

Angela R Brooks-Wilson

List of Publications by Year in descending order

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Version: 2024-02-01

187
papers

17,712
citations

31902

53
h-index

14702

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. <i>Breast Cancer</i> , 2022, 29, 38-49.	1.3	4
2	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
3	Functional MRI evaluation of cognitive effects of carotid stenosis revascularization. <i>Brain and Behavior</i> , 2022, 12, e2512.	1.0	2
4	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. <i>Scientific Reports</i> , 2022, 12, 6199.	1.6	2
5	B-Cell NHL Subtype Risk Associated with Autoimmune Conditions and PRS. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1103-1110.	1.1	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. <i>Leukemia and Lymphoma</i> , 2021, 62, 3147-3151.	0.6	1
8	Allele-Specific Transcript Abundance: A Pilot Study in Healthy Centenarians. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020, 75, 1068-1072.	1.7	0
9	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. <i>Human Molecular Genetics</i> , 2020, 29, 70-79.	1.4	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. <i>International Journal of Epidemiology</i> , 2020, 49, 216-232.	0.9	21
11	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
12	SimRVSequences: an R package to simulate genetic sequence data for pedigrees. <i>Bioinformatics</i> , 2020, 36, 2295-2297.	1.8	4
13	Tattoos and Hematologic Malignancies in British Columbia, Canada. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 2093-2095.	1.1	2
14	Birth Order, Sibship Size, Childhood Environment and Immune-Related Disorders, and Risk of Lymphoma in Lymphoid Cancer Families. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1168-1178.	1.1	3
15	Clinical and pathological associations of PTEN expression in ovarian cancer: a multicentre study from the Ovarian Tumour Tissue Analysis Consortium. <i>British Journal of Cancer</i> , 2020, 123, 793-802.	2.9	35
16	Dietary patterns in the healthy oldest old in the healthy aging study and the Canadian longitudinal study of aging: a cohort study. <i>BMC Geriatrics</i> , 2020, 20, 106.	1.1	20
17	In search of genetic factors predisposing to familial hairy cell leukemia (HCL): exome-sequencing of four multiplex HCL pedigrees. <i>Leukemia</i> , 2020, 34, 1934-1938.	3.3	3
18	Lipid Trait Variants and the Risk of Non-Hodgkin Lymphoma Subtypes: A Mendelian Randomization Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1074-1078.	1.1	13

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19	Ovarian Carcinoma Histotype: Strengths and Limitations of Integrating Morphology With Immunohistochemical Predictions. <i>International Journal of Gynecological Pathology</i> , 2019, 38, 353-362.	0.9	45
20	Genetic overlap between autoimmune diseases and non-Hodgkin lymphoma subtypes. <i>Genetic Epidemiology</i> , 2019, 43, 844-863.	0.6	28
21	Cohort Profile: The British Columbia Generations Project (BCGP). <i>International Journal of Epidemiology</i> , 2019, 48, 377-378k.	0.9	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. <i>Cancer Medicine</i> , 2019, 8, 2503-2513.	1.3	6
23	10-year follow-up of the Super-Seniors Study: compression of morbidity and genetic factors. <i>BMC Geriatrics</i> , 2019, 19, 58.	1.1	6
24	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
25	Genetic variants in genes related to inflammation, apoptosis and autophagy in breast cancer risk. <i>PLoS ONE</i> , 2019, 14, e0209010.	1.1	9
26	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. <i>Cancer Research</i> , 2019, 79, 467-481.	0.4	22
27	A comprehensive gene-environment interaction analysis in Ovarian Cancer using genome-wide significant common variants. <i>International Journal of Cancer</i> , 2019, 144, 2192-2205.	2.3	12
28	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. <i>Frontiers in Oncology</i> , 2019, 9, 1539.	1.3	6
29	Somatic Mitochondrial DNA Mutations in Diffuse Large B-Cell Lymphoma. <i>Scientific Reports</i> , 2018, 8, 3623.	1.6	4
30	Association of polygenic risk score with the risk of chronic lymphocytic leukemia and monoclonal B-cell lymphocytosis. <i>Blood</i> , 2018, 131, 2541-2551.	0.6	21
31	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. <i>British Journal of Cancer</i> , 2018, 118, 1123-1129.	2.9	15
32	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2018, 47, 450-459.	0.9	15
33	Racial/ethnic differences in the epidemiology of ovarian cancer: a pooled analysis of 12 case-control studies. <i>International Journal of Epidemiology</i> , 2018, 47, 460-472.	0.9	33
34	Simulating pedigrees ascertained for multiple disease-affected relatives. <i>Source Code for Biology and Medicine</i> , 2018, 13, 2.	1.7	6
35	The Super-Seniors Study: Phenotypic characterization of a healthy 85+ population. <i>PLoS ONE</i> , 2018, 13, e0197578.	1.1	15
36	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018, 13, e0197561.	1.1	9

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37	HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. <i>Cancer Research</i> , 2018, 78, 4086-4096.	0.4	34
38	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2473.	1.8	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. <i>Leukemia and Lymphoma</i> , 2017, 58, 2134-2143.	0.6	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. <i>Haematologica</i> , 2017, 102, e199-e202.	1.7	4
42	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. <i>Nature Communications</i> , 2017, 8, 14175.	5.8	75
43	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
44	Combined oral contraceptive use before the first birth and epithelial ovarian cancer risk. <i>British Journal of Cancer</i> , 2017, 116, 265-269.	2.9	8
45	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
46	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
47	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. <i>Lupus Science and Medicine</i> , 2017, 4, e000187.	1.1	15
48	Inherited Chromosomally Integrated Human Herpesvirus 6 and Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 425-427.	1.1	5
49	Effect of age on chronic inflammation and responsiveness to bacterial and viral challenges. <i>PLoS ONE</i> , 2017, 12, e0188881.	1.1	26
50	Lipid and Alzheimer's disease genes associated with healthy aging and longevity in healthy oldest-old. <i>Oncotarget</i> , 2017, 8, 20612-20621.	0.8	26
51	Polymorphisms of Insulin-Like Growth Factor 1 Pathway Genes and Breast Cancer Risk. <i>Frontiers in Oncology</i> , 2016, 6, 136.	1.3	8
52	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 884-895.	0.9	71
53	DNA repair variants and breast cancer risk. <i>Environmental and Molecular Mutagenesis</i> , 2016, 57, 269-281.	0.9	9
54	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. <i>Human Molecular Genetics</i> , 2016, 25, 3600-3612.	1.4	17

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55	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
56	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016, 135, 741-756.	1.8	19
57	A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1609-1618.	1.1	18
58	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 1619-1630.	0.9	111
59	Tea, coffee, and caffeinated beverage consumption and risk of epithelial ovarian cancers. <i>Cancer Epidemiology</i> , 2016, 45, 119-125.	0.8	20
60	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , 2016, 7, 10933.	5.8	94
61	Adult lifetime alcohol consumption and invasive epithelial ovarian cancer risk in a population-based case-control study. <i>Gynecologic Oncology</i> , 2016, 140, 277-284.	0.6	20
62	Genetic variation in vitamin D-related genes and risk of breast cancer among women of European and East Asian descent. <i>Tumor Biology</i> , 2016, 37, 6379-6387.	0.8	15
63	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. <i>Human Molecular Genetics</i> , 2016, 25, 1663-1676.	1.4	52
64	Evidence of a genetic link between endometriosis and ovarian cancer. <i>Fertility and Sterility</i> , 2016, 105, 35-43.e10.	0.5	37
65	Burden of Common Complex Disease Variants in the Exomes of Two Healthy Centenarian Brothers. <i>Gerontology</i> , 2016, 62, 58-62.	1.4	7
66	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	0.6	18
67	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. <i>Oncotarget</i> , 2016, 7, 69097-69110.	0.8	5
68	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. <i>Oncotarget</i> , 2016, 7, 72381-72394.	0.8	13
69	A targeted genetic association study of epithelial ovarian cancer susceptibility. <i>Oncotarget</i> , 2016, 7, 7381-7389.	0.8	7
70	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015, 39, 689-697.	0.6	22
71	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv279.	3.0	152
72	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	1.1	44

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73	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. <i>Nature Communications</i> , 2015, 6, 5751.	5.8	58
74	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2015, 24, 3595-3607.	1.4	40
75	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	9.4	221
76	Associations of Non-Hodgkin Lymphoma (NHL) Risk With Autoimmune Conditions According to Putative NHL Loci. <i>American Journal of Epidemiology</i> , 2015, 181, 406-421.	1.6	54
77	Genome-wide significant risk associations for mucinous ovarian carcinoma. <i>Nature Genetics</i> , 2015, 47, 888-897.	9.4	78
78	Network-Based Integration of GWAS and Gene Expression Identifies a <i>HOX</i> -Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	1.1	28
79	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. <i>Gynecologic Oncology</i> , 2015, 136, 542-548.	0.6	15
80	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	5.8	63
81	Common variants at the <i>CHEK2</i> gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	1.3	24
82	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015, 24, 5955-5964.	1.4	68
83	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 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- κ B Pathway: Genetic Association with <i>IL1A</i> and <i>TNFSF10</i> . <i>Cancer Research</i> , 2014, 74, 852-861.	0.4	48
87	Medical History, Lifestyle, Family History, and Occupational Risk Factors for Lymphoplasmacytic Lymphoma/Waldenstrom's Macroglobulinemia: The InterLymph Non-Hodgkin Lymphoma Subtypes Project. <i>Journal of the National Cancer Institute Monographs</i> , 2014, 2014, 87-97.	0.9	32
88	Gender and telomere length: Systematic review and meta-analysis. <i>Experimental Gerontology</i> , 2014, 51, 15-27.	1.2	394
89	Fasting insulin and endogenous hormones in relation to premenopausal breast density (Canada). <i>Cancer Causes and Control</i> , 2014, 25, 385-394.	0.8	12
90	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. <i>Human Genetics</i> , 2014, 133, 481-497.	1.8	23

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91	Rare and common variants in the Apolipoprotein E gene in healthy oldest old. <i>Neurobiology of Aging</i> , 2014, 35, 727.e1-727.e3.	1.5	11
92	Etiologic Heterogeneity Among Non-Hodgkin Lymphoma Subtypes: The InterLymph Non-Hodgkin Lymphoma Subtypes Project. <i>Journal of the National Cancer Institute Monographs</i> , 2014, 2014, 130-144.	0.9	265
93	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 1233-1238.	9.4	147
94	Functional characterization of genetic polymorphisms in the H2AFX distal promoter. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2014, 766-767, 37-43.	0.4	3
95	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. <i>American Journal of Human Genetics</i> , 2014, 95, 462-471.	2.6	96
96	Consortium analysis of gene and gene-folate interactions in purine and pyrimidine metabolism pathways with ovarian carcinoma risk. <i>Molecular Nutrition and Food Research</i> , 2014, 58, 2023-2035.	1.5	16
97	Occupational exposure and ovarian cancer risk. <i>Cancer Causes and Control</i> , 2014, 25, 829-841.	0.8	17
98	Abstract LB-272: Genome-wide association study identifies multiple susceptibility loci for diffuse large B-cell lymphoma. <i>Cancer Research</i> , 2014, 74, LB-272-LB-272.	0.4	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	CWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	9.4	326
102	Shared genetic factors for age at natural menopause in Iranian and European women. <i>Human Reproduction</i> , 2013, 28, 1987-1994.	0.4	15
103	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	9.4	493
104	Inherited common variants in mitochondrial DNA and invasive serous epithelial ovarian cancer risk. <i>BMC Research Notes</i> , 2013, 6, 425.	0.6	13
105	Genetics of healthy aging and longevity. <i>Human Genetics</i> , 2013, 132, 1323-1338.	1.8	274
106	Shift work, circadian gene variants and risk of breast cancer. <i>Cancer Epidemiology</i> , 2013, 37, 606-612.	0.8	52
107	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2013, 45, 868-876.	9.4	179
108	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013, 4, 1628.	5.8	144

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109	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	5.8	98
110	Genetic Polymorphisms at TIMP3 Are Associated with Survival of Adenocarcinoma of the Gastroesophageal Junction. <i>PLoS ONE</i> , 2013, 8, e59157.	1.1	23
111	Sex- and Subtype-Specific Analysis of H2AFX Polymorphisms in Non-Hodgkin Lymphoma. <i>PLoS ONE</i> , 2013, 8, e74619.	1.1	1
112	Non-Hodgkin Lymphoma Risk and Variants in Genes Controlling Lymphocyte Development. <i>PLoS ONE</i> , 2013, 8, e75170.	1.1	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. <i>Blood</i> , 2013, 122, 3111-3111.	0.6	2
114	Catenin Family Genes Are Not Commonly Mutated in Hereditary Diffuse Gastric Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 2272-2274.	1.1	21
115	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. <i>Twin Research and Human Genetics</i> , 2012, 15, 615-623.	0.3	8
116	PRRC2A and BCL2L11 gene variants influence risk of non-Hodgkin lymphoma: results from the InterLymph consortium. <i>Blood</i> , 2012, 120, 4645-4648.	0.6	34
117	BCL2 mutations in diffuse large B-cell lymphoma. <i>Leukemia</i> , 2012, 26, 1383-1390.	3.3	135
118	Genetic Variation in Cell Death Genes and Risk of Non-Hodgkin Lymphoma. <i>PLoS ONE</i> , 2012, 7, e31560.	1.1	21
119	The Relationship between Telomere Length and Mortality in Chronic Obstructive Pulmonary Disease (COPD). <i>PLoS ONE</i> , 2012, 7, e35567.	1.1	80
120	Absence of NR2E1 mutations in patients with aniridia. <i>Molecular Vision</i> , 2012, 18, 2770-82.	1.1	6
121	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	13.7	1,428
122	Cost-effective Prediction of Gender-Labeling Errors and Estimation of Gender-Labeling Error Rates in Candidate-Gene Association Studies. <i>Frontiers in Genetics</i> , 2011, 2, 31.	1.1	7
123	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. <i>PLoS ONE</i> , 2011, 6, e24987.	1.1	48
124	The prognostic effect of ethnicity for gastric and esophageal cancer: the population-based experience in British Columbia, Canada. <i>BMC Cancer</i> , 2011, 11, 164.	1.1	21
125	Comparison of Two Diverse Populations, British Columbia, Canada, and Ardabil, Iran, Indicates Several Variables Associated with Gastric and Esophageal Cancer Survival. <i>Journal of Gastrointestinal Cancer</i> , 2011, 42, 40-45.	0.6	11
126	Estimates of array and pool-construction variance for planning efficient DNA-pooling genome wide association studies. <i>BMC Medical Genomics</i> , 2011, 4, 81.	0.7	18

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127	Copy number alterations at polymorphic loci may be acquired somatically in patients with myelodysplastic syndromes. <i>Leukemia Research</i> , 2011, 35, 444-447.	0.4	11
128	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. <i>Clinical Cancer Research</i> , 2011, 17, 3742-3750.	3.2	47
129	GWAS of Follicular Lymphoma Reveals Allelic Heterogeneity at 6p21.32 and Suggests Shared Genetic Susceptibility with Diffuse Large B-cell Lymphoma. <i>PLoS Genetics</i> , 2011, 7, e1001378.	1.5	93
130	Polymorphisms in Stromal Genes and Susceptibility to Serous Epithelial Ovarian Cancer: A Report from the Ovarian Cancer Association Consortium. <i>PLoS ONE</i> , 2011, 6, e19642.	1.1	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 gastroesophageal junction. , 2011, , .		0
133	Letter to the Editor - Reply to Leiro-Fernandez <i>et al</i> .. <i>Pharmacogenomics</i> , 2010, 11, 1207-1208.	0.6	3
134	Elevated circulating t(14;18) translocation levels prior to diagnosis of follicular lymphoma. <i>Blood</i> , 2010, 116, 6146-6147.	0.6	17
135	Genetic variation in carboxylesterase genes and susceptibility to isoniazid-induced hepatotoxicity. <i>Pharmacogenomics Journal</i> , 2010, 10, 524-536.	0.9	49
136	Interaction between organochlorines and the AHR gene, and risk of non-Hodgkin lymphoma. <i>Cancer Causes and Control</i> , 2010, 21, 11-22.	0.8	36
137	GBV β /hepatitis G virus infection and non-Hodgkin lymphoma: a case control study. <i>International Journal of Cancer</i> , 2010, 126, 2885-2892.	2.3	51
138	Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. <i>Nature Genetics</i> , 2010, 42, 661-664.	9.4	152
139	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010, 42, 880-884.	9.4	235
140	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. <i>Nature Genetics</i> , 2010, 42, 874-879.	9.4	321
141	Tumor Necrosis Factor (TNF) and Lymphotoxin- α (LTA) Polymorphisms and Risk of Non-Hodgkin Lymphoma in the InterLymph Consortium. <i>American Journal of Epidemiology</i> , 2010, 171, 267-276.	1.6	128
142	BCL2 Is Highly Mutated In Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2010, 116, 4187-4187.	0.6	0
143	Genetic Variation in Healthy Oldest-Old. <i>PLoS ONE</i> , 2009, 4, e6641.	1.1	42
144	Impact of Genotype Misclassification on Genetic Association Estimates and the Bayesian Adjustment. <i>American Journal of Epidemiology</i> , 2009, 170, 994-1004.	1.6	7

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145	Prevalence and type distribution of human papillomavirus in 5,000 British Columbia women—implications for vaccination. <i>Cancer Causes and Control</i> , 2009, 20, 1387-1396.	0.8	35
146	Genetic variation in the NBS1, MRE11, RAD50 and BLM genes and susceptibility to non-Hodgkin lymphoma. <i>BMC Medical Genetics</i> , 2009, 10, 117.	2.1	27
147	Genetic variants at 6p21.33 are associated with susceptibility to follicular lymphoma. <i>Nature Genetics</i> , 2009, 41, 873-875.	9.4	142
148	Genetic variations of <i>NAT2</i> and <i>CYP2E1</i> and isoniazid hepatotoxicity in a diverse population. <i>Pharmacogenomics</i> , 2009, 10, 1433-1445.	0.6	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. <i>Haematologica</i> , 2009, 94, 423-427.	1.7	53
150	Diffuse large B-cell lymphoma: reduced CD20 expression is associated with an inferior survival. <i>Blood</i> , 2009, 113, 3773-3780.	0.6	133
151	Hepatitis C virus and risk of non-Hodgkin lymphoma in British Columbia, Canada. <i>International Journal of Cancer</i> , 2008, 122, 630-633.	2.3	27
152	Initial association of <i>NR2E1</i> with bipolar disorder and identification of candidate mutations in bipolar disorder, schizophrenia, and aggression through resequencing. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008, 147B, 880-889.	1.1	36
153	Reduced telomere length variation in healthy oldest old. <i>Mechanisms of Ageing and Development</i> , 2008, 129, 638-641.	2.2	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. <i>Blood</i> , 2008, 112, 3412-3424.	0.6	108
155	Incidence and Survival for Gastric and Esophageal Cancer Diagnosed in British Columbia, 1990 to 1999. <i>Canadian Journal of Gastroenterology & Hepatology</i> , 2008, 22, 143-148.	1.8	29
156	Genetic Variation in H2AFX Contributes to Risk of Non-Hodgkin Lymphoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007, 16, 1098-1106.	1.1	37
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