Antoinette Hollestelle

List of Publications by Year in Descending Order

105 papers	8,831 citations	38 h-index	93 g-index
114 ext. papers	10,834 ext. citations	11.4 avg, IF	4.2 L-index

#	Paper	IF	Citations
105	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
104	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3
103	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51	14.4	0
102	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. *Scientific Reports*, **2021**, 11, 19787	4.9	0
101	The predictive ability of the 313 variant-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	8.1	2
100	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. *American Journal of Human Genetics*, **2021**, 108, 1190-1203	11	1
99	Common Susceptibility Loci for Male Breast Cancer. *Journal of the National Cancer Institute*, **2021**, 113, 453-461	9.7	4
98	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
97	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
96	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. *Nature Genetics*, **2020**, 52, 572-581	36.3	76
95	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688	4.9	2
94	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
93	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
92	Another step forward towards unraveling the biological mechanisms driving breast cancer predisposition: a role for non-coding RNAs. *Non-coding RNA Investigation*, **2020**, 4, 3-3	0.6	
91	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 837-848	11	12
90	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228 951 Women of European Descent. *Journal of the National Cancer Institute*, **2020**, 112, 295-304	9.7	18
89	Addition of a 161-SNP polygenic risk score to family history-based risk prediction: impact on clinical management in non- breast cancer families. *Journal of Medical Genetics*, **2019**, 56, 581-589	5.8	21

88	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
87	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
86	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *Npj Breast Cancer*, **2019**, 5, 38	7.8	12
85	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
84	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 795-806	7.8	52
83	The BRCA2 c.68-7T□□A variant is not pathogenic: A model for clinical calibration of spliceogenicity. *Human Mutation*, **2018**, 39, 729-741	4.7	16
82	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. *International Journal of Cancer*, **2018**, 143, 746-757	7.5	9
81	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	10.1	32
80	The Prevalence of CD146 Expression in Breast Cancer Subtypes and Its Relation to Outcome. *Cancers*, **2018**, 10,	6.6	8
79	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101
78	Elucidating the Underlying Functional Mechanisms of Breast Cancer Susceptibility Through Post-GWAS Analyses. *Frontiers in Genetics*, **2018**, 9, 280	4.5	7
77	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
76	Low Tumor Mitochondrial DNA Content Is Associated with Better Outcome in Breast Cancer Patients Receiving Anthracycline-Based Chemotherapy. *Clinical Cancer Research*, **2017**, 23, 4735-4743	12.9	12
75	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
74	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
73	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. *Breast Cancer Research*, **2017**, 19, 119	8.3	26
72	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	6.3	51
71	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15

70	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. *Scientific Reports*, **2016**, 6, 36874	4.9	2
69	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
68	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
67	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). *Scientific Reports*, **2016**, 6, 32512	4.9	16
66	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. *Breast Cancer Research*, **2016**, 18, 104	8.3	44
65	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *Journal of Clinical Oncology*, **2016**, 34, 2750-60	2.2	107
64	GATA3 mRNA expression, but not mutation, associates with longer progression-free survival in ER-positive breast cancer patients treated with first-line tamoxifen for recurrent disease. *Cancer Letters*, **2016**, 376, 104-9	9.9	18
63	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. *Journal of Pathology: Clinical Research*, **2016**, 2, 138-53	5.3	16
62	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. *Nature Genetics*, **2016**, 48, 374-86	36.3	93
61	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. *PLoS ONE*, **2016**, 11, e0160316	3.7	11
60	The 29.5 kb APOBEC3B Deletion Polymorphism Is Not Associated with Clinical Outcome of Breast Cancer. *PLoS ONE*, **2016**, 11, e0161731	3.7	11
59	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. *International Journal of Cancer*, **2016**, 139, 1303-1317	7.5	26
58	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
57	Recurrent HOXB13 mutations in the Dutch population do not associate with increased breast cancer risk. *Scientific Reports*, **2016**, 6, 30026	4.9	1
56	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
55	Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22	8.3	31
54	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. *Carcinogenesis*, **2015**, 36, 256-71	4.6	12
53	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature Genetics*, **2015**, 47, 373-80	36.3	406

52	Identification of novel genetic markers of breast cancer survival. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	38
51	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. *BMC Medicine*, **2015**, 13, 156	11.4	37
50	Sensitivity to systemic therapy for metastatic breast cancer in CHEK2 1100delC mutation carriers. *Journal of Cancer Research and Clinical Oncology*, **2015**, 141, 1879-87	4.9	6
49	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 1680-91	4	17
48	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. *Human Molecular Genetics*, **2015**, 24, 285-98	5.6	35
47	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. *BMC Cancer*, **2015**, 15, 978	4.8	6
46	Common germline polymorphisms associated with breast cancer-specific survival. *Breast Cancer Research*, **2015**, 17, 58	8.3	24
45	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
44	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. *Journal of Pathology: Clinical Research*, **2015**, 1, 18-32	5.3	18
43	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
42	Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. *American Journal of Human Genetics*, **2015**, 96, 5-20	11	59
41	Tumor-associated inflammation as a potential prognostic tool in BRCA1/2-associated breast cancer. *Human Pathology*, **2015**, 46, 182-90	3.7	18
40	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46,450 cases and 42,461 controls from the breast cancer association consortium. *Human Molecular Genetics*, **2014**, 23, 1934-46	5.6	28
39	Survival and contralateral breast cancer in CHEK2 1100delC breast cancer patients: impact of adjuvant chemotherapy. *British Journal of Cancer*, **2014**, 111, 1004-13	8.7	43
38	CHEK2*1100delC homozygosity in the Netherlands--prevalence and risk of breast and lung cancer. *European Journal of Human Genetics*, **2014**, 22, 46-51	5.3	22
37	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. *Breast Cancer Research*, **2014**, 16, R51	8.3	12
36	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. *PLoS Genetics*, **2014**, 10, e1004285	6	38
35	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. *Nature Communications*, **2014**, 5, 4051	17.4	13

34	Growth and metastatic behavior of molecularly well-characterized human breast cancer cell lines in mice. *Breast Cancer Research and Treatment*, **2014**, 148, 19-31	4.4	2
33	Analysis of TP53 mutation status in human cancer cell lines: a reassessment. *Human Mutation*, **2014**, 35, 756-65	4.7	110
32	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium **2014**, n/a-n/a		1
31	miRNA expression profiling of 51 human breast cancer cell lines reveals subtype and driver mutation-specific miRNAs. *Breast Cancer Research*, **2013**, 15, R33	8.3	140
30	Loss of E-cadherin is not a necessity for epithelial to mesenchymal transition in human breast cancer. *Breast Cancer Research and Treatment*, **2013**, 138, 47-57	4.4	72
29	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
28	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
27	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
26	E-cadherin promotor methylation and mutation are inversely related to motility capacity of breast cancer cells. *Breast Cancer Research and Treatment*, **2012**, 136, 365-77	4.4	22
25	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. *Nature Genetics*, **2012**, 44, 1182-4	36.3	84
24	Genome-wide association analysis identifies three new breast cancer susceptibility loci. *Nature Genetics*, **2012**, 44, 312-8	36.3	237
23	9q31.2-rs865686 as a susceptibility locus for estrogen receptor-positive breast cancer: evidence from the Breast Cancer Association Consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2012**, 21, 1783-91	4	17
22	A 3Suntranslated region KRAS variant and triple-negative breast cancer: a case-control and genetic analysis. *Lancet Oncology, The*, **2011**, 12, 377-86	21.7	107
21	Prevalence of the variant allele rs61764370 T>G in the 3'UTR of KRAS among Dutch BRCA1, BRCA2 and non-BRCA1/BRCA2 breast cancer families. *Breast Cancer Research and Treatment*, **2011**, 128, 79-84	4.4	33
20	Confirmation of 5p12 as a susceptibility locus for progesterone-receptor-positive, lower grade breast cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 2222-31	4	27
19	Associations of breast cancer risk factors with tumor subtypes: a pooled analysis from the Breast Cancer Association Consortium studies. *Journal of the National Cancer Institute*, **2011**, 103, 250-63	9.7	513
18	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2011** , 20, 3289-303	5.6	140
17	Rare BRCA1 haplotypes including 3'UTR SNPs associated with breast cancer risk. *Cell Cycle*, **2011**, 10, 90-9	4.7	29

16	A genome-wide association scan on estrogen receptor-negative breast cancer. *Breast Cancer Research*, **2010**, 12, R93	8.3	32
15	Discovering moderate-risk breast cancer susceptibility genes. *Current Opinion in Genetics and Development*, **2010**, 20, 268-76	4.9	75
14	Distinct gene mutation profiles among luminal-type and basal-type breast cancer cell lines. *Breast Cancer Research and Treatment*, **2010**, 121, 53-64	4.4	207
13	Four human breast cancer cell lines with biallelic inactivating alpha-catenin gene mutations. *Breast Cancer Research and Treatment*, **2010**, 122, 125-33	4.4	34
12	Comment Re: MDA-MB-435 and M14 cell lines: identical but not M14 Melanoma?. *Cancer Research*, **2009**, 69, 7893	10.1	33
11	Low-risk susceptibility alleles in 40 human breast cancer cell lines. *BMC Cancer*, **2009**, 9, 236	4.8	20
10	Deleterious CHEK2 1100delC and L303X mutants identified among 38 human breast cancer cell lines. *Breast Cancer Research and Treatment*, **2009**, 113, 285-91	4.4	7
9	Exon expression arrays as a tool to identify new cancer genes. *PLoS ONE*, **2007**, 3, e3007	3.7	10
8	Phosphatidylinositol-3-OH kinase or RAS pathway mutations in human breast cancer cell lines. *Molecular Cancer Research*, **2007**, 5, 195-201	6.6	242
7	BRCA1 mutation analysis of 41 human breast cancer cell lines reveals three new deleterious mutants. *Cancer Research*, **2006**, 66, 41-5	10.1	195
6	Representational difference analysis as a tool in the search for new tumor suppressor genes. *Methods in Molecular Medicine*, **2005**, 103, 143-59		2
5	The CHEK2 1100delC mutation identifies families with a hereditary breast and colorectal cancer phenotype. *American Journal of Human Genetics*, **2003**, 72, 1308-14	11	169
4	Low-penetrance susceptibility to breast cancer due to CHEK2(*)1100delC in noncarriers of BRCA1 or BRCA2 mutations. *Nature Genetics*, **2002**, 31, 55-9	36.3	863
3	Common variants in breast cancer risk loci predispose to distinct tumor subtypes		1
2	Fine-mapping of 150 breast cancer risk regions identifies 178 high confidence target genes		2
1	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2