Ellen L Goode

List of Publications by Year
in descending order

146 papers	9,295 citations	47006 47 h-index	46799 89 g-index
149 all docs	149 docs citations	149 times ranked	14032 citing authors

#	Article	IF	Citations
1	DNA Methylation Profiles of Ovarian Clear Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 132-141.	2.5	12
2	MCM3 is a novel proliferation marker associated with longer survival for patients with tubo-ovarian high-grade serous carcinoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2022, 480, 855-871.	2.8	8
3	High Prediagnosis Inflammation-Related Risk Score Associated with Decreased Ovarian Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 443-452.	2.5	2
4	Functional analysis of the 1p34.3 risk locus implicates GNL2 in high-grade serous ovarian cancer. American Journal of Human Genetics, 2022, 109, 116-135.	6.2	3
5	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
6	Validated biomarker assays confirm that <scp>ARID1A</scp> loss is confounded with <scp>MMR</scp> deficiency, <scp>CD8⁺ TIL</scp> infiltration, and provides no independent prognostic value in endometriosisâ€associated ovarian carcinomas. Journal of Pathology, 2022, 256, 388-401.	4.5	15
7	Germline BRCA variants, lifestyle and ovarian cancer survival. Gynecologic Oncology, 2022, , .	1.4	2
8	CA-125 Levels Are Predictive of Survival in Low-Grade Serous Ovarian Cancerâ€”A Multicenter Analysis. Cancers, 2022, 14, 1954.	3.7	3
9	Molecular Subclasses of Clear Cell Ovarian Carcinoma and Their Impact on Disease Behavior and Outcomes. Clinical Cancer Research, 2022, 28, 4947-4956.	7.0	22
10	Population-based targeted sequencing of 54 candidate genes identifiesPALB2as a susceptibility gene for high-grade serous ovarian cancer. Journal of Medical Genetics, 2021, 58, 305-313.	3.2	26
11	Expanding Our Understanding of Ovarian Cancer Risk: The Role of Incomplete Pregnancies. Journal of the National Cancer Institute, 2021, 113, 301-308.	6.3	8
12	Refined cut-off for TP53 immunohistochemistry improves prediction of TP53 mutation status in ovarian mucinous tumors: implications for outcome analyses. Modern Pathology, 2021, 34, 194-206.	5.5	21
13	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
14	Circulating CD14 + HLAâ€ÐR lo/â^' monocytic cells as a biomarker for epithelial ovarian cancer progression. American Journal of Reproductive Immunology, 2021, 85, e13343.	1.2	4
15	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. Human Genetics and Genomics Advances, 2021, 2, 100042.	1.7	6
16	Identification of a Locus Near ULK1 Associated With Progression-Free Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1669-1680.	2.5	5
17	Frequent POLE-driven hypermutation in ovarian endometrioid cancer revealed by mutational signatures in RNA sequencing. BMC Medical Genomics, 2021, 14, 165.	1.5	10
18	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

#	Article	IF	Citations
19	Generating real-world evidence from unstructured clinical notes to examine clinical utility of genetic tests: use case in BRCAness. BMC Medical Informatics and Decision Making, 2021, 21, 3.	3.0	7
20	Multi-tissue transcriptome-wide association study identifies eight candidate genes and tissue-specific gene expression underlying endometrial cancer susceptibility. Communications Biology, 2021, 4, 1211.	4.4	11
21	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	1.6	270
22	BRCA1Promoter Methylation and Clinical Outcomes in Ovarian Cancer: An Individual Patient Data Meta-Analysis. Journal of the National Cancer Institute, 2020, 112, 1190-1203.	6.3	32
23	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	7.0	43
24	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
25	Menopausal hormone therapy prior to the diagnosis of ovarian cancer is associated with improved survival. Gynecologic Oncology, 2020, 158, 702-709.	1.4	15
26	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
27	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.9	49
28	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
29	Genes associated with bowel metastases in ovarian cancer. Gynecologic Oncology, 2019, 154, 495-504.	1.4	40
30	Going to extremes: determinants of extraordinary response and survival in patients with cancer. Nature Reviews Cancer, 2019, 19, 339-348.	28.4	35
31	Gene expression differences between matched pairs of ovarian cancer patient tumors and patient-derived xenografts. Scientific Reports, 2019, 9, 6314.	3.3	33
32	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
33	Joint exposure to smoking, excessive weight, and physical inactivity and survival of ovarian cancer patients, evidence from the Ovarian Cancer Association Consortium. Cancer Causes and Control, 2019, 30, 537-547.	1.8	16
34	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. Gynecologic Oncology, 2019, 153, 343-355.	1.4	28
35	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
36	Testing Mediation Effects in High-Dimensional Epigenetic Studies. Frontiers in Genetics, 2019, 10, 1195.	2.3	26

#	Article	IF	Citations
37	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
38	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
39	MyD88 and TLR4 Expression in Epithelial Ovarian Cancer. Mayo Clinic Proceedings, 2018, 93, 307-320.	3.0	22
40	Genomic Analysis Using Regularized Regression in High-Grade Serous Ovarian Cancer. Cancer Informatics, 2018, 17, 117693511875534.	1.9	5
41	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
42	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
43	Mediation analysis of alcohol consumption, DNA methylation, and epithelial ovarian cancer. Journal of Human Genetics, 2018, 63, 339-348.	2.3	18
44	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
45	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 395-404.	2.5	33
46	Epigenetics in ovarian cancer. Seminars in Cancer Biology, 2018, 51, 160-169.	9.6	86
47	Subject level clustering using a negative binomial model for small transcriptomic studies. BMC Bioinformatics, 2018, 19, 474.	2.6	8
48	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
49	Factors that influence survival in high-grade serous ovarian cancer: A complex relationship between molecular subtype, disease dissemination, and operability. Gynecologic Oncology, 2018, 150, 227-232.	1.4	40
50	Association of p16 expression with prognosis varies across ovarian carcinoma histotypes: an Ovarian Tumor Tissue Analysis consortium study. Journal of Pathology: Clinical Research, 2018, 4, 250-261.	3.0	70
51	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.9	54
52	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9
53	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
54	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

#	Article	IF	Citations
55	Assessment of data transformations for model-based clustering of RNA-Seq data. PLoS ONE, 2018, 13, e0191758.	2.5	5
56	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	6.4	23
57	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
58	Genetic Variants in Epigenetic Pathways and Risks of Multiple Cancers in the GAME-ON Consortium. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 816-825.	2.5	10
59	Bevacizumab May Differentially Improve Ovarian Cancer Outcome in Patients with Proliferative and Mesenchymal Molecular Subtypes. Clinical Cancer Research, 2017, 23, 3794-3801.	7.0	103
60	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
61	Pooled Clustering of High-Grade Serous Ovarian Cancer Gene Expression Leads to Novel Consensus Subtypes Associated with Survival and Surgical Outcomes. Clinical Cancer Research, 2017, 23, 4077-4085.	7.0	80
62	Predictors of pretreatment CA125 at ovarian cancer diagnosis: a pooled analysis in the Ovarian Cancer Association Consortium. Cancer Causes and Control, 2017, 28, 459-468.	1.8	20
63	Intraperitoneal disease dissemination patterns are associated with residual disease, extent of surgery, and molecular subtypes in advanced ovarian cancer. Gynecologic Oncology, 2017, 147, 503-508.	1.4	36
64	IL10 Release upon PD-1 Blockade Sustains Immunosuppression in Ovarian Cancer. Cancer Research, 2017, 77, 6667-6678.	0.9	126
65	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
66	History of Comorbidities and Survival of Ovarian Cancer Patients, Results from the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1470-1473.	2.5	10
67	The Association of Peripheral Blood Regulatory T-Cell Concentrations With Epithelial Ovarian Cancer: A Brief Report. International Journal of Gynecological Cancer, 2017, 27, 11-16.	2.5	9
68	An integrative approach to assess Xâ€chromosome inactivation using alleleâ€specific expression with applications to epithelial ovarian cancer. Genetic Epidemiology, 2017, 41, 898-914.	1.3	16
69	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	2.5	48
70	Germline miRNA DNA variants and the risk of colorectal cancer by subtype. Genes Chromosomes and Cancer, 2017, 56, 177-184.	2.8	7
71	EGFR as a prognostic biomarker and therapeutic target in ovarian cancer: evaluation of patient cohort and literature review. Genes and Cancer, 2017, 8, 589-599.	1.9	45
72	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. Oncotarget, 2017, 8, 46891-46899.	1.8	22

#	Article	IF	Citations
73	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. Oncotarget, 2017, 8, 64670-64684.	1.8	7
74	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
75	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
76	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
77	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
78	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
79	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
80	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
81	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
82	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
83	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
84	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
85	Drug discovery using clinical outcome-based Connectivity Mapping: application to ovarian cancer. BMC Genomics, 2016, 17, 811.	2.8	21
86	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
87	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. American Journal of Human Genetics, 2016, 98, 1159-1169.	6.2	32
88	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
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	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

#	Article	IF	Citations
91	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
92	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
93	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	2.5	9
94	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. Human Genetics, 2016, 135, 137-154.	3.8	8
95	PD-1 Blunts the Function of Ovarian Tumorâ€“Infiltrating Dendritic Cells by Inactivating NF-Î²B. Cancer Research, 2016, 76, 239-250.	0.9	84
96	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
97	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
98	Germline polymorphisms in an enhancer of PSIP1 are associated with progression-free survival in epithelial ovarian cancer. Oncotarget, 2016, 7, 6353-6368.	1.8	29
99	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	1.8	7
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	Leveraging global gene expression patterns to predict expression of unmeasured genes. BMC Genomics, 2015, 16, 1065.	2.8	3
102	Prior oral contraceptive use in ovarian cancer patients: assessing associations with overall and progression-free survival. BMC Cancer, 2015, 15, 711.	2.6	9
103	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
104	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
105	Intra-Gene DNA Methylation Variability Is a Clinically Independent Prognostic Marker in Womenâ€™s Cancers. PLoS ONE, 2015, 10, e0143178.	2.5	14
106	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. Genome Medicine, 2015, 7, 108.	8.2	138
107	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
108	Assessment of published models and prognostic variables in epithelial ovarian cancer at Mayo Clinic. Gynecologic Oncology, 2015, 137, 77-85.	1.4	15

#	Article	IF	Citations
109	TP53mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. Nucleic Acids Research, 2015, 43, 6945-6958.	14.5	46
110	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
111	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	1.4	15
112	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
113	Regulatory T cells, inherited variation, and clinical outcome in epithelial ovarian cancer. Cancer Immunology, Immunotherapy, 2015, 64, 1495-1504.	4.2	51
114	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
115	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
116	A functional variant in HOXA11-AS, a novel long non-coding RNA, inhibits the oncogenic phenotype of epithelial ovarian cancer. Oncotarget, 2015, 6, 34745-34757.	1.8	98
117	Serine protease inhibitor Kazal type 1 (SPINK1) drives proliferation and anoikis resistance in a subset of ovarian cancers. Oncotarget, 2015, 6, 35737-35754.	1.8	23
118	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
119	Prognostic and Therapeutic Relevance of Molecular Subtypes in High-Grade Serous Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	6.3	298
120	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
121	The contribution of deleterious germline mutations in BRCA1, BRCA2 and the mismatch repair genes to ovarian cancer in the population. Human Molecular Genetics, 2014, 23, 4703-4709.	2.9	112
122	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
123	A Review of the Application of Inflammatory Biomarkers in Epidemiologic Cancer Research. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1729-1751.	2.5	123
124	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	12.8	109
125	Aspirin, Nonaspirin Nonsteroidal Anti-inflammatory Drug, and Acetaminophen Use and Risk of Invasive Epithelial Ovarian Cancer: A Pooled Analysis in the Ovarian Cancer Association Consortium. Journal of the National Cancer Institute, 2014, 106, djt431-djt431.	6.3	186
126	Bevacizumab and improvement of progression-free survival (PFS) for patients with the mesenchymal molecular subtype of ovarian cancer.. Journal of Clinical Oncology, 2014, 32, 5509-5509.	1.6	16

#	Article	IF	Citations
127	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
128	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
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	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
133	Inherited Variants in Regulatory T Cell Genes and Outcome of Ovarian Cancer. PLoS ONE, 2013, 8, e53903.	2.5	20
134	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
135	Xenobioticâ€Metabolizing gene polymorphisms and ovarian cancer risk. Molecular Carcinogenesis, 2011, 50, 397-402.	2.7	29
136	Assessment of Hepatocyte Growth Factor in Ovarian Cancer Mortality. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1638-1648.	2.5	31
137	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
138	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
139	Inherited Determinants of Ovarian Cancer Survival. Clinical Cancer Research, 2010, 16, 995-1007.	7.0	56
140	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
141	No association between a candidate TCF7L2 variant and risk of breast or ovarian cancer. BMC Cancer, 2009, 9, 312.	2.6	16
142	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
143	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388.	5.1	73
144	Heritability of Longitudinal Measures of Body Mass Index and Lipid and Lipoprotein Levels in Aging Twins. Twin Research and Human Genetics, 2007, 10, 703-711.	0.6	92

#	Article	IF	Citations
145	Comparison of tagging single-nucleotide polymorphism methods in association analyses. BMC Proceedings, 2007, 1, S6.	1.6	5
146	Assessment and implications of linkage disequilibrium in genome-wide single-nucleotide polymorphism and microsatellite panels. Genetic Epidemiology, 2005, 29, S72-S76.	1.3	12