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	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
2	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
3	Functional MRI evaluation of cognitive effects of carotid stenosis revascularization. Brain and Behavior, 2022, 12, e2512.	2.2	2
4	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
5	B-Cell NHL Subtype Risk Associated with Autoimmune Conditions and PRS. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1103-1110.	2.5	4
6	Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217.		0
7	Anticipation in multiple-case lymphoid cancer families after controlling for ascertainment biases. Leukemia and Lymphoma, 2021, 62, 3147-3151.	1.3	1
8	Allele-Specific Transcript Abundance: A Pilot Study in Healthy Centenarians. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 1068-1072.	3.6	0
9	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
10	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
11	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
12	SimRVSequences: an R package to simulate genetic sequence data for pedigrees. Bioinformatics, 2020, 36, 2295-2297.	4.1	4
13	Tattoos and Hematologic Malignancies in British Columbia, Canada. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2093-2095.	2.5	2
14	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
15	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
16	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
17	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
18	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

#	Article	IF	Citations
19	Ovarian Carcinoma Histotype: Strengths and Limitations of Integrating Morphology With Immunohistochemical Predictions. International Journal of Gynecological Pathology, 2019, 38, 353-362.	1.4	45
20	Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863.	1.3	28
21	Cohort Profile: The British Columbia Generations Project (BCGP). International Journal of Epidemiology, 2019, 48, 377-378k.	1.9	18
22	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
23	10-year follow-up of the Super-Seniors Study: compression of morbidity and genetic factors. BMC Geriatrics, 2019, 19, 58.	2.7	6
24	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
25	Genetic variants in genes related to inflammation, apoptosis and autophagy in breast cancer risk. PLoS ONE, 2019, 14, e0209010.	2.5	9
26	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
27	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
28	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539.	2.8	6
29	Somatic Mitochondrial DNA Mutations in Diffuse Large B-Cell Lymphoma. Scientific Reports, 2018, 8, 3623.	3.3	4
30	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
31	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
32	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
33	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
34	Simulating pedigrees ascertained for multiple disease-affected relatives. Source Code for Biology and Medicine, 2018, 13, 2.	1.7	6
35	The Super-Seniors Study: Phenotypic characterization of a healthy 85+ population. PLoS ONE, 2018, 13, e0197578.	2.5	15
36	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9

#	Article	IF	Citations
37	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
38	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
39	Abstract 221: Inherited variants at 3q13.33 and 3p24.1 influences risk of diffuse large B-cell lymphoma. , 2018, , .		0
40	Nonrandom occurrence of lymphoid cancer types in 140 families. Leukemia and Lymphoma, 2017, 58, 2134-2143.	1.3	7
41	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
42	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	12.8	75
43	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
44	Combined oral contraceptive use before the first birth and epithelial ovarian cancer risk. British Journal of Cancer, 2017, 116, 265-269.	6.4	8
45	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
46	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
47	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	2.7	15
48	Inherited Chromosomally Integrated Human Herpesvirus 6 and Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 425-427.	2.5	5
49	Effect of age on chronic inflammation and responsiveness to bacterial and viral challenges. PLoS ONE, 2017, 12, e0188881.	2.5	26
50	Lipid and Alzheimerâ€™s disease genes associated with healthy aging and longevity in healthy oldest-old. Oncotarget, 2017, 8, 20612-20621.	1.8	26
51	Polymorphisms of Insulin-Like Growth Factor 1 Pathway Genes and Breast Cancer Risk. Frontiers in Oncology, 2016, 6, 136.	2.8	8
52	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
53	DNA repair variants and breast cancer risk. Environmental and Molecular Mutagenesis, 2016, 57, 269-281.	2.2	9
54	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

#	Article	IF	Citations
55	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
56	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
57	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
58	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
59	Tea, coffee, and caffeinated beverage consumption and risk of epithelial ovarian cancers. Cancer Epidemiology, 2016, 45, 119-125.	1.9	20
60	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	12.8	94
61	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
62	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
63	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
64	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	1.0	37
65	Burden of Common Complex Disease Variants in the Exomes of Two Healthy Centenarian Brothers. Gerontology, 2016, 62, 58-62.	2.8	7
66	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
67	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
68	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
69	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	1.8	7
70	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
71	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
72	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44

#	Article	IF	Citations
73	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	12.8	58
74	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
75	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
76	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
77	Genome-wide significant risk associations for mucinous ovarian carcinoma. Nature Genetics, 2015, 47, 888-897.	21.4	78
78	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
79	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	1.4	15
80	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
81	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
82	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
83	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
84	Abstract 2792: Polymorphisms in vitamin D-related genes and risk of breast cancer. , 2015, , .		0
85	Abstract 4629: Multiple myeloma susceptibility loci examined in African and European ancestry populations. , 2015, , .		0
86	Risk of Ovarian Cancer and the NF-Î°B Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.9	48
87	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
88	Gender and telomere length: Systematic review and meta-analysis. Experimental Gerontology, 2014, 51, 15-27.	2.8	394
89	Fasting insulin and endogenous hormones in relation to premenopausal breast density (Canada). Cancer Causes and Control, 2014, 25, 385-394.	1.8	12
90	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23

#	Article	IF	Citations
91	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
92	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
93	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	21.4	147
94	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
95	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
96	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
97	Occupational exposure and ovarian cancer risk. Cancer Causes and Control, 2014, 25, 829-841.	1.8	17
98	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
99	Abstract 5072: Meta-analysis of genome-wide association studies identifies novel susceptibility loci for follicular lymphoma. , 2014, , .		0
100	Abstract 5071: A genome-wide association study suggests evidence of variants at 6p21.32 associated with marginal zone lymphoma. , 2014, , .		1
101	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
102	Shared genetic factors for age at natural menopause in Iranian and European women. Human Reproduction, 2013, 28, 1987-1994.	0.9	15
103	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
104	Inherited common variants in mitochondrial DNA and invasive serous epithelial ovarian cancer risk. BMC Research Notes, 2013, 6, 425.	1.4	13
105	Genetics of healthy aging and longevity. Human Genetics, 2013, 132, 1323-1338.	3.8	274
106	Shift work, circadian gene variants and risk of breast cancer. Cancer Epidemiology, 2013, 37, 606-612.	1.9	52
107	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	21.4	179
108	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144

#	Article	IF	Citations
109	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
110	Genetic Polymorphisms at TIMP3 Are Associated with Survival of Adenocarcinoma of the Gastroesophageal Junction. PLoS ONE, 2013, 8, e59157.	2.5	23
111	Sex- and Subtype-Specific Analysis of H2AFX Polymorphisms in Non-Hodgkin Lymphoma. PLoS ONE, 2013, 8, e74619.	2.5	1
112	Non-Hodgkin Lymphoma Risk and Variants in Genes Controlling Lymphocyte Development. PLoS ONE, 2013, 8, e75170.	2.5	10
113	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
114	Catenin Family Genes Are Not Commonly Mutated in Hereditary Diffuse Gastric Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 2272-2274.	2.5	21
115	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. Twin Research and Human Genetics, 2012, 15, 615-623.	0.6	8
116	PRRC2A and BCL2L11 gene variants influence risk of non-Hodgkin lymphoma: results from the InterLymph consortium. Blood, 2012, 120, 4645-4648.	1.4	34
117	BCL2 mutations in diffuse large B-cell lymphoma. Leukemia, 2012, 26, 1383-1390.	7.2	135
118	Genetic Variation in Cell Death Genes and Risk of Non-Hodgkin Lymphoma. PLoS ONE, 2012, 7, e31560.	2.5	21
119	The Relationship between Telomere Length and Mortality in Chronic Obstructive Pulmonary Disease (COPD). PLoS ONE, 2012, 7, e35567.	2.5	80
120	Absence of NR2E1 mutations in patients with aniridia. Molecular Vision, 2012, 18, 2770-82.	1.1	6
121	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
122	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
123	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
124	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
125	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
126	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

#	Article	IF	Citations
127	Copy number alterations at polymorphic loci may be acquired somatically in patients with myelodysplastic syndromes. Leukemia Research, 2011, 35, 444-447.	0.8	11
128	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	7.0	47
129	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
130	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
131	Abstract 4676: Survival of gastric cancer differs by ethnicity: A population-based experience from British Columbia, Canada. , 2011, , .		0
132	Abstract 4673: Host genetic polymorphisms at TIMP3 are associated with survival of patients with adenocarcinoma of esophagus and gastoesophageal junction. , 2011, , .		0
133	Letter to the Editor - Reply to Leiro-Fernandez et al.. Pharmacogenomics, 2010, 11, 1207-1208.	1.3	3
134	Elevated circulating t(14;18) translocation levels prior to diagnosis of follicular lymphoma. Blood, 2010, 116, 6146-6147.	1.4	17
135	Genetic variation in carboxylesterase genes and susceptibility to isoniazid-induced hepatotoxicity. Pharmacogenomics Journal, 2010, 10, 524-536.	2.0	49
136	Interaction between organochlorines and the AHR gene, and risk of non-Hodgkin lymphoma. Cancer Causes and Control, 2010, 21, 11-22.	1.8	36
137	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
138	Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. Nature Genetics, 2010, 42, 661-664.	21.4	152
139	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
140	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
141	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
142	BCL2 Is Highly Mutated In Diffuse Large B-Cell Lymphoma. Blood, 2010, 116, 4187-4187.	1.4	0
143	Genetic Variation in Healthy Oldest-Old. PLoS ONE, 2009, 4, e6641.	2.5	42
144	Impact of Genotype Misclassification on Genetic Association Estimates and the Bayesian Adjustment. American Journal of Epidemiology, 2009, 170, 994-1004.	3.4	7

#	Article	IF	Citations
145	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
146	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
147	Genetic variants at 6p21.33 are associated with susceptibility to follicular lymphoma. Nature Genetics, 2009, 41, 873-875.	21.4	142
148	Genetic variations of NAT2 and CYP2E1 and isoniazid hepatotoxicity in a diverse population. Pharmacogenomics, 2009, 10, 1433-1445.	1.3	69
149	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
150	Diffuse large B-cell lymphoma: reduced CD20 expression is associated with an inferior survival. Blood, 2009, 113, 3773-3780.	1.4	133
151	Hepatitis C virus and risk of nonâ€Hodgkin lymphoma in British Columbia, Canada. International Journal of Cancer, 2008, 122, 630-633.	5.1	27
152	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
153	Reduced telomere length variation in healthy oldest old. Mechanisms of Ageing and Development, 2008, 129, 638-641.	4.6	59
154	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
155	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
156	Genetic Variation in H2AFX Contributes to Risk of Nonâ€"Hodgkin Lymphoma. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1098-1106.	2.5	37
157	A Survey of Genomic Properties for the Detection of Regulatory Polymorphisms. PLoS Computational Biology, 2007, 3, e106.	3.2	24
158	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
159	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
160	Organochlorines and risk of nonâ€Hodgkin lymphoma. International Journal of Cancer, 2007, 121, 2767-2775.	5.1	121
161	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
162	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

#	Article	IF	Citations
163	Allogeneic Stem Cell Transplant in First Complete Remission Overcomes the Poor Prognosis Associated with the FLT-3 Internal Tandem Duplication in Acute Myeloid Leukemia.. Blood, 2007, 110, 3491-3491.	1.4	0
164	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
165	Identifying related cancer types based on their incidence among people with multiple cancers. Emerging Themes in Epidemiology, 2006, 3, 17.	2.7	12
166	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
167	Analysis of long-lived C. elegans daf-2 mutants using serial analysis of gene expression. Genome Research, 2005, 15, 603-615.	5.5	180
168	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
169	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
170	The Genome Sequence of the SARS-Associated Coronavirus. Science, 2003, 300, 1399-1404.	12.6	1,842
171	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
172	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
173	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
174	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
175	Cholesterol efflux regulatory protein, Tangier disease and familial high-density lipoprotein deficiency. Current Opinion in Lipidology, 2000, 11, 117-122.	2.7	111
176	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
177	Mutations in ABC1 in Tangier disease and familial high-density lipoprotein deficiency. Nature Genetics, 1999, 22, 336-345.	21.4	1,609
178	Mutations in the ABC 1 gene in familial HDL deficiency with defective cholesterol efflux. Lancet, The, 1999, 354, 1341-1346.	13.7	345
179	Unexpectedly low loss of heterozygosity in genetically unstable Werner syndrome cell lines. Genes Chromosomes and Cancer, 1997, 18, 133-142.	2.8	8
180	A new polymorphic marker (D10S97) tightly linked to the multiple endocrine neoplasia type 2A (MEN2A) locus. Human Genetics, 1993, 90, 516-20.	3.8	1

#	Article	IF	Citations
181	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
182	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
183	Human repeat element-mediated PCR: Cloning and mapping of chromosome 10 DNA markers. Genomics, 1992, 13, 409-414.	2.9	10
184	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
185	Isolation of DNA fragments from a human chromosomal subregion by Alu PCR differential hybridization. Genomics, 1991, 9, 241-246.	2.9	15
186	Two polymorphisms at the D10S94 locus. Nucleic Acids Research, 1990, 18, 4959-4959.	14.5	2
187	Rapid cloning and characterization of new chromosome 10 DNA markers by Alu element-mediated PCR. Genomics, 1990, 7, 614-620.	2.9	74