

Simon A Gayther

List of Publications by Citations

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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.

229
papers

14,997
citations

64
h-index

116
g-index

245
ext. papers

17,471
ext. citations

9.9
avg, IF

5.2
L-index

#	Paper	IF	Citations
229	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. <i>Genome Research</i> , 2010 , 20, 440-6	9.7	638
228	Association between endometriosis and risk of histological subtypes of ovarian cancer: a pooled analysis of case-control studies. <i>Lancet Oncology, The</i> , 2012 , 13, 385-94	21.7	612
227	Mutations truncating the EP300 acetylase in human cancers. <i>Nature Genetics</i> , 2000 , 24, 300-3	36.3	482
226	Germline mutations of the BRCA1 gene in breast and ovarian cancer families provide evidence for a genotype-phenotype correlation. <i>Nature Genetics</i> , 1995 , 11, 428-33	36.3	439
225	Association between BRCA1 and BRCA2 mutations and survival in women with invasive epithelial ovarian cancer. <i>JAMA - Journal of the American Medical Association</i> , 2012 , 307, 382-90	27.4	427
224	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
223	Pathology of breast and ovarian cancers among BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 134-47	4	411
222	Variation of risks of breast and ovarian cancer associated with different germline mutations of the BRCA2 gene. <i>Nature Genetics</i> , 1997 , 15, 103-5	36.3	377
221	Principles for the post-GWAS functional characterization of cancer risk loci. <i>Nature Genetics</i> , 2011 , 43, 513-8	36.3	326
220	Two percent of men with early-onset prostate cancer harbor germline mutations in the BRCA2 gene. <i>American Journal of Human Genetics</i> , 2003 , 72, 1-12	11	293
219	Association of type and location of BRCA1 and BRCA2 mutations with risk of breast and ovarian cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 313, 1347-61	27.4	286
218	Multiple loci with different cancer specificities within the 8q24 gene desert. <i>Journal of the National Cancer Institute</i> , 2008 , 100, 962-6	9.7	283
217	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
216	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. <i>Nature Genetics</i> , 2010 , 42, 885-92	36.3	276
215	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
214	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. <i>Lancet Oncology, The</i> , 2013 , 14, 853-62	21.7	248
213	An epigenetic signature in peripheral blood predicts active ovarian cancer. <i>PLoS ONE</i> , 2009 , 4, e8274	3.7	245

212	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
211	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	239
210	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010 , 42, 880-4	36.3	210
209	Contribution of BRCA1 mutations to ovarian cancer. <i>New England Journal of Medicine</i> , 1997 , 336, 1125-30	39.2	208
208	Contribution of Germline Mutations in the RAD51B, RAD51C, and RAD51D Genes to Ovarian Cancer in the Population. <i>Journal of Clinical Oncology</i> , 2015 , 33, 2901-7	2.2	200
207	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017 , 49, 680-691	36.3	190
206	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 126-135	4	183
205	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015 , 47, 164-71	36.3	177
204	A polymorphic stop codon in BRCA2. <i>Nature Genetics</i> , 1996 , 14, 253-4	36.3	136
203	The BRCA1- Δ 11q Alternative Splice Isoform Bypasses Germline Mutations and Promotes Therapeutic Resistance to PARP Inhibition and Cisplatin. <i>Cancer Research</i> , 2016 , 76, 2778-90	10.1	136
202	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
201	Risk models for familial ovarian and breast cancer. <i>Genetic Epidemiology</i> , 2000 , 18, 173-90	2.6	128
200	The contribution of BRCA1 and BRCA2 to ovarian cancer. <i>Molecular Oncology</i> , 2009 , 3, 138-50	7.9	125
199	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
198	Polymorphisms in DNA repair genes and epithelial ovarian cancer risk. <i>International Journal of Cancer</i> , 2005 , 117, 611-8	7.5	112
197	The contribution of germline BRCA1 and BRCA2 mutations to familial ovarian cancer: no evidence for other ovarian cancer-susceptibility genes. <i>American Journal of Human Genetics</i> , 1999 , 65, 1021-9	11	109
196	Germline mutation in BRCA1 or BRCA2 and ten-year survival for women diagnosed with epithelial ovarian cancer. <i>Clinical Cancer Research</i> , 2015 , 21, 652-7	12.9	107
195	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

194	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016 , 48, 374-86	36.3	93
193	Cost-effectiveness of Population-Based BRCA1, BRCA2, RAD51C, RAD51D, BRIP1, PALB2 Mutation Testing in Unselected General Population Women. <i>Journal of the National Cancer Institute</i> , 2018 , 110, 714-725	9.7	92
192	Common breast cancer susceptibility variants in LSP1 and RAD51L1 are associated with mammographic density measures that predict breast cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 1156-66	4	92
191	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
190	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
189	CA125 expression pattern, prognosis and correlation with serum CA125 in ovarian tumor patients. From The Danish "MALOVA" Ovarian Cancer Study. <i>Gynecologic Oncology</i> , 2007 , 104, 508-15	4.9	90
188	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013 , 4, 1627	17.4	85
187	BRCA1 and BRCA2 mutation prevalence and clinical characteristics of a population-based series of ovarian cancer cases from Denmark. <i>Clinical Cancer Research</i> , 2008 , 14, 3761-7	12.9	77
186	Frequent loss of BRCA1 mRNA and protein expression in sporadic ovarian cancers. <i>International Journal of Cancer</i> , 2000 , 87, 317-21	7.5	77
185	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
184	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020 , 52, 572-581	36.3	76
183	Aberrant splicing of the TSG101 and FHIT genes occurs frequently in multiple malignancies and in normal tissues and mimics alterations previously described in tumours. <i>Oncogene</i> , 1997 , 15, 2119-26	9.2	75
182	Tagging single nucleotide polymorphisms in cell cycle control genes and susceptibility to invasive epithelial ovarian cancer. <i>Cancer Research</i> , 2007 , 67, 3027-35	10.1	75
181	The sex hormone system in carriers of BRCA1/2 mutations: a case-control study. <i>Lancet Oncology</i> , 2013 , 14, 1226-32	21.7	73
180	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2012 , 14, R33	8.3	70
179	LIN28B polymorphisms influence susceptibility to epithelial ovarian cancer. <i>Cancer Research</i> , 2011 , 71, 3896-903	10.1	70
178	Cigarette smoking and risk of ovarian cancer: a pooled analysis of 21 case-control studies. <i>Cancer Causes and Control</i> , 2013 , 24, 989-1004	2.8	69
177	Histopathology, FIGO stage, and BRCA mutation status of ovarian cancers from the Gilda Radner Familial Ovarian Cancer Registry. <i>International Journal of Gynecological Pathology</i> , 2004 , 23, 29-34	3.2	68

176	Contribution of BRCA1 and BRCA2 mutations to inherited ovarian cancer. <i>Human Mutation</i> , 2007 , 28, 1207-15	4.7	67
175	Senescent fibroblasts promote neoplastic transformation of partially transformed ovarian epithelial cells in a three-dimensional model of early stage ovarian cancer. <i>Neoplasia</i> , 2010 , 12, 317-25	6.4	66
174	Consortium analysis of 7 candidate SNPs for ovarian cancer. <i>International Journal of Cancer</i> , 2008 , 123, 380-388	7.5	66
173	Prognostic value of estrogen receptor and progesterone receptor tumor expression in Danish ovarian cancer patients: from the SMALOVAS ovarian cancer study. <i>Oncology Reports</i> , 2007 , 18, 1051-9	3.5	66
172	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. <i>Nature Medicine</i> , 2015 , 21, 1357-63	50.5	65
171	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	65
170	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018 , 9, 4079	17.4	65
169	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
168	ESR1/SYNE1 polymorphism and invasive epithelial ovarian cancer risk: an Ovarian Cancer Association Consortium study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 245-50	4	64
167	Common variants in mismatch repair genes and risk of invasive ovarian cancer. <i>Carcinogenesis</i> , 2006 , 27, 2235-42	4.6	64
166	Increased frequency of TP53 mutations in BRCA1 and BRCA2 ovarian tumours. <i>Genes Chromosomes and Cancer</i> , 1999 , 25, 91-6	5	64
165	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. <i>Nature Genetics</i> , 2020 , 52, 790-799	36.3	62
164	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. <i>Human Molecular Genetics</i> , 2014 , 23, 5294-302	5.6	61
163	A breast/ovarian cancer patient with germline mutations in both BRCA1 and BRCA2. <i>Nature Genetics</i> , 1997 , 15, 14-5	36.3	60
162	Role of genetic polymorphisms and ovarian cancer susceptibility. <i>Molecular Oncology</i> , 2009 , 3, 171-81	7.9	59
161	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
160	Biomarker-based ovarian carcinoma typing: a histologic investigation in the ovarian tumor tissue analysis consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013 , 22, 1677-86	4	53
159	The clonal evolution of metastases from primary serous epithelial ovarian cancers. <i>International Journal of Cancer</i> , 2009 , 124, 1579-86	7.5	53

158	Single nucleotide polymorphisms in the TP53 region and susceptibility to invasive epithelial ovarian cancer. <i>Cancer Research</i> , 2009 , 69, 2349-57	10.1	52
157	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 1242-1250	9.7	51
156	Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. <i>International Journal of Cancer</i> , 2011 , 128, 2063-74	7.5	49
155	Genetic epidemiology of ovarian cancer and prospects for polygenic risk prediction. <i>Gynecologic Oncology</i> , 2017 , 147, 705-713	4.9	48
154	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015 , 24, 5955-64	5.6	48
153	The inherited genetics of ovarian and endometrial cancer. <i>Current Opinion in Genetics and Development</i> , 2010 , 20, 231-8	4.9	47
152	Tagging single nucleotide polymorphisms in the BRIP1 gene and susceptibility to breast and ovarian cancer. <i>PLoS ONE</i> , 2007 , 2, e268	3.7	47
151	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45
150	The role of KRAS rs61764370 in invasive epithelial ovarian cancer: implications for clinical testing. <i>Clinical Cancer Research</i> , 2011 , 17, 3742-50	12.9	45
149	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
148	Vitamin D receptor rs2228570 polymorphism and invasive ovarian carcinoma risk: pooled analysis in five studies within the Ovarian Cancer Association Consortium. <i>International Journal of Cancer</i> , 2011 , 128, 936-43	7.5	44
147	Common variants at the 19p13.1 and ZNF365 loci are associated with ER subtypes of breast cancer and ovarian cancer risk in BRCA1 and BRCA2 mutation carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 645-57	4	44
146	Evaluation of candidate stromal epithelial cross-talk genes identifies association between risk of serous ovarian cancer and TERT, a cancer susceptibility "hot-spot". <i>PLoS Genetics</i> , 2010 , 6, e1001016	6	42
145	Ovarian cancer and genetic susceptibility in relation to the BRCA1 and BRCA2 genes. Occurrence, clinical importance and intervention. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2006 , 85, 93-105	3.8	42
144	Functional polymorphisms in the TERT promoter are associated with risk of serous epithelial ovarian and breast cancers. <i>PLoS ONE</i> , 2011 , 6, e24987	3.7	41
143	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015 , 6, 8234	17.4	40
142	Stromal Expression of Fibroblast Activation Protein Alpha (FAP) Predicts Platinum Resistance and Shorter Recurrence in patients with Epithelial Ovarian Cancer. <i>Cancer Microenvironment</i> , 2015 , 8, 23-31	6.1	39
141	A molecular genetic and statistical approach for the diagnosis of dual-site cancers. <i>Journal of the National Cancer Institute</i> , 2004 , 96, 1441-6	9.7	39

140	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
139	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. <i>IScience</i> , 2019 , 17, 242-255	6.1	38
138	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
137	Association between invasive ovarian cancer susceptibility and 11 best candidate SNPs from breast cancer genome-wide association study. <i>Human Molecular Genetics</i> , 2009 , 18, 2297-304	5.6	37
136	Genetic variation at 9p22.2 and ovarian cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Journal of the National Cancer Institute</i> , 2011 , 103, 105-16	9.7	37
135	Risk of ovarian cancer and the NF- κ B pathway: genetic association with IL1A and TNFSF10. <i>Cancer Research</i> , 2014 , 74, 852-61	10.1	36
134	In vitro three-dimensional modeling of fallopian tube secretory epithelial cells. <i>BMC Cell Biology</i> , 2013 , 14, 43		35
133	Ovarian cancer risk associated with inherited inflammation-related variants. <i>Cancer Research</i> , 2012 , 72, 1064-9	10.1	35
132	PPM1D Mosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	34
131	Common variants in RB1 gene and risk of invasive ovarian cancer. <i>Cancer Research</i> , 2006 , 66, 10220-6	10.1	34
130	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. <i>Nature Genetics</i> , 2019 , 51, 815-823	36.3	33
129	Modelling genetic and clinical heterogeneity in epithelial ovarian cancers. <i>Carcinogenesis</i> , 2011 , 32, 1540-6	4.6	33
128	Predicting clinical outcome in patients diagnosed with synchronous ovarian and endometrial cancer. <i>Clinical Cancer Research</i> , 2008 , 14, 5840-8	12.9	33
127	Association between common germline genetic variation in 94 candidate genes or regions and risks of invasive epithelial ovarian cancer. <i>PLoS ONE</i> , 2009 , 4, e5983	3.7	33
126	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020 , 11, 3353	17.4	32
125	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
124	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2015 , 24, 3595-607	5.6	32
123	Microcell-mediated chromosome transfer identifies EPB41L3 as a functional suppressor of epithelial ovarian cancers. <i>Neoplasia</i> , 2010 , 12, 579-89	6.4	32

122	Ovarian cancer susceptibility alleles and risk of ovarian cancer in BRCA1 and BRCA2 mutation carriers. <i>Human Mutation</i> , 2012 , 33, 690-702	4.7	31
121	A gene (DLG2) located at 17q12-q21 encodes a new homologue of the Drosophila tumor suppressor dlg-A. <i>Genomics</i> , 1995 , 28, 25-31	4.3	31
120	HNF1B variants associate with promoter methylation and regulate gene networks activated in prostate and ovarian cancer. <i>Oncotarget</i> , 2016 , 7, 74734-74746	3.3	31
119	The effects of common genetic variants in oncogenes on ovarian cancer survival. <i>Clinical Cancer Research</i> , 2008 , 14, 5833-9	12.9	30
118	A modified medium that significantly improves the growth of human normal ovarian surface epithelial (OSE) cells in vitro. <i>Laboratory Investigation</i> , 2004 , 84, 923-31	5.9	30
117	Breast cancer information on the web. <i>Nature Genetics</i> , 1995 , 11, 238-9	36.3	30
116	Germline whole exome sequencing and large-scale replication identifies a likely high grade serous ovarian cancer susceptibility gene. <i>Oncotarget</i> , 2017 , 8, 50930-50940	3.3	30
115	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016 , 139, 2655-2670	7.5	30
114	Evaluation of polygenic risk scores for ovarian cancer risk prediction in a prospective cohort study. <i>Journal of Medical Genetics</i> , 2018 , 55, 546-554	5.8	30
113	BRCA1/2 mutation status influences somatic genetic progression in inherited and sporadic epithelial ovarian cancer cases. <i>Cancer Research</i> , 2003 , 63, 417-23	10.1	30
112	Identification of a novel splice-site mutation of the BRCA1 gene in two breast cancer families: screening reveals low frequency in Icelandic breast cancer patients. <i>Human Mutation</i> , 1998 , Suppl 1, S195-7	4.7	28
111	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
110	Down-regulation of ARID1A is sufficient to initiate neoplastic transformation along with epigenetic reprogramming in non-tumorigenic endometriotic cells. <i>Cancer Letters</i> , 2017 , 401, 11-19	9.9	27
109	PAX8 expression in ovarian surface epithelial cells. <i>Human Pathology</i> , 2015 , 46, 948-56	3.7	27
108	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
107	ABO blood group and risk of epithelial ovarian cancer within the Ovarian Cancer Association Consortium. <i>Cancer Causes and Control</i> , 2012 , 23, 1805-10	2.8	27
106	Recruitment of newly diagnosed ovarian cancer patients proved challenging in a multicentre biobanking study. <i>Journal of Clinical Epidemiology</i> , 2011 , 64, 525-30	5.7	27
105	Master transcription factors form interconnected circuitry and orchestrate transcriptional networks in oesophageal adenocarcinoma. <i>Gut</i> , 2020 , 69, 630-640	19.2	27

104	The genetics of inherited breast cancer. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 1998 , 3, 365-76.4	26
103	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
102	Vascular endothelial growth factor gene polymorphisms and ovarian cancer survival. <i>Gynecologic Oncology</i> , 2010 , 119, 479-83	4.9 25
101	Apparent human BRCA1 knockout caused by mispriming during polymerase chain reaction: implications for genetic testing. <i>Genes Chromosomes and Cancer</i> , 2001 , 31, 96-8	5 25
100	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1574-84	4 24
99	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
98	Mutations of the BRCA1 and BRCA2 genes and the possibilities for predictive testing. <i>Trends in Molecular Medicine</i> , 1997 , 3, 168-74	24
97	Effects of common germ-line genetic variation in cell cycle genes on ovarian cancer survival. <i>Clinical Cancer Research</i> , 2008 , 14, 1090-5	12.9 24
96	The PAX8 cistrome in epithelial ovarian cancer. <i>Oncotarget</i> , 2017 , 8, 108316-108332	3.3 24
95	Association Between Menopausal Estrogen-Only Therapy and Ovarian Carcinoma Risk. <i>Obstetrics and Gynecology</i> , 2016 , 127, 828-836	4.9 24
94	Clues to the function of the tumour susceptibility gene BRCA2. <i>Disease Markers</i> , 1998 , 14, 1-8	3.2 23
93	Genetic variation in TYMS in the one-carbon transfer pathway is associated with ovarian carcinoma types in the Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 1822-30	4 22
92	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
91	A combination of the immunohistochemical markers CK7 and SATB2 is highly sensitive and specific for distinguishing primary ovarian mucinous tumors from colorectal and appendiceal metastases. <i>Modern Pathology</i> , 2019 , 32, 1834-1846	9.8 21
90	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
89	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. <i>Human Genetics</i> , 2014 , 133, 481-97	6.3 21
88	Common variants of the BRCA1 wild-type allele modify the risk of breast cancer in BRCA1 mutation carriers. <i>Human Molecular Genetics</i> , 2011 , 20, 4732-47	5.6 21
87	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015 , 36, 1341-53	4.6 20

86	Molecular Analysis of Mixed Endometrioid and Serous Adenocarcinoma of the Endometrium. <i>PLoS ONE</i> , 2015 , 10, e0130909	3.7	20
85	Large-scale evaluation of common variation in regulatory T cell-related genes and ovarian cancer outcome. <i>Cancer Immunology Research</i> , 2014 , 2, 332-40	12.5	20
84	Analysis of over 10,000 Cases finds no association between previously reported candidate polymorphisms and ovarian cancer outcome. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013 , 22, 987-92	4	20
83	Polymorphism in the GALNT1 gene and epithelial ovarian cancer in non-Hispanic white women: the Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 600-4 ⁴		20
82	Mismatch repair gene polymorphisms and survival in invasive ovarian cancer patients. <i>European Journal of Cancer</i> , 2008 , 44, 2259-65	7.5	20
81	Estrogen receptor beta rs1271572 polymorphism and invasive ovarian carcinoma risk: pooled analysis within the Ovarian Cancer Association Consortium. <i>PLoS ONE</i> , 2011 , 6, e20703	3.7	20
80	Inherited variants in regulatory T cell genes and outcome of ovarian cancer. <i>PLoS ONE</i> , 2013 , 8, e53903	3.7	19
79	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. <i>Cell Reports</i> , 2019 , 29, 3726-3735.e4	10.6	19
78	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
77	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
76	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015 , 39, 689-97	2.6	18
75	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. <i>Fertility and Sterility</i> , 2011 , 95, 40-5	4.8	18
74	Genetic variation in insulin-like growth factor 2 may play a role in ovarian cancer risk. <i>Human Molecular Genetics</i> , 2011 , 20, 2263-72	5.6	18
73	MicroRNA processing and binding site polymorphisms are not replicated in the Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011 , 20, 1793-7	4	18
72	Protein expression levels of carcinoembryonic antigen (CEA) in Danish ovarian cancer patients: from the Danish MALOVA ovarian cancer study. <i>Pathology</i> , 2008 , 40, 487-92	1.6	18
71	Expression level of Wilms tumor 1 (WT1) protein has limited prognostic value in epithelial ovarian cancer: from the Danish "MALOVA" ovarian cancer study. <i>Gynecologic Oncology</i> , 2007 , 106, 318-24	4.9	18
70	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016 , 135, 741-56	6.3	18
69	NPPB is a novel candidate biomarker expressed by cancer-associated fibroblasts in epithelial ovarian cancer. <i>International Journal of Cancer</i> , 2015 , 136, 1390-401	7.5	17

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