

Ellen L Goode

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

140
papers

6,545
citations

40
h-index

77
g-index

149
ext. papers

8,162
ext. citations

8.1
avg. IF

4.48
L-index

#	Paper	IF	Citations
140	Validated biomarker assays confirm ARID1A loss is confounded with MMR deficiency, CD8 TIL infiltration, and provides no independent prognostic value in endometriosis-associated ovarian carcinomas.. <i>Journal of Pathology</i> , 2021 ,	9.4	3
139	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> , 2021 ,	5.1	2
138	DNA Methylation Profiles of Ovarian Clear Cell Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 ,	4	2
137	Multi-tissue transcriptome-wide association study identifies eight candidate genes and tissue-specific gene expression underlying endometrial cancer susceptibility. <i>Communications Biology</i> , 2021 , 4, 1211	6.7	2
136	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, 100042-100042	0.8	2
135	Identification of a Locus Near Associated With Progression-Free Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 1669-1680	4	2
134	Frequent POLE-driven hypermutation in ovarian endometrioid cancer revealed by mutational signatures in RNA sequencing. <i>BMC Medical Genomics</i> , 2021 , 14, 165	3.7	2
133	Population-based targeted sequencing of 54 candidate genes identifies as a susceptibility gene for high-grade serous ovarian cancer. <i>Journal of Medical Genetics</i> , 2021 , 58, 305-313	5.8	12
132	Expanding Our Understanding of Ovarian Cancer Risk: The Role of Incomplete Pregnancies. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 301-308	9.7	3
131	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	9.8	6
130	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , 2021 , 148, 307-319	7.5	13
129	Circulating CD14 HLA-DR monocytic cells as a biomarker for epithelial ovarian cancer progression. <i>American Journal of Reproductive Immunology</i> , 2021 , 85, e13343	3.8	1
128	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	6.3	5
127	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	3.6	1
126	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	12.9	21
125	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	8.7	16
124	Menopausal hormone therapy prior to the diagnosis of ovarian cancer is associated with improved survival. <i>Gynecologic Oncology</i> , 2020 , 158, 702-709	4.9	5

123	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020 , 11, 3353	17.4	32
122	Cancer Risks Associated With Germline Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020 , 38, 674-685	2.2	133
121	BRCA1 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	9.7	12
120	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45
119	Genes associated with bowel metastases in ovarian cancer. <i>Gynecologic Oncology</i> , 2019 , 154, 495-504	4.9	21
118	Going to extremes: determinants of extraordinary response and survival in patients with cancer. <i>Nature Reviews Cancer</i> , 2019 , 19, 339-348	31.3	17
117	Gene expression differences between matched pairs of ovarian cancer patient tumors and patient-derived xenografts. <i>Scientific Reports</i> , 2019 , 9, 6314	4.9	22
116	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	4.8	4
115	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	2.8	9
114	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019 , 153, 343-355	4.9	16
113	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 1117-1126	4	8
112	Testing Mediation Effects in High-Dimensional Epigenetic Studies. <i>Frontiers in Genetics</i> , 2019 , 10, 1195	4.5	9
111	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. <i>Human Molecular Genetics</i> , 2019 , 28, 1331-1342	5.6	11
110	A comprehensive gene-environment interaction analysis in Ovarian Cancer using genome-wide significant common variants. <i>International Journal of Cancer</i> , 2019 , 144, 2192-2205	7.5	11
109	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	10.1	28
108	MyD88 and TLR4 Expression in Epithelial Ovarian Cancer. <i>Mayo Clinic Proceedings</i> , 2018 , 93, 307-320	6.4	14
107	Genomic Analysis Using Regularized Regression in High-Grade Serous Ovarian Cancer. <i>Cancer Informatics</i> , 2018 , 17, 1176935118755341	2.4	3
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	8.7	10

105	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	4.8	40
104	Mediation analysis of alcohol consumption, DNA methylation, and epithelial ovarian cancer. <i>Journal of Human Genetics</i> , 2018 , 63, 339-348	4.3	12
103	Robust Tests for Additive Gene-Environment Interaction in Case-Control Studies Using Gene-Environment Independence. <i>American Journal of Epidemiology</i> , 2018 , 187, 366-377	3.8	7
102	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018 , 27, 395-404	4	25
101	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	5.3	38
100	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	10.1	32
99	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018 , 13, e0197561	3.7	9
98	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018 , 9, 3166	17.4	70
97	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	3
96	Assessment of data transformations for model-based clustering of RNA-Seq data. <i>PLoS ONE</i> , 2018 , 13, e0191758	3.7	2
95	Epigenetics in ovarian cancer. <i>Seminars in Cancer Biology</i> , 2018 , 51, 160-169	12.7	57
94	Subject level clustering using a negative binomial model for small transcriptomic studies. <i>BMC Bioinformatics</i> , 2018 , 19, 474	3.6	4
93	Transcriptomic Characterization of Endometrioid, Clear Cell, and High-Grade Serous Epithelial Ovarian Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018 , 27, 1101-1109	4	9
92	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	4.9	26
91	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017 , 116, 524-535	8.7	18
90	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	7.5	18
89	Genetic Variants in Epigenetic Pathways and Risks of Multiple Cancers in the GAME-ON Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 816-825	4	7
88	Bevacizumab May Differentially Improve Ovarian Cancer Outcome in Patients with Proliferative and Mesenchymal Molecular Subtypes. <i>Clinical Cancer Research</i> , 2017 , 23, 3794-3801	12.9	62

87	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017 , 49, 680-691	36.3	190
86	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 ^{12.9}		54
85	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	2.8	13
84	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	4.9	19
83	IL10 Release upon PD-1 Blockade Sustains Immunosuppression in Ovarian Cancer. <i>Cancer Research</i> , 2017 , 77, 6667-6678	10.1	79
82	Dose-Response Association of CD8+ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. <i>JAMA Oncology</i> , 2017 , 3, e173290	13.4	152
81	History of Comorbidities and Survival of Ovarian Cancer Patients, Results from the Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1470-1473	4	8
80	The Association of Peripheral Blood Regulatory T-Cell Concentrations With Epithelial Ovarian Cancer: A Brief Report. <i>International Journal of Gynecological Cancer</i> , 2017 , 27, 11-16	3.5	5
79	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	2.6	7
78	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1427-1435	4	25
77	Germline miRNA DNA variants and the risk of colorectal cancer by subtype. <i>Genes Chromosomes and Cancer</i> , 2017 , 56, 177-184	5	6
76	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	2.9	24
75	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. <i>Oncotarget</i> , 2017 , 8, 46891-46899	3.3	17
74	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	3.3	5
73	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	4	42
72	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, 1052-67 ^{24.4}		104
71	Drug discovery using clinical outcome-based Connectivity Mapping: application to ovarian cancer. <i>BMC Genomics</i> , 2016 , 17, 811	4.5	17
70	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016 , 7, 12675	17.4	53

69	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	11	17
68	Expression signature distinguishing two tumour transcriptome classes associated with progression-free survival among rare histological types of epithelial ovarian cancer. <i>British Journal of Cancer</i> , 2016 , 114, 1412-20	8.7	5
67	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	8.7	28
66	Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 780-90	4	8
65	Molecular classification of high grade endometrioid and clear cell ovarian cancer using TCGA gene expression signatures. <i>Gynecologic Oncology</i> , 2016 , 141, 95-100	4.9	34
64	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, 71-9	2.8	17
63	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 446-54	4	6
62	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. <i>Human Genetics</i> , 2016 , 135, 137-54	6.3	6
61	PD-1 Blunts the Function of Ovarian Tumor-Infiltrating Dendritic Cells by Inactivating NF- κ B. <i>Cancer Research</i> , 2016 , 76, 239-50	10.1	62
60	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	3.3	4
59	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. <i>Oncotarget</i> , 2016 , 7, 72381-72394	3.3	11
58	Germline polymorphisms in an enhancer of PSIP1 are associated with progression-free survival in epithelial ovarian cancer. <i>Oncotarget</i> , 2016 , 7, 6353-68	3.3	19
57	A targeted genetic association study of epithelial ovarian cancer susceptibility. <i>Oncotarget</i> , 2016 , 7, 7381-9	3.9	7
56	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	4.5	15
55	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016 , 45, 884-95	7.8	45
54	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. <i>Human Molecular Genetics</i> , 2016 , 25, 3600-3612	5.6	9
53	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016 , 53, 800-811	5.8	121
52	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	3.2	18

51	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, 1114-14	4	27
50	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016 , 135, 741-56	6.3	18
49	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016 , 48, 667-674	36.3	56
48	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016 , 45, 1619-1630	7.8	77
47	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015 , 47, 164-71	36.3	177
46	Assessment of published models and prognostic variables in epithelial ovarian cancer at Mayo Clinic. <i>Gynecologic Oncology</i> , 2015 , 137, 77-85	4.9	12
45	TP53 mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. <i>Nucleic Acids Research</i> , 2015 , 43, 6945-58	20.1	37
44	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, 5264-76	12.9	24
43	Evaluating the ovarian cancer gonadotropin hypothesis: a candidate gene study. <i>Gynecologic Oncology</i> , 2015 , 136, 542-8	4.9	12
42	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015 , 24, 5955-64	5.6	48
41	Regulatory T cells, inherited variation, and clinical outcome in epithelial ovarian cancer. <i>Cancer Immunology, Immunotherapy</i> , 2015 , 64, 1495-504	7.4	36
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,	9.7	47
39	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 1478-92	5.6	46
38	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	4.9	27
37	Leveraging global gene expression patterns to predict expression of unmeasured genes. <i>BMC Genomics</i> , 2015 , 16, 1065	4.5	2
36	Prior oral contraceptive use in ovarian cancer patients: assessing associations with overall and progression-free survival. <i>BMC Cancer</i> , 2015 , 15, 711	4.8	7
35	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015 , 39, 689-97	2.6	18
34	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015 , 10, e0128106	3.7	15

33	Intra-Gene DNA Methylation Variability Is a Clinically Independent Prognostic Marker in Women's Cancers. <i>PLoS ONE</i> , 2015 , 10, e0143178	3.7	10
32	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. <i>Genome Medicine</i> , 2015 , 7, 108	14.4	110
31	A functional variant in HOXA11-AS, a novel long non-coding RNA, inhibits the oncogenic phenotype of epithelial ovarian cancer. <i>Oncotarget</i> , 2015 , 6, 34745-57	3.3	92
30	Serine protease inhibitor Kazal type 1 (SPINK1) drives proliferation and anoikis resistance in a subset of ovarian cancers. <i>Oncotarget</i> , 2015 , 6, 35737-54	3.3	14
29	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 2015 , 2,		22
28	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, 4703-9	5.6	90
27	Kernel canonical correlation analysis for assessing gene-gene interactions and application to ovarian cancer. <i>European Journal of Human Genetics</i> , 2014 , 22, 126-31	5.3	27
26	A review of the application of inflammatory biomarkers in epidemiologic cancer research. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 1729-51	4	88
25	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. <i>Nature Communications</i> , 2014 , 5, 5303	17.4	84
24	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	9.7	149
23	Prognostic and therapeutic relevance of molecular subtypes in high-grade serous ovarian cancer. <i>Journal of the National Cancer Institute</i> , 2014 , 106,	9.7	215
22	Tumor hypomethylation at 6p21.3 associates with longer time to recurrence of high-grade serous epithelial ovarian cancer. <i>Cancer Research</i> , 2014 , 74, 3084-91	10.1	23
21	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	2.2	14
20	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013 , 45, 362-70, 370e1-2	36.3	267
19	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, 371-84, 384e1-2	36.3	422
18	Combined and interactive effects of environmental and GWAS-identified risk factors in ovarian cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013 , 22, 880-90	4	37
17	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. <i>Endocrine-Related Cancer</i> , 2013 , 20, 251-62	5.7	135
16	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013 , 4, 1628	17.4	124

15	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013 , 4, 1627	17.4	85
14	Inherited variants in regulatory T cell genes and outcome of ovarian cancer. <i>PLoS ONE</i> , 2013 , 8, e53903	3.7	19
13	Association between endometriosis and risk of histological subtypes of ovarian cancer: a pooled analysis of case-control studies. <i>Lancet Oncology</i> , 2012 , 13, 385-94	21.7	612
12	Xenobiotic-Metabolizing gene polymorphisms and ovarian cancer risk. <i>Molecular Carcinogenesis</i> , 2011 , 50, 397-402	5	24
11	Assessment of hepatocyte growth factor in ovarian cancer mortality. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011 , 20, 1638-48	4	30
10	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010 , 42, 880-4	36.3	210
9	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. <i>Nature Genetics</i> , 2010 , 42, 874-9	36.3	277
8	Inherited determinants of ovarian cancer survival. <i>Clinical Cancer Research</i> , 2010 , 16, 995-1007	12.9	50
7	Candidate gene analysis using imputed genotypes: cell cycle single-nucleotide polymorphisms and ovarian cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009 , 18, 935-44	4	31
6	No association between a candidate TCF7L2 variant and risk of breast or ovarian cancer. <i>BMC Cancer</i> , 2009 , 9, 312	4.8	13
5	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. <i>Nature Genetics</i> , 2009 , 41, 996-1000	36.3	240
4	Consortium analysis of 7 candidate SNPs for ovarian cancer. <i>International Journal of Cancer</i> , 2008 , 123, 380-388	7.5	66
3	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, 703-11	2.2	56
2	Comparison of tagging single-nucleotide polymorphism methods in association analyses. <i>BMC Proceedings</i> , 2007 , 1 Suppl 1, S6	2.3	5
1	Assessment and implications of linkage disequilibrium in genome-wide single-nucleotide polymorphism and microsatellite panels. <i>Genetic Epidemiology</i> , 2005 , 29 Suppl 1, S72-6	2.6	12