841.	1.8	17

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109	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	2.9	17
110	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. Human Molecular Genetics, 2020, 29, 70-79.	2.9	17
111	Consortium analysis of gene and geneâ€"folate interactions in purine and pyrimidine metabolism pathways with ovarian carcinoma risk. Molecular Nutrition and Food Research, 2014, 58, 2023-2035.	3.3	16
112	Isolation of DNA fragments from a human chromosomal subregion by Alu PCR differential hybridization. Genomics, 1991, 9, 241-246.	2.9	15
113	Shared genetic factors for age at natural menopause in Iranian and European women. Human Reproduction, 2013, 28, 1987-1994.	0.9	15
114	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	1.4	15
115	Genetic variation in vitamin D-related genes and risk of breast cancer among women of European and East Asian descent. Tumor Biology, 2016, 37, 6379-6387.	1.8	15
116	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	2.7	15
117	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129.	6.4	15
118	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2018, 47, 450-459.	1.9	15
119	The Super-Seniors Study: Phenotypic characterization of a healthy 85+ population. PLoS ONE, 2018, 13, e0197578.	2.5	15
120	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
121	A cluster of CpG islands at D10S94, near the locus responsible for multiple endocrine neoplasia type 2A (MEN2A). Genomics, 1992, 13, 339-343.	2.9	14
122	Inherited common variants in mitochondrial DNA and invasive serous epithelial ovarian cancer risk. BMC Research Notes, 2013, 6, 425.	1.4	13
123	Lipid Trait Variants and the Risk of Non-Hodgkin Lymphoma Subtypes: A Mendelian Randomization Study. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1074-1078.	2.5	13
124	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	1.8	13
125	Additional RFLPs at D10S94 and the Development of PCR-based variant detection systems: Implications for disease genotype prediction in MEN 2A, MEN 2B, and MTC1 families. Genomics, 1992, 13, 233-234.	2.9	12
126	Identifying related cancer types based on their incidence among people with multiple cancers. Emerging Themes in Epidemiology, 2006, 3, 17.	2.7	12

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127	Fasting insulin and endogenous hormones in relation to premenopausal breast density (Canada). Cancer Causes and Control, 2014, 25, 385-394.	1.8	12
128	A comprehensive geneâ€“environment interaction analysis in Ovarian Cancer using genomeâ€wide significant common variants. International Journal of Cancer, 2019, 144, 2192-2205.	5.1	12
129	Mutation and evolutionary analyses identify NR2E1-candidate-regulatory mutations in humans with severe cortical malformations. Genes, Brain and Behavior, 2007, 6, 503-516.	2.2	11
130	Comparison of Two Diverse Populations, British Columbia, Canada, and Ardabil, Iran, Indicates Several Variables Associated with Gastric and Esophageal Cancer Survival. Journal of Gastrointestinal Cancer, 2011, 42, 40-45.	1.3	11
131	Copy number alterations at polymorphic loci may be acquired somatically in patients with myelodysplastic syndromes. Leukemia Research, 2011, 35, 444-447.	0.8	11
132	Rare and common variants in the Apolipoprotein E gene in healthy oldest old. Neurobiology of Aging, 2014, 35, 727.e1-727.e3.	3.1	11
133	Human repeat element-mediated PCR: Cloning and mapping of chromosome 10 DNA markers. Genomics, 1992, 13, 409-414.	2.9	10
134	Genomic and Yeast Artificial Chromosome Long-Range Regular Article Linking Six Loci in 10q11.2 and Spanning the Multiple Endocrine Neoplasia Type 2A (MEN2A) Region. Genomics, 1993, 17, 611-617.	2.9	10
135	Non-Hodgkin Lymphoma Risk and Variants in Genes Controlling Lymphocyte Development. PLoS ONE, 2013, 8, e75170.	2.5	10
136	DNA repair variants and breast cancer risk. Environmental and Molecular Mutagenesis, 2016, 57, 269-281.	2.2	9
137	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9
138	Genetic variants in genes related to inflammation, apoptosis and autophagy in breast cancer risk. PLoS ONE, 2019, 14, e0209010.	2.5	9
139	Unexpectedly low loss of heterozygosity in genetically unstable Werner syndrome cell lines. Genes Chromosomes and Cancer, 1997, 18, 133-142.	2.8	8
140	A systematic evaluation of the ataxia telangiectasia mutated gene does not show an association with nonâ€Hodgkin lymphoma. International Journal of Cancer, 2007, 121, 1967-1975.	5.1	8
141	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. Twin Research and Human Genetics, 2012, 15, 615-623.	0.6	8
142	Polymorphisms of Insulin-Like Growth Factor 1 Pathway Genes and Breast Cancer Risk. Frontiers in Oncology, 2016, 6, 136.	2.8	8
143	Combined oral contraceptive use before the first birth and epithelial ovarian cancer risk. British Journal of Cancer, 2017, 116, 265-269.	6.4	8
144	Impact of Genotype Misclassification on Genetic Association Estimates and the Bayesian Adjustment. American Journal of Epidemiology, 2009, 170, 994-1004.	3.4	7

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145	Costâ€“Effective Prediction of Gender-Labeling Errors and Estimation of Gender-Labeling Error Rates in Candidate-Gene Association Studies. Frontiers in Genetics, 2011, 2, 31.	2.3	7
146	Burden of Common Complex Disease Variants in the Exomes of Two Healthy Centenarian Brothers. Gerontology, 2016, 62, 58-62.	2.8	7
147	Nonrandom occurrence of lymphoid cancer types in 140 families. Leukemia and Lymphoma, 2017, 58, 2134-2143.	1.3	7
148	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	1.8	7
149	Simulating pedigrees ascertained for multiple disease-affected relatives. Source Code for Biology and Medicine, 2018, 13, 2.	1.7	6
150	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. Cancer Medicine, 2019, 8, 2503-2513.	2.8	6
151	10-year follow-up of the Super-Seniors Study: compression of morbidity and genetic factors. BMC Geriatrics, 2019, 19, 58.	2.7	6
152	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539.	2.8	6
153	Absence of NR2E1 mutations in patients with aniridia. Molecular Vision, 2012, 18, 2770-82.	1.1	6
154	Inherited Chromosomally Integrated Human Herpesvirus 6 and Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 425-427.	2.5	5
155	Polymorphisms in Stromal Genes and Susceptibility to Serous Epithelial Ovarian Cancer: A Report from the Ovarian Cancer Association Consortium. PLoS ONE, 2011, 6, e19642.	2.5	5
156	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	1.8	5
157	Genetic polymorphism at BCL2 as a predictor for rituximab, cyclophosphamide, doxorubicin, vincristine and prednisone efficacy in patients with diffuse large B-cell lymphoma. Haematologica, 2017, 102, e199-e202.	3.5	4
158	Somatic Mitochondrial DNA Mutations in Diffuse Large B-Cell Lymphoma. Scientific Reports, 2018, 8, 3623.	3.3	4
159	SimRVSequences: an R package to simulate genetic sequence data for pedigrees. Bioinformatics, 2020, 36, 2295-2297.	4.1	4
160	Interactions between exposure to polycyclic aromatic hydrocarbons and xenobiotic metabolism genes, and risk of breast cancer. Breast Cancer, 2022, 29, 38-49.	2.9	4
161	Abstract LB-272: Genome-wide association study identifies multiple susceptibility loci for diffuse large B-cell lymphoma. Cancer Research, 2014, 74, LB-272-LB-272.	0.9	4
162	B-Cell NHL Subtype Risk Associated with Autoimmune Conditions and PRS. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1103-1110.	2.5	4

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163	Letter to the Editor - Reply to Leiro-Fernandez et al.. Pharmacogenomics, 2010, 11, 1207-1208.	1.3	3
164	Functional characterization of genetic polymorphisms in the H2AFX distal promoter. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2014, 766-767, 37-43.	1.0	3
165	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	4.1	3
166	Birth Order, Sibship Size, Childhood Environment and Immune-Related Disorders, and Risk of Lymphoma in Lymphoid Cancer Families. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1168-1178.	2.5	3
167	In search of genetic factors predisposing to familial hairy cell leukemia (HCL): exome-sequencing of four multiplex HCL pedigrees. Leukemia, 2020, 34, 1934-1938.	7.2	3
168	Two polymorphisms at the D10S94 locus. Nucleic Acids Research, 1990, 18, 4959-4959.	14.5	2
169	Tattoos and Hematologic Malignancies in British Columbia, Canada. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2093-2095.	2.5	2
170	CD20 Mutations at the Rituximab Binding Site Are Rare and Are Not a Significant Cause of R-CHOP Resistance in Patients with De Novo Diffuse Large B-Cell Lymphoma.. Blood, 2007, 110, 686-686.	1.4	2
171	A Meta-Analysis Of Genome-Wide Association Studies Of Multiple Myeloma In Cases and Controls Of European Origin Identifies a Risk Locus In 12q23.1. Blood, 2013, 122, 3111-3111.	1.4	2
172	Functional MRI evaluation of cognitive effects of carotid stenosis revascularization. Brain and Behavior, 2022, 12, e2512.	2.2	2
173	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	3.3	2
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175	Sex- and Subtype-Specific Analysis of H2AFX Polymorphisms in Non-Hodgkin Lymphoma. PLoS ONE, 2013, 8, e74619.	2.5	1
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