Brooke L Fridley

List of Publications by Year
in descending order

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240 papers	13,867 citations	28274 55 h-index	29157 104 g-index
244 all docs	244 docs citations	244 times ranked	20176 citing authors

#	Article	IF	Citations
1	Association between endometriosis and risk of histological subtypes of ovarian cancer: a pooled analysis of caseâ€“control studies. Lancet Oncology, The, 2012, 13, 385-394.	10.7	753
2	FKBP51 Affects Cancer Cell Response to Chemotherapy by Negatively Regulating Akt. Cancer Cell, 2009, 16, 259-266.	16.8	643
3	Association Between <emph type="ital">BRCA1</emph> and <emph type="ital">BRCA2</emph> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. JAMA - Journal of the American Medical Association, 2012, 307, 382.	7.4	546
4	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
5	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
6	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	10.7	335
7	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
8	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
9	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. Journal of the National Cancer Institute, 2015, 107, .	6.3	311
10	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
11	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.	1.6	266
12	Dose-Response Association of CD8⁺ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. JAMA Oncology, 2017, 3, e173290.	7.1	260
13	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
14	Genome-wide association study of glioma and meta-analysis. Human Genetics, 2012, 131, 1877-1888.	3.8	222
15	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
16	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
17	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
18	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. Endocrine-Related Cancer, 2013, 20, 251-262.	3.1	169

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19	Gemcitabine and Cytosine Arabinoside Cytotoxicity: Association with Lymphoblastoid Cell Expression. Cancer Research, 2008, 68, 7050-7058.	0.9	155
20	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
21	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. Genome Medicine, 2015, 7, 108.	8.2	138
22	Germline Mutation in BRCA1 or BRCA2 and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	7.0	138
23	Host genetic variation contributes to phenotypic diversity in myeloproliferative disorders. Blood, 2008, 111, 2785-2789.	1.4	135
24	Radiation pharmacogenomics: A genome-wide association approach to identify radiation response biomarkers using human lymphoblastoid cell lines. Genome Research, 2010, 20, 1482-1492.	5.5	135
25	A low-frequency variant at 8q24.21 is strongly associated with risk of oligodendroglial tumors and astrocytomas with IDH1 or IDH2 mutation. Nature Genetics, 2012, 44, 1122-1125.	21.4	131
26	Gene set analysis of SNP data: benefits, challenges, and future directions. European Journal of Human Genetics, 2011, 19, 837-843.	2.8	128
27	Integrative clustering of multi-level â€˜omic data based on non-negative matrix factorization algorithm. PLoS ONE, 2017, 12, e0176278.	2.5	116
28	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.	2.9	112
29	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
30	Genomic Association Analysis Suggests Chromosome 12 Locus Influencing Antihypertensive Response to Thiazide Diuretic. Hypertension, 2008, 52, 359-365.	2.7	106
31	Functional Genetic Polymorphisms in the Aromatase GeneCYP19Vary the Response of Breast Cancer Patients to Neoadjuvant Therapy with Aromatase Inhibitors. Cancer Research, 2010, 70, 319-328.	0.9	102
32	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
33	Familial Aggregation of Irritable Bowel Syndrome: A Family Caseâ€“Control Study. American Journal of Gastroenterology, 2010, 105, 833-841.	0.4	91
34	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	2.9	90
35	Genetic Variation Predicting Cisplatin Cytotoxicity Associated with Overall Survival in Lung Cancer Patients Receiving Platinum-Based Chemotherapy. Clinical Cancer Research, 2011, 17, 5801-5811.	7.0	87
36	Cigarette smoking and risk of ovarian cancer: a pooled analysis of 21 caseâ€“control studies. Cancer Causes and Control, 2013, 24, 989-1004.	1.8	84

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37	PurBayes: estimating tumor cellularity and subclonality in next-generation sequencing data. Bioinformatics, 2013, 29, 1888-1889.	4.1	82
38	Toll-like Receptor Polymorphisms and Age-Related Macular Degeneration. , 2008, 49, 1652.		79
39	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
40	Distinct germ line polymorphisms underlie glioma morphologic heterogeneity. Cancer Genetics, 2011, 204, 13-18.	0.4	77
41	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
42	Evidence for a time-dependent association between FOLR1 expression and survival from ovarian carcinoma: implications for clinical testing. An Ovarian Tumour Tissue Analysis consortium study. British Journal of Cancer, 2014, 111, 2297-2307.	6.4	76
43	ESR1/SYNE1 Polymorphism and Invasive Epithelial Ovarian Cancer Risk: An Ovarian Cancer Association Consortium Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 245-250.	2.5	75
44	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.9	75
45	Gemcitabine and Arabinosylcytosin Pharmacogenomics: Genome-Wide Association and Drug Response Biomarkers. PLoS ONE, 2009, 4, e7765.	2.5	75
46	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
47	Biomarker-Based Ovarian Carcinoma Typing: A Histologic Investigation in the Ovarian Tumor Tissue Analysis Consortium. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1677-1686.	2.5	70
48	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
49	Complement Component 3 (C3) Haplotypes and Risk of Advanced Age-Related Macular Degeneration. , 2009, 50, 3386.		65
50	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.	2.5	64
51	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
52	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. Journal of the National Cancer Institute, 2015, 107, djv246.	6.3	63
53	Primary Biliary Cirrhosis Is Associated With a Genetic Variant in the 3â€² Flanking Region of the CTLA4 Gene. Gastroenterology, 2008, 135, 1200-1206.	1.3	62
54	Inherited Variants in Mitochondrial Biogenesis Genes May Influence Epithelial Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1131-1145.	2.5	62

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55	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
56	Acetaminophen-NAPQI Hepatotoxicity: A Cell Line Model System Genome-Wide Association Study. Toxicological Sciences, 2011, 120, 33-41.	3.1	61
57	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.	2.9	60
58	Comparison of normalization approaches for gene expression studies completed with high-throughput sequencing. PLoS ONE, 2018, 13, e0206312.	2.5	60
59	Molecular classification of high grade endometrioid and clear cell ovarian cancer using TCGA gene expression signatures. Gynecologic Oncology, 2016, 141, 95-100.	1.4	58
60	Platinum Sensitivityâ€“Related Germline Polymorphism Discovered via a Cell-Based Approach and Analysis of Its Association with Outcome in Ovarian Cancer Patients. Clinical Cancer Research, 2011, 17, 5490-5500.	7.0	57
61	Genome-Wide Study of Response to Platinum, Taxane, and Combination Therapy in Ovarian Cancer: In vitro Phenotypes, Inherited Variation, and Disease Recurrence. Frontiers in Genetics, 2016, 7, 37.	2.3	57
62	Inherited Determinants of Ovarian Cancer Survival. Clinical Cancer Research, 2010, 16, 995-1007.	7.0	56
63	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.	1.4	55
64	Combined and Interactive Effects of Environmental and GWAS-Identified Risk Factors in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 880-890.	2.5	54
65	FKBP5 genetic variation. Pharmacogenetics and Genomics, 2013, 23, 156-166.	1.5	54
66	Self-Contained Gene-Set Analysis of Expression Data: An Evaluation of Existing and Novel Methods. PLoS ONE, 2010, 5, e12693.	2.5	52
67	Associations of High-Grade Glioma With Glioma Risk Alleles and Histories of Allergy and Smoking. American Journal of Epidemiology, 2011, 174, 574-581.	3.4	52
68	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
69	TSPYL5 SNPs: Association with Plasma Estradiol Concentrations and Aromatase Expression. Molecular Endocrinology, 2013, 27, 657-670.	3.7	49
70	Bayesian variable and model selection methods for genetic association studies. Genetic Epidemiology, 2009, 33, 27-37.	1.3	48
71	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
72	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

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73	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	7.0	47
74	Thiopurine pharmacogenomics: association of SNPs with clinical response and functional validation of candidate genes. Pharmacogenomics, 2014, 15, 433-447.	1.3	47
75	Genome-wide gene-set analysis for identification of pathways associated with alcohol dependence. International Journal of Neuropsychopharmacology, 2013, 16, 271-278.	2.1	46
76	Ovarian Cancer Risk Associated with Inherited Inflammation-Related Variants. Cancer Research, 2012, 72, 1064-1069.	0.9	45
77	Interacting alleles of the coinhibitory immunoreceptor genes cytotoxic T-lymphocyte antigen 4 and programmed cell-death 1 influence risk and features of primary biliary cirrhosis. Hepatology, 2007, 47, 563-570.	7.3	44
78	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
79	PPM1DMosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. Journal of the National Cancer Institute, 2016, 108, djv347.	6.3	43
80	Differential roles of ERRFI1 in EGFR and AKT pathway regulation affect cancer proliferation. EMBO Reports, 2018, 19, .	4.5	43
81	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.	1.8	43
82	Confirmation of Linkage to and Localization of Familial Colon Cancer Risk Haplotype on Chromosome 9q22. Cancer Research, 2010, 70, 5409-5418.	0.9	42
83	Genetic regulation of dihydropyrimidinase and its possible implication in altered uracil catabolism. Pharmacogenetics and Genomics, 2007, 17, 973-987.	1.5	42
84	Evaluation of Clustering and Genotype Distribution for Replication in Genome Wide Association Studies: The Age-Related Eye Disease Study. PLoS ONE, 2008, 3, e3813.	2.5	41
85	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.	2.6	40
86	A <scp>B</scp>ayesian Integrative Genomic Model for Pathway Analysis of Complex Traits. Genetic Epidemiology, 2012, 36, 352-359.	1.3	40
87	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
88	Cell cycle genes and ovarian cancer susceptibility: a tagSNP analysis. British Journal of Cancer, 2009, 101, 1461-1468.	6.4	39
89	Recreational physical inactivity and mortality in women with invasive epithelial ovarian cancer: evidence from the Ovarian Cancer Association Consortium. British Journal of Cancer, 2016, 115, 95-101.	6.4	39
90	Betaine-homocysteine methyltransferase: Human liver genotypeâ€“phenotype correlation. Molecular Genetics and Metabolism, 2011, 102, 126-133.	1.1	38

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91	Inherited variant on chromosome 11q23 increases susceptibility to IDH-mutated but not IDH-normal gliomas regardless of grade or histology. Neuro-Oncology, 2013, 15, 535-541.	1.2	38
92	HNF1B variants associate with promoter methylation and regulate gene networks activated in prostate and ovarian cancer. Oncotarget, 2016, 7, 74734-74746.	1.8	38
93	Genome-wide association analyses of genetic, phenotypic, and environmental risks in the age-related eye disease study. Molecular Vision, 2010, 16, 2811-21.	1.1	38
94	Candidate Gene Analysis Using Imputed Genotypes: Cell Cycle Single-Nucleotide Polymorphisms and Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 935-944.	2.5	37
95	Identification of Novel Variants in Colorectal Cancer Families by High-Throughput Exome Sequencing. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1239-1251.	2.5	37
96	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	1.0	37
97	Genetic variation in platinating agent and taxane pathway genes as predictors of outcome and toxicity in advanced non-small-cell lung cancer. Pharmacogenomics, 2014, 15, 1565-1574.	1.3	36
98	Proteasome Î² Subunit Pharmacogenomics: Gene Resequencing and Functional Genomics. Clinical Cancer Research, 2008, 14, 3503-3513.	7.0	35
99	ABO blood group and risk of epithelial ovarian cancer within the Ovarian Cancer Association Consortium. Cancer Causes and Control, 2012, 23, 1805-1810.	1.8	35
100	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.	3.3	35
101	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	5.1	35
102	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.	3.8	34
103	Meta-analysis of 8q24 for seven cancers reveals a locus between NOV and ENPP2 associated with cancer development. BMC Medical Genetics, 2011, 12, 156.	2.1	33
104	Gemcitabine metabolic pathway genetic polymorphisms and response in patients with non-small cell lung cancer. Pharmacogenetics and Genomics, 2012, 22, 105-116.	1.5	33
105	Kernel canonical correlation analysis for assessing geneâ€“gene interactions and application to ovarian cancer. European Journal of Human Genetics, 2014, 22, 126-131.	2.8	33
106	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.	7.0	33
107	Modulation of Breast Cancer Risk Biomarkers by High-Dose Omega-3 Fatty Acids: Phase II Pilot Study in Postmenopausal Women. Cancer Prevention Research, 2015, 8, 922-931.	1.5	33
108	Use of the gamma method for self-contained gene-set analysis of SNP data. European Journal of Human Genetics, 2012, 20, 565-571.	2.8	32

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109	Survival Is Associated With Genetic Variation in Inflammatory Pathway Genes Among Patients With Resected and Unresected Pancreatic Cancer. Annals of Surgery, 2013, 257, 1096-1102.	4.2	32
110	Contribution of FKBP5 Genetic Variation to Gemcitabine Treatment and Survival in Pancreatic Adenocarcinoma. PLoS ONE, 2013, 8, e70216.	2.5	32
111	Tumor Hypomethylation at 6p21.3 Associates with Longer Time to Recurrence of High-Grade Serous Epithelial Ovarian Cancer. Cancer Research, 2014, 74, 3084-3091.	0.9	32
112	Integrative genomic analysis identifies epigenetic marks that mediate genetic risk for epithelial ovarian cancer. BMC Medical Genomics, 2014, 7, 8.	1.5	32
113	Chronic Recreational Physical Inactivity and Epithelial Ovarian Cancer Risk: Evidence from the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1114-1124.	2.5	32
114	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.	3.4	32
115	Integrative clustering methods for high-dimensional molecular data. Translational Cancer Research, 2014, 3, 202-216.	1.0	32
116	Assessment of Hepatocyte Growth Factor in Ovarian Cancer Mortality. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1638-1648.	2.5	31
117	Identification of a novel percent mammographic density locus at 12q24. Human Molecular Genetics, 2012, 21, 3299-3305.	2.9	31
118	Genetic variations associated with gemcitabine treatment outcome in pancreatic cancer. Pharmacogenetics and Genomics, 2016, 26, 527-537.	1.5	31
119	Comprehensive Cross-Population Analysis of High-Grade Serous Ovarian Cancer Supports No More Than Three Subtypes. G3: Genes, Genomes, Genetics, 2016, 6, 4097-4103.	1.8	31
120	Genetic regulation of Î²-ureidopropionase and its possible implication in altered uracil catabolism. Pharmacogenetics and Genomics, 2008, 18, 25-35.	1.5	30
121	Discovery of genetic biomarkers contributing to variation in drug response of cytidine analogues using human lymphoblastoid cell lines. BMC Genomics, 2014, 15, 93.	2.8	30
122	Data augmentation for a Bayesian spatial model involving censored observations. Environmetrics, 2007, 18, 107-123.	1.4	29
123	Risk of Ovarian Cancer and Inherited Variants in Relapse-Associated Genes. PLoS ONE, 2010, 5, e8884.	2.5	29
124	Xenobioticâ€Metabolizing gene polymorphisms and ovarian cancer risk. Molecular Carcinogenesis, 2011, 50, 397-402.	2.7	29
125	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
126	Gender Bias in Human Systemic Lupus Erythematosus: A Problem of Steroid Receptor Action?. Frontiers in Immunology, 2018, 9, 611.	4.8	28

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127	Transcriptomic Characterization of Endometrioid, Clear Cell, and High-Grade Serous Epithelial Ovarian Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1101-1109.	2.5	26
128	Predictors of survival trajectories among women with epithelial ovarian cancer. Gynecologic Oncology, 2020, 156, 459-466.	1.4	26
129	Modulation of Breast Cancer Risk Biomarkers by High-Dose Omega-3 Fatty Acids: Phase II Pilot Study in Premenopausal Women. Cancer Prevention Research, 2015, 8, 912-921.	1.5	25
130	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	3.1	25
131	Cigarette smoking is associated with adverse survival among women with ovarian cancer: Results from a pooled analysis of 19 studies. International Journal of Cancer, 2017, 140, 2422-2435.	5.1	25
132	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
133	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.	2.5	24
134	Colorectal Cancer Linkage on Chromosomes 4q21, 8q13, 12q24, and 15q22. PLoS ONE, 2012, 7, e38175.	2.5	24
135	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
136	Oxidized mitochondrial DNA released after inflammasome activation is a disease biomarker for myelodysplastic syndromes. Blood Advances, 2021, 5, 2216-2228.	5.2	24
137	Polymorphisms in ABCB1 and ERCC2 associated with ovarian cancer outcome. International Journal of Molecular Epidemiology and Genetics, 2011, 2, 185-95.	0.4	24
138	Polymorphism in the GALNT1 Gene and Epithelial Ovarian Cancer in Non-Hispanic White Women: The Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 600-604.	2.5	23
139	Inflammation-Related Gene Variants as Risk Factors for Pancreatic Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1251-1254.	2.5	23
140	SSBP2 Variants Are Associated with Survival in Glioblastoma Patients. Clinical Cancer Research, 2012, 18, 3154-3162.	7.0	23
141	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23
142	InterSIM: Simulation tool for multiple integrative â€˜omic datasetsâ€™. Computer Methods and Programs in Biomedicine, 2016, 128, 69-74.	4.7	23
143	Comparison of penalty functions for sparse canonical correlation analysis. Computational Statistics and Data Analysis, 2012, 56, 245-254.	1.2	22
144	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22

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145	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. Oncotarget, 2017, 8, 46891-46899.	1.8	22
146	Genome-Wide Investigation of Regional Blood-Based DNA Methylation Adjusted for Complete Blood Counts Implicates BNC2 in Ovarian Cancer. Genetic Epidemiology, 2014, 38, 457-466.	1.3	21
147	Large-Scale Evaluation of Common Variation in Regulatory T Cellâ€“Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	3.4	21
148	Methylation of leukocyte DNA and ovarian cancer: relationships with disease status and outcome. BMC Medical Genomics, 2014, 7, 21.	1.5	21
149	Drug discovery using clinical outcome-based Connectivity Mapping: application to ovarian cancer. BMC Genomics, 2016, 17, 811.	2.8	21
150	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1117-1126.	2.5	21
151	Challenges and Opportunities in the Statistical Analysis of Multiplex Immunofluorescence Data. Cancers, 2021, 13, 3031.	3.7	21
152	Polymorphisms in NF-Îºb Inhibitors and Risk of Epithelial Ovarian Cancer. BMC Cancer, 2009, 9, 170.	2.6	20
153	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. Fertility and Sterility, 2011, 95, 40-45.	1.0	20
154	Gene set analysis of purine and pyrimidine antimetabolites cancer therapies. Pharmacogenetics and Genomics, 2011, 21, 701-712.	1.5	20
155	Analysis of Over 10,000 Cases Finds No Association between Previously Reported Candidate Polymorphisms and Ovarian Cancer Outcome. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 987-992.	2.5	20
156	The association between socioeconomic status and tumour stage at diagnosis of ovarian cancer: A pooled analysis of 18 case-control studies. Cancer Epidemiology, 2016, 41, 71-79.	1.9	20
157	Inherited Variants in Regulatory T Cell Genes and Outcome of Ovarian Cancer. PLoS ONE, 2013, 8, e53903.	2.5	20
158	MicroRNA Processing and Binding Site Polymorphisms Are Not Replicated in the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1793-1797.	2.5	19
159	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
160	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. Human Molecular Genetics, 2019, 28, 1331-1342.	2.9	19
161	Utilizing Genotype Imputation for the Augmentation of Sequence Data. PLoS ONE, 2010, 5, e11018.	2.5	19
162	Integrative Gene Set Analysis: Application to Platinum Pharmacogenomics. OMICS A Journal of Integrative Biology, 2014, 18, 34-41.	2.0	18

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163	Metformin pharmacogenomics: a genome-wide association study to identify genetic and epigenetic biomarkers involved in metformin anticancer response using human lymphoblastoid cell lines. Human Molecular Genetics, 2016, 25, ddw301.	2.9	18
164	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
165	Mediation analysis of alcohol consumption, DNA methylation, and epithelial ovarian cancer. Journal of Human Genetics, 2018, 63, 339-348.	2.3	18
166	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	3.8	18
167	Variation at 8q24 and 9p24 and Risk of Epithelial Ovarian Cancer. Twin Research and Human Genetics, 2010, 13, 43-56.	0.6	17
168	Simultaneous Analysis of Multiple Data Types in Pharmacogenomic Studies Using Weighted Sparse Canonical Correlation Analysis. OMICS A Journal of Integrative Biology, 2012, 16, 363-373.	2.0	17
169	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
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