

Hiltrud Brauch

List of Publications by Year in Descending Order

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Version: 2024-04-26

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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.

88
papers

11,003
citations

43
h-index

90
g-index

90
ext. papers

13,295
ext. citations

14.7
avg, IF

3.76
L-index

#	Paper	IF	Citations
88	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. <i>Breast Cancer Research</i> , 2022 , 24, 2	8.3	3
87	(Z)-Endoxifen and Early Recurrence of Breast Cancer: An Explorative Analysis in a Prospective Brazilian Study.. <i>Journal of Personalized Medicine</i> , 2022 , 12,	3.6	3
86	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 329-337	9.7	14
85	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021 , 12, 1078	17.4	4
84	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021 , 384, 428-439	59.2	143
83	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. <i>Breast Cancer Research</i> , 2021 , 23, 86	8.3	1
82	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	36.3	76
81	Obesity Alters Endoxifen Plasma Levels in Young Breast Cancer Patients: A Pharmacometric Simulation Approach. <i>Clinical Pharmacology and Therapeutics</i> , 2020 , 108, 661-670	6.1	9
80	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. <i>Genetic Epidemiology</i> , 2020 , 44, 442-468	2.6	9
79	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020 , 11, 312	17.4	20
78	Downregulation of 15-hydroxyprostaglandin dehydrogenase during acquired tamoxifen resistance and association with poor prognosis in ER ϵ positive breast cancer. <i>Exploration of Targeted Anti-tumor Therapy</i> , 2020 , 1, 355-371	2.5	2
77	The Influences of Adherence to Tamoxifen and CYP2D6 Pharmacogenetics on Plasma Concentrations of the Active Metabolite (Z)-Endoxifen in Breast Cancer. <i>Clinical and Translational Science</i> , 2020 , 13, 284-292	4.9	11
76	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020 , 52, 56-73	36.3	56
75	Gene Expression Signatures of BRCAness and Tumor Inflammation Define Subgroups of Early-Stage Hormone Receptor-Positive Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2020 , 26, 6523-6534	12.9	4
74	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020 , 107, 837-848	11	12
73	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019 , 9, 12524	4.9	2
72	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45

71	Tamoxifen Pharmacogenetics and Metabolism: The Same Is Not the Same. <i>Journal of Clinical Oncology</i> , 2019 , 37, 1981-1982	2.2	11
70	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019 , 10, 1741	17.4	47
69	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019 , 120, 647-657	8.7	28
68	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019 , 5, 38	7.8	12
67	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019 , 104, 21-34	11	363
66	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. <i>Cancer Medicine</i> , 2018 , 7, 1978-1987	4.8	40
65	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. <i>Journal of the National Cancer Institute</i> , 2018 , 110, 855-862	9.7	145
64	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018 , 9, 3166	17.4	70
63	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	36.3	101
62	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017 , 49, 834-841	36.3	257
61	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
60	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186
59	Improved Prediction of Endoxifen Metabolism by CYP2D6 Genotype in Breast Cancer Patients Treated with Tamoxifen. <i>Frontiers in Pharmacology</i> , 2017 , 8, 582	5.6	37
58	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016 , 141, 386-401	4.9	15
57	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016 , 25, 3863-3876	5.6	24
56	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 1503-1510	4	42
55	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016 , 6, 1052-67	24.4	104
54	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64

53	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016 , 7, 12675	17.4	53
52	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, 32512	4.9	16
51	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016 , 34, 2750-60	2.2	107
50	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2016 , 23, 77-91	5.7	41
49	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016 , 53, 298-309	5.8	83
48	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016 , 48, 374-86	36.3	93
47	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	65
46	Profiles of miRNAs matched to biology in aromatase inhibitor resistant breast cancer. <i>Oncotarget</i> , 2016 , 7, 71235-71254	3.3	10
45	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016 , 11, e0160316	3.7	11
44	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016 , 139, 1303-1317	7.5	26
43	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016 , 53, 800-811	5.8	121
42	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, 64	8.3	25
41	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016 , 48, 667-674	36.3	56
40	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016 , 99, 903-911	11	43
39	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015 , 47, 373-80	36.3	406
38	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015 , 97, 22-34	11	26
37	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. <i>Human Genetics</i> , 2015 , 134, 231-45	6.3	30
36	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226

35	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	74
34	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2015 , 22, 851-61	5.7	19
33	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, 1680-91	4	17
32	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, 285-98	5.6	35
31	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 1478-92	5.6	46
30	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015 , 5, 17369	4.9	27
29	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	324
28	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
27	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	11	59
26	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
25	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014 , 23, 6034-46	5.6	11
24	ERBB4 promoter polymorphism is associated with poor distant disease-free survival in high-risk early breast cancer. <i>PLoS ONE</i> , 2014 , 9, e102388	3.7	5
23	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
22	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , 2014 , 10, e1004285	6	38
21	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 6096-111	5.6	48
20	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014 , 16, 3419	8.3	82
19	Prediction of tamoxifen outcome by genetic variation of CYP2D6 in post-menopausal women with early breast cancer. <i>British Journal of Clinical Pharmacology</i> , 2014 , 77, 695-703	3.8	38
18	Fine-scale mapping of the FGFR2 breast cancer risk locus: putative functional variants differentially bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013 , 93, 1046-60	11	80

17	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, 371-84, 384e1-2	36.3	422
16	Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. <i>American Journal of Human Genetics</i> , 2013 , 92, 489-503	11	167
15	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013 , 45, 392-8, 398e1-2	36.3	327
14	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013 , 45, 353-61, 361e1-2	36.3	813
13	A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. <i>Breast Cancer Research and Treatment</i> , 2013 , 138, 529-542	4.4	14
12	Night work and breast cancer estrogen receptor status--results from the German GENICA study. <i>Scandinavian Journal of Work, Environment and Health</i> , 2013 , 39, 448-55	4.3	37
11	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012 , 44, 312-8	36.3	237
10	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012 , 21, 5373-84	5.6	143
9	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011 , 43, 1210-4	36.3	253
8	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. <i>Nature Genetics</i> , 2010 , 42, 885-92	36.3	276
7	Association between CYP2D6 polymorphisms and outcomes among women with early stage breast cancer treated with tamoxifen. <i>JAMA - Journal of the American Medical Association</i> , 2009 , 302, 1429-36	27.4	405
6	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. <i>PLoS Genetics</i> , 2008 , 4, e1000054	6	280
5	A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007 , 39, 352-8	36.3	557
4	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007 , 447, 1087-93	36.3	1957
3	Common variants in breast cancer risk loci predispose to distinct tumor subtypes		1
2	Combining genome-wide studies of breast, prostate, ovarian and endometrial cancers maps cross-cancer susceptibility loci and identifies new genetic associations		2
1	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2