Ian G Campbell

List of Publications by Year
in descending order

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134 papers	7,867 citations	53660 45 h-index	58464 82 g-index
141 all docs	141 docs citations	141 times ranked	13618 citing authors

#	Article	IF	Citations
1	Mutation of the PIK3CA Gene in Ovarian and Breast Cancer. Cancer Research, 2004, 64, 7678-7681.	0.4	864
2	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
3	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
4	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
5	Dose-Response Association of CD8⁺ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. JAMA Oncology, 2017, 3, e173290.	3.4	260
6	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244
7	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
8	Exome Sequencing Identifies Rare Deleterious Mutations in DNA Repair Genes FANCC and BLM as Potential Breast Cancer Susceptibility Alleles. PLoS Genetics, 2012, 8, e1002894.	1.5	186
9	Monogenic and polygenic determinants of sarcoma risk: an international genetic study. Lancet Oncology, The, 2016, 17, 1261-1271.	5.1	161
10	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
11	Panel Testing for Familial Breast Cancer: Calibrating the Tension Between Research and Clinical Care. Journal of Clinical Oncology, 2016, 34, 1455-1459.	0.8	154
12	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
13	Molecular profiling of low grade serous ovarian tumours identifies novel candidate driver genes. Oncotarget, 2015, 6, 37663-37677.	0.8	142
14	Mutational landscape of mucinous ovarian carcinoma and its neoplastic precursors. Genome Medicine, 2015, 7, 87.	3.6	126
15	Mutational Signature Analysis Reveals NTHL1 Deficiency to Cause a Multi-tumor Phenotype. Cancer Cell, 2019, 35, 256-266.e5.	7.7	123
16	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
17	The molecular origin and taxonomy of mucinous ovarian carcinoma. Nature Communications, 2019, 10, 3935.	5.8	110
18	<scp>RNF43</scp> is a tumour suppressor gene mutated in mucinous tumours of the ovary. Journal of Pathology, 2013, 229, 469-476.	2.1	102

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19	Inferring copy number and genotype in tumour exome data. BMC Genomics, 2014, 15, 732.	1.2	102
20	Genomic Classification of Serous Ovarian Cancer with Adjacent Borderline Differentiates RAS Pathway and TP53-Mutant Tumors and Identifies NRAS as an Oncogenic Driver. Clinical Cancer Research, 2014, 20, 6618-6630.	3.2	96
21	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
22	FANCMc.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. Human Molecular Genetics, 2015, 24, 5345-5355.	1.4	91
23	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
24	Methylenetetrahydrofolate reductase polymorphism and susceptibility to breast cancer. Breast Cancer Research, 2002, 4, R14.	2.2	89
25	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
26	Loss of heterozygosity: what is it good for?. BMC Medical Genomics, 2015, 8, 45.	0.7	85
27	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.	1.1	82
28	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
29	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
30	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
31	Clonal Mutations in the Cancer-Associated Fibroblasts: The Case against Genetic Coevolution. Cancer Research, 2009, 69, 6765-6769.	0.4	70
32	No association of the MDM2 SNP309 polymorphism with risk of breast or ovarian cancer. Cancer Letters, 2006, 240, 195-197.	3.2	68
33	Analysis of RAD51C germline mutations in high-risk breast and ovarian cancer families and ovarian cancer patients. Human Mutation, 2012, 33, 95-99.	1.1	64
34	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
35	Relationship of the Breast Ductal Carcinoma In Situ Immune Microenvironment with Clinicopathological and Genetic Features. Clinical Cancer Research, 2017, 23, 5210-5217.	3.2	61
36	Identification of copy number alterations associated with the progression of DCIS to invasive ductal carcinoma. Breast Cancer Research and Treatment, 2012, 133, 889-898.	1.1	60

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37	Pre-Invasive Ovarian Mucinous Tumors Are Characterized by CDKN2A and RAS Pathway Aberrations. Clinical Cancer Research, 2012, 18, 5267-5277.	3.2	57
38	Are there any more ovarian tumor suppressor genes? A new perspective using ultra highâ€resolution copy number and loss of heterozygosity analysis. Genes Chromosomes and Cancer, 2009, 48, 931-942.	1.5	56
39	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
40	Genomic analysis of lowâ€grade serous ovarian carcinoma to identify key drivers and therapeutic vulnerabilities. Journal of Pathology, 2021, 253, 41-54.	2.1	54
41	Whole genome SNP arrays using DNA derived from formalin-fixed, paraffin-embedded ovarian tumor tissue. Human Mutation, 2005, 26, 384-389.	1.1	52
42	Breast ductal carcinoma in situ carry mutational driver events representative of invasive breast cancer. Modern Pathology, 2017, 30, 952-963.	2.9	50
43	Rare variants in XRCC2 as breast cancer susceptibility alleles: TableÂ1. Journal of Medical Genetics, 2012, 49, 618-620.	1.5	49
44	Therapeutic options for mucinous ovarian carcinoma. Gynecologic Oncology, 2020, 156, 552-560.	0.6	49
45	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
46	Molecular analysis of PALB2â€associated breast cancers. Journal of Pathology, 2018, 245, 53-60.	2.1	46
47	Population-based genetic testing of asymptomatic women for breast and ovarian cancer susceptibility. Genetics in Medicine, 2019, 21, 913-922.	1.1	45
48	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
49	Copy number analysis of ductal carcinoma in situ with and without recurrence. Modern Pathology, 2015, 28, 1174-1184.	2.9	40
50	Compromized DNA repair as a basis for identification of cancer radiotherapy patients with extreme radiosensitivity. Cancer Letters, 2016, 383, 212-219.	3.2	39
51	Copy number analysis by low coverage whole genome sequencing using ultra low-input DNA from formalin-fixed paraffin embedded tumor tissue. Genome Medicine, 2016, 8, 121.	3.6	39
52	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
53	Atypical ductal hyperplasia: update on diagnosis, management, and molecular landscape. Breast Cancer Research, 2018, 20, 39.	2.2	38
54	COMPLEXO: identifying the missing heritability of breast cancer via next generation collaboration. Breast Cancer Research, 2013, 15, 402.	2.2	36

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55	Prevalence of PALB2 mutations in Australian familial breast cancer cases and controls. Breast Cancer Research, 2015, 17, 111.	2.2	36
56	Mutational Landscape of Ovarian Adult Granulosa Cell Tumors from Whole Exome and Targeted TERT Promoter Sequencing. Molecular Cancer Research, 2019, 17, 177-185.	1.5	36
57	A simple consensus approach improves somatic mutation prediction accuracy. Genome Medicine, 2013, 5, 90.	3.6	33
58	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
59	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
60	Largeâ€scale genomic analysis of ovarian carcinomas. Molecular Oncology, 2009, 3, 157-164.	2.1	31
61	Genetic changes in tumour microenvironments. Journal of Pathology, 2011, 223, 450-458.	2.1	31
62	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.	2.2	31
63	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
64	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
65	MicroRNA Genes and Their Target 3â€²-Untranslated Regions Are Infrequently Somatically Mutated in Ovarian Cancers. PLoS ONE, 2012, 7, e35805.	1.1	27
66	Genetic analysis of benign ovarian tumors. International Journal of Cancer, 2003, 105, 499-505.	2.3	26
67	Reevaluation of the BRCA2 truncating allele c.9976Aâ€‰>â€‰T (p.Lys3326Ter) in a familial breast cancer context. Scientific Reports, 2015, 5, 14800.	1.6	26
68	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.	1.9	26
69	â€œA Natural Progressionâ€: Australian Women's Attitudes About an Individualized Breast Screening Model. Cancer Prevention Research, 2019, 12, 383-390.	0.7	26
70	Combined Tumor Sequencing and Case-Control Analyses of RAD51C in Breast Cancer. Journal of the National Cancer Institute, 2019, 111, 1332-1338.	3.0	26
71	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
72	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

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73	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24
74	Exome sequencing of familial high-grade serous ovarian carcinoma reveals heterogeneity for rare candidate susceptibility genes. Nature Communications, 2020, 11, 1640.	5.8	24
75	BARD1 variants are not associated with breast cancer risk in Australian familial breast cancer. Breast Cancer Research and Treatment, 2008, 111, 505-509.	1.1	23
76	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	2.9	23
77	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
78	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
79	MyD88 and TLR4 Expression in Epithelial Ovarian Cancer. Mayo Clinic Proceedings, 2018, 93, 307-320.	1.4	22
80	Prospective validation of the NCI Breast Cancer Risk Assessment Tool (Gail Model) on 40,000 Australian women. Breast Cancer Research, 2018, 20, 155.	2.2	22
81	Atypical ductal hyperplasia is a multipotent precursor of breast carcinoma. Journal of Pathology, 2019, 248, 326-338.	2.1	21
82	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.	2.9	21
83	Evaluating the breast cancer predisposition role of rare variants in genes associated with low-penetrance breast cancer risk SNPs. Breast Cancer Research, 2018, 20, 3.	2.2	19
84	Mutations in RECQL are not associated with breast cancer risk in an Australian population. Nature Genetics, 2018, 50, 1346-1348.	9.4	19
85	The genetic architecture of breast papillary lesions as a predictor of progression to carcinoma. Npj Breast Cancer, 2020, 6, 9.	2.3	19
86	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
87	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
88	Low-grade fibromatosis-like spindle cell carcinomas of the breast are molecularly exiguous. Journal of Clinical Pathology, 2015, 68, 362-367.	1.0	18
89	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
90	Mutation of the ST7 tumor suppressor gene on 7q31.1 is rare in breast, ovarian and colorectal cancers. Nature Genetics, 2001, 29, 379-380.	9.4	17

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91	Bioinformatics Pipelines for Targeted Resequencing and Whole-Exome Sequencing of Human and Mouse Genomes: A Virtual Appliance Approach for Instant Deployment. PLoS ONE, 2014, 9, e95217.	1.1	17
92	Refinement of an ovarian cancer tumour suppressor gene locus on chromosome arm 22q and mutation analysis ofCYP2D6,SREBP2 andNAGA. International Journal of Cancer, 2000, 87, 798-802.	2.3	16
93	Reevaluation of RINT1 as a breast cancer predisposition gene. Breast Cancer Research and Treatment, 2016, 159, 385-392.	1.1	16
94	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	0.6	15
95	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
96	Molecular comparison of interval and screenâ€detected breast cancers. Journal of Pathology, 2019, 248, 243-252.	2.1	15
97	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
98	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
99	Assessment of DNA methylation profiling and copy number variation as indications of clonal relationship in ipsilateral and contralateral breast cancers to distinguish recurrent breast cancer from a second primary tumour. BMC Cancer, 2015, 15, 669.	1.1	14
100	Genetic and epigenetic analysis of the TIMP-3 gene in ovarian cancer. Cancer Letters, 2007, 247, 91-97.	3.2	13
101	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
102	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
103	Genetic and Epigenetic Analysis of the Putative Tumor Suppressor km23 in Primary Ovarian, Breast, and Colorectal Cancers. Clinical Cancer Research, 2006, 12, 3713-3715.	3.2	12
104	Investigation of monogenic causes of familial breast cancer: data from the BEACCON case-control study. Npj Breast Cancer, 2021, 7, 76.	2.3	12
105	A functionally impaired missense variant identified in French Canadian families implicates FANCI as a candidate ovarian cancer-predisposing gene. Genome Medicine, 2021, 13, 186.	3.6	12
106	No germline mutations in the histone acetyltransferase gene EP300 in BRCA1 and BRCA2 negative families with breast cancer and gastric, pancreatic, or colorectal cancer. Breast Cancer Research, 2004, 6, R366-71.	2.2	9
107	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
108	Prohibitin 3' untranslated region polymorphism and breast cancer risk. Cancer Epidemiology Biomarkers and Prevention, 2003, 12, 1273-4.	1.1	9

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109	Molecular characterization of low-grade serous ovarian carcinoma identifies genomic aberrations according to hormone receptor expression. Npj Precision Oncology, 2022, 6, .	2.3	9
110	Highâ€resolution copy number arrays in cancer and the problem of normal genome copy number variation. Genes Chromosomes and Cancer, 2008, 47, 933-938.	1.5	7
111	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. Npj Breast Cancer, 2021, 7, 52.	2.3	7
112	Analysis of KLLN as a high-penetrance breast cancer predisposition gene. Breast Cancer Research and Treatment, 2012, 134, 543-547.	1.1	6
113	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
114	Primary mucinous ovarian neoplasms rarely show germ cell histogenesis. Histopathology, 2021, 78, 640-642.	1.6	6
115	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
116	Estimating the proportion of pathogenic variants from breast cancer caseâ€“control data: Application to calibration of ACMG/AMP variant classification criteria. Human Mutation, 2022, 43, 882-888.	1.1	6
117	Appraisal of the technologies and review of the genomic landscape of ductal carcinoma in situ of the breast. Breast Cancer Research, 2015, 17, 80.	2.2	5
118	Germline whole exome sequencing of a family with appendiceal mucinous tumours presenting with pseudomyxoma peritonei. BMC Cancer, 2020, 20, 369.	1.1	5
119	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
120	Discussion: Ovarian Cancer Prevention. Gynecologic Oncology, 2003, 88, S67-S70.	0.6	4
121	Searching for candidate genes in familial BRCAX mutation carriers with prostate cancer. Urologic Oncology: Seminars and Original Investigations, 2016, 34, 120.e9-120.e16.	0.8	4
122	The TP53 mutation rate differs in breast cancers that arise in women with high or low mammographic density. Npj Breast Cancer, 2020, 6, 34.	2.3	4
123	Breast cancer risk and the BRCA1 interacting protein CTIP. Breast Cancer Research and Treatment, 2008, 112, 351-352.	1.1	3
124	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
125	Genomic Aberrations of BRCA1-Mutated Fallopian Tube Carcinomas. American Journal of Pathology, 2014, 184, 1871-1876.	1.9	2
126	Evaluation of two population screening programmes for BRCA1/2 founder mutations in the Australian Jewish community: a protocol paper. BMJ Open, 2021, 11, e041186.	0.8	2

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127	Development and pilot testing of an online decision aid for women considering risk-stratified breast screening. Journal of Community Genetics, 2022, 13, 137-141.	0.5	2
128	The Clinical and Psychosocial Outcomes for Women Who Received Unexpected Clinically Actionable Germline Information Identified through Research: An Exploratory Sequential Mixed-Methods Comparative Study. Journal of Personalized Medicine, 2022, 12, 1112.	1.1	2
129	Pharmacogenomics and functional imaging to predict irinotecan pharmacokinetics and pharmacodynamics: the predict IR study. Cancer Chemotherapy and Pharmacology, 2021, 88, 39-52.	1.1	1
130	Evaluation of pharmacogenomics and hepatic nuclear imagingâ€“related covariates by population pharmacokinetic models of irinotecan and its metabolites. European Journal of Clinical Pharmacology, 2021, , 1.	0.8	1
131	Contribution of large genomic rearrangements inPALB2to familial breast cancer: implications for genetic testing. Journal of Medical Genetics, 2023, 60, 112-118.	1.5	1
132	Unselected Women's Experiences of Receiving Genetic Research Results for Hereditary Breast and Ovarian Cancer: A Qualitative Study. Genetic Testing and Molecular Biomarkers, 2021, 25, 741-748.	0.3	1
133	Genomic Analysis. , 2016, , 83-106.		0
134	Integration of tumour sequencing and caseâ€“control data to assess pathogenicity of RAD51C missense variants in familial breast cancer. Npj Breast Cancer, 2022, 8, 10.	2.3	0