Julie M Cunningham

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

146 papers	8,164 citations	47 h-index	88 g-index
157 ext. papers	10,106 ext. citations	8.5 avg, IF	4.52 L-index

#	Paper	IF	Citations
146	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
145	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
144	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. *Nature Genetics*, **2010**, 42, 874-9	36.3	277
143	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. *Nature Genetics*, **2013**, 45, 362-70, 370e1-2	36.3	267
142	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	4.8	253
141	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. *Nature Genetics*, **2009**, 41, 996-1000	36.3	240
140	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	239
139	Common variants at 19p13 are associated with susceptibility to ovarian cancer. *Nature Genetics*, **2010**, 42, 880-4	36.3	210
138	Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk. *PLoS Genetics*, **2013**, 9, e1003212	6	209
137	Contribution of Germline Mutations in the RAD51B, RAD51C, and RAD51D Genes to Ovarian Cancer in the Population. *Journal of Clinical Oncology*, **2015**, 33, 2901-7	2.2	200
136	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
135	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
134	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
133	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. *Nature Genetics*, **2015**, 47, 164-71	36.3	177
132	Microsatellite instability and mutation analysis of hMSH2 and hMLH1 in patients with sporadic, familial and hereditary colorectal cancer. *Human Molecular Genetics*, **1996**, 5, 1245-52	5.6	164
131	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. *Nature Genetics*, **2013**, 45, 868-76	36.3	147
130	Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. *Nature Genetics*, **2010**, 42, 661-4	36.3	137

129	The contributions of breast density and common genetic variation to breast cancer risk. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	128
128	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. *Nature Communications*, **2013**, 4, 1628	17.4	124
127	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
126	miRNA expression in colon polyps provides evidence for a multihit model of colon cancer. *PLoS ONE* , **2011**, 6, e20465	3.7	115
125	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, 1052-67	24.4	104
124	Genome-wide association study identifies a novel susceptibility locus at 6p21.3 among familial CLL. *Blood*, **2011**, 117, 1911-6	2.2	102
123	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101
122	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, 969-78	4	93
121	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, 4703-9	5.6	90
120	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. *Nature Communications*, **2013**, 4, 1627	17.4	85
119	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. *Nature Communications*, **2014**, 5, 5303	17.4	84
118	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	36.3	83
117	Telomere length varies by DNA extraction method: implications for epidemiologic research. *Cancer Epidemiology Biomarkers and Prevention*, **2013**, 22, 2047-54	4	81
116	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. *International Journal of Epidemiology*, **2016**, 45, 1619-1630	7.8	77
115	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. *Nature Communications*, **2016**, 7, 10933	17.4	70
114	LIN28B polymorphisms influence susceptibility to epithelial ovarian cancer. *Cancer Research*, **2011**, 71, 3896-903	10.1	70
113	Genetic variation in the one-carbon transfer pathway and ovarian cancer risk. *Cancer Research*, **2008** , 68, 2498-506	10.1	67
112	Consortium analysis of 7 candidate SNPs for ovarian cancer. *International Journal of Cancer*, **2008**, 123, 380-388	7.5	66

111	Base resolution methylome profiling: considerations in platform selection, data preprocessing and analysis. *Epigenomics*, **2015**, 7, 813-28	4.4	65
110	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
109	Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia. *Blood*, **2012**, 120, 843-6	2.2	63
108	Strong evidence of a genetic determinant for mammographic density, a major risk factor for breast cancer. *Cancer Research*, **2007**, 67, 8412-8	10.1	62
107	Epigenetics in ovarian cancer. *Seminars in Cancer Biology*, **2018**, 51, 160-169	12.7	57
106	Five endometrial cancer risk loci identified through genome-wide association analysis. *Nature Genetics*, **2016**, 48, 667-674	36.3	56
105	Biomarker-based ovarian carcinoma typing: a histologic investigation in the ovarian tumor tissue analysis consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2013**, 22, 1677-86	4	53
104	Inherited variants in mitochondrial biogenesis genes may influence epithelial ovarian cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 1131-45	4	50
103	DNA methylation profiling: comparison of genome-wide sequencing methods and the Infinium Human Methylation 450 Bead Chip. *Epigenomics*, **2015**, 7, 1287-302	4.4	49
102	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, 3038-47	5.6	49
101	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. *Human Molecular Genetics*, **2015**, 24, 5955-64	5.6	48
100	The oncogenic transcription factor IRF4 is regulated by a novel CD30/NF-B positive feedback loop in peripheral T-cell lymphoma. *Blood*, **2015**, 125, 3118-27	2.2	47
99	The androgen receptor CAG and GGN repeat polymorphisms and prostate cancer susceptibility in African-American men: results from the Flint Men Health Study. *Journal of Human Genetics*, **2008**, 53, 220-226	4.3	47
98	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. *Human Molecular Genetics*, **2015**, 24, 1478-92	5.6	46
97	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	8.3	46
96	Genome linkage screen for prostate cancer susceptibility loci: results from the Mayo Clinic Familial Prostate Cancer Study. *Prostate*, **2003**, 57, 335-46	4.2	46
95	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019**, 10, 431	17.4	45
94	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. *Cancer Research*, **2015**, 75, 2457-67	10.1	45

93	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. *International Journal of Epidemiology*, **2016**, 45, 884-95	7.8	45
92	Effects of Age and Estrogen on Skeletal Gene Expression in Humans as Assessed by RNA Sequencing. *PLoS ONE*, **2015**, 10, e0138347	3.7	43
91	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	4	42
90	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. *Nature Communications*, **2015**, 6, 8234	17.4	40
89	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. *Cancer Medicine*, **2018**, 7, 1978-1987	4.8	40
88	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	4.9	39
87	TP53 mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. *Nucleic Acids Research*, **2015**, 43, 6945-58	20.1	37
86	DNA methylation changes in epithelial ovarian cancer histotypes. *Genomics*, **2015**, 106, 311-21	4.3	37
85	Regulatory T cells, inherited variation, and clinical outcome in epithelial ovarian cancer. *Cancer Immunology, Immunotherapy*, **2015**, 64, 1495-504	7.4	36
84	PPM1D Mosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	34
83	Use of FFPE-derived DNA in next generation sequencing: DNA extraction methods. *PLoS ONE*, **2019**, 14, e0211400	3.7	32
82	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. *Human Molecular Genetics*, **2015**, 24, 3595-607	5.6	32
81	Does □synuclein have a dual and opposing effect in preclinical vs. clinical Parkinson□ disease?. *Parkinsonism and Related Disorders*, **2014**, 20, 584-9; discussion 584	3.6	31
80	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. *Human Genetics*, **2015**, 134, 231-45	6.3	30
79	Performance of amplified DNA in an Illumina GoldenGate BeadArray assay. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 1781-9	4	30
78	Germline whole exome sequencing and large-scale replication identifies as a likely high grade serous ovarian cancer susceptibility gene. *Oncotarget*, **2017**, 8, 50930-50940	3.3	30
77	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	4.8	29
76	Identification of a novel percent mammographic density locus at 12q24. *Human Molecular Genetics*, **2012**, 21, 3299-305	5.6	28

75	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	4.7	27
74	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	6.6	27
73	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	4.9	27
72	ABO blood group and risk of epithelial ovarian cancer within the Ovarian Cancer Association Consortium. *Cancer Causes and Control*, **2012**, 23, 1805-10	2.8	27
71	Evidence of a genetic link between endometriosis and ovarian cancer. *Fertility and Sterility*, **2016**, 105, 35-43.e1-10	4.8	26
70	Assessing associations between the AURKA-HMMR-TPX2-TUBG1 functional module and breast cancer risk in BRCA1/2 mutation carriers. *PLoS ONE*, **2015**, 10, e0120020	3.7	26
69	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, 1574-84	4	24
68	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. *Clinical Cancer Research*, **2015**, 21, 5264-76	12.9	24
67	Evaluation of a new high-dimensional miRNA profiling platform. *BMC Medical Genomics*, **2009**, 2, 57	3.7	24
66	Tumor hypomethylation at 6p21.3 associates with longer time to recurrence of high-grade serous epithelial ovarian cancer. *Cancer Research*, **2014**, 74, 3084-91	10.1	23
65	Risk Prediction for Epithelial Ovarian Cancer in 11 United States-Based Case-Control Studies: Incorporation of Epidemiologic Risk Factors and 17 Confirmed Genetic Loci. *American Journal of Epidemiology*, **2016**, 184, 579-589	3.8	23
64	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, 1822-30	4	22
63	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). *Journal of Genetics and Genome Research*, **2015**, 2,		22
62	The association of telomere length with colorectal cancer differs by the age of cancer onset. *Clinical and Translational Gastroenterology*, **2014**, 5, e52	4.2	21
61	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. *Carcinogenesis*, **2015**, 36, 1341-53	4.6	20
60	Accumulating evidence for a role of TCF7L2 variants in bipolar disorder with elevated body mass index. *Bipolar Disorders*, **2016**, 18, 124-35	3.8	20
59	Germline polymorphisms in an enhancer of PSIP1 are associated with progression-free survival in epithelial ovarian cancer. *Oncotarget*, **2016**, 7, 6353-68	3.3	19
58	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. *British Journal of Cancer*, **2017**, 116, 524-535	8.7	18

57	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. *Genetic Epidemiology*, **2015**, 39, 689-97	2.6	18
56	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. *Human Genetics*, **2016**, 135, 741-56	6.3	18
55	Bioinformatics and DNA-extraction strategies to reliably detect genetic variants from FFPE breast tissue samples. *BMC Genomics*, **2019**, 20, 689	4.5	17
54	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. *Oncotarget*, **2017**, 8, 46891-46899	3.3	17
53	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15
52	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. *PLoS ONE*, **2015**, 10, e0128106	3.7	15
51	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	5	13
50	Evaluating the ovarian cancer gonadotropin hypothesis: a candidate gene study. *Gynecologic Oncology*, **2015**, 136, 542-8	4.9	12
49	DNA methylation and RNA expression profiles in lung adenocarcinomas of never-smokers. *Cancer Genetics*, **2015**, 208, 253-60	2.3	12
48	BRCA1 Promoter Methylation and Clinical Outcomes in Ovarian Cancer: An Individual Patient Data Meta-Analysis. *Journal of the National Cancer Institute*, **2020**, 112, 1190-1203	9.7	12
47	Population-based targeted sequencing of 54 candidate genes identifies as a susceptibility gene for high-grade serous ovarian cancer. *Journal of Medical Genetics*, **2021**, 58, 305-313	5.8	12
46	Variation in NF-B signaling pathways and survival in invasive epithelial ovarian cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 1421-7	4	11
45	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. *Oncotarget*, **2016**, 7, 72381-72394	3.3	11
44	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. *Human Molecular Genetics*, **2019**, 28, 1331-1342	5.6	11
43	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. *British Journal of Cancer*, **2018**, 118, 1123-1129	8.7	10
42	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	6.6	10
41	Intra-Gene DNA Methylation Variability Is a Clinically Independent Prognostic Marker in Women Cancers. *PLoS ONE*, **2015**, 10, e0143178	3.7	10
40	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. *PLoS ONE*, **2018**, 13, e0197561	3.7	9

39	Germline copy number variation and ovarian cancer survival. *Frontiers in Genetics*, **2012**, 3, 142	4.5	9
38	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. *Human Molecular Genetics*, **2016**, 25, 3600-3612	5.6	9
37	Transcriptomic Characterization of Endometrioid, Clear Cell, and High-Grade Serous Epithelial Ovarian Carcinoma. *Cancer Epidemiology Biomarkers and Prevention*, **2018**, 27, 1101-1109	4	9
36	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. *Cancer Epidemiology Biomarkers and Prevention*, **2019**, 28, 1117-1126	4	8
35	Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 780-90	4	8
34	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	4	7
33	A targeted genetic association study of epithelial ovarian cancer susceptibility. *Oncotarget*, **2016**, 7, 7381-9	3.3	7
32	Effect of catechol-O-methyltransferase (rs4680) single-nucleotide polymorphism on opioid-induced hyperalgesia in adults with chronic pain. *Molecular Pain*, **2019**, 15, 1744806919848929	3.4	6
31	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 446-54	4	6
30	Associations of catechol-O-methyltransferase (rs4680) single nucleotide polymorphisms with opioid use and dose among adults with chronic pain. *Pain*, **2019**, 160, 263-268	8	6
29	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. *Oncotarget*, **2017**, 8, 64670-64684	3.3	5
28	Whole Exome Sequencing Among 26 Patients With Indeterminate Acute Liver Failure: A Pilot Study. *Clinical and Translational Gastroenterology*, **2019**, 10, e00087	4.2	5
27	Epigenetic and senescence markers indicate an accelerated ageing-like state in women with preeclamptic pregnancies. *EBioMedicine*, **2021**, 70, 103536	8.8	5
26	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. *Oncotarget*, **2016**, 7, 69097-69110	3.3	4
25	Clinical validation of genetic variants associated with chemotherapy-related lymphoblastoid cell toxicity. *Oncotarget*, **2017**, 8, 78133-78143	3.3	4
24	Genomic Analysis Using Regularized Regression in High-Grade Serous Ovarian Cancer. *Cancer Informatics*, **2018**, 17, 1176935118755341	2.4	3
23	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	3
22	Association of germline variation with the survival of women with pathogenic variants and breast cancer. *Npj Breast Cancer*, **2020**, 6, 44	7.8	3

21	Widespread Non-Canonical Epigenetic Modifications in MMTV-NeuT Breast Cancer. *Neoplasia*, **2015**, 17, 348-57	6.4	2
20	DNA Methylation Profiles of Ovarian Clear Cell Carcinoma. *Cancer Epidemiology Biomarkers and Prevention*, **2021**,	4	2
19	Use of FFPE-Derived DNA in Next Generation Sequencing: DNA extraction methods		2
18	Identification of a Locus Near Associated With Progression-Free Survival in Ovarian Cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2021**, 30, 1669-1680	4	2
17	The association of copy number variation and percent mammographic density. *BMC Research Notes*, **2015**, 8, 297	2.3	1
16	Genetic polymorphisms and correlation with treatment induced cardiotoxicity and prognosis in breast cancer patients.. *Clinical Cancer Research*, **2022**,	12.9	1
15	Association of Gene-Gene Interactions with Venous Thromboembolism (VTE): A Pathway-Directed Candidate-Gene Case-Control Study.. *Blood*, **2009**, 114, 150-150	2.2	1
14	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	2.2	1
13	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	2.2	1
12	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	3.9	1
11	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	5.8	0
10	Somatic mutations in benign breast disease tissues and association with breast cancer risk. *BMC Medical Genomics*, **2021**, 14, 185	3.7	0
9	A Large Scale Evaluation of Genetic Variation in Immune and Inflammation Genes and Risk of Non-Hodgkin Lymphoma.. *Blood*, **2006**, 108, 817-817	2.2	
8	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	2.2	
7	Association of Gene-Environment Interactions with Venous Thromboembolism (VTE): A Pathway-Directed Candidate-Gene Case-Control Study. *Blood*, **2010**, 116, 480-480	2.2	
6	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	2.2	
5	Identification of Venous Thromboembolism (VTE)-Associated Novel Variants in the ABO Gene Using Targeted Deep Sequencing. *Blood*, **2011**, 118, 709-709	2.2	
4	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	2.2	

3	CXCR5 Polymorphisms in Non-Hodgkin Lymphoma (NHL) Risk and Prognosis.. *Blood*, **2012**, 120, 2702-2702	2.2
2	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	2.2
1	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	2.2