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	MCM3 is a novel proliferation marker associated with longer survival for patients with tubo-ovarian high-grade serous carcinoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2022, 480, 855-871.	1.4	8
2	Functional analysis of the 1p34.3 risk locus implicates GNL2 in high-grade serous ovarian cancer. American Journal of Human Genetics, 2022, 109, 116-135.	2.6	3
3	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
4	Validated biomarker assays confirm that <scp>ARID1A</scp> loss is confounded with <scp>MMR</scp> deficiency, <scp>CD8⁺ TIL</scp> infiltration, and provides no independent prognostic value in endometriosisâ€associated ovarian carcinomas. Journal of Pathology, 2022, 256, 388-401.	2.1	15
5	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. Cell Reports Medicine, 2022, 3, 100542.	3.3	26
6	Molecular Subclasses of Clear Cell Ovarian Carcinoma and Their Impact on Disease Behavior and Outcomes. Clinical Cancer Research, 2022, 28, 4947-4956.	3.2	22
7	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.	1.5	26
8	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
9	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube. Cell Reports, 2021, 35, 108978.	2.9	48
10	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. Human Genetics and Genomics Advances, 2021, 2, 100042.	1.0	6
11	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	1.1	16
12	Risks and Function of Breast Cancer Susceptibility Alleles. Cancers, 2021, 13, 3953.	1.7	8
13	Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123.	4.7	30
14	Human iPSC-derived fallopian tube organoids with BRCA1 mutation recapitulate early-stage carcinogenesis. Cell Reports, 2021, 37, 110146.	2.9	21
15	Master transcription factors form interconnected circuitry and orchestrate transcriptional networks in oesophageal adenocarcinoma. Gut, 2020, 69, 630-640.	6.1	68
16	Identification of novel epithelial ovarian cancer loci in women of African ancestry. International Journal of Cancer, 2020, 146, 2987-2998.	2.3	18
17	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. American Journal of Human Genetics, 2020, 107, 622-635.	2.6	14
18	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	9.4	174

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19	Rare Germline Genetic Variants and the Risks of Epithelial Ovarian Cancer. Cancers, 2020, 12, 3046.	1.7	22
20	Offspring sex and risk of epithelial ovarian cancer: a multinational pooled analysis of 12 caseâ€“control studies. European Journal of Epidemiology, 2020, 35, 1025-1042.	2.5	2
21	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
22	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	3.2	43
23	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.	2.9	35
24	Menopausal hormone therapy prior to the diagnosis of ovarian cancer is associated with improved survival. Gynecologic Oncology, 2020, 158, 702-709.	0.6	15
25	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
26	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. Journal of the National Cancer Institute, 2020, 112, 1242-1250.	3.0	106
27	Lineage-Specific Epigenomic and Genomic Activation of Oncogene HNF4A Promotes Gastrointestinal Adenocarcinomas. Cancer Research, 2020, 80, 2722-2736.	0.4	37
28	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. Nature Communications, 2020, 11, 2020.	5.8	52
29	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.	0.4	49
30	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. IScience, 2019, 17, 242-255.	1.9	60
31	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. BMC Genomics, 2019, 20, 745.	1.2	40
32	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
33	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.	2.9	54
34	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. Cancer Medicine, 2019, 8, 2503-2513.	1.3	6
35	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.	9.4	89
36	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. Gynecologic Oncology, 2019, 153, 343-355.	0.6	28

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37	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. Cell Reports, 2019, 29, 3726-3735.e4.	2.9	39
38	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. Human Molecular Genetics, 2019, 28, 1331-1342.	1.4	19
39	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.4	22
40	A comprehensive geneâ€“environment interaction analysis in Ovarian Cancer using genomeâ€wide significant common variants. International Journal of Cancer, 2019, 144, 2192-2205.	2.3	12
41	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129.	2.9	15
42	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
43	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2018, 47, 450-459.	0.9	15
44	Robust Tests for Additive Gene-Environment Interaction in Case-Control Studies Using Gene-Environment Independence. American Journal of Epidemiology, 2018, 187, 366-377.	1.6	8
45	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 395-404.	1.1	33
46	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079.	5.8	121
47	Evaluation of polygenic risk scores for ovarian cancer risk prediction in a prospective cohort study. Journal of Medical Genetics, 2018, 55, 546-554.	1.5	38
48	Transcriptomic Characterization of Endometrioid, Clear Cell, and High-Grade Serous Epithelial Ovarian Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1101-1109.	1.1	26
49	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.	1.3	70
50	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.	0.4	54
51	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
52	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	1.8	3
53	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	2.9	23
54	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.	2.3	25

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55	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.	3.2	42
56	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
57	Use of common analgesic medications and ovarian cancer survival: results from a pooled analysis in the Ovarian Cancer Association Consortium. British Journal of Cancer, 2017, 116, 1223-1228.	2.9	13
58	Integration of Population-Level Genotype Data with Functional Annotation Reveals Over-Representation of Long Noncoding RNAs at Ovarian Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 116-125.	1.1	6
59	Genetic epidemiology of ovarian cancer and prospects for polygenic risk prediction. Gynecologic Oncology, 2017, 147, 705-713.	0.6	69
60	History of Comorbidities and Survival of Ovarian Cancer Patients, Results from the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1470-1473.	1.1	10
61	An integrative approach to assess Xâ€chromosome inactivation using alleleâ€specific expression with applications to epithelial ovarian cancer. Genetic Epidemiology, 2017, 41, 898-914.	0.6	16
62	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. Breast Cancer Research and Treatment, 2017, 161, 117-134.	1.1	18
63	No Evidence That Genetic Variation in the Myeloid-Derived Suppressor Cell Pathway Influences Ovarian Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 420-424.	1.1	3
64	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
65	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.	0.8	43
66	Characterization of fusion genes in common and rare epithelial ovarian cancer histologic subtypes. Oncotarget, 2017, 8, 46891-46899.	0.8	22
67	The PAX8 cistrome in epithelial ovarian cancer. Oncotarget, 2017, 8, 108316-108332.	0.8	38
68	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	0.9	71
69	Association Between Menopausal Estrogen-Only Therapy and Ovarian Carcinoma Risk. Obstetrics and Gynecology, 2016, 127, 828-836.	1.2	39
70	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	1.4	17
71	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	1.8	19
72	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.	0.4	208

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73	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	0.9	111
74	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	2.3	43
75	A splicing variant of TERT identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. International Journal of Cancer, 2016, 139, 2646-2654.	2.3	7
76	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
77	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
78	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
79	Assessment of Multifactor Geneâ€“Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 780-790.	1.1	10
80	PPM1DMosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. Journal of the National Cancer Institute, 2016, 108, djv347.	3.0	43
81	The association between socioeconomic status and tumour stage at diagnosis of ovarian cancer: A pooled analysis of 18 case-control studies. Cancer Epidemiology, 2016, 41, 71-79.	0.8	20
82	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
83	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	1.1	9
84	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77
85	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
86	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	0.8	5
87	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	0.8	13
88	HNF1B variants associate with promoter methylation and regulate gene networks activated in prostate and ovarian cancer. Oncotarget, 2016, 7, 74734-74746.	0.8	38
89	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
90	Identification of novel candidate biomarkers of epithelial ovarian cancer by profiling the secretomes of threeâ€dimensional genetic models of ovarian carcinogenesis. International Journal of Cancer, 2015, 137, 1806-1817.	2.3	20

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91	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
92	Molecular Analysis of Mixed Endometrioid and Serous Adenocarcinoma of the Endometrium. PLoS ONE, 2015, 10, e0130909.	1.1	23
93	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
94	Germline Mutation in BRCA1 or BRCA2 and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	3.2	138
95	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
96	PAX8 expression in ovarian surface epithelial cells. Human Pathology, 2015, 46, 948-956.	1.1	36
97	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.	1.1	28
98	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.	3.2	33
99	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
100	NPPB is a novel candidate biomarker expressed by cancerâ€associated fibroblasts in epithelial ovarian cancer. International Journal of Cancer, 2015, 136, 1390-1401.	2.3	24
101	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
102	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24
103	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. Nature Medicine, 2015, 21, 1357-1363.	15.2	90
104	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
105	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.	0.8	266
106	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. Journal of the National Cancer Institute, 2015, 107, .	3.0	311
107	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
108	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.	0.8	98

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109	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
110	Variation in NF-Î²B Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1421-1427.	1.1	13
111	Src as a novel therapeutic target for endometriosis. Gynecologic Oncology, 2014, 135, 100-107.	0.6	8
112	Risk of Ovarian Cancer and the NF-Î²B Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.4	48
113	Large-Scale Evaluation of Common Variation in Regulatory T Cellâ€“Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	1.6	21
114	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	1.8	23
115	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.	1.4	112
116	Kernel canonical correlation analysis for assessing geneâ€“gene interactions and application to ovarian cancer. European Journal of Human Genetics, 2014, 22, 126-131.	1.4	33
117	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. Human Molecular Genetics, 2014, 23, 5294-5302.	1.4	71
118	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	5.1	335
119	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
120	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.	9.4	493
121	In vitro three-dimensional modeling of fallopian tube secretory epithelial cells. BMC Cell Biology, 2013, 14, 43.	3.0	40
122	Cigarette smoking and risk of ovarian cancer: a pooled analysis of 21 caseâ€“control studies. Cancer Causes and Control, 2013, 24, 989-1004.	0.8	84
123	The sex hormone system in carriers of BRCA1/2 mutations: a case-control study. Lancet Oncology, The, 2013, 14, 1226-1232.	5.1	98
124	Biomarker-Based Ovarian Carcinoma Typing: A Histologic Investigation in the Ovarian Tumor Tissue Analysis Consortium. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1677-1686.	1.1	70
125	Combined and Interactive Effects of Environmental and GWAS-Identified Risk Factors in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 880-890.	1.1	54
126	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. Endocrine-Related Cancer, 2013, 20, 251-262.	1.6	169

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127	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
128	Analysis of Over 10,000 Cases Finds No Association between Previously Reported Candidate Polymorphisms and Ovarian Cancer Outcome. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 987-992.	1.1	20
129	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	5.8	98
130	Inherited Variants in Regulatory T Cell Genes and Outcome of Ovarian Cancer. PLoS ONE, 2013, 8, e53903.	1.1	20
131	Gene Set Analysis of Survival Following Ovarian Cancer Implicates Macrolide Binding and Intracellular Signaling Genes. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 529-536.	1.1	7
132	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.	1.1	101
133	Ovarian Cancer Risk Associated with Inherited Inflammation-Related Variants. Cancer Research, 2012, 72, 1064-1069.	0.4	45
134	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.	1.1	47
135	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.	1.1	513
136	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. Twin Research and Human Genetics, 2012, 15, 615-623.	0.3	8
137	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.	3.8	546
138	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.	5.1	753
139	ABO blood group and risk of epithelial ovarian cancer within the Ovarian Cancer Association Consortium. Cancer Causes and Control, 2012, 23, 1805-1810.	0.8	35
140	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.	2.2	78
141	Ovarian cancer susceptibility alleles and risk of ovarian cancer inBRCA1andBRCA2mutation carriers. Human Mutation, 2012, 33, 690-702.	1.1	34
142	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. Fertility and Sterility, 2011, 95, 40-45.	0.5	20
143	Recruitment of newly diagnosed ovarian cancer patients proved challenging in a multicentre biobanking study. Journal of Clinical Epidemiology, 2011, 64, 525-530.	2.4	30
144	Principles for the post-GWAS functional characterisation of risk loci. Nature Precedings, 2011, , .	0.1	0

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145	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. PLoS ONE, 2011, 6, e24987.	1.1	48
146	Principles for the post-GWAS functional characterization of cancer risk loci. Nature Genetics, 2011, 43, 513-518.	9.4	392
147	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.	2.3	49
148	Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. International Journal of Cancer, 2011, 128, 2063-2074.	2.3	54
149	Genetic variation in insulin-like growth factor 2 may play a role in ovarian cancer risk. Human Molecular Genetics, 2011, 20, 2263-2272.	1.4	22
150	Prostate Cancer Susceptibility Polymorphism rs2660753 Is Not Associated with Invasive Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1028-1031.	1.1	0
151	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	3.2	47
152	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.4	75
153	Modelling genetic and clinical heterogeneity in epithelial ovarian cancers. Carcinogenesis, 2011, 32, 1540-1549.	1.3	36
154	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.	1.4	32
155	MicroRNA Processing and Binding Site Polymorphisms Are Not Replicated in the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1793-1797.	1.1	19
156	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.	3.0	40
157	Polymorphisms in Stromal Genes and Susceptibility to Serous Epithelial Ovarian Cancer: A Report from the Ovarian Cancer Association Consortium. PLoS ONE, 2011, 6, e19642.	1.1	5
158	Estrogen Receptor Beta rs1271572 Polymorphism and Invasive Ovarian Carcinoma Risk: Pooled Analysis within the Ovarian Cancer Association Consortium. PLoS ONE, 2011, 6, e20703.	1.1	21
159	Vascular endothelial growth factor gene polymorphisms and ovarian cancer survival. Gynecologic Oncology, 2010, 119, 479-483.	0.6	26
160	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	9.4	235
161	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	9.4	321
162	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.	9.4	309

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163	Principles for the post-GWAS functional characterisation of risk loci. Nature Precedings, 2010, , .	0.1	1
164	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.	1.1	23
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