Marjanka K Schmidt

List of Publications by Citations

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#	Paper	IF	Citations
272	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
271	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
270	Subtyping of breast cancer by immunohistochemistry to investigate a relationship between subtype and short and long term survival: a collaborative analysis of data for 10,159 cases from 12 studies. <i>PLoS Medicine</i> , 2010 , 7, e1000279	11.6	616
269	A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007 , 39, 352-	8 36.3	557
268	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, 250-63	9.7	513
267	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
266	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
265	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
264	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
263	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. <i>Nature Genetics</i> , 2009 , 41, 585-	99 6.3	393
262	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
261	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
260	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
259	Risk reduction of contralateral breast cancer and survival after contralateral prophylactic mastectomy in BRCA1 or BRCA2 mutation carriers. <i>British Journal of Cancer</i> , 2005 , 93, 287-92	8.7	269
258	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
257	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
256	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012 , 44, 312-8	36.3	237

255	Somatic mutations in the chromatin remodeling gene ARID1A occur in several tumor types. <i>Human Mutation</i> , 2012 , 33, 100-3	4.7	230
254	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
253	The 70-gene prognosis-signature predicts disease outcome in breast cancer patients with 1-3 positive lymph nodes in an independent validation study. <i>Breast Cancer Research and Treatment</i> , 2009 , 116, 295-302	4.4	222
252	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. <i>Genetics in Medicine</i> , 2019 , 21, 1708-1718	8.1	192
251	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778	36.3	186
250	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
249	Annexin A1 regulates TGF-beta signaling and promotes metastasis formation of basal-like breast cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6340-5	11.5	151
248	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
247	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, 3289-303	5.6	140
246	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. <i>Journal of Clinical Oncology</i> , 2012 , 30, 4308-16	2.2	134
245	Calibration and discriminatory accuracy of prognosis calculation for breast cancer with the online Adjuvant! program: a hospital-based retrospective cohort study. <i>Lancet Oncology, The</i> , 2009 , 10, 1070-6	21.7	133
244	An aCGH classifier derived from BRCA1-mutated breast cancer and benefit of high-dose platinum-based chemotherapy in HER2-negative breast cancer patients. <i>Annals of Oncology</i> , 2011 , 22, 1561-1570	10.3	131
243	PREDICT Plus: development and validation of a prognostic model for early breast cancer that includes HER2. <i>British Journal of Cancer</i> , 2012 , 107, 800-7	8.7	130
242	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
241	The 70-gene prognosis signature predicts early metastasis in breast cancer patients between 55 and 70 years of age. <i>Annals of Oncology</i> , 2010 , 21, 717-722	10.3	115
240	Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. <i>PLoS Genetics</i> , 2013 , 9, e1003284	6	112
239	Gene-environment interaction and risk of breast cancer. British Journal of Cancer, 2016, 114, 125-33	8.7	108
238	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016 , 34, 2750-60	2.2	107

237	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, 1052-6	5 7 4·4	104
236	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
235	An updated PREDICT breast cancer prognostication and treatment benefit prediction model with independent validation. <i>Breast Cancer Research</i> , 2017 , 19, 58	8.3	100
234	Common breast cancer susceptibility loci are associated with triple-negative breast cancer. <i>Cancer Research</i> , 2011 , 71, 6240-9	10.1	100
233	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
232	19p13.1 is a triple-negative-specific breast cancer susceptibility locus. <i>Cancer Research</i> , 2012 , 72, 1795-	8 03 .1	93
231	Breast cancer survival and tumor characteristics in premenopausal women carrying the CHEK2*1100delC germline mutation. <i>Journal of Clinical Oncology</i> , 2007 , 25, 64-9	2.2	92
230	Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk. <i>PLoS Genetics</i> , 2013 , 9, e1003173	6	90
229	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
228	The single-nucleotide polymorphism 309 in the MDM2 gene contributes to the Li-Fraumeni syndrome and related phenotypes. <i>European Journal of Human Genetics</i> , 2007 , 15, 110-4	5.3	85
227	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
226	Independent prognostic value of screen detection in invasive breast cancer. <i>Journal of the National Cancer Institute</i> , 2011 , 103, 585-97	9.7	83
225	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
224	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
223	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016 , 13, e1002105	11.6	80
222	Breast tumors induced by high-dose radiation display similar genetic profiles. <i>Breast Cancer Research</i> , 2005 , 7, 1	8.3	78
221	Genetic determinants of breast cancer characteristics and outcome in women under 50 years of age. <i>Breast Cancer Research</i> , 2005 , 7, 1	8.3	78
220	Clinical outcome for BRCA1 and BRCA2 mutation carriers after contralateral prophylactic mastectomy. <i>Breast Cancer Research</i> , 2005 , 7, 1	8.3	78

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219	Use of insulin and insulin analogs and risk of cancer - systematic review and meta-analysis of observational studies. <i>Current Drug Safety</i> , 2013 , 8, 333-48	1.4	77	
218	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	
217	Weekly supplementation with iron and vitamin A during pregnancy increases hemoglobin concentration but decreases serum ferritin concentration in Indonesian pregnant women. <i>Journal of Nutrition</i> , 2001 , 131, 85-90	4.1	76	
216	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 2009, 18, 1	13 ţ.g	75	
215	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012 , 21, 3926-39	5.6	75	
214	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015 , 107,	9.7	74	
213	Do MDM2 SNP309 and TP53 R72P interact in breast cancer susceptibility? A large pooled series from the breast cancer association consortium. <i>Cancer Research</i> , 2007 , 67, 9584-90	10.1	69	
212	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011 , 20, 4693-706	5.6	66	
211	Impact of Age at Primary Breast Cancer on Contralateral Breast Cancer Risk in BRCA1/2 Mutation Carriers. <i>Journal of Clinical Oncology</i> , 2016 , 34, 409-18	2.2	65	
210	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	
209	Worse breast cancer prognosis of BRCA1/BRCA2 mutation carriers: what's the evidence? A systematic review with meta-analysis. <i>PLoS ONE</i> , 2015 , 10, e0120189	3.7	65	
208	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020 , 17, 687-705	19.4	64	
207	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64	
206	Identification of women with an increased risk of developing radiation-induced breast cancer: a case only study. <i>Breast Cancer Research</i> , 2007 , 9, R26	8.3	60	
205	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	
204	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020 , 52, 56-73	36.3	56	
203	CHEK2*1100delC homozygosity is associated with a high breast cancer risk in women. <i>Journal of Medical Genetics</i> , 2011 , 48, 860-3	5.8	54	
202	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2018 , 47, 526-536	7.8	53	

201	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
200	Five polymorphisms and breast cancer risk: results from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009 , 18, 1610-6	4	53
199	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	7.8	52
198	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017 , 19, 599)- 60 ₂ 3	51
197	Assessment of PD-L1 expression across breast cancer molecular subtypes, in relation to mutation rate, -like status, tumor-infiltrating immune cells and survival. <i>OncoImmunology</i> , 2018 , 7, e1509820	7.2	51
196	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017 , 77, 2789-2799	10.1	49
195	Comparison of 6q25 breast cancer hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). <i>PLoS ONE</i> , 2012 , 7, e42380	3.7	49
194	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
193	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
192	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2014 , 16, 3416	8.3	46
191	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45
190	Cancer-immune interactions in ER-positive breast cancers: PI3K pathway alterations and tumor-infiltrating lymphocytes. <i>Breast Cancer Research</i> , 2019 , 21, 90	8.3	45
189	Long-term impact of the 70-gene signature on breast cancer outcome. <i>Breast Cancer Research and Treatment</i> , 2014 , 143, 587-92	4.4	45
188	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, 104	8.3	44
187	Mammographic screening detects low-risk tumor biology breast cancers. <i>Breast Cancer Research and Treatment</i> , 2014 , 144, 103-11	4.4	44
186	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. <i>EBioMedicine</i> , 2015 , 2, 681-9	8.8	44
185	Family history, genetic testing, and clinical risk prediction: pooled analysis of CHEK2 1100delC in 1,828 bilateral breast cancers and 7,030 controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009 , 18, 230-4	4	44
184	Nutritional status and linear growth of Indonesian infants in west java are determined more by prenatal environment than by postnatal factors. <i>Journal of Nutrition</i> , 2002 , 132, 2202-7	4.1	43

(2016-2016)

183	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
182	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. <i>Journal of Medical Genetics</i> , 2011 , 48, 477-84	5.8	42
181	Cancer risk among insulin users: comparing analogues with human insulin in the CARING five-country cohort study. <i>Diabetologia</i> , 2017 , 60, 1691-1703	10.3	41
180	Breast Cancer Survival of BRCA1/BRCA2 Mutation Carriers in a Hospital-Based Cohort of Young Women. <i>Journal of the National Cancer Institute</i> , 2017 , 109,	9.7	40
179	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	38
178	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , 2014 , 10, e1004285	6	38
177	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , 2015 , 13, 156	11.4	37
176	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
175	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
174	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
173	Treatment with insulin (analogues) and breast cancer risk in diabetics; a systematic review and meta-analysis of in vitro, animal and human evidence. <i>Breast Cancer Research</i> , 2015 , 17, 100	8.3	35
172	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , 2014 , 23, 2490-7	5.6	35
171	Weekly vitamin A and iron supplementation during pregnancy increases vitamin A concentration of breast milk but not iron status in Indonesian lactating women. <i>Journal of Nutrition</i> , 2001 , 131, 2664-9	4.1	35
170	Subsequent risk of ipsilateral and contralateral invasive breast cancer after treatment for ductal carcinoma in situ: incidence and the effect of radiotherapy in a population-based cohort of 10,090 women. <i>Breast Cancer Research and Treatment</i> , 2016 , 159, 553-63	4.4	34
169	11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012 , 33, 1123-32	4.7	33
168	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020 , 11, 3353	17.4	32
167	Cause-specific Mortality in a Population-based Cohort of 9799 Women Treated for Ductal Carcinoma In Situ. <i>Annals of Surgery</i> , 2018 , 267, 952-958	7.8	31
166	Exceptions to the rule of informed consent for research with an intervention. <i>BMC Medical Ethics</i> , 2016 , 17, 9	2.9	31

165	Use of metformin and survival of diabetic women with breast cancer. Current Drug Safety, 2013, 8, 357-0	6 3 .4	31
164	Association between polymorphisms of the renin-angiotensin system genes and breast cancer risk: a meta-analysis. <i>Breast Cancer Research and Treatment</i> , 2011 , 130, 561-8	4.4	31
163	Missense variants in ATM in 26,101 breast cancer cases and 29,842 controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 2143-51	4	31
162	A trial of consent procedures for future research with clinically derived biological samples. <i>British Journal of Cancer</i> , 2009 , 101, 1505-12	8.7	31
161	Combined effects of single nucleotide polymorphisms TP53 R72P and MDM2 SNP309, and p53 expression on survival of breast cancer patients. <i>Breast Cancer Research</i> , 2009 , 11, R89	8.3	31
160	Mental and psychomotor development in Indonesian infants of mothers supplemented with vitamin A in addition to iron during pregnancy. <i>British Journal of Nutrition</i> , 2004 , 91, 279-86	3.6	31
159	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016 , 18, 22	8.3	31
158	Vitamin A and iron supplementation of Indonesian pregnant women benefits vitamin A status of their infants. <i>British Journal of Nutrition</i> , 2001 , 86, 607-15	3.6	30
157	Diabetes and Breast Cancer Subtypes. <i>PLoS ONE</i> , 2017 , 12, e0170084	3.7	29
156	Alcohol consumption and survival after a breast cancer diagnosis: a literature-based meta-analysis and collaborative analysis of data for 29,239 cases. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 934-45	4	29
155	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
154	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, 1934-46	5.6	28
153	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021 , 596, 393-39	930.4	28
152	The Influence of Adjuvant Systemic Regimens on Contralateral Breast Cancer Risk and Receptor Subtype. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 709-718	9.7	27
151	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017 , 46, 1814-1822	7.8	27
150	Confirmation of 5p12 as a susceptibility locus for progesterone-receptor-positive, lower grade breast cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011 , 20, 2222-31	4	27
149	Obtaining 'fresh' consent for genetic research with biological samples archived 10 years ago. <i>European Journal of Cancer</i> , 2009 , 45, 1168-1174	7.5	27
148	The spectrum of ATM missense variants and their contribution to contralateral breast cancer. Breast Cancer Research and Treatment, 2008 , 107, 243-8	4.4	27

(2013-2002)

147	Randomised double-blind trial of the effect of vitamin A supplementation of Indonesian pregnant women on morbidity and growth of their infants during the first year of life. <i>European Journal of Clinical Nutrition</i> , 2002 , 56, 338-46	5.2	27	
146	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	
145	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017 , 19, 119	8.3	26	
144	Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. <i>International Journal of Cancer</i> , 2015 , 136, E685-96	7.5	26	
143	Opt-out plus, the patients' choice: preferences of cancer patients concerning information and consent regimen for future research with biological samples archived in the context of treatment. <i>Journal of Clinical Pathology</i> , 2009 , 62, 275-8	3.9	26	
142	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	
141	Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016 , 18, 98	8.3	26	
140	The prognostic value of the tumour-stroma ratio in primary operable invasive cancer of the breast: a validation study. <i>Breast Cancer Research and Treatment</i> , 2017 , 166, 435-445	4.4	25	
139	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	
138	Risk factors for metachronous contralateral breast cancer: A systematic review and meta-analysis. <i>Breast</i> , 2019 , 44, 1-14	3.6	25	
137	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	
136	Prognostic Impact of Breast-Conserving Therapy Versus Mastectomy of BRCA1/2 Mutation Carriers Compared With Noncarriers in a Consecutive Series of Young Breast Cancer Patients. <i>Annals of Surgery</i> , 2019 , 270, 364-372	7.8	24	
135	Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. <i>Genetic Epidemiology</i> , 2014 , 38, 84-93	2.6	24	
134	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015 , 17, 58	8.3	24	
133	Genetic variants in TGFEI and PAI-1 as possible risk factors for cardiovascular disease after radiotherapy for breast cancer. <i>Radiotherapy and Oncology</i> , 2012 , 102, 115-21	5.3	24	
132	Clinicopathological Risk Factors for an Invasive Breast Cancer Recurrence after Ductal Carcinoma -A Nested Case-Control Study. <i>Clinical Cancer Research</i> , 2018 , 24, 3593-3601	12.9	23	
131	Accuracy of the online prognostication tools PREDICT and Adjuvant! for early-stage breast cancer patients younger than 50 years. <i>European Journal of Cancer</i> , 2017 , 78, 37-44	7.5	22	
130	Inferior survival for young patients with contralateral compared to unilateral breast cancer: a nationwide population-based study in the Netherlands. <i>Breast Cancer Research and Treatment</i> , 2013 , 139, 811-9	4.4	21	

129	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016 , 7, 80140-80163	3.3	21
128	Candidate genetic modifiers for breast and ovarian cancer risk in BRCA1 and BRCA2 mutation carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 308-16	4	20
127	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020 , 11, 312	17.4	20
126	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. <i>British Journal of Cancer</i> , 2014 , 110, 1088-100	8.7	20
125	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. <i>Scientific Reports</i> , 2018 , 8, 6574	4.9	19
124	Optimized outcome prediction in breast cancer by combining the 70-gene signature with clinical risk prediction algorithms. <i>Breast Cancer Research and Treatment</i> , 2014 , 145, 697-705	4.4	19
123	SNP-SNP interaction analysis of NF- B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015 , 6, 37979-94	3.3	19
122	Determinants of weight and length of Indonesian neonates. <i>European Journal of Clinical Nutrition</i> , 2002 , 56, 947-51	5.2	19
121	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	5.3	18
120	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016 , 11, e0153788	3.7	18
119	The prognostic value of the tumor-stroma ratio is most discriminative in patients with grade III or triple-negative breast cancer. <i>International Journal of Cancer</i> , 2020 , 146, 2296-2304	7.5	18
118	Predictors of an Invasive Breast Cancer Recurrence after DCIS: A Systematic Review and Meta-analyses. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 835-845	4	17
117	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. <i>Breast Cancer Research</i> , 2015 , 17, 18	8.3	17
116	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
115	Validation of the BOADICEA model and a 313-variant polygenic risk score for breast cancer risk prediction in a Dutch prospective cohort. <i>Genetics in Medicine</i> , 2020 , 22, 1803-1811	8.1	17
114	Excess breast cancer risk in first degree relatives of CHEK2*1100delC positive familial breast cancer cases. <i>European Journal of Cancer</i> , 2013 , 49, 1993-9	7.5	17
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101	Variants of uncertain clinical significance in hereditary breast and ovarian cancer genes: best practices in functional analysis for clinical annotation. <i>Journal of Medical Genetics</i> , 2020 , 57, 509-518	5.8	14
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91	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
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61	The association of diabetes mellitus and insulin treatment with expression of insulin-related proteins in breast tumors. <i>BMC Cancer</i> , 2018 , 18, 224	4.8	6
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36	Effectiveness of a multicentre nasopharyngeal carcinoma awareness programme in Indonesia. <i>BMJ Open</i> , 2016 , 6, e008571	3	2
35	Abstract 2030: The role of genetic variation in calcium-activated potassium channels in breast cancer patients treated with tamoxifen 2016 ,		2
34	Prospective Evaluation of a Breast Cancer Risk Model Integrating Classical Risk Factors and Polygenic Risk in 15 Cohorts from Six Countries		2
33	Combining genome-wide studies of breast, prostate, ovarian and endometrial cancers maps cross-cancer susceptibility loci and identifies new genetic associations		2
32	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. <i>Npj Breast Cancer</i> , 2021 , 7, 52	7.8	2
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28	Prognostic Value of Stromal Tumor-Infiltrating Lymphocytes in Young, Node-Negative, Triple-Negative Breast Cancer Patients Who Did Not Receive (neo)Adjuvant Systemic Therapy Journal of Clinical Oncology, 2022 , JCO2101536	2.2	2
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26	The BIO-PIN paradigm: 'access to' or 'return of' results?. <i>Nature Reviews Cancer</i> , 2011 , 11, 895; author reply 895	31.3	1
25	Enhancing the BOADICEA cancer risk prediction model to incorporate new data on RAD51C, RAD51D, BARD1, updates to tumour pathology and cancer incidences		1
24	Outcome without any adjuvant systemic treatment in stage I ER+/HER2- breast cancer patients included in the MINDACT trial. <i>Annals of Oncology</i> , 2021 ,	10.3	1
23	Familial versus Sporadic Breast Cancer: Different Treatments for Similar Tumors?. <i>Advances in Breast Cancer Research</i> , 2015 , 04, 87-99	0.1	1
22	Common variants in breast cancer risk loci predispose to distinct tumor subtypes		1

21	Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers		1
20	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1
19	Genomic profiling defines variable clonal relatedness between invasive breast cancer and primary ductal carcinoma in situ		1
18	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	11	1
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6	Letter to the editor regarding: 'Association between BRCA mutational status and survival in patients with breast cancer: a systematic review and meta-analysis'. <i>Breast Cancer Research and Treatment</i> , 2021 , 188, 821-823	4.4	O
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LIST OF PUBLICATIONS

- Towards implementation of comprehensive breast cancer risk prediction tools in health care for personalised prevention.. *Preventive Medicine*, **2022**, 107075
- 4.3 0
- Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51
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- Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. *Obstetrical and Gynecological Survey*, **2015**, 70, 758-762²⁻⁴