Ian G Campbell

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

131 papers	5,587 citations	39 h-index	71 g-index
141 ext. papers	6,906 ext. citations	9 avg, IF	4.67 L-index

#	Paper	IF	Citations
131	Integration of tumour sequencing and case-control data to assess pathogenicity of RAD51C missense variants in familial breast cancer.. *Npj Breast Cancer*, **2022**, 8, 10	7.8	
130	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
129	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3
128	Development and pilot testing of an online decision aid for women considering risk-stratified breast screening.. *Journal of Community Genetics*, **2022**, 13, 137	2.5	0
127	Validated biomarker assays confirm ARID1A loss is confounded with MMR deficiency, CD8 TIL infiltration, and provides no independent prognostic value in endometriosis-associated ovarian carcinomas.. *Journal of Pathology*, **2021**,	9.4	3
126	Pharmacogenomics and functional imaging to predict irinotecan pharmacokinetics and pharmacodynamics: the predict IR study. *Cancer Chemotherapy and Pharmacology*, **2021**, 88, 39-52	3.5	
125	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	7.8	2
124	Evaluation of two population screening programmes for founder mutations in the Australian Jewish community: a protocol paper. *BMJ Open*, **2021**, 11, e041186	3	1
123	Investigation of monogenic causes of familial breast cancer: data from the BEACCON case-control study. *Npj Breast Cancer*, **2021**, 7, 76	7.8	3
122	Population-based targeted sequencing of 54 candidate genes identifies as a susceptibility gene for high-grade serous ovarian cancer. *Journal of Medical Genetics*, **2021**, 58, 305-313	5.8	12
121	Primary mucinous ovarian neoplasms rarely show germ cell histogenesis. *Histopathology*, **2021**, 78, 640-643	7.3	2
120	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	9.8	6
119	Genomic analysis of low-grade serous ovarian carcinoma to identify key drivers and therapeutic vulnerabilities. *Journal of Pathology*, **2021**, 253, 41-54	9.4	15
118	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. *Nature Communications*, **2021**, 12, 1078	17.4	4
117	Breast and Prostate Cancer Risks for Male BRCA1 and BRCA2 Pathogenic Variant Carriers Using Polygenic Risk Scores. *Journal of the National Cancer Institute*, **2021**,	9.7	3
116	Evaluation of pharmacogenomics and hepatic nuclear imaging-related covariates by population pharmacokinetic models of irinotecan and its metabolites. *European Journal of Clinical Pharmacology*, **2021**, 1	2.8	0
115	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	1.6	0

114	A functionally impaired missense variant identified in French Canadian families implicates FANCI as a candidate ovarian cancer-predisposing gene. *Genome Medicine*, **2021**, 13, 186	14.4	2
113	Germline whole exome sequencing of a family with appendiceal mucinous tumours presenting with pseudomyxoma peritonei. *BMC Cancer*, **2020**, 20, 369	4.8	2
112	The genetic architecture of breast papillary lesions as a predictor of progression to carcinoma. *Npj Breast Cancer*, **2020**, 6, 9	7.8	13
111	Characterization of the Cancer Spectrum in Men With Germline BRCA1 and BRCA2 Pathogenic Variants: Results From the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). *JAMA Oncology*, **2020**, 6, 1218-1230	13.4	25
110	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
109	Exome sequencing of familial high-grade serous ovarian carcinoma reveals heterogeneity for rare candidate susceptibility genes. *Nature Communications*, **2020**, 11, 1640	17.4	10
108	Association of Genomic Domains in and with Prostate Cancer Risk and Aggressiveness. *Cancer Research*, **2020**, 80, 624-638	10.1	22
107	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
106	Therapeutic options for mucinous ovarian carcinoma. *Gynecologic Oncology*, **2020**, 156, 552-560	4.9	21
105	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	8.1	34
104	The TP53 mutation rate differs in breast cancers that arise in women with high or low mammographic density. *Npj Breast Cancer*, **2020**, 6, 34	7.8	1
103	The molecular origin and taxonomy of mucinous ovarian carcinoma. *Nature Communications*, **2019**, 10, 3935	17.4	59
102	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019** , 10, 431	17.4	45
101	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	9.8	21
100	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	4.8	4
99	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
98	"A Natural Progression": Australian Women's Attitudes About an Individualized Breast Screening Model. *Cancer Prevention Research*, **2019**, 12, 383-390	3.2	10
97	Atypical ductal hyperplasia is a multipotent precursor of breast carcinoma. *Journal of Pathology*, **2019**, 248, 326-338	9.4	12

96	Combined Tumor Sequencing and Case-Control Analyses of RAD51C in Breast Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 1332-1338	9.7	16
95	Molecular comparison of interval and screen-detected breast cancers. *Journal of Pathology*, **2019**, 248, 243-252	9.4	8
94	Mutational Signature Analysis Reveals NTHL1 Deficiency to Cause a Multi-tumor Phenotype. *Cancer Cell*, **2019**, 35, 256-266.e5	24.3	72
93	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *Npj Breast Cancer*, **2019**, 5, 38	7.8	12
92	Mutational Landscape of Ovarian Adult Granulosa Cell Tumors from Whole Exome and Targeted Promoter Sequencing. *Molecular Cancer Research*, **2019**, 17, 177-185	6.6	18
91	Population-based genetic testing of asymptomatic women for breast and ovarian cancer susceptibility. *Genetics in Medicine*, **2019**, 21, 913-922	8.1	26
90	MyD88 and TLR4 Expression in Epithelial Ovarian Cancer. *Mayo Clinic Proceedings*, **2018**, 93, 307-320	6.4	14
89	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. *British Journal of Cancer*, **2018**, 118, 1123-1129	8.7	10
88	Molecular analysis of PALB2-associated breast cancers. *Journal of Pathology*, **2018**, 245, 53-60	9.4	22
87	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	8.3	11
86	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. *PLoS ONE*, **2018**, 13, e0197561	3.7	9
85	Atypical ductal hyperplasia: update on diagnosis, management, and molecular landscape. *Breast Cancer Research*, **2018**, 20, 39	8.3	21
84	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	3
83	Prospective validation of the NCI Breast Cancer Risk Assessment Tool (Gail Model) on 40,000 Australian women. *Breast Cancer Research*, **2018**, 20, 155	8.3	16
82	Mutations in RECQL are not associated with breast cancer risk in an Australian population. *Nature Genetics*, **2018**, 50, 1346-1348	36.3	12
81	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. *British Journal of Cancer*, **2017**, 116, 524-535	8.7	18
80	Relationship of the Breast Ductal Carcinoma Immune Microenvironment with Clinicopathological and Genetic Features. *Clinical Cancer Research*, **2017**, 23, 5210-5217	12.9	41
79	Breast ductal carcinoma in situ carry mutational driver events representative of invasive breast cancer. *Modern Pathology*, **2017**, 30, 952-963	9.8	37

78	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
77	Dose-Response Association of CD8+ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. *JAMA Oncology*, **2017**, 3, e173290	13.4	152
76	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
75	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	2.2	101
74	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15
73	Reevaluation of RINT1 as a breast cancer predisposition gene. *Breast Cancer Research and Treatment*, **2016**, 159, 385-92	4.4	16
72	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, 1052-67	24.4	104
71	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
70	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	14.4	27
69	Panel Testing for Familial Breast Cancer: Calibrating the Tension Between Research and Clinical Care. *Journal of Clinical Oncology*, **2016**, 34, 1455-9	2.2	125
68	Searching for candidate genes in familial BRCAX mutation carriers with prostate cancer. *Urologic Oncology: Seminars and Original Investigations*, **2016**, 34, 120.e9-16	2.8	3
67	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. *Journal of Medical Genetics*, **2016**, 53, 298-309	5.8	83
66	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	65
65	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. *Oncotarget*, **2016**, 7, 69097-69110	3.3	4
64	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. *Oncotarget*, **2016**, 7, 72381-72394	3.3	11
63	Genomic Analysis **2016**, 83-106		
62	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. *International Journal of Epidemiology*, **2016**, 45, 884-95	7.8	45
61	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	8.3	25

60	Compromized DNA repair as a basis for identification of cancer radiotherapy patients with extreme radiosensitivity. *Cancer Letters*, **2016**, 383, 212-219	9.9	28
59	Monogenic and polygenic determinants of sarcoma risk: an international genetic study. *Lancet Oncology, The*, **2016**, 17, 1261-71	21.7	121
58	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. *Nature Genetics*, **2015**, 47, 164-71	36.3	177
57	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, 1574-84	4	24
56	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. *Clinical Cancer Research*, **2015**, 21, 5264-76	12.9	24
55	FANCM c.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, 5345-55	5.6	68
54	Low-grade fibromatosis-like spindle cell carcinomas of the breast are molecularly exiguous. *Journal of Clinical Pathology*, **2015**, 68, 362-7	3.9	15
53	Evaluating the ovarian cancer gonadotropin hypothesis: a candidate gene study. *Gynecologic Oncology*, **2015**, 136, 542-8	4.9	12
52	Enhanced GAB2 Expression Is Associated with Improved Survival in High-Grade Serous Ovarian Cancer and Sensitivity to PI3K Inhibition. *Molecular Cancer Therapeutics*, **2015**, 14, 1495-503	6.1	13
51	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. *Nature Communications*, **2015**, 6, 8234	17.4	40
50	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. *Carcinogenesis*, **2015**, 36, 1341-53	4.6	20
49	Loss of heterozygosity: what is it good for?. *BMC Medical Genomics*, **2015**, 8, 45	3.7	48
48	Prevalence of PALB2 mutations in Australian familial breast cancer cases and controls. *Breast Cancer Research*, **2015**, 17, 111	8.3	26
47	Copy number analysis of ductal carcinoma in situ with and without recurrence. *Modern Pathology*, **2015**, 28, 1174-84	9.8	28
46	Appraisal of the technologies and review of the genomic landscape of ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2015**, 17, 80	8.3	5
45	Reevaluation of the BRCA2 truncating allele c.9976A > T (p.Lys3326Ter) in a familial breast cancer context. *Scientific Reports*, **2015**, 5, 14800	4.9	21
44	Mutational landscape of mucinous ovarian carcinoma and its neoplastic precursors. *Genome Medicine*, **2015**, 7, 87	14.4	100
43	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	4.8	11

42	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. *Genetic Epidemiology*, **2015**, 39, 689-97	2.6	18
41	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. *PLoS ONE*, **2015**, 10, e0128106	3.7	15
40	Molecular profiling of low grade serous ovarian tumours identifies novel candidate driver genes. *Oncotarget*, **2015**, 6, 37663-77	3.3	98
39	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). *Journal of Genetics and Genome Research*, **2015**, 2,		22
38	Genomic aberrations of BRCA1-mutated fallopian tube carcinomas. *American Journal of Pathology*, **2014**, 184, 1871-6	5.8	2
37	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	3.7	15
36	Variation in NF-B signaling pathways and survival in invasive epithelial ovarian cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 1421-7	4	11
35	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, 6618-30	12.9	66
34	Inferring copy number and genotype in tumour exome data. *BMC Genomics*, **2014**, 15, 732	4.5	82
33	COMPLEXO: identifying the missing heritability of breast cancer via next generation collaboration. *Breast Cancer Research*, **2013**, 15, 402	8.3	30
32	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
31	A simple consensus approach improves somatic mutation prediction accuracy. *Genome Medicine*, **2013**, 5, 90	14.4	29
30	RNF43 is a tumour suppressor gene mutated in mucinous tumours of the ovary. *Journal of Pathology*, **2013**, 229, 469-76	9.4	81
29	Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk. *PLoS Genetics*, **2013**, 9, e1003212	6	209
28	Analysis of RAD51C germline mutations in high-risk breast and ovarian cancer families and ovarian cancer patients. *Human Mutation*, **2012**, 33, 95-9	4.7	53
27	Rare variants in XRCC2 as breast cancer susceptibility alleles. *Journal of Medical Genetics*, **2012**, 49, 618-23	5.8	37
26	Analysis of KLLN as a high-penetrance breast cancer predisposition gene. *Breast Cancer Research and Treatment*, **2012**, 134, 543-7	4.4	3
25	Identification of copy number alterations associated with the progression of DCIS to invasive ductal carcinoma. *Breast Cancer Research and Treatment*, **2012**, 133, 889-98	4.4	56

24	Exome sequencing identifies rare deleterious mutations in DNA repair genes FANCC and BLM as potential breast cancer susceptibility alleles. *PLoS Genetics*, **2012**, 8, e1002894	6	144
23	Pre-invasive ovarian mucinous tumors are characterized by CDKN2A and RAS pathway aberrations. *Clinical Cancer Research*, **2012**, 18, 5267-77	12.9	46
22	MicroRNA genes and their target 3N-untranslated regions are infrequently somatically mutated in ovarian cancers. *PLoS ONE*, **2012**, 7, e35805	3.7	25
21	Genetic changes in tumour microenvironments. *Journal of Pathology*, **2011**, 223, 450-8	9.4	28
20	Clonal mutations in the cancer-associated fibroblasts: the case against genetic coevolution. *Cancer Research*, **2009**, 69, 6765-8; discussion 6769	10.1	66
19	Are there any more ovarian tumor suppressor genes? A new perspective using ultra high-resolution copy number and loss of heterozygosity analysis. *Genes Chromosomes and Cancer*, **2009**, 48, 931-42	5	51
18	Large-scale genomic analysis of ovarian carcinomas. *Molecular Oncology*, **2009**, 3, 157-64	7.9	29
17	BARD1 variants are not associated with breast cancer risk in Australian familial breast cancer. *Breast Cancer Research and Treatment*, **2008**, 111, 505-9	4.4	20
16	Breast cancer risk and the BRCA1 interacting protein CTIP. *Breast Cancer Research and Treatment*, **2008**, 112, 351-2	4.4	3
15	High-resolution copy number arrays in cancer and the problem of normal genome copy number variation. *Genes Chromosomes and Cancer*, **2008**, 47, 933-8	5	6
14	Genetic and epigenetic analysis of the TIMP-3 gene in ovarian cancer. *Cancer Letters*, **2007**, 247, 91-7	9.9	10
13	Genetic and epigenetic analysis of the putative tumor suppressor km23 in primary ovarian, breast, and colorectal cancers. *Clinical Cancer Research*, **2006**, 12, 3713-5	12.9	11
12	No association of the MDM2 SNP309 polymorphism with risk of breast or ovarian cancer. *Cancer Letters*, **2006**, 240, 195-7	9.9	63
11	Whole genome SNP arrays using DNA derived from formalin-fixed, paraffin-embedded ovarian tumor tissue. *Human Mutation*, **2005**, 26, 384-9	4.7	49
10	Mutation of the PIK3CA gene in ovarian and breast cancer. *Cancer Research*, **2004**, 64, 7678-81	10.1	779
9	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	8.3	9
8	Discussion: Ovarian Cancer Prevention. *Gynecologic Oncology*, **2003**, 88, S67-S70	4.9	3
7	Genetic analysis of benign ovarian tumors. *International Journal of Cancer*, **2003**, 105, 499-505	7.5	21

6	Prohibitin 3Nuntranslated region polymorphism and breast cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2003**, 12, 1273-4	4	9
5	Methylenetetrahydrofolate reductase polymorphism and susceptibility to breast cancer. *Breast Cancer Research*, **2002**, 4, R14	8.3	79
4	Mutation of the ST7 tumor suppressor gene on 7q31.1 is rare in breast, ovarian and colorectal cancers. *Nature Genetics*, **2001**, 29, 379-80	36.3	16
3	Refinement of an ovarian cancer tumour suppressor gene locus on chromosome arm 22q and mutation analysis of CYP2D6, SREBP2 and NAGA. *International Journal of Cancer*, **2000**, 87, 798-802	7.5	15
2	Polygenic Risk Modelling for Prediction of Epithelial Ovarian Cancer Risk		1
1	The genetic analysis of a founder Northern American population of European descent identifies FANCI as a candidate familial ovarian cancer risk gene		1