

Ellen L Goode

List of Publications by Year in descending order

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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	Association between endometriosis and risk of histological subtypes of ovarian cancer: a pooled analysis of case-control studies. <i>Lancet Oncology</i> , The, 2012, 13, 385-394.	10.7	753
2	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.	21.4	493
3	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	21.4	356
4	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	21.4	326
5	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. <i>Nature Genetics</i> , 2010, 42, 874-879.	21.4	321
6	Prognostic and Therapeutic Relevance of Molecular Subtypes in High-Grade Serous Ovarian Cancer. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	6.3	298
7	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. <i>Nature Genetics</i> , 2009, 41, 996-1000.	21.4	276
8	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020, 38, 674-685.	1.6	270
9	Dose-Response Association of CD8 ⁺ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. <i>JAMA Oncology</i> , 2017, 3, e173290.	7.1	260
10	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010, 42, 880-884.	21.4	235
11	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	21.4	221
12	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. <i>Journal of the National Cancer Institute</i> , 2014, 106, djt431-djt431.	6.3	186
13	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	12.8	178
14	<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.	3.2	174
15	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. <i>Endocrine-Related Cancer</i> , 2013, 20, 251-262.	3.1	169
16	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	9.4	157
17	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013, 4, 1628.	12.8	144
18	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. <i>Genome Medicine</i> , 2015, 7, 108.	8.2	138

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19	IL10 Release upon PD-1 Blockade Sustains Immunosuppression in Ovarian Cancer. <i>Cancer Research</i> , 2017, 77, 6667-6678.	0.9	126
20	A Review of the Application of Inflammatory Biomarkers in Epidemiologic Cancer Research. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1729-1751.	2.5	123
21	The contribution of deleterious germline mutations in BRCA1, BRCA2 and the mismatch repair genes to ovarian cancer in the population. <i>Human Molecular Genetics</i> , 2014, 23, 4703-4709.	2.9	112
22	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 1619-1630.	1.9	111
23	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. <i>Nature Communications</i> , 2014, 5, 5303.	12.8	109
24	Bevacizumab May Differentially Improve Ovarian Cancer Outcome in Patients with Proliferative and Mesenchymal Molecular Subtypes. <i>Clinical Cancer Research</i> , 2017, 23, 3794-3801.	7.0	103
25	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	12.8	98
26	A functional variant in <i>HOXA11-AS</i> , a novel long non-coding RNA, inhibits the oncogenic phenotype of epithelial ovarian cancer. <i>Oncotarget</i> , 2015, 6, 34745-34757.	1.8	98
27	Heritability of Longitudinal Measures of Body Mass Index and Lipid and Lipoprotein Levels in Aging Twins. <i>Twin Research and Human Genetics</i> , 2007, 10, 703-711.	0.6	92
28	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
29	Epigenetics in ovarian cancer. <i>Seminars in Cancer Biology</i> , 2018, 51, 160-169.	9.6	86
30	PD-1 Blunts the Function of Ovarian Tumor-Infiltrating Dendritic Cells by Inactivating NF- κ B. <i>Cancer Research</i> , 2016, 76, 239-250.	0.9	84
31	Pooled Clustering of High-Grade Serous Ovarian Cancer Gene Expression Leads to Novel Consensus Subtypes Associated with Survival and Surgical Outcomes. <i>Clinical Cancer Research</i> , 2017, 23, 4077-4085.	7.0	80
32	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
33	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016, 48, 667-674.	21.4	77
34	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	12.8	75
35	Consortium analysis of 7 candidate SNPs for ovarian cancer. <i>International Journal of Cancer</i> , 2008, 123, 380-388.	5.1	73
36	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.	1.9	71

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37	Association of p16 expression with prognosis varies across ovarian carcinoma histotypes: an Ovarian Tumor Tissue Analysis consortium study. <i>Journal of Pathology: Clinical Research</i> , 2018, 4, 250-261.	3.0	70
38	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015, 24, 5955-5964.	2.9	68
39	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1503-1510.	2.5	64
40	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv246.	6.3	63
41	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. <i>Cancer Medicine</i> , 2018, 7, 1978-1987.	2.8	62
42	Molecular classification of high grade endometrioid and clear cell ovarian cancer using TCGA gene expression signatures. <i>Gynecologic Oncology</i> , 2016, 141, 95-100.	1.4	58
43	Genome-Wide Study of Response to Platinum, Taxane, and Combination Therapy in Ovarian Cancer: In vitro Phenotypes, Inherited Variation, and Disease Recurrence. <i>Frontiers in Genetics</i> , 2016, 7, 37.	2.3	57
44	Inherited Determinants of Ovarian Cancer Survival. <i>Clinical Cancer Research</i> , 2010, 16, 995-1007.	7.0	56
45	Combined and Interactive Effects of Environmental and GWAS-Identified Risk Factors in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 880-890.	2.5	54
46	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.9	54
47	Regulatory T cells, inherited variation, and clinical outcome in epithelial ovarian cancer. <i>Cancer Immunology, Immunotherapy</i> , 2015, 64, 1495-1504.	4.2	51
48	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 1478-1492.	2.9	50
49	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2019, 79, 505-517.	0.9	49
50	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1427-1435.	2.5	48
51	<i>TP53</i> mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. <i>Nucleic Acids Research</i> , 2015, 43, 6945-6958.	14.5	46
52	EGFR as a prognostic biomarker and therapeutic target in ovarian cancer: evaluation of patient cohort and literature review. <i>Genes and Cancer</i> , 2017, 8, 589-599.	1.9	45
53	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	2.5	44
54	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). <i>Clinical Cancer Research</i> , 2020, 26, 5411-5423.	7.0	43

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55	Factors that influence survival in high-grade serous ovarian cancer: A complex relationship between molecular subtype, disease dissemination, and operability. <i>Gynecologic Oncology</i> , 2018, 150, 227-232.	1.4	40
56	Genes associated with bowel metastases in ovarian cancer. <i>Gynecologic Oncology</i> , 2019, 154, 495-504.	1.4	40
57	Recreational physical inactivity and mortality in women with invasive epithelial ovarian cancer: evidence from the Ovarian Cancer Association Consortium. <i>British Journal of Cancer</i> , 2016, 115, 95-101.	6.4	39
58	Candidate Gene Analysis Using Imputed Genotypes: Cell Cycle Single-Nucleotide Polymorphisms and Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 935-944.	2.5	37
59	Intraperitoneal disease dissemination patterns are associated with residual disease, extent of surgery, and molecular subtypes in advanced ovarian cancer. <i>Gynecologic Oncology</i> , 2017, 147, 503-508.	1.4	36
60	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015, 5, 17369.	3.3	35
61	Going to extremes: determinants of extraordinary response and survival in patients with cancer. <i>Nature Reviews Cancer</i> , 2019, 19, 339-348.	28.4	35
62	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.	6.4	35
63	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , 2021, 148, 307-319.	5.1	35
64	Kernel canonical correlation analysis for assessing gene-gene interactions and application to ovarian cancer. <i>European Journal of Human Genetics</i> , 2014, 22, 126-131.	2.8	33
65	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. <i>Clinical Cancer Research</i> , 2015, 21, 5264-5276.	7.0	33
66	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 395-404.	2.5	33
67	Gene expression differences between matched pairs of ovarian cancer patient tumors and patient-derived xenografts. <i>Scientific Reports</i> , 2019, 9, 6314.	3.3	33
68	Tumor Hypomethylation at 6p21.3 Associates with Longer Time to Recurrence of High-Grade Serous Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2014, 74, 3084-3091.	0.9	32
69	Chronic Recreational Physical Inactivity and Epithelial Ovarian Cancer Risk: Evidence from the Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1114-1124.	2.5	32
70	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. <i>American Journal of Human Genetics</i> , 2016, 98, 1159-1169.	6.2	32
71	<i>BRCA1</i> Promoter Methylation and Clinical Outcomes in Ovarian Cancer: An Individual Patient Data Meta-Analysis. <i>Journal of the National Cancer Institute</i> , 2020, 112, 1190-1203.	6.3	32
72	Assessment of Hepatocyte Growth Factor in Ovarian Cancer Mortality. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1638-1648.	2.5	31

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73	Comprehensive Cross-Population Analysis of High-Grade Serous Ovarian Cancer Supports No More Than Three Subtypes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4097-4103.	1.8	31
74	Xenobioticâ€Metabolizing gene polymorphisms and ovarian cancer risk. <i>Molecular Carcinogenesis</i> , 2011, 50, 397-402.	2.7	29
75	Germline polymorphisms in an enhancer of <i>PSIP1</i> are associated with progression-free survival in epithelial ovarian cancer. <i>Oncotarget</i> , 2016, 7, 6353-6368.	1.8	29
76	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	1.4	28
77	Transcriptomic Characterization of Endometrioid, Clear Cell, and High-Grade Serous Epithelial Ovarian Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1101-1109.	2.5	26
78	Testing Mediation Effects in High-Dimensional Epigenetic Studies. <i>Frontiers in Genetics</i> , 2019, 10, 1195.	2.3	26
79	Population-based targeted sequencing of 54 candidate genes identifies <i>PALB2</i> as a susceptibility gene for high-grade serous ovarian cancer. <i>Journal of Medical Genetics</i> , 2021, 58, 305-313.	3.2	26
80	Cigarette smoking is associated with adverse survival among women with ovarian cancer: Results from a pooled analysis of 19 studies. <i>International Journal of Cancer</i> , 2017, 140, 2422-2435.	5.1	25
81	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
82	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017, 116, 524-535.	6.4	23
83	Serine protease inhibitor Kazal type 1 (SPINK1) drives proliferation and anoikis resistance in a subset of ovarian cancers. <i>Oncotarget</i> , 2015, 6, 35737-35754.	1.8	23
84	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	2.8	23
85	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015, 39, 689-697.	1.3	22
86	MyD88 and TLR4 Expression in Epithelial Ovarian Cancer. <i>Mayo Clinic Proceedings</i> , 2018, 93, 307-320.	3.0	22
87	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. <i>Oncotarget</i> , 2017, 8, 46891-46899.	1.8	22
88	Molecular Subclasses of Clear Cell Ovarian Carcinoma and Their Impact on Disease Behavior and Outcomes. <i>Clinical Cancer Research</i> , 2022, 28, 4947-4956.	7.0	22
89	Drug discovery using clinical outcome-based Connectivity Mapping: application to ovarian cancer. <i>BMC Genomics</i> , 2016, 17, 811.	2.8	21
90	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1117-1126.	2.5	21

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91	Refined cut-off for TP53 immunohistochemistry improves prediction of TP53 mutation status in ovarian mucinous tumors: implications for outcome analyses. <i>Modern Pathology</i> , 2021, 34, 194-206.	5.5	21
92	The association between socioeconomic status and tumour stage at diagnosis of ovarian cancer: A pooled analysis of 18 case-control studies. <i>Cancer Epidemiology</i> , 2016, 41, 71-79.	1.9	20
93	Predictors of pretreatment CA125 at ovarian cancer diagnosis: a pooled analysis in the Ovarian Cancer Association Consortium. <i>Cancer Causes and Control</i> , 2017, 28, 459-468.	1.8	20
94	Inherited Variants in Regulatory T Cell Genes and Outcome of Ovarian Cancer. <i>PLoS ONE</i> , 2013, 8, e53903.	2.5	20
95	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016, 135, 741-756.	3.8	19
96	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. <i>Human Molecular Genetics</i> , 2019, 28, 1331-1342.	2.9	19
97	Mediation analysis of alcohol consumption, DNA methylation, and epithelial ovarian cancer. <i>Journal of Human Genetics</i> , 2018, 63, 339-348.	2.3	18
98	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. <i>Human Genetics</i> , 2021, 140, 1353-1365.	3.8	18
99	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.	2.9	17
100	No association between a candidate TCF7L2 variant and risk of breast or ovarian cancer. <i>BMC Cancer</i> , 2009, 9, 312.	2.6	16
101	An integrative approach to assess X chromosome inactivation using allele-specific expression with applications to epithelial ovarian cancer. <i>Genetic Epidemiology</i> , 2017, 41, 898-914.	1.3	16
102	Joint exposure to smoking, excessive weight, and physical inactivity and survival of ovarian cancer patients, evidence from the Ovarian Cancer Association Consortium. <i>Cancer Causes and Control</i> , 2019, 30, 537-547.	1.8	16
103	Bevacizumab and improvement of progression-free survival (PFS) for patients with the mesenchymal molecular subtype of ovarian cancer. <i>Journal of Clinical Oncology</i> , 2014, 32, 5509-5509.	1.6	16
104	Assessment of published models and prognostic variables in epithelial ovarian cancer at Mayo Clinic. <i>Gynecologic Oncology</i> , 2015, 137, 77-85.	1.4	15
105	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. <i>Gynecologic Oncology</i> , 2015, 136, 542-548.	1.4	15
106	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. <i>British Journal of Cancer</i> , 2018, 118, 1123-1129.	6.4	15
107	Menopausal hormone therapy prior to the diagnosis of ovarian cancer is associated with improved survival. <i>Gynecologic Oncology</i> , 2020, 158, 702-709.	1.4	15
108	Validated biomarker assays confirm that <i>ARID1A</i> loss is confounded with <i>MMR</i> deficiency, <i>CD8</i> ⁺ TIL infiltration, and provides no independent prognostic value in endometriosis-associated ovarian carcinomas. <i>Journal of Pathology</i> , 2022, 256, 388-401.	4.5	15

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109	Intra-Gene DNA Methylation Variability Is a Clinically Independent Prognostic Marker in Women's Cancers. PLoS ONE, 2015, 10, e0143178.	2.5	14
110	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
111	Assessment and implications of linkage disequilibrium in genome-wide single-nucleotide polymorphism and microsatellite panels. Genetic Epidemiology, 2005, 29, S72-S76.	1.3	12
112	A comprehensive gene-environment interaction analysis in Ovarian Cancer using genome-wide significant common variants. International Journal of Cancer, 2019, 144, 2192-2205.	5.1	12
113	DNA Methylation Profiles of Ovarian Clear Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 132-141.	2.5	12
114	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
115	Assessment of Multifactor Gene-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
116	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
117	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
118	Frequent POLE-driven hypermutation in ovarian endometrioid cancer revealed by mutational signatures in RNA sequencing. BMC Medical Genomics, 2021, 14, 165.	1.5	10
119	Prior oral contraceptive use in ovarian cancer patients: assessing associations with overall and progression-free survival. BMC Cancer, 2015, 15, 711.	2.6	9
120	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	2.5	9
121	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
122	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9
123	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
124	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
125	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
126	Subject level clustering using a negative binomial model for small transcriptomic studies. BMC Bioinformatics, 2018, 19, 474.	2.6	8

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127	Expanding Our Understanding of Ovarian Cancer Risk: The Role of Incomplete Pregnancies. <i>Journal of the National Cancer Institute</i> , 2021, 113, 301-308.	6.3	8
128	MCM3 is a novel proliferation marker associated with longer survival for patients with tubo-ovarian high-grade serous carcinoma. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2022, 480, 855-871.	2.8	8
129	Germline miRNA DNA variants and the risk of colorectal cancer by subtype. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 177-184.	2.8	7
130	Generating real-world evidence from unstructured clinical notes to examine clinical utility of genetic tests: use case in BRCAness. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 3.	3.0	7
131	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. <i>Oncotarget</i> , 2017, 8, 64670-64684.	1.8	7
132	A targeted genetic association study of epithelial ovarian cancer susceptibility. <i>Oncotarget</i> , 2016, 7, 7381-7389.	1.8	7
133	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.	2.8	6
134	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100042.	1.7	6
135	Comparison of tagging single-nucleotide polymorphism methods in association analyses. <i>BMC Proceedings</i> , 2007, 1, S6.	1.6	5
136	Genomic Analysis Using Regularized Regression in High-Grade Serous Ovarian Cancer. <i>Cancer Informatics</i> , 2018, 17, 117693511875534.	1.9	5
137	Identification of a Locus Near <i>ULK1</i> Associated With Progression-Free Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1669-1680.	2.5	5
138	Assessment of data transformations for model-based clustering of RNA-Seq data. <i>PLoS ONE</i> , 2018, 13, e0191758.	2.5	5
139	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.	1.8	5
140	Circulating CD14 + HLA-DR ^{lo} monocytic cells as a biomarker for epithelial ovarian cancer progression. <i>American Journal of Reproductive Immunology</i> , 2021, 85, e13343.	1.2	4
141	Leveraging global gene expression patterns to predict expression of unmeasured genes. <i>BMC Genomics</i> , 2015, 16, 1065.	2.8	3
142	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2473.	4.1	3
143	Functional analysis of the 1p34.3 risk locus implicates GNL2 in high-grade serous ovarian cancer. <i>American Journal of Human Genetics</i> , 2022, 109, 116-135.	6.2	3
144	CA-125 Levels Are Predictive of Survival in Low-Grade Serous Ovarian Cancer—A Multicenter Analysis. <i>Cancers</i> , 2022, 14, 1954.	3.7	3

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145	High Prediagnosis Inflammation-Related Risk Score Associated with Decreased Ovarian Cancer Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 443-452.	2.5	2
146	Germline BRCA variants, lifestyle and ovarian cancer survival. <i>Gynecologic Oncology</i> , 2022, , .	1.4	2