Susan J Ramus

List of Publications by Year
in descending order

228 papers	16,987 citations	14655 66 h-index	18647 119 g-index
244 all docs	244 docs citations	244 times ranked	20611 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	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
5	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
6	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
7	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	10.7	335
8	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
9	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
10	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
11	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
12	Multiple Loci With Different Cancer Specificities Within the 8q24 Gene Desert. Journal of the National Cancer Institute, 2008, 100, 962-966.	6.3	306
13	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. PLoS ONE, 2009, 4, e8274.	2.5	291
14	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
15	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	1.6	270
16	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
17	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
18	Dose-Response Association of CD8⁺ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. JAMA Oncology, 2017, 3, e173290.	7.1	260

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19	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	3.5	244
20	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2017, 109, .	6.3	242
21	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
22	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	2.5	224
23	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
24	Aspirin, Nonaspirin Nonsteroidal Anti-inflammatory Drug, and Acetaminophen Use and Risk of Invasive Epithelial Ovarian Cancer: A Pooled Analysis in the Ovarian Cancer Association Consortium. Journal of the National Cancer Institute, 2014, 106, djt431-djt431.	6.3	186
25	An Immunohistochemical Algorithm for Ovarian Carcinoma Typing. International Journal of Gynecological Pathology, 2016, 35, 430-441.	1.4	180
26	The Contribution of BRCA1 and BRCA2 to Ovarian Cancer. Molecular Oncology, 2009, 3, 138-150.	4.6	178
27	Common Breast Cancer Susceptibility Alleles and the Risk of Breast Cancer for BRCA1 and BRCA2 Mutation Carriers: Implications for Risk Prediction. Cancer Research, 2010, 70, 9742-9754.	0.9	169
28	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. Endocrine-Related Cancer, 2013, 20, 251-262.	3.1	169
29	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
30	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
31	Oral contraceptive use and ovarian cancer risk among carriers of BRCA1 or BRCA2 mutations. British Journal of Cancer, 2004, 91, 1911-1915.	6.4	138
32	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
33	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
34	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
35	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
36	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

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37	Genetic intra-tumour heterogeneity in epithelial ovarian cancer and its implications for molecular diagnosis of tumours. Journal of Pathology, 2007, 211, 286-295.	4.5	108
38	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
39	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
40	The sex hormone system in carriers of BRCA1/2 mutations: a case-control study. Lancet Oncology, The, 2013, 14, 1226-1232.	10.7	98
41	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
42	Candidate tumor-suppressor genes on chromosome arm 8p in early-onset and high-grade breast cancers. Oncogene, 2004, 23, 5697-5702.	5.9	97
43	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
44	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	1.6	90
45	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	5.0	88
46	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
47	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	3.5	85
48	Frequent loss of BRCA1 mRNA and protein expression in sporadic ovarian cancers. International Journal of Cancer, 2000, 87, 317-321.	5.1	84
49	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
50	Histopathology of familial ovarian tumors in women from families with and without germline BRCA1 mutations. Human Pathology, 2000, 31, 1420-1424.	2.0	82
51	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	2.4	82
52	Efficient molecular subtype classification of highâ€grade serous ovarian cancer. Journal of Pathology, 2015, 236, 272-277.	4.5	81
53	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
54	Genome-wide significant risk associations for mucinous ovarian carcinoma. Nature Genetics, 2015, 47, 888-897.	21.4	78

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55	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
56	Assessing the usefulness of a novel MRI-based breast density estimation algorithm in a cohort of women at high genetic risk of breast cancer: the UK MARIBS study. Breast Cancer Research, 2009, 11, R80.	5.0	77
57	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
58	Common origins of MDA-MB-435 cells from various sources with those shown to have melonoma properties. Clinical and Experimental Metastasis, 2004, 21, 543-552.	3.3	76
59	Contribution ofBRCA1andBRCA2mutations to inherited ovarian cancer. Human Mutation, 2007, 28, 1207-1215.	2.5	76
60	Evidence for a time-dependent association between FOLR1 expression and survival from ovarian carcinoma: implications for clinical testing. An Ovarian Tumour Tissue Analysis consortium study. British Journal of Cancer, 2014, 111, 2297-2307.	6.4	76
61	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
62	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.9	75
63	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
64	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388.	5.1	73
65	Common breast cancer susceptibility alleles are associated with tumour subtypes in BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2011, 13, R110.	5.0	71
66	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
67	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
68	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
69	Role of genetic polymorphisms and ovarian cancer susceptibility. Molecular Oncology, 2009, 3, 171-181.	4.6	69
70	Increased frequency ofTP53 mutations inBRCA1 andBRCA2 ovarian tumours. , 1999, 25, 91-96.		68
71	The clonal evolution of metastases from primary serous epithelial ovarian cancers. International Journal of Cancer, 2009, 124, 1579-1586.	5.1	68
72	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68

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73	Common variants in mismatch repair genes and risk of invasive ovarian cancer. Carcinogenesis, 2006, 27, 2235-2242.	2.8	67
74	Association Between Single-Nucleotide Polymorphisms in Hormone Metabolism and DNA Repair Genes and Epithelial Ovarian Cancer: Results from Two Australian Studies and an Additional Validation Set. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 2557-2565.	2.5	65
75	Inhibition of the Nuclear Export Receptor XPO1 as a Therapeutic Target for Platinum-Resistant Ovarian Cancer. Clinical Cancer Research, 2017, 23, 1552-1563.	7.0	65
76	Single Nucleotide Polymorphisms in the TP53 Region and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2009, 69, 2349-2357.	0.9	63
77	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
78	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	5.0	57
79	Tagging Single Nucleotide Polymorphisms in the BRIP1 Gene and Susceptibility to Breast and Ovarian Cancer. PLoS ONE, 2007, 2, e268.	2.5	54
80	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
81	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
82	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
83	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
84	Molecular Classification of Epithelial Ovarian Cancer Based on Methylation Profiling: Evidence for Survival Heterogeneity. Clinical Cancer Research, 2019, 25, 5937-5946.	7.0	50
85	Progesterone receptor variation and risk of ovarian cancer is limited to the invasive endometrioid subtype: results from the ovarian cancer association consortium pooled analysis. British Journal of Cancer, 2008, 98, 282-288.	6.4	49
86	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
87	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
88	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
89	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
90	Risk of Ovarian Cancer and the NF-ÎºB Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.9	48

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91	Validating genetic risk associations for ovarian cancer through the international Ovarian Cancer Association Consortium. British Journal of Cancer, 2009, 100, 412-420.	6.4	47
92	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	7.0	47
93	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
94	Ovarian Cancer Risk Associated with Inherited Inflammation-Related Variants. Cancer Research, 2012, 72, 1064-1069.	0.9	45
95	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
96	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	5.1	43
97	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
98	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
99	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
100	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
101	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	5.0	42
102	Predicting Clinical Outcome in Patients Diagnosed with Synchronous Ovarian and Endometrial Cancer. Clinical Cancer Research, 2008, 14, 5840-5848.	7.0	41
103	Ovarian cancer survival in Ashkenazi Jewish patients with BRCA1 and BRCA2 mutations. European Journal of Surgical Oncology, 2001, 27, 278-281.	1.0	40
104	Morphological predictors of BRCA1 germline mutations in young women with breast cancer. British Journal of Cancer, 2011, 104, 903-909.	6.4	40
105	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
106	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
107	Common Variants in RB1 Gene and Risk of Invasive Ovarian Cancer. Cancer Research, 2006, 66, 10220-10226.	0.9	39
108	Cell cycle genes and ovarian cancer susceptibility: a tagSNP analysis. British Journal of Cancer, 2009, 101, 1461-1468.	6.4	39

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109	Association Between Menopausal Estrogen-Only Therapy and Ovarian Carcinoma Risk. Obstetrics and Gynecology, 2016, 127, 828-836.	2.4	39
110	Microcell-Mediated Chromosome Transfer Identifies EPB41L3 as a Functional Suppressor of Epithelial Ovarian Cancers. Neoplasia, 2010, 12, 579-IN18.	5.3	38
111	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
112	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
113	Candidate Gene Analysis Using Imputed Genotypes: Cell Cycle Single-Nucleotide Polymorphisms and Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 935-944.	2.5	37
114	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	1.0	37
115	Complete mutation detection using unlabeled chemical cleavage. Human Mutation, 1992, 1, 63-69.	2.5	36
116	COMPLEXO: identifying the missing heritability of breast cancer via next generation collaboration. Breast Cancer Research, 2013, 15, 402.	5.0	36
117	Complex CGH alterations on chromosome arm 8p at candidate tumor suppressor gene loci in breast cancer cell lines. Cancer Genetics and Cytogenetics, 2005, 160, 134-140.	1.0	35
118	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
119	Going to extremes: determinants of extraordinary response and survival in patients with cancer. Nature Reviews Cancer, 2019, 19, 339-348.	28.4	35
120	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
121	Simultaneous screening for Î²-thalassemia mutations by chemical cleavage of mismatch. Genomics, 1991, 11, 48-53.	2.9	34
122	Ovarian cancer susceptibility alleles and risk of ovarian cancer inBRCA1andBRCA2mutation carriers. Human Mutation, 2012, 33, 690-702.	2.5	34
123	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
124	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
125	Comprehensive epithelial tubo-ovarian cancer risk prediction model incorporating genetic and epidemiological risk factors. Journal of Medical Genetics, 2022, 59, 632-643.	3.2	33
126	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

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127	The Effects of Common Genetic Variants in Oncogenes on Ovarian Cancer Survival. Clinical Cancer Research, 2008, 14, 5833-5839.	7.0	32
128	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	5.0	31
129	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
130	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. Journal of the National Cancer Institute, 2019, 111, 350-364.	6.3	30
131	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
132	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
133	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
134	Vascular endothelial growth factor gene polymorphisms and ovarian cancer survival. Gynecologic Oncology, 2010, 119, 479-483.	1.4	26
135	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	5.0	26
136	Enhanced GAB2 Expression Is Associated with Improved Survival in High-Grade Serous Ovarian Cancer and Sensitivity to PI3K Inhibition. Molecular Cancer Therapeutics, 2015, 14, 1495-1503.	4.1	26
137	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
138	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
139	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
140	Tagging single-nucleotide polymorphisms in candidate oncogenes and susceptibility to ovarian cancer. British Journal of Cancer, 2009, 100, 993-1001.	6.4	24
141	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
142	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
143	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
144	A Nonsynonymous Polymorphism in IRS1 Modifies Risk of Developing Breast and Ovarian Cancers in BRCA1 and Ovarian Cancer in BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1362-1370.	2.5	23

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145	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23
146	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	6.4	23
147	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
148	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
149	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
150	MyD88 and TLR4 Expression in Epithelial Ovarian Cancer. Mayo Clinic Proceedings, 2018, 93, 307-320.	3.0	22
151	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
152	Rare Germline Genetic Variants and the Risks of Epithelial Ovarian Cancer. Cancers, 2020, 12, 3046.	3.7	22
153	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
154	Refined cut-off for TP53 immunohistochemistry improves prediction of TP53 mutation status in ovarian mucinous tumors: implications for outcome analyses. Modern Pathology, 2021, 34, 194-206.	5.5	21
155	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
156	Mismatch repair gene polymorphisms and survival in invasive ovarian cancer patients. European Journal of Cancer, 2008, 44, 2259-2265.	2.8	20
157	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. Fertility and Sterility, 2011, 95, 40-45.	1.0	20
158	A Kallikrein 15 (KLK15) single nucleotide polymorphism located close to a novel exon shows evidence of association with poor ovarian cancer survival. BMC Cancer, 2011, 11, 119.	2.6	20
159	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.	2.5	20
160	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.	1.9	20
161	Inherited Variants in Regulatory T Cell Genes and Outcome of Ovarian Cancer. PLoS ONE, 2013, 8, e53903.	2.5	20
162	MicroRNA Processing and Binding Site Polymorphisms Are Not Replicated in the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1793-1797.	2.5	19

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163	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
164	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2019, 121, 180-192.	6.4	19
165	BRCA1 promoter deletions in young women with breast cancer and a strong family history: A population-based study. European Journal of Cancer, 2007, 43, 823-827.	2.8	18
166	Polymorphism in theIL18Gene and Epithelial Ovarian Cancer in Non-Hispanic White Women. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 3567-3572.	2.5	18
167	Risk of ovarian cancer in women with first-degree relatives with cancer. Acta Obstetricia Et Gynecologica Scandinavica, 2009, 88, 449-456.	2.8	18
168	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
169	Genotype and Intellectual Phenotype in Untreated Phenylketonuria Patients. Pediatric Research, 1999, 45, 474-481.	2.3	18
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