Julie M Cunningham

List of Publications by Year
in descending order

149 papers	11,498 citations	31902 53 h-index	33814 99 g-index
157 all docs	157 docs citations	157 times ranked	17224 citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
2	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
3	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
4	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
5	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
6	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	9.4	321
7	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. Journal of the National Cancer Institute, 2015, 107, .	3.0	311
8	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
9	Human colon cancer profiles show differential microRNA expression depending on mismatch repair status and are characteristic of undifferentiated proliferative states. BMC Cancer, 2009, 9, 401.	1.1	281
10	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278
11	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	9.4	276
12	Contribution of Germline Mutations in the RAD51B, RAD51C, and RAD51D Genes to Ovarian Cancer in the Population. Journal of Clinical Oncology, 2015, 33, 2901-2907.	0.8	266
13	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244
14	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	9.4	235
15	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
16	Microsatellite instability and mutation analysis of hMSH2 and hMLH1 in patients with sporadic, familial and hereditary colorectal cancer. Human Molecular Genetics, 1996, 5, 1245-1252.	1.4	193
17	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
18	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	9.4	179

#	Article	IF	Citations
19	The Contributions of Breast Density and Common Genetic Variation to Breast Cancer Risk. Journal of the National Cancer Institute, 2015, 107, .	3.0	174
20	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
21	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
22	Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. Nature Genetics, 2010, 42, 661-664.	9.4	152
23	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
24	miRNA Expression in Colon Polyps Provides Evidence for a Multihit Model of Colon Cancer. PLoS ONE, 2011, 6, e20465.	1.1	127
25	Genome-wide association study identifies a novel susceptibility locus at 6p21.3 among familial CLL. Blood, 2011, 117, 1911-1916.	0.6	118
26	The contribution of deleterious germline mutations in BRCA1, BRCA2 and the mismatch repair genes to ovarian cancer in the population. Human Molecular Genetics, 2014, 23, 4703-4709.	1.4	112
27	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	0.9	111
28	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	5.8	109
29	Evaluation of Genetic Variations in the Androgen and Estrogen Metabolic Pathways as Risk Factors for Sporadic and Familial Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 969-978.	1.1	101
30	Telomere Length Varies By DNA Extraction Method: Implications for Epidemiologic Research. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 2047-2054.	1.1	100
31	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	5.8	98
32	Base resolution methylome profiling: considerations in platform selection, data preprocessing and analysis. Epigenomics, 2015, 7, 813-828.	1.0	97
33	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94
34	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
35	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
36	Epigenetics in ovarian cancer. Seminars in Cancer Biology, 2018, 51, 160-169.	4.3	86

#	Article	IF	Citations
37	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
38	Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia. Blood, 2012, 120, 843-846.	0.6	76
39	Genetic Variation in the One-Carbon Transfer Pathway and Ovarian Cancer Risk. Cancer Research, 2008, 68, 2498-2506.	0.4	75
40	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.4	75
41	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388.	2.3	73
42	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	0.9	71
43	Biomarker-Based Ovarian Carcinoma Typing: A Histologic Investigation in the Ovarian Tumor Tissue Analysis Consortium. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1677-1686.	1.1	70
44	Strong Evidence of a Genetic Determinant for Mammographic Density, a Major Risk Factor for Breast Cancer. Cancer Research, 2007, 67, 8412-8418.	0.4	69
45	The oncogenic transcription factor IRF4 is regulated by a novel CD30/NF-ÎºB positive feedback loop in peripheral T-cell lymphoma. Blood, 2015, 125, 3118-3127.	0.6	68
46	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
47	DNA methylation profiling: comparison of genome-wide sequencing methods and the Infinium Human Methylation 450 Bead Chip. Epigenomics, 2015, 7, 1287-1302.	1.0	66
48	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1503-1510.	1.1	64
49	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
50	Inherited Variants in Mitochondrial Biogenesis Genes May Influence Epithelial Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1131-1145.	1.1	62
51	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	1.3	62
52	Use of FFPE-derived DNA in next generation sequencing: DNA extraction methods. PLoS ONE, 2019, 14, e0211400.	1.1	62
53	Effects of Age and Estrogen on Skeletal Gene Expression in Humans as Assessed by RNA Sequencing. PLoS ONE, 2015, 10, e0138347.	1.1	62
54	Epigenome-wide ovarian cancer analysis identifies a methylation profile differentiating clear-cell histology with epigenetic silencing of the HERG K+ channel. Human Molecular Genetics, 2013, 22, 3038-3047.	1.4	60

#	Article	IF	Citations
55	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	2.2	57
56	ABCB1 (MDR1) polymorphisms and ovarian cancer progression and survival: A comprehensive analysis from the Ovarian Cancer Association Consortium and The Cancer Genome Atlas. Gynecologic Oncology, 2013, 131, 8-14.	0.6	55
57	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.4	55
58	The androgen receptor CAG and GGN repeat polymorphisms and prostate cancer susceptibility in African-American men: results from the Flint Menâ€™s Health Study. Journal of Human Genetics, 2008, 53, 220-226.	1.1	52
59	Regulatory T cells, inherited variation, and clinical outcome in epithelial ovarian cancer. Cancer Immunology, Immunotherapy, 2015, 64, 1495-1504.	2.0	51
60	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50
61	Genome linkage screen for prostate cancer susceptibility loci: Results from the Mayo Clinic familial prostate cancer study. Prostate, 2003, 57, 335-346.	1.2	48
62	DNA methylation changes in epithelial ovarian cancer histotypes. Genomics, 2015, 106, 311-321.	1.3	48
63	TP53mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. Nucleic Acids Research, 2015, 43, 6945-6958.	6.5	46
64	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
65	PPM1DMosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. Journal of the National Cancer Institute, 2016, 108, djv347.	3.0	43
66	Germline whole exome sequencing and large-scale replication identifies FANCM as a likely high grade serous ovarian cancer susceptibility gene. Oncotarget, 2017, 8, 50930-50940.	0.8	43
67	Does Î±-synuclein have a dual and opposing effect in preclinical vs. clinical Parkinson's disease?. Parkinsonism and Related Disorders, 2014, 20, 584-589.	1.1	41
68	Genetic association with overall survival of taxane-treated lung cancer patients - a genome-wide association study in human lymphoblastoid cell lines followed by a clinical association study. BMC Cancer, 2012, 12, 422.	1.1	40
69	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
70	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	0.5	37
71	Bioinformatics and DNA-extraction strategies to reliably detect genetic variants from FFPE breast tissue samples. BMC Genomics, 2019, 20, 689.	1.2	37
72	Pharmacogenomics of antidepressant induced mania: A review and meta-analysis of the serotonin transporter gene (5HTTLPR) association. Journal of Affective Disorders, 2012, 136, e21-e29.	2.0	36

#	Article	IF	Citations
73	ABO blood group and risk of epithelial ovarian cancer within the Ovarian Cancer Association Consortium. Cancer Causes and Control, 2012, 23, 1805-1810.	0.8	35
74	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	1.6	35
75	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
76	Global transcriptional profiling using RNA sequencing and DNA methylation patterns in highly enriched mesenchymal cells from young versus elderly women. Bone, 2015, 76, 49-57.	1.4	34
77	Candidate locus analysis of the TERTâ€“CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	1.8	34
78	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. Clinical Cancer Research, 2015, 21, 5264-5276.	3.2	33
79	Tumor Hypomethylation at 6p21.3 Associates with Longer Time to Recurrence of High-Grade Serous Epithelial Ovarian Cancer. Cancer Research, 2014, 74, 3084-3091.	0.4	32
80	Risk Prediction for Epithelial Ovarian Cancer in 11 United Statesâ€“Based Case-Control Studies: Incorporation of Epidemiologic Risk Factors and 17 Confirmed Genetic Loci. American Journal of Epidemiology, 2016, 184, 555-569.	1.6	32
81	BRCA1Promoter Methylation and Clinical Outcomes in Ovarian Cancer: An Individual Patient Data Meta-Analysis. Journal of the National Cancer Institute, 2020, 112, 1190-1203.	3.0	32
82	Identification of a novel percent mammographic density locus at 12q24. Human Molecular Genetics, 2012, 21, 3299-3305.	1.4	31
83	Performance of Amplified DNA in an Illumina GoldenGate BeadArray Assay. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1781-1789.	1.1	30
84	Germline polymorphisms in an enhancer of PSIP1 are associated with progression-free survival in epithelial ovarian cancer. Oncotarget, 2016, 7, 6353-6368.	0.8	29
85	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.	1.1	28
86	Accumulating evidence for a role of <scp>TCF</scp>7L2 variants in bipolar disorder with elevated body mass index. Bipolar Disorders, 2016, 18, 124-135.	1.1	27
87	Transcriptomic Characterization of Endometrioid, Clear Cell, and High-Grade Serous Epithelial Ovarian Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1101-1109.	1.1	26
88	Population-based targeted sequencing of 54 candidate genes identifiesPALB2as a susceptibility gene for high-grade serous ovarian cancer. Journal of Medical Genetics, 2021, 58, 305-313.	1.5	26
89	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
90	Evaluation of a new high-dimensional miRNA profiling platform. BMC Medical Genomics, 2009, 2, 57.	0.7	24

#	Article	IF	Citations
91	Genetic Variation in TYMS in the One-Carbon Transfer Pathway Is Associated with Ovarian Carcinoma Types in the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1822-1830.	1.1	24
92	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24
93	The Association of Telomere Length with Colorectal Cancer Differs by the Age of Cancer Onset. Clinical and Translational Gastroenterology, 2014, 5, e52.	1.3	23
94	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	2.9	23
95	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
96	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
97	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. Oncotarget, 2017, 8, 46891-46899.	0.8	22
98	Molecular Subclasses of Clear Cell Ovarian Carcinoma and Their Impact on Disease Behavior and Outcomes. Clinical Cancer Research, 2022, 28, 4947-4956.	3.2	22
99	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1117-1126.	1.1	21
100	Epigenetic and senescence markers indicate an accelerated ageing-like state in women with preeclamptic pregnancies. EBioMedicine, 2021, 70, 103536.	2.7	20
101	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	1.8	19
102	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. Human Molecular Genetics, 2019, 28, 1331-1342.	1.4	19
103	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
104	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	1.4	17
105	A genome wide association study suggests the association of muskelin with early onset bipolar disorder: Implications for a GABAergic epileptogenic neurogenesis model. Journal of Affective Disorders, 2017, 208, 120-129.	2.0	17
106	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	0.6	15
107	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129.	2.9	15
108	A search for germline APC mutations in early onset colorectal cancer or familial colorectal cancer with normal DNA mismatch repair. Genes Chromosomes and Cancer, 2001, 30, 181-186.	1.5	14

#	Article	IF	Citations
109	Intra-Gene DNA Methylation Variability Is a Clinically Independent Prognostic Marker in Womenâ€™s Cancers. PLoS ONE, 2015, 10, e0143178.	1.1	14
110	DNA methylation and RNA expression profiles in lung adenocarcinomas of never-smokers. Cancer Genetics, 2015, 208, 253-260.	0.2	14
111	Variation in NF-ÎºB Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1421-1427.	1.1	13
112	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	0.8	13
113	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	1.1	12
114	DNA Methylation Profiles of Ovarian Clear Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 132-141.	1.1	12
115	Germline Copy Number Variation and Ovarian Cancer Survival. Frontiers in Genetics, 2012, 3, 142.	1.1	11
116	Assessment of Multifactor Geneâ€“Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 780-790.	1.1	10
117	Associations of catechol-O-methyltransferase (rs4680) single nucleotide polymorphisms with opioid use and dose among adults with chronic pain. Pain, 2019, 160, 263-268.	2.0	10
118	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	1.1	9
119	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
120	Effect of catechol-O-methyltransferase (rs4680) single-nucleotide polymorphism on opioid-induced hyperalgesia in adults with chronic pain. Molecular Pain, 2019, 15, 174480691984892.	1.0	9
121	Whole Exome Sequencing Among 26 Patients With Indeterminate Acute Liver Failure: A Pilot Study. Clinical and Translational Gastroenterology, 2019, 10, e00087.	1.3	9
122	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. Oncotarget, 2017, 8, 64670-64684.	0.8	7
123	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	0.8	7
124	Clinical validation of genetic variants associated with in vitro chemotherapy-related lymphoblastoid cell toxicity. Oncotarget, 2017, 8, 78133-78143.	0.8	6
125	Genomic Analysis Using Regularized Regression in High-Grade Serous Ovarian Cancer. Cancer Informatics, 2018, 17, 117693511875534.	0.9	5
126	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44.	2.3	5

#	Article	IF	Citations
127	Identification of a Locus Near ULK1 Associated With Progression-Free Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1669-1680.	1.1	5
128	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	0.8	5
129	Genetic Polymorphisms and Correlation with Treatment-Induced Cardiotoxicity and Prognosis in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 1854-1862.	3.2	5
130	Effects of the ABCB1 c.3435C>T (rs1045642) Polymorphism on Heat Pain Perception in Opioid-Free Adults With Chronic Pain. Anesthesia and Analgesia, 2021, 133, 1028-1035.	1.1	4
131	Widespread Non-Canonical Epigenetic Modifications in MMTV-NeuT Breast Cancer. Neoplasia, 2015, 17, 348-357.	2.3	3
132	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	1.8	3
133	Identification of Two Genetic Loci Associated with Leukopenia after Chemotherapy in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 3342-3355.	3.2	3
134	The association of copy number variation and percent mammographic density. BMC Research Notes, 2015, 8, 297.	0.6	2
135	Somatic mutations in benign breast disease tissues and association with breast cancer risk. BMC Medical Genomics, 2021, 14, 185.	0.7	2
136	Germline BRCA variants, lifestyle and ovarian cancer survival. Gynecologic Oncology, 2022, , .	0.6	2
137	Association of Gene-Gene Interactions with Venous Thromboembolism (VTE): A Pathway-Directed Candidate-Gene Case-Control Study.. Blood, 2009, 114, 150-150.	0.6	1
138	Association of Gene-Environment Interactions with Venous Thromboembolism (VTE): A Merged/Imputed Genome-Wide Scan/Candidate-Gene Case-Control Study. Blood, 2011, 118, 2295-2295.	0.6	1
139	A Genome-Wide Association Study (GWAS) Of Event-Free Survival In Diffuse Large B-Cell Lymphoma (DLBCL) Treated With Rituximab and Anthracycline-Based Chemotherapy: A Lysa and Iowa/Mayo Clinic SPORE Multistage Study. Blood, 2013, 122, 76-76.	0.6	1
140	Buffy Coat DNA Methylation Profile Is Representative of Methylation Patterns in White Blood Cell Types in Normal Pregnancy. Frontiers in Bioengineering and Biotechnology, 2021, 9, 782843.	2.0	1
141	A Large Scale Evaluation of Genetic Variation in Immune and Inflammation Genes and Risk of Non-Hodgkin Lymphoma.. Blood, 2006, 108, 817-817.	0.6	0
142	Investigation of CLL-Susceptibility Loci with Monoclonal B-Cell Lymphocytosis (MBL) Risk and Confirmation of Recently Reported CLL-Susceptibility Loci. Blood, 2010, 116, 2443-2443.	0.6	0
143	Association of Gene-Environment Interactions with Venous Thromboembolism (VTE): A Pathway-Directed Candidate-Gene Case-Control Study. Blood, 2010, 116, 480-480.	0.6	0
144	Association of Gene-Gene Interactions with Venous Thromboembolism (VTE): A Merged/Imputed Genome-Wide Scan/Candidate-Gene Case-Control Study. Blood, 2011, 118, 1242-1242.	0.6	0

#	Article	IF	Citations
145	Identification of Venous Thromboembolism (VTE)-Associated Novel Variants in the ABO Gene Using Targeted Deep Sequencing. Blood, 2011, 118, 709-709.	0.6	0
146	Single Nucleotide Polymorphisms (SNPs) in Genes for Glutathione-Related Metabolism, Cyclin D1, and DNA Repair As Predictive Biomarkers in Mantle Cell Lymphoma Patients Treated with R-HyperCVAD with Ten Year Clinical Follow-up,. Blood, 2011, 118, 3650-3650.	0.6	0
147	CXCR5 Polymorphisms in Non-Hodgkin Lymphoma (NHL) Risk and Prognosis.. Blood, 2012, 120, 2702-2702.	0.6	0
148	Comparison Of Single Nucleotide Mutations (SNVs) and Copy Number Variants (CNVs) Detection In Formalin Fixed Paraffin Embedded (FFPE) and Paired Frozen Tumor Tissues Using Target Capture and Sequencing Approach. Blood, 2013, 122, 1784-1784.	0.6	0
149	Copy Number Abnormalities Of The Interferon Regulatory Factor-4 (IRF4) Gene Are Associated With IRF4/MUM1 Expression In Peripheral T-Cell Lymphomas. Blood, 2013, 122, 3016-3016.	0.6	0