

Simon A Gayther

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.

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	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes.. <i>Cell Reports Medicine</i> , 2022 , 3, 100542	18	5
228	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
227	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021 , 7, eabf6133	13.3	2
226	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
225	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube. <i>Cell Reports</i> , 2021 , 35, 108978	10.6	7
224	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	9.8	2
223	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. <i>Genetics in Medicine</i> , 2021 , 23, 1726-1737	8.1	2
222	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
221	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021 , 12, 1078	17.4	4
220	Risks and Function of Breast Cancer Susceptibility Alleles. <i>Cancers</i> , 2021 , 13,	6.6	1
219	Human iPSC-derived fallopian tube organoids with BRCA1 mutation recapitulate early-stage carcinogenesis.. <i>Cell Reports</i> , 2021 , 37, 110146	10.6	0
218	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
217	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
216	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
215	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
214	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020 , 11, 3353	17.4	32
213	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

212	Lineage-Specific Epigenomic and Genomic Activation of Oncogene HNF4A Promotes Gastrointestinal Adenocarcinomas. <i>Cancer Research</i> , 2020 , 80, 2722-2736	10.1	14
211	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. <i>Nature Communications</i> , 2020 , 11, 2020	17.4	17
210	Identification of novel epithelial ovarian cancer loci in women of African ancestry. <i>International Journal of Cancer</i> , 2020 , 146, 2987-2998	7.5	8
209	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. <i>American Journal of Human Genetics</i> , 2020 , 107, 622-635	11	5
208	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. <i>Nature Genetics</i> , 2020 , 52, 790-799	36.3	62
207	Rare Germline Genetic Variants and the Risks of Epithelial Ovarian Cancer. <i>Cancers</i> , 2020 , 12,	6.6	5
206	Offspring sex and risk of epithelial ovarian cancer: a multinational pooled analysis of 12 case-control studies. <i>European Journal of Epidemiology</i> , 2020 , 35, 1025-1042	12.1	2
205	Master transcription factors form interconnected circuitry and orchestrate transcriptional networks in oesophageal adenocarcinoma. <i>Gut</i> , 2020 , 69, 630-640	19.2	27
204	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45
203	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
202	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
201	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
200	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
199	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
198	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. <i>BMC Genomics</i> , 2019 , 20, 745	4.5	10
197	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
196	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
195	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. <i>Cancer Research</i> , 2019 , 79, 467-481	10.1	11

194	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
193	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
192	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
191	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
190	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2018 , 47, 450-459	7.8	8
189	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
188	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
187	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
186	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
185	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018 , 13, e0197561	3.7	9
184	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
183	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018 , 9, 4079	17.4	65
182	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
181	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
180	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
179	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
178	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
177	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017 , 49, 680-691	36.3	190

176	Use of common analgesic medications and ovarian cancer survival: results from a pooled analysis in the Ovarian Cancer Association Consortium. <i>British Journal of Cancer</i> , 2017 , 116, 1223-1228	8.7	11
175	Integration of Population-Level Genotype Data with Functional Annotation Reveals Over-Representation of Long Noncoding RNAs at Ovarian Cancer Susceptibility Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 116-125	4	5
174	Genetic epidemiology of ovarian cancer and prospects for polygenic risk prediction. <i>Gynecologic Oncology</i> , 2017 , 147, 705-713	4.9	48
173	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
172	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
171	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. <i>Breast Cancer Research and Treatment</i> , 2017 , 161, 117-134	4.4	15
170	No Evidence That Genetic Variation in the Myeloid-Derived Suppressor Cell Pathway Influences Ovarian Cancer Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 420-424	4	3
169	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
168	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
167	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. <i>Oncotarget</i> , 2017 , 8, 46891-46899	3.3	17
166	The PAX8 cistrome in epithelial ovarian cancer. <i>Oncotarget</i> , 2017 , 8, 108316-108332	3.3	24
165	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016 , 141, 386-401	4.9	15
164	A splicing variant of TERT identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. <i>International Journal of Cancer</i> , 2016 , 139, 2646-2654	7.5	6
163	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, 1052-674.4	7.4	104
162	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
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	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
159	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

158	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
157	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
156	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 446-54	4	6
155	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
154	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
153	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
152	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
151	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
150	Association Between Menopausal Estrogen-Only Therapy and Ovarian Carcinoma Risk. <i>Obstetrics and Gynecology</i> , 2016 , 127, 828-836	4.9	24
149	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
148	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016 , 135, 741-56	6.3	18
147	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
146	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
145	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
144	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015 , 47, 164-71	36.3	177
143	PAX8 expression in ovarian surface epithelial cells. <i>Human Pathology</i> , 2015 , 46, 948-56	3.7	27
142	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
141	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

140	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
139	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
138	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
137	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015 , 36, 1341-53	4.6	20
136	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
135	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015 , 24, 5955-64	5.6	48
134	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
133	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
132	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
131	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015 , 39, 689-97	2.6	18
130	Identification of novel candidate biomarkers of epithelial ovarian cancer by profiling the secretomes of three-dimensional genetic models of ovarian carcinogenesis. <i>International Journal of Cancer</i> , 2015 , 137, 1806-17	7.5	14
129	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015 , 10, e0128106	3.7	15
128	Molecular Analysis of Mixed Endometrioid and Serous Adenocarcinoma of the Endometrium. <i>PLoS ONE</i> , 2015 , 10, e0130909	3.7	20
127	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
126	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
125	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
124	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
123	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

122	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
121	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
120	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
119	Variation in NF- κ B signaling pathways and survival in invasive epithelial ovarian cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 1421-7	4	11
118	Src as a novel therapeutic target for endometriosis. <i>Gynecologic Oncology</i> , 2014 , 135, 100-7	4.9	7
117	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
116	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
115	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. <i>Lancet Oncology</i> , 2013 , 14, 853-62	21.7	248
114	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
113	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
112	In vitro three-dimensional modeling of fallopian tube secretory epithelial cells. <i>BMC Cell Biology</i> , 2013 , 14, 43		35
111	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
110	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
109	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
108	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
107	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
106	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
105	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

104	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013 , 4, 1627	17.4	85
103	Inherited variants in regulatory T cell genes and outcome of ovarian cancer. <i>PLoS ONE</i> , 2013 , 8, e53903	3.7	19
102	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
101	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
100	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
99	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
98	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
97	Gene set analysis of survival following ovarian cancer implicates macrolide binding and intracellular signaling genes. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 529-36	4	7
96	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
95	Ovarian cancer risk associated with inherited inflammation-related variants. <i>Cancer Research</i> , 2012 , 72, 1064-9	10.1	35
94	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
93	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
92	Genome-wide association study for ovarian cancer susceptibility using pooled DNA. <i>Twin Research and Human Genetics</i> , 2012 , 15, 615-623	2.2	8
91	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
90	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
89	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
88	Principles for the post-GWAS functional characterization of cancer risk loci. <i>Nature Genetics</i> , 2011 , 43, 513-8	36.3	326
87	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

86	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
85	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
84	Prostate cancer susceptibility polymorphism rs2660753 is not associated with invasive ovarian cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011 , 20, 1028-31	4	
83	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
82	LIN28B polymorphisms influence susceptibility to epithelial ovarian cancer. <i>Cancer Research</i> , 2011 , 71, 3896-903	10.1	70
81	Modelling genetic and clinical heterogeneity in epithelial ovarian cancers. <i>Carcinogenesis</i> , 2011 , 32, 1540-9	4.6	33
80	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
79	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
78	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
77	Polymorphisms in stromal genes and susceptibility to serous epithelial ovarian cancer: a report from the Ovarian Cancer Association Consortium. <i>PLoS ONE</i> , 2011 , 6, e19642	3.7	4
76	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
75	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010 , 42, 880-4	36.3	210
74	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
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