Simon A Gayther

List of Publications by Year
in descending order

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232 papers	19,370 citations	14655 66 h-index	14759 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 caseâ€“control studies. Lancet Oncology, The, 2012, 13, 385-394.	10.7	753
2	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. Genome Research, 2010, 20, 440-446.	5.5	740
3	Association Between <emph type="ital">BRCA1</emph> and <emph type="ital">BRCA2</emph> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. JAMA - Journal of the American Medical Association, 2012, 307, 382.	7.4	546
4	Mutations truncating the EP300 acetylase in human cancers. Nature Genetics, 2000, 24, 300-303.	21.4	543
5	Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 134-147.	2.5	513
6	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
7	Germline mutations of the BRCA1 gene in breast and ovarian cancer families provide evidence for a genotypeâ€“phenotype correlation. Nature Genetics, 1995, 11, 428-433.	21.4	484
8	Variation of risks of breast and ovarian cancer associated with different germline mutations of the BRCA2 gene. Nature Genetics, 1997, 15, 103-105.	21.4	422
9	Principles for the post-GWAS functional characterization of cancer risk loci. Nature Genetics, 2011, 43, 513-518.	21.4	392
10	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	7.4	390
11	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
12	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	10.7	335
13	Two Percent of Men with Early-Onset Prostate Cancer Harbor Germline Mutations in the BRCA2 Gene. American Journal of Human Genetics, 2003, 72, 1-12.	6.2	332
14	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
15	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
16	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. Journal of the National Cancer Institute, 2015, 107, .	6.3	311
17	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	21.4	309
18	Multiple Loci With Different Cancer Specificities Within the 8q24 Gene Desert. Journal of the National Cancer Institute, 2008, 100, 962-966.	6.3	306

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19	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. PLoS ONE, 2009, 4, e8274.	2.5	291
20	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	2.5	278
21	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
22	Contribution of Germline Mutations in the RAD51B, RAD51C, and RAD51D Genes to Ovarian Cancer in the Population. Journal of Clinical Oncology, 2015, 33, 2901-2907.	1.6	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.	21.4	265
24	Contribution ofBRCA1Mutations to Ovarian Cancer. New England Journal of Medicine, 1997, 336, 1125-1130.	27.0	236
25	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
26	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
27	The BRCA1-Î”11q Alternative Splice Isoform Bypasses Germline Mutations and Promotes Therapeutic Resistance to PARP Inhibition and Cisplatin. Cancer Research, 2016, 76, 2778-2790.	0.9	208
28	The Contribution of BRCA1 and BRCA2 to Ovarian Cancer. Molecular Oncology, 2009, 3, 138-150.	4.6	178
29	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	21.4	174
30	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. Endocrine-Related Cancer, 2013, 20, 251-262.	3.1	169
31	Risk models for familial ovarian and breast cancer. Genetic Epidemiology, 2000, 18, 173-190.	1.3	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.	9.4	157
33	A polymorphic stop codon in BRCA2. Nature Genetics, 1996, 14, 253-254.	21.4	152
34	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
35	Germline Mutation in BRCA1 or BRCA2 and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	7.0	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.	6.3	138

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37	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
38	Polymorphisms in DNA repair genes and epithelial ovarian cancer risk. International Journal of Cancer, 2005, 117, 611-618.	5.1	123
39	CA125 expression pattern, prognosis and correlation with serum CA125 in ovarian tumor patients. Gynecologic Oncology, 2007, 104, 508-515.	1.4	122
40	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079.	12.8	121
41	The Contribution of Germline BRCA1 and BRCA2 Mutations to Familial Ovarian Cancer: No Evidence for Other Ovarian Cancerâ€“Susceptibility Genes. American Journal of Human Genetics, 1999, 65, 1021-1029.	6.2	116
42	The contribution of deleterious germline mutations in BRCA1, BRCA2 and the mismatch repair genes to ovarian cancer in the population. Human Molecular Genetics, 2014, 23, 4703-4709.	2.9	112
43	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	1.9	111
44	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. Journal of the National Cancer Institute, 2020, 112, 1242-1250.	6.3	106
45	Common Breast Cancer Susceptibility Variants in LSP1 and RAD51L1 Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1156-1166.	2.5	101
46	The sex hormone system in carriers of BRCA1/2 mutations: a case-control study. Lancet Oncology, The, 2013, 14, 1226-1232.	10.7	98
47	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
48	A functional variant in HOXA11-AS, a novel long non-coding RNA, inhibits the oncogenic phenotype of epithelial ovarian cancer. Oncotarget, 2015, 6, 34745-34757.	1.8	98
49	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
50	BRCA1 and BRCA2 Mutation Prevalence and Clinical Characteristics of a Population-Based Series of Ovarian Cancer Cases from Denmark. Clinical Cancer Research, 2008, 14, 3761-3767.	7.0	92
51	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. Nature Medicine, 2015, 21, 1357-1363.	30.7	90
52	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nature Genetics, 2019, 51, 815-823.	21.4	89
53	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
54	Frequent loss of BRCA1 mRNA and protein expression in sporadic ovarian cancers. International Journal of Cancer, 2000, 87, 317-321.	5.1	84

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55	Cigarette smoking and risk of ovarian cancer: a pooled analysis of 21 caseâ€“control studies. Cancer Causes and Control, 2013, 24, 989-1004.	1.8	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. Oncogene, 1997, 15, 2119-2126.	5.9	78
57	Tagging Single Nucleotide Polymorphisms in Cell Cycle Control Genes and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2007, 67, 3027-3035.	0.9	78
58	Senescent Fibroblasts Promote Neoplastic Transformation of Partially Transformed Ovarian Epithelial Cells in a Three-dimensional Model of Early Stage Ovarian Cancer. Neoplasia, 2010, 12, 317-IN3.	5.3	78
59	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	5.0	78
60	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
61	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
62	Contribution ofBRCA1andBRCA2mutations to inherited ovarian cancer. Human Mutation, 2007, 28, 1207-1215.	2.5	76
63	ESR1/SYNE1 Polymorphism and Invasive Epithelial Ovarian Cancer Risk: An Ovarian Cancer Association Consortium Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 245-250.	2.5	75
64	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.9	75
65	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
66	Histopathology, FIGO Stage, and BRCA Mutation Status of Ovarian Cancers from the Gilda Radner Familial Ovarian Cancer Registry. International Journal of Gynecological Pathology, 2004, 23, 29-34.	1.4	74
67	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388.	5.1	73
68	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. Human Molecular Genetics, 2014, 23, 5294-5302.	2.9	71
69	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	1.9	71
70	Biomarker-Based Ovarian Carcinoma Typing: A Histologic Investigation in the Ovarian Tumor Tissue Analysis Consortium. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1677-1686.	2.5	70
71	Association of p16 expression with prognosis varies across ovarian carcinoma histotypes: an Ovarian Tumor Tissue Analysis consortium study. Journal of Pathology: Clinical Research, 2018, 4, 250-261.	3.0	70
72	Role of genetic polymorphisms and ovarian cancer susceptibility. Molecular Oncology, 2009, 3, 171-181.	4.6	69

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73	Genetic epidemiology of ovarian cancer and prospects for polygenic risk prediction. Gynecologic Oncology, 2017, 147, 705-713.	1.4	69
74	Prognostic value of estrogen receptor and progesterone receptor tumor expression in Danish ovarian cancer patients: from the 'MALOVA' ovarian cancer study. Oncology Reports, 2007, 18, 1051-9.	2.6	69
75	Increased frequency ofTP53 mutations inBRCA1 andBRCA2 ovarian tumours. , 1999, 25, 91-96.		68
76	The clonal evolution of metastases from primary serous epithelial ovarian cancers. International Journal of Cancer, 2009, 124, 1579-1586.	5.1	68
77	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
78	Master transcription factors form interconnected circuitry and orchestrate transcriptional networks in oesophageal adenocarcinoma. Gut, 2020, 69, 630-640.	12.1	68
79	A breast/ovarian cancer patient with germline mutations in both BRCA1 and BRCA2. Nature Genetics, 1997, 15, 14-15.	21.4	67
80	Common variants in mismatch repair genes and risk of invasive ovarian cancer. Carcinogenesis, 2006, 27, 2235-2242.	2.8	67
81	The inherited genetics of ovarian and endometrial cancer. Current Opinion in Genetics and Development, 2010, 20, 231-238.	3.3	64
82	Single Nucleotide Polymorphisms in the TP53 Region and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2009, 69, 2349-2357.	0.9	63
83	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
84	Stromal Expression of Fibroblast Activation Protein Alpha (FAP) Predicts Platinum Resistance and Shorter Recurrence in patients with Epithelial Ovarian Cancer. Cancer Microenvironment, 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. IScience, 2019, 17, 242-255.	4.1	60
86	Tagging Single Nucleotide Polymorphisms in the BRIP1 Gene and Susceptibility to Breast and Ovarian Cancer. PLoS ONE, 2007, 2, e268.	2.5	54
87	Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. International Journal of Cancer, 2011, 128, 2063-2074.	5.1	54
88	Combined and Interactive Effects of Environmental and GWAS-Identified Risk Factors in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 880-890.	2.5	54
89	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.9	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. Modern Pathology, 2019, 32, 1834-1846.	5.5	54

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91	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. Nature Communications, 2020, 11, 2020.	12.8	52
92	Vitamin D receptor rs2228570 polymorphism and invasive ovarian carcinoma risk: Pooled analysis in five studies within the Ovarian Cancer Association Consortium. International Journal of Cancer, 2011, 128, 936-943.	5.1	49
93	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.9	49
94	Evaluation of Candidate Stromal Epithelial Cross-Talk Genes Identifies Association between Risk of Serous Ovarian Cancer and TERT, a Cancer Susceptibility â€œHot-Spotâ€• PLoS Genetics, 2010, 6, e1001016.	3.5	48
95	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. PLoS ONE, 2011, 6, e24987.	2.5	48
96	Risk of Ovarian Cancer and the NF-Îºb Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.9	48
97	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube. Cell Reports, 2021, 35, 108978.	6.4	48
98	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	7.0	47
99	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. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 645-657.	2.5	47
100	Ovarian cancer and genetic susceptibility in relation to the BRCA1 and BRCA2 genes. Occurrence, clinical importance and intervention. Acta Obstetricia Et Gynecologica Scandinavica, 2006, 85, 93-105.	2.8	45
101	Ovarian Cancer Risk Associated with Inherited Inflammation-Related Variants. Cancer Research, 2012, 72, 1064-1069.	0.9	45
102	A Molecular Genetic and Statistical Approach for the Diagnosis of Dual-Site Cancers. Journal of the National Cancer Institute, 2004, 96, 1441-1446.	6.3	44
103	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
104	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	5.1	43
105	PPM1DMosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. Journal of the National Cancer Institute, 2016, 108, djv347.	6.3	43
106	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	7.0	43
107	Germline whole exome sequencing and large-scale replication identifies FANCM as a likely high grade serous ovarian cancer susceptibility gene. Oncotarget, 2017, 8, 50930-50940.	1.8	43
108	Association between invasive ovarian cancer susceptibility and 11 best candidate SNPs from breast cancer genome-wide association study. Human Molecular Genetics, 2009, 18, 2297-2304.	2.9	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. Cancer Letters, 2017, 401, 11-19.	7.2	42
110	Predicting Clinical Outcome in Patients Diagnosed with Synchronous Ovarian and Endometrial Cancer. Clinical Cancer Research, 2008, 14, 5840-5848.	7.0	41
111	Genetic Variation at 9p22.2 and Ovarian Cancer Risk for BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2011, 103, 105-116.	6.3	40
112	In vitro three-dimensional modeling of fallopian tube secretory epithelial cells. BMC Cell Biology, 2013, 14, 43.	3.0	40
113	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
114	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. BMC Genomics, 2019, 20, 745.	2.8	40
115	Common Variants in RB1 Gene and Risk of Invasive Ovarian Cancer. Cancer Research, 2006, 66, 10220-10226.	0.9	39
116	Association Between Menopausal Estrogen-Only Therapy and Ovarian Carcinoma Risk. Obstetrics and Gynecology, 2016, 127, 828-836.	2.4	39
117	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. Cell Reports, 2019, 29, 3726-3735.e4.	6.4	39
118	Microcell-Mediated Chromosome Transfer Identifies EPB41L3 as a Functional Suppressor of Epithelial Ovarian Cancers. Neoplasia, 2010, 12, 579-IN18.	5.3	38
119	Evaluation of polygenic risk scores for ovarian cancer risk prediction in a prospective cohort study. Journal of Medical Genetics, 2018, 55, 546-554.	3.2	38
120	Association between Common Germline Genetic Variation in 94 Candidate Genes or Regions and Risks of Invasive Epithelial Ovarian Cancer. PLoS ONE, 2009, 4, e5983.	2.5	38
121	HNF1B variants associate with promoter methylation and regulate gene networks activated in prostate and ovarian cancer. Oncotarget, 2016, 7, 74734-74746.	1.8	38
122	The PAX8 cistrome in epithelial ovarian cancer. Oncotarget, 2017, 8, 108316-108332.	1.8	38
123	Lineage-Specific Epigenomic and Genomic Activation of Oncogene HNF4A Promotes Gastrointestinal Adenocarcinomas. Cancer Research, 2020, 80, 2722-2736.	0.9	37
124	Modelling genetic and clinical heterogeneity in epithelial ovarian cancers. Carcinogenesis, 2011, 32, 1540-1549.	2.8	36
125	PAX8 expression in ovarian surface epithelial cells. Human Pathology, 2015, 46, 948-956.	2.0	36
126	ABO blood group and risk of epithelial ovarian cancer within the Ovarian Cancer Association Consortium. Cancer Causes and Control, 2012, 23, 1805-1810.	1.8	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. British Journal of Cancer, 2020, 123, 793-802.	6.4	35
128	Ovarian cancer susceptibility alleles and risk of ovarian cancer inBRCA1andBRCA2mutation carriers. Human Mutation, 2012, 33, 690-702.	2.5	34
129	Breast cancer information on the web. Nature Genetics, 1995, 11, 238-239.	21.4	33
130	A Gene (DLG2) Located at 17q12-q21 Encodes a New Homologue of the Drosophila Tumor Suppressor dlg-A. Genomics, 1995, 28, 25-31.	2.9	33
131	The genetics of inherited breast cancer. Journal of Mammary Gland Biology and Neoplasia, 1998, 3, 365-376.	2.7	33
132	Kernel canonical correlation analysis for assessing geneâ€“gene interactions and application to ovarian cancer. European Journal of Human Genetics, 2014, 22, 126-131.	2.8	33
133	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. Clinical Cancer Research, 2015, 21, 5264-5276.	7.0	33
134	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 395-404.	2.5	33
135	BRCA1/2 mutation status influences somatic genetic progression in inherited and sporadic epithelial ovarian cancer cases. Cancer Research, 2003, 63, 417-23.	0.9	33
136	The Effects of Common Genetic Variants in Oncogenes on Ovarian Cancer Survival. Clinical Cancer Research, 2008, 14, 5833-5839.	7.0	32
137	Common variants of the BRCA1 wild-type allele modify the risk of breast cancer in BRCA1 mutation carriers. Human Molecular Genetics, 2011, 20, 4732-4747.	2.9	32
138	Mutations of the BRCA1 and BRCA2 genes and the possibilities for predictive testing. Trends in Molecular Medicine, 1997, 3, 168-174.	2.6	30
139	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. Human Mutation, 1998, 11, S195-S197.	2.5	30
140	A modified medium that significantly improves the growth of human normal ovarian surface epithelial (OSE) cells in vitro. Laboratory Investigation, 2004, 84, 923-931.	3.7	30
141	Recruitment of newly diagnosed ovarian cancer patients proved challenging in a multicentre biobanking study. Journal of Clinical Epidemiology, 2011, 64, 525-530.	5.0	30
142	Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123.	10.3	30
143	Apparent humanBRCA1 knockout caused by mispriming during polymerase chain reaction: Implications for genetic testing. Genes Chromosomes and Cancer, 2001, 31, 96-98.	2.8	29
144	Effects of Common Germ-Line Genetic Variation in Cell Cycle Genes on Ovarian Cancer Survival. Clinical Cancer Research, 2008, 14, 1090-1095.	7.0	29

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145	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	2.5	28
146	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. Gynecologic Oncology, 2019, 153, 343-355.	1.4	28
147	Clues to the Function of the Tumour Susceptibility Gene BRCA2. Disease Markers, 1998, 14, 1-8.	1.3	26
148	Vascular endothelial growth factor gene polymorphisms and ovarian cancer survival. Gynecologic Oncology, 2010, 119, 479-483.	1.4	26
149	Transcriptomic Characterization of Endometrioid, Clear Cell, and High-Grade Serous Epithelial Ovarian Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1101-1109.	2.5	26
150	Population-based targeted sequencing of 54 candidate genes identifiesPALB2as a susceptibility gene for high-grade serous ovarian cancer. Journal of Medical Genetics, 2021, 58, 305-313.	3.2	26
151	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. Cell Reports Medicine, 2022, 3, 100542.	6.5	26
152	Cigarette smoking is associated with adverse survival among women with ovarian cancer: Results from a pooled analysis of 19 studies. International Journal of Cancer, 2017, 140, 2422-2435.	5.1	25
153	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
154	Genetic Variation in TYMS in the One-Carbon Transfer Pathway Is Associated with Ovarian Carcinoma Types in the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1822-1830.	2.5	24
155	NPPB is a novel candidate biomarker expressed by cancerâ€associated fibroblasts in epithelial ovarian cancer. International Journal of Cancer, 2015, 136, 1390-1401.	5.1	24
156	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
157	Polymorphism in the GALNT1 Gene and Epithelial Ovarian Cancer in Non-Hispanic White Women: The Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 600-604.	2.5	23
158	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23
159	Molecular Analysis of Mixed Endometrioid and Serous Adenocarcinoma of the Endometrium. PLoS ONE, 2015, 10, e0130909.	2.5	23
160	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	6.4	23
161	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
162	Genetic variation in insulin-like growth factor 2 may play a role in ovarian cancer risk. Human Molecular Genetics, 2011, 20, 2263-2272.	2.9	22

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163	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
164	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
165	Rare Germline Genetic Variants and the Risks of Epithelial Ovarian Cancer. Cancers, 2020, 12, 3046.	3.7	22
166	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. Oncotarget, 2017, 8, 46891-46899.	1.8	22
167	Molecular Subclasses of Clear Cell Ovarian Carcinoma and Their Impact on Disease Behavior and Outcomes. Clinical Cancer Research, 2022, 28, 4947-4956.	7.0	22
168	Large-Scale Evaluation of Common Variation in Regulatory T Cellâ€“Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	3.4	21
169	Estrogen Receptor Beta rs1271572 Polymorphism and Invasive Ovarian Carcinoma Risk: Pooled Analysis within the Ovarian Cancer Association Consortium. PLoS ONE, 2011, 6, e20703.	2.5	21
170	Human iPSC-derived fallopian tube organoids with BRCA1 mutation recapitulate early-stage carcinogenesis. Cell Reports, 2021, 37, 110146.	6.4	21
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