

# Antoinette Hollestelle

## List of Publications by Citations

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**Version:** 2024-04-23

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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.

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	Low-penetrance susceptibility to breast cancer due to CHEK2(*)1100delC in noncarriers of BRCA1 or BRCA2 mutations. <i>Nature Genetics</i> , <b>2002</b> , 31, 55-9	36.3	863
104	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , <b>2013</b> , 45, 353-61, 361e1-2	36.3	813
103	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , <b>2017</b> , 551, 92-94	50.4	643
102	Associations of breast cancer risk factors with tumor subtypes: a pooled analysis from the Breast Cancer Association Consortium studies. <i>Journal of the National Cancer Institute</i> , <b>2011</b> , 103, 250-63	9.7	513
101	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , <b>2013</b> , 45, 371-84, 384e1-2	36.3	422
100	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , <b>2015</b> , 47, 373-80	36.3	406
99	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , <b>2019</b> , 104, 21-34	11	363
98	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , <b>2013</b> , 45, 392-8, 398e1-2	36.3	327
97	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , <b>2015</b> , 107,	9.7	324
96	Phosphatidylinositol-3-OH kinase or RAS pathway mutations in human breast cancer cell lines. <i>Molecular Cancer Research</i> , <b>2007</b> , 5, 195-201	6.6	242
95	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , <b>2012</b> , 44, 312-8	36.3	237
94	Distinct gene mutation profiles among luminal-type and basal-type breast cancer cell lines. <i>Breast Cancer Research and Treatment</i> , <b>2010</b> , 121, 53-64	4.4	207
93	BRCA1 mutation analysis of 41 human breast cancer cell lines reveals three new deleterious mutants. <i>Cancer Research</i> , <b>2006</b> , 66, 41-5	10.1	195
92	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , <b>2017</b> , 49, 1767-1778	36.3	186
91	The CHEK2 1100delC mutation identifies families with a hereditary breast and colorectal cancer phenotype. <i>American Journal of Human Genetics</i> , <b>2003</b> , 72, 1308-14	11	169
90	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , <b>2021</b> , 384, 428-439	59.2	143
89	miRNA expression profiling of 51 human breast cancer cell lines reveals subtype and driver mutation-specific miRNAs. <i>Breast Cancer Research</i> , <b>2013</b> , 15, R33	8.3	140

88	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , <b>2011</b> , 20, 3289-303	5.6	140
87	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , <b>2016</b> , 53, 800-811	5.8	121
86	Analysis of TP53 mutation status in human cancer cell lines: a reassessment. <i>Human Mutation</i> , <b>2014</b> , 35, 756-65	4.7	110
85	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. <i>Journal of Clinical Oncology</i> , <b>2016</b> , 34, 2750-60	2.2	107
84	A 35untranslated region KRAS variant and triple-negative breast cancer: a case-control and genetic analysis. <i>Lancet Oncology</i> , <b>2011</b> , 12, 377-86	21.7	107
83	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , <b>2018</b> , 50, 968-978	36.3	101
82	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , <b>2016</b> , 48, 374-86	36.3	93
81	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. <i>Nature Genetics</i> , <b>2012</b> , 44, 1182-4	36.3	84
80	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , <b>2020</b> , 52, 572-581	36.3	76
79	Discovering moderate-risk breast cancer susceptibility genes. <i>Current Opinion in Genetics and Development</i> , <b>2010</b> , 20, 268-76	4.9	75
78	Loss of E-cadherin is not a necessity for epithelial to mesenchymal transition in human breast cancer. <i>Breast Cancer Research and Treatment</i> , <b>2013</b> , 138, 47-57	4.4	72
77	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , <b>2016</b> , 7, 11375	17.4	64
76	Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 5-20	11	59
75	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , <b>2020</b> , 52, 56-73	36.3	56
74	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , <b>2016</b> , 7, 12675	17.4	53
73	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , <b>2019</b> , 48, 795-806	7.8	52
72	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , <b>2017</b> , 19, 599-603		51
71	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , <b>2017</b> , 77, 2789-2799	10.1	49

70	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , <b>2019</b> , 10, 1741	17.4	47
69	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , <b>2016</b> , 18, 104	8.3	44
68	Survival and contralateral breast cancer in CHEK2 1100delC breast cancer patients: impact of adjuvant chemotherapy. <i>British Journal of Cancer</i> , <b>2014</b> , 111, 1004-13	8.7	43
67	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , <b>2015</b> , 107,	9.7	38
66	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004285	6	38
65	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , <b>2015</b> , 13, 156	11.4	37
64	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 2966-84	5.6	36
63	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 285-98	5.6	35
62	Four human breast cancer cell lines with biallelic inactivating alpha-catenin gene mutations. <i>Breast Cancer Research and Treatment</i> , <b>2010</b> , 122, 125-33	4.4	34
61	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. <i>Breast Cancer Research and Treatment</i> , <b>2011</b> , 128, 79-84	4.4	33
60	Comment Re: MDA-MB-435 and M14 cell lines: identical but not M14 Melanoma?. <i>Cancer Research</i> , <b>2009</b> , 69, 7893	10.1	33
59	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , <b>2018</b> , 78, 5419-5430	10.1	32
58	A genome-wide association scan on estrogen receptor-negative breast cancer. <i>Breast Cancer Research</i> , <b>2010</b> , 12, R93	8.3	32
57	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , <b>2016</b> , 18, 22	8.3	31
56	Rare BRCA1 haplotypes including 3'UTR SNPs associated with breast cancer risk. <i>Cell Cycle</i> , <b>2011</b> , 10, 90-9	4.7	29
55	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , <b>2019</b> , 120, 647-657	8.7	28
54	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. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 1934-46	5.6	28
53	Confirmation of 5p12 as a susceptibility locus for progesterone-receptor-positive, lower grade breast cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2011</b> , 20, 2222-31	4	27

52	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , <b>2017</b> , 19, 119	8.3	26
51	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , <b>2016</b> , 139, 1303-1317	7.5	26
50	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , <b>2016</b> , 18, 64	8.3	25
49	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , <b>2015</b> , 17, 58	8.3	24
48	CHEK2*1100delC homozygosity in the Netherlands--prevalence and risk of breast and lung cancer. <i>European Journal of Human Genetics</i> , <b>2014</b> , 22, 46-51	5.3	22
47	E-cadherin promotor methylation and mutation are inversely related to motility capacity of breast cancer cells. <i>Breast Cancer Research and Treatment</i> , <b>2012</b> , 136, 365-77	4.4	22
46	Addition of a 161-SNP polygenic risk score to family history-based risk prediction: impact on clinical management in non- breast cancer families. <i>Journal of Medical Genetics</i> , <b>2019</b> , 56, 581-589	5.8	21
45	Low-risk susceptibility alleles in 40 human breast cancer cell lines. <i>BMC Cancer</i> , <b>2009</b> , 9, 236	4.8	20
44	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. <i>Cancer Letters</i> , <b>2016</b> , 376, 104-9	9.9	18
43	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , <b>2015</b> , 1, 18-32	5.3	18
42	Tumor-associated inflammation as a potential prognostic tool in BRCA1/2-associated breast cancer. <i>Human Pathology</i> , <b>2015</b> , 46, 182-90	3.7	18
41	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228 951 Women of European Descent. <i>Journal of the National Cancer Institute</i> , <b>2020</b> , 112, 295-304	9.7	18
40	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2015</b> , 24, 1680-91	4	17
39	9q31.2-rs865686 as a susceptibility locus for estrogen receptor-positive breast cancer: evidence from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2012</b> , 21, 1783-91	4	17
38	The BRCA2 c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , <b>2018</b> , 39, 729-741	4.7	16
37	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , <b>2016</b> , 6, 32512	4.9	16
36	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , <b>2016</b> , 2, 138-53	5.3	16
35	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , <b>2016</b> , 141, 386-401	4.9	15

34	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , <b>2014</b> , 5, 4051	17.4	13
33	Low Tumor Mitochondrial DNA Content Is Associated with Better Outcome in Breast Cancer Patients Receiving Anthracycline-Based Chemotherapy. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 4735-4743	12.9	12
32	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. <i>Carcinogenesis</i> , <b>2015</b> , 36, 256-71	4.6	12
31	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , <b>2019</b> , 5, 38	7.8	12
30	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , <b>2014</b> , 16, R51	8.3	12
29	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , <b>2020</b> , 107, 837-848	11	12
28	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , <b>2016</b> , 11, e0160316	3.7	11
27	The 29.5 kb APOBEC3B Deletion Polymorphism Is Not Associated with Clinical Outcome of Breast Cancer. <i>PLoS ONE</i> , <b>2016</b> , 11, e0161731	3.7	11
26	Exon expression arrays as a tool to identify new cancer genes. <i>PLoS ONE</i> , <b>2007</b> , 3, e3007	3.7	10
25	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. <i>Genetic Epidemiology</i> , <b>2020</b> , 44, 442-468	2.6	9
24	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. <i>International Journal of Cancer</i> , <b>2018</b> , 143, 746-757	7.5	9
23	The Prevalence of CD146 Expression in Breast Cancer Subtypes and Its Relation to Outcome. <i>Cancers</i> , <b>2018</b> , 10,	6.6	8
22	Deleterious CHEK2 1100delC and L303X mutants identified among 38 human breast cancer cell lines. <i>Breast Cancer Research and Treatment</i> , <b>2009</b> , 113, 285-91	4.4	7
21	Elucidating the Underlying Functional Mechanisms of Breast Cancer Susceptibility Through Post-GWAS Analyses. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 280	4.5	7
20	Sensitivity to systemic therapy for metastatic breast cancer in CHEK2 1100delC mutation carriers. <i>Journal of Cancer Research and Clinical Oncology</i> , <b>2015</b> , 141, 1879-87	4.9	6
19	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. <i>BMC Cancer</i> , <b>2015</b> , 15, 978	4.8	6
18	Common Susceptibility Loci for Male Breast Cancer. <i>Journal of the National Cancer Institute</i> , <b>2021</b> , 113, 453-461	9.7	4
17	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , <b>2021</b> , 12, 1078	17.4	4

16	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. <i>Breast Cancer Research</i> , <b>2022</b> , 24, 2	8.3	3
15	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , <b>2020</b> , 10, 9688	4.9	2
14	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , <b>2016</b> , 6, 36874	4.9	2
13	Growth and metastatic behavior of molecularly well-characterized human breast cancer cell lines in mice. <i>Breast Cancer Research and Treatment</i> , <b>2014</b> , 148, 19-31	4.4	2
12	Representational difference analysis as a tool in the search for new tumor suppressor genes. <i>Methods in Molecular Medicine</i> , <b>2005</b> , 103, 143-59		2
11	Fine-mapping of 150 breast cancer risk regions identifies 178 high confidence target genes		2
10	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2
9	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. <i>Genetics in Medicine</i> , <b>2021</b> , 23, 1726-1737	8.1	2
8	Common variants in breast cancer risk loci predispose to distinct tumor subtypes		1
7	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 1190-1203	11	1
6	Recurrent HOXB13 mutations in the Dutch population do not associate with increased breast cancer risk. <i>Scientific Reports</i> , <b>2016</b> , 6, 30026	4.9	1
5	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium <b>2014</b> , n/a-n/a		1
4	Rare germline copy number variants (CNVs) and breast cancer risk.. <i>Communications Biology</i> , <b>2022</b> , 5, 65	6.7	0
3	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , <b>2021</b> , 11, 19787	4.9	0
2	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. <i>Genome Medicine</i> , <b>2022</b> , 14, 51	14.4	0
1	Another step forward towards unraveling the biological mechanisms driving breast cancer predisposition: a role for non-coding RNAs. <i>Non-coding RNA Investigation</i> , <b>2020</b> , 4, 3-3	0.6	