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	A Question-and-Answer System to Extract Data From Free-Text Oncological Pathology Reports (CancerBERT Network): Development Study. Journal of Medical Internet Research, 2022, 24, e27210.	4.3	10
2	Mitochondrial DNA sequence variation and risk of glioma. Mitochondrion, 2022, 63, 32-36.	3.4	2
3	Summarizing internal dynamics boosts differential analysis and functional interpretation of super enhancers. Nucleic Acids Research, 2022, 50, 3115-3127.	14.5	4
4	Tumor immune cell clustering and its association with survival in African American women with ovarian cancer. PLoS Computational Biology, 2022, 18, e1009900.	3.2	8
5	spatialGE: quantification and visualization of the tumor microenvironment heterogeneity using spatial transcriptomics. Bioinformatics, 2022, 38, 2645-2647.	4.1	12
6	Identification of Two Genetic Loci Associated with Leukopenia after Chemotherapy in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 3342-3355.	7.0	3
7	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
8	Oxidized mitochondrial DNA released after inflammasome activation is a disease biomarker for myelodysplastic syndromes. Blood Advances, 2021, 5, 2216-2228.	5.2	24
9	Enabling Precision Medicine in Cancer Care Through a Molecular Data Warehouse: The Moffitt Experience. JCO Clinical Cancer Informatics, 2021, 5, 561-569.	2.1	7
10	Challenges and Opportunities in the Statistical Analysis of Multiplex Immunofluorescence Data. Cancers, 2021, 13, 3031.	3.7	21
11	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
12	Statistical and Bioinformatics Analysis of Data from Bulk and Single-Cell RNA Sequencing Experiments. Methods in Molecular Biology, 2021, 2194, 143-175.	0.9	12
13	DNA Methylation in Ovarian Cancer Susceptibility. Cancers, 2021, 13, 108.	3.7	10
14	Statistical genomics in rare cancer. Seminars in Cancer Biology, 2020, 61, 1-10.	9.6	15
15	Predictors of survival trajectories among women with epithelial ovarian cancer. Gynecologic Oncology, 2020, 156, 459-466.	1.4	26
16	Ontogeny Related Changes in the Pediatric Liver Metabolome. Frontiers in Pediatrics, 2020, 8, 549.	1.9	3
17	Nonlinear mixed-effects models for modeling in vitro drug response data to determine problematic cancer cell lines. Scientific Reports, 2019, 9, 14421.	3.3	8
18	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

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19	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
20	Genomic Analysis Using Regularized Regression in High-Grade Serous Ovarian Cancer. Cancer Informatics, 2018, 17, 117693511875534.	1.9	5
21	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
22	Expression of Sestrin Genes in Radiotherapy for Prostate Cancer and Its Association With Fatigue: A Proof-of-Concept Study. Biological Research for Nursing, 2018, 20, 218-226.	1.9	8
23	Ontogeny-related pharmacogene changes in the pediatric liver transcriptome. Pharmacogenetics and Genomics, 2018, 28, 86-94.	1.5	12
24	Differential roles of ERRFI1 in EGFR and AKT pathway regulation affect cancer proliferation. EMBO Reports, 2018, 19, .	4.5	43
25	Mediation analysis of alcohol consumption, DNA methylation, and epithelial ovarian cancer. Journal of Human Genetics, 2018, 63, 339-348.	2.3	18
26	Sestrin family of genes and their role in cancer-related fatigue. Supportive Care in Cancer, 2018, 26, 2071-2074.	2.2	2
27	Robust Tests for Additive Gene-Environment Interaction in Case-Control Studies Using Gene-Environment Independence. American Journal of Epidemiology, 2018, 187, 366-377.	3.4	8
28	Subject level clustering using a negative binomial model for small transcriptomic studies. BMC Bioinformatics, 2018, 19, 474.	2.6	8
29	Comparison of normalization approaches for gene expression studies completed with high-throughput sequencing. PLoS ONE, 2018, 13, e0206312.	2.5	60
30	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
31	Gender Bias in Human Systemic Lupus Erythematosus: A Problem of Steroid Receptor Action?. Frontiers in Immunology, 2018, 9, 611.	4.8	28
32	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9
33	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
34	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
35	Assessment of data transformations for model-based clustering of RNA-Seq data. PLoS ONE, 2018, 13, e0191758.	2.5	5
36	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

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37	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
38	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
39	Integrative clustering of multi-level â€˜omic data based on non-negative matrix factorization algorithm. PLoS ONE, 2017, 12, e0176278.	2.5	116
40	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
41	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. Oncotarget, 2017, 8, 46891-46899.	1.8	22
42	Genetic variations associated with gemcitabine treatment outcome in pancreatic cancer. Pharmacogenetics and Genomics, 2016, 26, 527-537.	1.5	31
43	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
44	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
45	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
46	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
47	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
48	InterSIM: Simulation tool for multiple integrative â€˜omic datasetsâ€™. Computer Methods and Programs in Biomedicine, 2016, 128, 69-74.	4.7	23
49	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
50	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
51	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
52	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
53	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
54	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

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55	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
56	Drug discovery using clinical outcome-based Connectivity Mapping: application to ovarian cancer. BMC Genomics, 2016, 17, 811.	2.8	21
57	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
58	Expression signature distinguishing two tumour transcriptome classes associated with progression-free survival among rare histological types of epithelial ovarian cancer. British Journal of Cancer, 2016, 114, 1412-1420.	6.4	8
59	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
60	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
61	Assessment of Multifactor Geneâ€“Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 780-790.	2.5	10
62	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
63	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
64	Clinical and Emergent Biomarkers and Their Relationship to the Prognosis of Ovarian Cancer. Oncology, 2016, 90, 59-68.	1.9	9
65	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
66	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	2.5	9
67	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	1.0	37
68	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
69	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
70	HNF1B variants associate with promoter methylation and regulate gene networks activated in prostate and ovarian cancer. Oncotarget, 2016, 7, 74734-74746.	1.8	38
71	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	1.8	7
72	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

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73	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
74	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
75	Intra-Gene DNA Methylation Variability Is a Clinically Independent Prognostic Marker in Womenâ€™s Cancers. PLoS ONE, 2015, 10, e0143178.	2.5	14
76	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
77	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. Genome Medicine, 2015, 7, 108.	8.2	138
78	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
79	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
80	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
81	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
82	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	1.4	15
83	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
84	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
85	Genome-wide association analysis identified splicing single nucleotide polymorphism in CFLAR predictive of triptolide chemo-sensitivity. BMC Genomics, 2015, 16, 483.	2.8	7
86	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
87	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
88	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
89	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
90	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

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91	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
92	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	3.1	25
93	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
94	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
95	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
96	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
97	Variation in NF-ÎºB Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1421-1427.	2.5	13
98	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
99	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
100	Individualizing Care for Ovarian Cancer Patients Using Big Data. Journal of the National Cancer Institute, 2014, 106, .	6.3	1
101	Thiopurine pharmacogenomics: association of SNPs with clinical response and functional validation of candidate genes. Pharmacogenomics, 2014, 15, 433-447.	1.3	47
102	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
103	Risk of Ovarian Cancer and the NF-ÎºB Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.9	48
104	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
105	Acquired chromosomal anomalies in chronic lymphocytic leukemia patients compared with more than 50,000 quasi-normal participants. Cancer Genetics, 2014, 207, 19-30.	0.4	5
106	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
107	Integrative genomic analysis identifies epigenetic marks that mediate genetic risk for epithelial ovarian cancer. BMC Medical Genomics, 2014, 7, 8.	1.5	32
108	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23

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109	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
110	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
111	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
112	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
113	Integrative Gene Set Analysis: Application to Platinum Pharmacogenomics. OMICS A Journal of Integrative Biology, 2014, 18, 34-41.	2.0	18
114	Methylation of leukocyte DNA and ovarian cancer: relationships with disease status and outcome. BMC Medical Genomics, 2014, 7, 21.	1.5	21
115	Integrative clustering methods for high-dimensional molecular data. Translational Cancer Research, 2014, 3, 202-216.	1.0	32
116	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	10.7	335
117	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
118	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
119	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
120	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
121	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
122	Genome-wide gene-set analysis for identification of pathways associated with alcohol dependence. International Journal of Neuropsychopharmacology, 2013, 16, 271-278.	2.1	46
123	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
124	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
125	TSPYL5 SNPs: Association with Plasma Estradiol Concentrations and Aromatase Expression. Molecular Endocrinology, 2013, 27, 657-670.	3.7	49
126	PurBayes: estimating tumor cellularity and subclonality in next-generation sequencing data. Bioinformatics, 2013, 29, 1888-1889.	4.1	82

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127	Bayesian genomic models for the incorporation of pathway topology knowledge into association studies. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 505-16.	0.6	2
128	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
129	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
130	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. Endocrine-Related Cancer, 2013, 20, 251-262.	3.1	169
131	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
132	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
133	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
134	Soft truncation thresholding for gene set analysis of RNA-seq data: Application to a vaccine study. Scientific Reports, 2013, 3, 2898.	3.3	15
135	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
136	FKBP5 genetic variation. Pharmacogenetics and Genomics, 2013, 23, 156-166.	1.5	54
137	Contribution of FKBP5 Genetic Variation to Gemcitabine Treatment and Survival in Pancreatic Adenocarcinoma. PLoS ONE, 2013, 8, e70216.	2.5	32
138	Genome-wide association study for biomarker identification of Rapamycin and Everolimus using a lymphoblastoid cell line system. Frontiers in Genetics, 2013, 4, 166.	2.3	12
139	Abstract 2271: Metformin pharmacogenomics: A genome-wide associate study to identify genetic and epigenetic biomarkers involved in metformin response.. , 2013, , .		1
140	Inherited Variants in Regulatory T Cell Genes and Outcome of Ovarian Cancer. PLoS ONE, 2013, 8, e53903.	2.5	20
141	Abstract 4844: Polymorphisms in regulatory T cell related genes and ovarian cancer survival.. , 2013, , .		0
142	Gene Set Analysis of Survival Following Ovarian Cancer Implicates Macrolide Binding and Intracellular Signaling Genes. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 529-536.	2.5	7
143	Identification of a novel percent mammographic density locus at 12q24. Human Molecular Genetics, 2012, 21, 3299-3305.	2.9	31
144	Common Variation in Nemo-Like Kinase Is Associated with Risk of Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 523-528.	2.5	8

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145	SSBP2 Variants Are Associated with Survival in Glioblastoma Patients. Clinical Cancer Research, 2012, 18, 3154-3162.	7.0	23
146	Ovarian Cancer Risk Associated with Inherited Inflammation-Related Variants. Cancer Research, 2012, 72, 1064-1069.	0.9	45
147	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
148	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
149	Human Liver Methionine Cycle:MAT1AandGNMTGene Resequencing, Functional Genomics, and Hepatic Genotype-Phenotype Correlation. Drug Metabolism and Disposition, 2012, 40, 1984-1992.	3.3	16
150	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
151	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
152	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
153	Genome-wide association study of glioma and meta-analysis. Human Genetics, 2012, 131, 1877-1888.	3.8	222
154	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
155	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
156	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
157	Colorectal Cancer Linkage on Chromosomes 4q21, 8q13, 12q24, and 15q22. PLoS ONE, 2012, 7, e38175.	2.5	24
158	Identifying the Genetic Variation of Gene Expression Using Gene Sets: Application of Novel Gene Set eQTL Approach to PharmGKB and KEGG. PLoS ONE, 2012, 7, e43301.	2.5	6
159	Regular Multivitamin Supplement Use, Single Nucleotide Polymorphisms in ATIC, SHMT2, and SLC46A1, and Risk of Ovarian Carcinoma. Frontiers in Genetics, 2012, 3, 33.	2.3	4
160	Germline Copy Number Variation and Ovarian Cancer Survival. Frontiers in Genetics, 2012, 3, 142.	2.3	11
161	Localization of Association Signal from Risk and Protective Variants in Sequencing Studies. Frontiers in Genetics, 2012, 3, 173.	2.3	9
162	A <scp>B</scp>ayesian Integrative Genomic Model for Pathway Analysis of Complex Traits. Genetic Epidemiology, 2012, 36, 352-359.	1.3	40

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163	Comparison of penalty functions for sparse canonical correlation analysis. Computational Statistics and Data Analysis, 2012, 56, 245-254.	1.2	22
164	Genetic Association Studies of Copy-Number Variation: Should Assignment of Copy Number States Precede Testing?. PLoS ONE, 2012, 7, e34262.	2.5	10
165	European American Stratification in Ovarian Cancer Case Control Data: The Utility of Genome-Wide Data for Inferring Ancestry. PLoS ONE, 2012, 7, e35235.	2.5	3
166	Association of TNFSF8 Polymorphisms With Peripheral Neutrophil Count. Mayo Clinic Proceedings, 2011, 86, 1075-1081.	3.0	2
167	Distinct germ line polymorphisms underlie glioma morphologic heterogeneity. Cancer Genetics, 2011, 204, 13-18.	0.4	77
168	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. Fertility and Sterility, 2011, 95, 40-45.	1.0	20
169	Mycophenolic acid response biomarkers: A cell line model system-based genome-wide screen. International Immunopharmacology, 2011, 11, 1057-1064.	3.8	10
170	Betaine-homocysteine methyltransferase: Human liver genotypeâ€“phenotype correlation. Molecular Genetics and Metabolism, 2011, 102, 126-133.	1.1	38
171	A Latent Model for Prioritization of SNPs for Functional Studies. PLoS ONE, 2011, 6, e20764.	2.5	7
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