

# Antoinette Hollestelle

## List of Articles by Year in descending order

Source: [//exaly.com/author-pdf/7739181/publications.pdf](https://exaly.com/author-pdf/7739181/publications.pdf)

Version: 2025-02-01

115

PR articles

10,726

PR citations

75816

39

PR h-index

31651

100

g-index

122

documents

12484

doc citations

69917

43

h-index

23248

citing authors

#	ARTICLE	IF	CITATIONS
1	The benefit of adding polygenic risk scores, lifestyle factors, and breast density to family history and genetic status for breast cancer risk and surveillance classification of unaffected women from germline CHEK2 c.1100delC families. <i>Breast</i> , 2024, 73, 103611.	2.3	7
2	Expression and Localization of Ferritin-Heavy Chain Predicts Recurrence for Breast Cancer Patients with a BRCA1/2 Mutation. <i>Cancers</i> , 2024, 16, 28.	3.8	3
3	Functional Homologous Recombination (HR) Screening Shows the Majority of BRCA1/2-Mutant Breast and Ovarian Cancer Cell Lines Are HR-Proficient. <i>Cancers</i> , 2024, 16, 741.	3.8	8
4	Genetic drivers and cellular selection of female mosaic X chromosome loss. <i>Nature</i> , 2024, 631, 134-141.	37.9	32
5	Cancer risks for other sites in addition to breast in CHEK2 c.1100delC families. <i>Genetics in Medicine</i> , 2024, 26, 101171.	4.2	10
6	Cohort profile: a nationwide study in Dutch CHEK2 c.1100delC families using the infrastructure of the Hereditary Breast and Ovarian cancer study Netherlands â€“ Hebon-CHEK2. <i>BMJ Open</i> , 2024, 14, e086688.	1.9	1
7	Polygenic score distribution differences across European ancestry populations: implications for breast cancer risk prediction. <i>Breast Cancer Research</i> , 2024, 26, .	4.8	11
8	Clinical applicability of the Polygenic Risk Score for breast cancer risk prediction in familial cases. <i>Journal of Medical Genetics</i> , 2023, 60, 327-336.	3.8	34
9	FANCM missense variants and breast cancer risk: a case-control association study of 75,156 European women. <i>European Journal of Human Genetics</i> , 2023, 31, 578-587.	3.0	10
10	Genome-wide analyses characterize shared heritability among cancers and identify novel cancer susceptibility regions. <i>Journal of the National Cancer Institute</i> , 2023, 115, 712-732.	4.6	29
11	Breast cancer genomes from CHEK2 c.1100delC mutation carriers lack somatic TP53 mutations and display a unique structural variant size distribution profile. <i>Breast Cancer Research</i> , 2023, 25, .	4.8	7
12	Spectrum and Frequency of Germline FANCM Protein-Truncating Variants in 44,803 European Female Breast Cancer Cases. <i>Cancers</i> , 2023, 15, 3313. <a href="#">Association of the</a>	3.8	1
13	<a href="#">CHEK2</a> <a href="#">c.1100delC</a>	2.6	5
14	Evaluation of European-based polygenic risk score for breast cancer in Ashkenazi Jewish women in Israel. <i>Journal of Medical Genetics</i> , 2023, 60, 1186-1197.	3.8	3
15	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, .	4.4	12
16	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, .	4.8	26
17	Identifying Transcripts with Tandem Duplications from RNA-Sequencing Data to Predict BRCA1-Type Primary Breast Cancer. <i>Cancers</i> , 2022, 14, 753.	3.8	1
18	A pipeline for copy number profiling of single circulating tumour cells to assess inpatient tumour heterogeneity. <i>Molecular Oncology</i> , 2022, 16, 2981-3000.	4.1	8

#	ARTICLE	IF	CITATIONS
19	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, .	9.6	51
20	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. <i>Cancers</i> , 2022, 14, 3363.	3.8	3
21	Physical activity, sedentary time and breast cancer risk: a Mendelian randomisation study. <i>British Journal of Sports Medicine</i> , 2022, 56, 1157-1170.	10.6	61
22	Progression-free survival and overall survival after BRCA1/2-associated epithelial ovarian cancer: A matched cohort study. <i>PLoS ONE</i> , 2022, 17, e0275015.	2.3	5
23	Common Susceptibility Loci for Male Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2021, 113, 453-461.	4.6	20
24	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021, 12, .	13.7	37
25	Breast Cancer Risk Genes Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	34.6	956
26	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> , 2021, 23, 1726-1737.	4.2	29
27	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> , 2021, 108, 1190-1203.	6.5	7
28	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , 2021, 11, .	3.4	3
29	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> , 2020, 112, 295-304.	4.6	48
30	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	25.2	166
31	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	6.5	56
32	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	25.2	437
33	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, .	3.4	4
34	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	3.1	42
35	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, .	6.4	42
36	Addition of a 161-SNP polygenic risk score to family history-based risk prediction: impact on clinical management in non-BRCA1/2 breast cancer families. <i>Journal of Medical Genetics</i> , 2019, 56, 581-589.	3.8	45

#	ARTICLE	IF	CITATIONS
37	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, .	13.7	116
38	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	5.5	62
39	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	6.5	989
40	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 795-806.	4.9	91
41	The BRCA2 c.68-7T>>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018, 39, 729-741.	4.5	20
42	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. <i>International Journal of Cancer</i> , 2018, 143, 746-757.	4.3	27
43	Elucidating the Underlying Functional Mechanisms of Breast Cancer Susceptibility Through Post-GWAS Analyses. <i>Frontiers in Genetics</i> , 2018, 9, .	2.3	15
44	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	3.8	64
45	The Prevalence of CD146 Expression in Breast Cancer Subtypes and Its Relation to Outcome. <i>Cancers</i> , 2018, 10, 134.	3.8	24
46	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	25.2	226
47	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	3.8	87
48	Low Tumor Mitochondrial DNA Content Is Associated with Better Outcome in Breast Cancer Patients Receiving Anthracycline-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2017, 23, 4735-4743.	6.8	17
49	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	37.9	1,398
50	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	25.2	394
51	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017, 19, .	4.8	45
52	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	2.3	12
53	The 29.5 kb APOBEC3B Deletion Polymorphism Is Not Associated with Clinical Outcome of Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0161731.	2.3	17
54	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	4.3	53

#	ARTICLE	IF	CITATIONS
55	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	3.8	204
56	Recurrent HOXB13 mutations in the Dutch population do not associate with increased breast cancer risk. <i>Scientific Reports</i> , 2016, 6, .	3.4	3
57	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> , 2016, 18, .	4.8	37
58	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, .	4.8	54
59	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016, 6, .	3.4	2
60	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, .	13.7	103
61	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, .	13.7	88
62	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> , 2016, 6, .	3.4	21
63	Prognostic value of automated Ki67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , 2016, 18, .	4.8	66
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. <i>Cancer Letters</i> , 2016, 376, 104-109.	8.6	26
65	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2016, 2, 138-153.	3.3	19
66	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	25.2	148
67	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	3.0	20
68	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> , 2015, 15, .	2.9	10
69	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, .	4.8	29
70	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	4.6	482
71	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> , 2015, 1, 18-32.	3.3	25
72	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	2.9	40

#	ARTICLE	IF	CITATIONS
73	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> , 2015, 96, 5-20.	6.5	81
74	Tumor-associated inflammation as a potential prognostic tool in BRCA1/2-associated breast cancer. <i>Human Pathology</i> , 2015, 46, 182-190.	2.3	27
75	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> , 2015, 36, 256-271.	2.8	18
76	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	25.2	573
77	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	4.6	65
78	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , 2015, 13, .	7.1	57
79	Sensitivity to systemic therapy for metastatic breast cancer in CHEK2 1100delC mutation carriers. <i>Journal of Cancer Research and Clinical Oncology</i> , 2015, 141, 1879-1887.	2.3	11
80	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	1.1	25
81	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298.	2.9	39
82	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	3.2	44
83	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, .	13.7	16
84	Growth and metastatic behavior of molecularly well-characterized human breast cancer cell lines in mice. <i>Breast Cancer Research and Treatment</i> , 2014, 148, 19-31.	2.4	6
85	Analysis of TP53 Mutation Status in Human Cancer Cell Lines: A Reassessment. <i>Human Mutation</i> , 2014, 35, 756-765.	4.5	199
86	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> , 2014, 23, 1934-1946.	2.9	34
87	Survival and contralateral breast cancer in CHEK2 1100delC breast cancer patients: impact of adjuvant chemotherapy. <i>British Journal of Cancer</i> , 2014, 111, 1004-1013.	5.5	68
88	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014, 16, .	4.8	14
89	miRNA expression profiling of 51 human breast cancer cell lines reveals subtype and driver mutation-specific miRNAs. <i>Breast Cancer Research</i> , 2013, 15, .	4.8	195
90	Loss of E-cadherin is not a necessity for epithelial to mesenchymal transition in human breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 138, 47-57.	2.4	123

#	ARTICLE	IF	CITATIONS
91	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	25.2	514
92	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	25.2	396
93	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	25.2	1,020
94	CHEK2*1100delC homozygosity in the Netherlands prevalence and risk of breast and lung cancer. <i>European Journal of Human Genetics</i> , 2013, 22, 46-51.	3.0	37
95	E-cadherin promotor methylation and mutation are inversely related to motility capacity of breast cancer cells. <i>Breast Cancer Research and Treatment</i> , 2012, 136, 365-377.	2.4	27
96	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. <i>Nature Genetics</i> , 2012, 44, 1182-1184.	25.2	104
97	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	25.2	271
98	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> , 2012, 21, 1783-1791.	1.1	17
99	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptor-Positive, Lower Grade Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 2222-2231.	1.1	27
100	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> , 2011, 103, 250-263.	4.6	626
101	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> , 2011, 20, 3289-3303.	2.9	156
102	A 3'-untranslated region KRAS variant and triple-negative breast cancer: a case-control and genetic analysis. <i>Lancet Oncology</i> , The, 2011, 12, 377-386.	27.4	138
103	A genome-wide association scan on estrogen receptor-negative breast cancer. <i>Breast Cancer Research</i> , 2010, 12, .	4.8	35
104	Discovering moderate-risk breast cancer susceptibility genes. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 268-276.	3.2	107
105	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> , 2010, 128, 79-84.	2.4	35
106	Comment Re: MDA-MB-435 and M14 Cell Lines: Identical but not M14 Melanoma?. <i>Cancer Research</i> , 2009, 69, 7893-7893.	3.8	36
107	Low-risk susceptibility alleles in 40 human breast cancer cell lines. <i>BMC Cancer</i> , 2009, 9, .	2.9	27
108	Distinct gene mutation profiles among luminal-type and basal-type breast cancer cell lines. <i>Breast Cancer Research and Treatment</i> , 2009, 121, 53-64.	2.4	264

#	ARTICLE	IF	CITATIONS
109	Four human breast cancer cell lines with biallelic inactivating $\beta$ -catenin gene mutations. <i>Breast Cancer Research and Treatment</i> , 2009, 122, 125-133.	2.4	40
110	Exon Expression Arrays as a Tool to Identify New Cancer Genes. <i>PLoS ONE</i> , 2008, 3, e3007.	2.3	13
111	Deleterious CHEK2 1100delC and L303X mutants identified among 38 human breast cancer cell lines. <i>Breast Cancer Research and Treatment</i> , 2008, 113, 285-291.	2.4	9
112	Phosphatidylinositol-3-OH Kinase or RAS Pathway Mutations in Human Breast Cancer Cell Lines. <i>Molecular Cancer Research</i> , 2007, 5, 195-201.	3.1	293
113	Low-penetrance susceptibility to breast cancer due to CHEK2*1100delC in noncarriers of BRCA1 or BRCA2 mutations. <i>Nature Genetics</i> , 2002, 31, 55-59.	25.2	1,052
114	Outcomes for ER-positive CHEK2 c.1100delC breast cancer patients compared with breast cancer patients without the variant. <i>Breast</i> , 0, 85, 104666.	2.3	0
115	Large-scale meta-analysis and precision functional assays identify FANCM regions in which PTVs confer different risks for ER-negative and triple-negative breast cancer. <i>Breast</i> , 0, 85, 104619.	2.3	0