

# Simon A Gayther

## List of Publications by Year in descending order

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232  
papers

19,370  
citations

14614

66  
h-index

14702

127  
g-index

245  
all docs

245  
docs citations

245  
times ranked

22933  
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.	5.1	753
2	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. <i>Genome Research</i> , 2010, 20, 440-446.	2.4	740
3	Association Between <i>BRCA1</i> and <i>BRCA2</i> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2012, 307, 382.	3.8	546
4	Mutations truncating the EP300 acetylase in human cancers. <i>Nature Genetics</i> , 2000, 24, 300-303.	9.4	543
5	Pathology of Breast and Ovarian Cancers among <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Results from the Consortium of Investigators of Modifiers of <i>BRCA1/2</i> (CIMBA). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 134-147.	1.1	513
6	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.	9.4	493
7	Germline mutations of the <i>BRCA1</i> gene in breast and ovarian cancer families provide evidence for a genotype-phenotype correlation. <i>Nature Genetics</i> , 1995, 11, 428-433.	9.4	484
8	Variation of risks of breast and ovarian cancer associated with different germline mutations of the <i>BRCA2</i> gene. <i>Nature Genetics</i> , 1997, 15, 103-105.	9.4	422
9	Principles for the post-GWAS functional characterization of cancer risk loci. <i>Nature Genetics</i> , 2011, 43, 513-518.	9.4	392
10	Association of Type and Location of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Risk of Breast and Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1347.	3.8	390
11	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
12	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. <i>Lancet Oncology</i> , The, 2013, 14, 853-862.	5.1	335
13	Two Percent of Men with Early-Onset Prostate Cancer Harbor Germline Mutations in the <i>BRCA2</i> Gene. <i>American Journal of Human Genetics</i> , 2003, 72, 1-12.	2.6	332
14	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	9.4	326
15	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. <i>Nature Genetics</i> , 2010, 42, 874-879.	9.4	321
16	Germline Mutations in the <i>BRIP1</i> , <i>BARD1</i> , <i>PALB2</i> , and <i>NBN</i> Genes in Women With Ovarian Cancer. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	311
17	A locus on 19p13 modifies risk of breast cancer in <i>BRCA1</i> mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. <i>Nature Genetics</i> , 2010, 42, 885-892.	9.4	309
18	Multiple Loci With Different Cancer Specificities Within the 8q24 Gene Desert. <i>Journal of the National Cancer Institute</i> , 2008, 100, 962-966.	3.0	306

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19	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. PLoS ONE, 2009, 4, e8274.	1.1	291
20	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278
21	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	9.4	276
22	Contribution of Germline Mutations in the <i>RAD51B</i> , <i>RAD51C</i> , and <i>RAD51D</i> Genes to Ovarian Cancer in the Population. Journal of Clinical Oncology, 2015, 33, 2901-2907.	0.8	266
23	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
24	Contribution of BRCA1 Mutations to Ovarian Cancer. New England Journal of Medicine, 1997, 336, 1125-1130.	13.9	236
25	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	9.4	235
26	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
27	The BRCA1- $\Delta$ 11q Alternative Splice Isoform Bypasses Germline Mutations and Promotes Therapeutic Resistance to PARP Inhibition and Cisplatin. Cancer Research, 2016, 76, 2778-2790.	0.4	208
28	The Contribution of <i>BRCA1</i> and <i>BRCA2</i> to Ovarian Cancer. Molecular Oncology, 2009, 3, 138-150.	2.1	178
29	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	9.4	174
30	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. Endocrine-Related Cancer, 2013, 20, 251-262.	1.6	169
31	Risk models for familial ovarian and breast cancer. , 2000, 18, 173-190.		157
32	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
33	A polymorphic stop codon in BRCA2. Nature Genetics, 1996, 14, 253-254.	9.4	152
34	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
35	Germline Mutation in <i>BRCA1</i> or <i>BRCA2</i> and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	3.2	138
36	Cost-effectiveness of Population-Based BRCA1, BRCA2, RAD51C, RAD51D, BRIP1, PALB2 Mutation Testing in Unselected General Population Women. Journal of the National Cancer Institute, 2018, 110, 714-725.	3.0	138

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37	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	9.4	125
38	Polymorphisms in DNA repair genes and epithelial ovarian cancer risk. <i>International Journal of Cancer</i> , 2005, 117, 611-618.	2.3	123
39	CA125 expression pattern, prognosis and correlation with serum CA125 in ovarian tumor patients. <i>Gynecologic Oncology</i> , 2007, 104, 508-515.	0.6	122
40	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018, 9, 4079.	5.8	121
41	The Contribution of Germline BRCA1 and BRCA2 Mutations to Familial Ovarian Cancer: No Evidence for Other Ovarian Cancer-Related Susceptibility Genes. <i>American Journal of Human Genetics</i> , 1999, 65, 1021-1029.	2.6	116
42	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.	1.4	112
43	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 1619-1630.	0.9	111
44	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in <i>RAD51C</i> and <i>RAD51D</i> . <i>Journal of the National Cancer Institute</i> , 2020, 112, 1242-1250.	3.0	106
45	Common Breast Cancer Susceptibility Variants in <i>LSP1</i> and <i>RAD51L1</i> Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1156-1166.	1.1	101
46	The sex hormone system in carriers of BRCA1/2 mutations: a case-control study. <i>Lancet Oncology</i> , The, 2013, 14, 1226-1232.	5.1	98
47	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	5.8	98
48	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.	0.8	98
49	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
50	<i>BRCA1</i> and <i>BRCA2</i> Mutation Prevalence and Clinical Characteristics of a Population-Based Series of Ovarian Cancer Cases from Denmark. <i>Clinical Cancer Research</i> , 2008, 14, 3761-3767.	3.2	92
51	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. <i>Nature Medicine</i> , 2015, 21, 1357-1363.	15.2	90
52	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.	9.4	89
53	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
54	Frequent loss of BRCA1 mRNA and protein expression in sporadic ovarian cancers. <i>International Journal of Cancer</i> , 2000, 87, 317-321.	2.3	84

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55	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.	0.8	84
56	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, 2119-2126.	2.6	78
57	Tagging Single Nucleotide Polymorphisms in Cell Cycle Control Genes and Susceptibility to Invasive Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2007, 67, 3027-3035.	0.4	78
58	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-IN3.	2.3	78
59	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.	2.2	78
60	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
61	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	3.0	77
62	Contribution of BRCA1 and BRCA2 mutations to inherited ovarian cancer. <i>Human Mutation</i> , 2007, 28, 1207-1215.	1.1	76
63	ESR1/SYNE1 Polymorphism and Invasive Epithelial Ovarian Cancer Risk: An Ovarian Cancer Association Consortium Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 245-250.	1.1	75
64	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2011, 71, 3896-3903.	0.4	75
65	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	5.8	75
66	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.	0.9	74
67	Consortium analysis of 7 candidate SNPs for ovarian cancer. <i>International Journal of Cancer</i> , 2008, 123, 380-388.	2.3	73
68	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. <i>Human Molecular Genetics</i> , 2014, 23, 5294-5302.	1.4	71
69	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.	0.9	71
70	Biomarker-Based Ovarian Carcinoma Typing: A Histologic Investigation in the Ovarian Tumor Tissue Analysis Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 1677-1686.	1.1	70
71	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.	1.3	70
72	Role of genetic polymorphisms and ovarian cancer susceptibility. <i>Molecular Oncology</i> , 2009, 3, 171-181.	2.1	69

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73	Genetic epidemiology of ovarian cancer and prospects for polygenic risk prediction. <i>Gynecologic Oncology</i> , 2017, 147, 705-713.	0.6	69
74	Prognostic value of estrogen receptor and progesterone receptor tumor expression in Danish ovarian cancer patients: from the 'MALOVA' ovarian cancer study. <i>Oncology Reports</i> , 2007, 18, 1051-9.	1.2	69
75	Increased frequency of TP53 mutations in BRCA1 and BRCA2 ovarian tumours. , 1999, 25, 91-96.		68
76	The clonal evolution of metastases from primary serous epithelial ovarian cancers. <i>International Journal of Cancer</i> , 2009, 124, 1579-1586.	2.3	68
77	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015, 24, 5955-5964.	1.4	68
78	Master transcription factors form interconnected circuitry and orchestrate transcriptional networks in oesophageal adenocarcinoma. <i>Gut</i> , 2020, 69, 630-640.	6.1	68
79	A breast/ovarian cancer patient with germline mutations in both BRCA1 and BRCA2. <i>Nature Genetics</i> , 1997, 15, 14-15.	9.4	67
80	Common variants in mismatch repair genes and risk of invasive ovarian cancer. <i>Carcinogenesis</i> , 2006, 27, 2235-2242.	1.3	67
81	The inherited genetics of ovarian and endometrial cancer. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 231-238.	1.5	64
82	Single Nucleotide Polymorphisms in the TP53 Region and Susceptibility to Invasive Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2009, 69, 2349-2357.	0.4	63
83	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	5.8	63
84	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.	3.1	62
85	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.	1.9	60
86	Tagging Single Nucleotide Polymorphisms in the BRIP1 Gene and Susceptibility to Breast and Ovarian Cancer. <i>PLoS ONE</i> , 2007, 2, e268.	1.1	54
87	Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. <i>International Journal of Cancer</i> , 2011, 128, 2063-2074.	2.3	54
88	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.	1.1	54
89	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.	0.4	54
90	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.	2.9	54

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91	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. <i>Nature Communications</i> , 2020, 11, 2020.	5.8	52
92	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, 936-943.	2.3	49
93	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.	0.4	49
94	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.	1.5	48
95	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. <i>PLoS ONE</i> , 2011, 6, e24987.	1.1	48
96	Risk of Ovarian Cancer and the NF- $\kappa$ B Pathway: Genetic Association with <i>IL1A</i> and <i>TNFSF10</i> . <i>Cancer Research</i> , 2014, 74, 852-861.	0.4	48
97	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube. <i>Cell Reports</i> , 2021, 35, 108978.	2.9	48
98	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. <i>Clinical Cancer Research</i> , 2011, 17, 3742-3750.	3.2	47
99	Common Variants at the 19p13.1 and <i>ZNF365</i> Loci Are Associated with ER Subtypes of Breast Cancer and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 645-657.	1.1	47
100	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.	1.3	45
101	Ovarian Cancer Risk Associated with Inherited Inflammation-Related Variants. <i>Cancer Research</i> , 2012, 72, 1064-1069.	0.4	45
102	A Molecular Genetic and Statistical Approach for the Diagnosis of Dual-Site Cancers. <i>Journal of the National Cancer Institute</i> , 2004, 96, 1441-1446.	3.0	44
103	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	1.1	44
104	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016, 139, 2655-2670.	2.3	43
105	<i>PPM1D</i> Mosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv347.	3.0	43
106	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.	3.2	43
107	Germline whole exome sequencing and large-scale replication identifies FANCM as a likely high grade serous ovarian cancer susceptibility gene. <i>Oncotarget</i> , 2017, 8, 50930-50940.	0.8	43
108	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, 2297-2304.	1.4	42

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109	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.	3.2	42
110	Predicting Clinical Outcome in Patients Diagnosed with Synchronous Ovarian and Endometrial Cancer. <i>Clinical Cancer Research</i> , 2008, 14, 5840-5848.	3.2	41
111	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, 105-116.	3.0	40
112	In vitro three-dimensional modeling of fallopian tube secretory epithelial cells. <i>BMC Cell Biology</i> , 2013, 14, 43.	3.0	40
113	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2015, 24, 3595-3607.	1.4	40
114	GENAVI: a shiny web application for gene expression normalization, analysis and visualization. <i>BMC Genomics</i> , 2019, 20, 745.	1.2	40
115	Common Variants in RB1 Gene and Risk of Invasive Ovarian Cancer. <i>Cancer Research</i> , 2006, 66, 10220-10226.	0.4	39
116	Association Between Menopausal Estrogen-Only Therapy and Ovarian Carcinoma Risk. <i>Obstetrics and Gynecology</i> , 2016, 127, 828-836.	1.2	39
117	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.	2.9	39
118	Microcell-Mediated Chromosome Transfer Identifies EPB41L3 as a Functional Suppressor of Epithelial Ovarian Cancers. <i>Neoplasia</i> , 2010, 12, 579-IN18.	2.3	38
119	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.	1.5	38
120	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.	1.1	38
121	<i>HNF1B</i> variants associate with promoter methylation and regulate gene networks activated in prostate and ovarian cancer. <i>Oncotarget</i> , 2016, 7, 74734-74746.	0.8	38
122	The PAX8 cistrome in epithelial ovarian cancer. <i>Oncotarget</i> , 2017, 8, 108316-108332.	0.8	38
123	Lineage-Specific Epigenomic and Genomic Activation of Oncogene HNF4A Promotes Gastrointestinal Adenocarcinomas. <i>Cancer Research</i> , 2020, 80, 2722-2736.	0.4	37
124	Modelling genetic and clinical heterogeneity in epithelial ovarian cancers. <i>Carcinogenesis</i> , 2011, 32, 1540-1549.	1.3	36
125	PAX8 expression in ovarian surface epithelial cells. <i>Human Pathology</i> , 2015, 46, 948-956.	1.1	36
126	ABO blood group and risk of epithelial ovarian cancer within the Ovarian Cancer Association Consortium. <i>Cancer Causes and Control</i> , 2012, 23, 1805-1810.	0.8	35



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127	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.	2.9	35
128	Ovarian cancer susceptibility alleles and risk of ovarian cancer in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. <i>Human Mutation</i> , 2012, 33, 690-702.	1.1	34
129	Breast cancer information on the web. <i>Nature Genetics</i> , 1995, 11, 238-239.	9.4	33
130	A Gene ( <i>DLG2</i> ) Located at 17q12-q21 Encodes a New Homologue of the Drosophila Tumor Suppressor <i>dlg-A</i> . <i>Genomics</i> , 1995, 28, 25-31.	1.3	33
131	The genetics of inherited breast cancer. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 1998, 3, 365-376.	1.0	33
132	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.	1.4	33
133	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.	3.2	33
134	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 395-404.	1.1	33
135	<i>BRCA1/2</i> mutation status influences somatic genetic progression in inherited and sporadic epithelial ovarian cancer cases. <i>Cancer Research</i> , 2003, 63, 417-23.	0.4	33
136	The Effects of Common Genetic Variants in Oncogenes on Ovarian Cancer Survival. <i>Clinical Cancer Research</i> , 2008, 14, 5833-5839.	3.2	32
137	Common variants of the <i>BRCA1</i> wild-type allele modify the risk of breast cancer in <i>BRCA1</i> mutation carriers. <i>Human Molecular Genetics</i> , 2011, 20, 4732-4747.	1.4	32
138	Mutations of the <i>BRCA1</i> and <i>BRCA2</i> genes and the possibilities for predictive testing. <i>Trends in Molecular Medicine</i> , 1997, 3, 168-174.	2.6	30
139	Identification of a novel splice-site mutation of the <i>BRCA1</i> gene in two breast cancer families: Screening reveals low frequency in Icelandic breast cancer patients. <i>Human Mutation</i> , 1998, 11, S195-S197.	1.1	30
140	A modified medium that significantly improves the growth of human normal ovarian surface epithelial (OSE) cells in vitro. <i>Laboratory Investigation</i> , 2004, 84, 923-931.	1.7	30
141	Recruitment of newly diagnosed ovarian cancer patients proved challenging in a multicentre biobanking study. <i>Journal of Clinical Epidemiology</i> , 2011, 64, 525-530.	2.4	30
142	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	4.7	30
143	Apparent human <i>BRCA1</i> knockout caused by mispriming during polymerase chain reaction: Implications for genetic testing. <i>Genes Chromosomes and Cancer</i> , 2001, 31, 96-98.	1.5	29
144	Effects of Common Germ-Line Genetic Variation in Cell Cycle Genes on Ovarian Cancer Survival. <i>Clinical Cancer Research</i> , 2008, 14, 1090-1095.	3.2	29

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145	Network-Based Integration of GWAS and Gene Expression Identifies a <i>HOX</i> -Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	1.1	28
146	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	0.6	28
147	Clues to the Function of the Tumour Susceptibility Gene BRCA2. <i>Disease Markers</i> , 1998, 14, 1-8.	0.6	26
148	Vascular endothelial growth factor gene polymorphisms and ovarian cancer survival. <i>Gynecologic Oncology</i> , 2010, 119, 479-483.	0.6	26
149	Transcriptomic Characterization of Endometrioid, Clear Cell, and High-Grade Serous Epithelial Ovarian Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1101-1109.	1.1	26
150	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.	1.5	26
151	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. <i>Cell Reports Medicine</i> , 2022, 3, 100542.	3.3	26
152	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.	2.3	25
153	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
154	Genetic Variation in <i>TYMS</i> 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, 1822-1830.	1.1	24
155	NPPB is a novel candidate biomarker expressed by cancer-associated fibroblasts in epithelial ovarian cancer. <i>International Journal of Cancer</i> , 2015, 136, 1390-1401.	2.3	24
156	Common variants at the <i>CHEK2</i> gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	1.3	24
157	Polymorphism in the <i>GALNT1</i> Gene and Epithelial Ovarian Cancer in Non-Hispanic White Women: The Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 600-604.	1.1	23
158	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. <i>Human Genetics</i> , 2014, 133, 481-497.	1.8	23
159	Molecular Analysis of Mixed Endometrioid and Serous Adenocarcinoma of the Endometrium. <i>PLoS ONE</i> , 2015, 10, e0130909.	1.1	23
160	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017, 116, 524-535.	2.9	23
161	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	1.4	23
162	Genetic variation in insulin-like growth factor 2 may play a role in ovarian cancer risk. <i>Human Molecular Genetics</i> , 2011, 20, 2263-2272.	1.4	22

#	ARTICLE	IF	CITATIONS
163	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015, 39, 689-697.	0.6	22
164	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. <i>Cancer Research</i> , 2019, 79, 467-481.	0.4	22
165	Rare Germline Genetic Variants and the Risks of Epithelial Ovarian Cancer. <i>Cancers</i> , 2020, 12, 3046.	1.7	22
166	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. <i>Oncotarget</i> , 2017, 8, 46891-46899.	0.8	22
167	Molecular Subclasses of Clear Cell Ovarian Carcinoma and Their Impact on Disease Behavior and Outcomes. <i>Clinical Cancer Research</i> , 2022, 28, 4947-4956.	3.2	22
168	Large-Scale Evaluation of Common Variation in Regulatory T Cellâ€Related Genes and Ovarian Cancer Outcome. <i>Cancer Immunology Research</i> , 2014, 2, 332-340.	1.6	21
169	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.	1.1	21
170	Human iPSC-derived fallopian tube organoids with BRCA1 mutation recapitulate early-stage carcinogenesis. <i>Cell Reports</i> , 2021, 37, 110146.	2.9	21
171	Mismatch repair gene polymorphisms and survival in invasive ovarian cancer patients. <i>European Journal of Cancer</i> , 2008, 44, 2259-2265.	1.3	20
172	Protein expression levels of carcinoembryonic antigen (CEA) in Danish ovarian cancer patients: from the Danish â€MALOVAâ€ ovarian cancer study. <i>Pathology</i> , 2008, 40, 487-492.	0.3	20
173	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. <i>Fertility and Sterility</i> , 2011, 95, 40-45.	0.5	20
174	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, 987-992.	1.1	20
175	Identification of novel candidate biomarkers of epithelial ovarian cancer by profiling the secretomes of threeâ€dimensional genetic models of ovarian carcinogenesis. <i>International Journal of Cancer</i> , 2015, 137, 1806-1817.	2.3	20
176	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.	0.8	20
177	Inherited Variants in Regulatory T Cell Genes and Outcome of Ovarian Cancer. <i>PLoS ONE</i> , 2013, 8, e53903.	1.1	20
178	Expression level of Wilms tumor 1 (WT1) protein has limited prognostic value in epithelial ovarian cancer From the Danish â€MALOVAâ€ Ovarian Cancer Study. <i>Gynecologic Oncology</i> , 2007, 106, 318-324.	0.6	19
179	MicroRNA Processing and Binding Site Polymorphisms Are Not Replicated in the Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1793-1797.	1.1	19
180	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016, 135, 741-756.	1.8	19

#	ARTICLE	IF	CITATIONS
181	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. <i>Human Molecular Genetics</i> , 2019, 28, 1331-1342.	1.4	19
182	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	5.8	19
183	Localisation of the human blue cone pigment gene to chromosome band 7q31.3-32. <i>Human Genetics</i> , 1994, 93, 79-80.	1.8	18
184	Risk of ovarian cancer in women with first-degree relatives with cancer. <i>Acta Obstetricia Et Gynecologica Scandinavica</i> , 2009, 88, 449-456.	1.3	18
185	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	0.6	18
186	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.	1.1	18
187	Identification of novel epithelial ovarian cancer loci in women of African ancestry. <i>International Journal of Cancer</i> , 2020, 146, 2987-2998.	2.3	18
188	Functional complementation studies identify candidate genes and common genetic variants associated with ovarian cancer survival. <i>Human Molecular Genetics</i> , 2009, 18, 1869-1878.	1.4	17
189	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.	1.4	17
190	Distribution of p53 expression in tissue from 774 Danish ovarian tumour patients and its prognostic significance in ovarian carcinomas. <i>Apmis</i> , 2008, 116, 400-409.	0.9	16
191	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.	0.6	16
192	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.	1.1	16
193	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. <i>British Journal of Cancer</i> , 2018, 118, 1123-1129.	2.9	15
194	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.	0.9	15
195	Menopausal hormone therapy prior to the diagnosis of ovarian cancer is associated with improved survival. <i>Gynecologic Oncology</i> , 2020, 158, 702-709.	0.6	15
196	Validated biomarker assays confirm that <i>ARID1A</i> loss is confounded with <i>MMR</i> deficiency, <i>CD8</i> <sup>+</sup> TIL infiltration, and provides no independent prognostic value in endometriosis-associated ovarian carcinomas. <i>Journal of Pathology</i> , 2022, 256, 388-401.	2.1	15
197	Idiopathic slow-transit constipation is not associated with mutations of the RET proto-oncogene or GDNF. <i>Diseases of the Colon and Rectum</i> , 2000, 43, 851-857.	0.7	14
198	Association Study of Prostate Cancer Susceptibility Variants with Risks of Invasive Ovarian, Breast, and Colorectal Cancer. <i>Cancer Research</i> , 2008, 68, 8837-8842.	0.4	14

#	ARTICLE	IF	CITATIONS
199	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.	2.6	14
200	Variation in NF- $\kappa$ B Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1421-1427.	1.1	13
201	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.	2.9	13
202	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. <i>Oncotarget</i> , 2016, 7, 72381-72394.	0.8	13
203	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.	2.3	12
204	Chromosomes 6 and 18 induce neoplastic suppression in epithelial ovarian cancer cells. <i>International Journal of Cancer</i> , 2009, 124, 1037-1044.	2.3	11
205	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, 780-790.	1.1	10
206	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.	1.1	10
207	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 446-454.	1.1	9
208	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018, 13, e0197561.	1.1	9
209	Screening for the BRCA1-ins6kbEx13 mutation: potential for misdiagnosis. <i>Human Mutation</i> , 2007, 28, 525-526.	1.1	8
210	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. <i>Twin Research and Human Genetics</i> , 2012, 15, 615-623.	0.3	8
211	Src as a novel therapeutic target for endometriosis. <i>Gynecologic Oncology</i> , 2014, 135, 100-107.	0.6	8
212	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.	1.6	8
213	Risks and Function of Breast Cancer Susceptibility Alleles. <i>Cancers</i> , 2021, 13, 3953.	1.7	8
214	A polymorphism in the GALNT2 gene and ovarian cancer risk in four population based case-control studies. <i>International Journal of Molecular Epidemiology and Genetics</i> , 2010, 1, 272-7.	0.4	8
215	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.	1.4	8
216	Gene Set Analysis of Survival Following Ovarian Cancer Implicates Macrolide Binding and Intracellular Signaling Genes. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 529-536.	1.1	7

#	ARTICLE	IF	CITATIONS
217	A splicing variant of <i>TERT</i> identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. <i>International Journal of Cancer</i> , 2016, 139, 2646-2654.	2.3	7
218	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.	1.1	6
219	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.	1.3	6
220	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.	1.0	6
221	Ovarian cancer aetiology: facts and fiction. <i>Journal of Family Planning and Reproductive Health Care</i> , 2006, 32, 82-86.	0.9	5
222	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.	1.1	5
223	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.	0.8	5
224	Genetic mutations in gynaecological cancers. <i>Reviews in Gynaecological and Perinatal Practice</i> , 2006, 6, 115-125.	0.3	4
225	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.	1.1	3
226	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2473.	1.8	3
227	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.	2.6	3
228	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.	2.5	2
229	Principles for the post-GWAS functional characterisation of risk loci. <i>Nature Precedings</i> , 2010, , .	0.1	1
230	Germline rearrangement at the locus detected by PFGE. <i>Cancer Genetics and Cytogenetics</i> , 1992, 63, 123.	1.0	0
231	Principles for the post-GWAS functional characterisation of risk loci. <i>Nature Precedings</i> , 2011, , .	0.1	0
232	Prostate Cancer Susceptibility Polymorphism rs2660753 Is Not Associated with Invasive Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1028-1031.	1.1	0