Marjanka K Schmidt

List of Publications by Year
in descending order

285	22,447	11651 70	11308 136
papers	citations	h-index	g-index

306	306	306	25786
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
3	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. PLoS Medicine, 2010, 7, e1000279.	8.4	764
4	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
5	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, 250-263.	6.3	596
6	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
7	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
8	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
9	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
10	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
11	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
12	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	21.4	434
13	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
14	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
15	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	2.4	415
16	Genome-wide association studies identify four ER negativeâ€"specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
17	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
18	Risk reduction of contralateral breast cancer and survival after contralateral prophylactic mastectomy in BRCA1 or BRCA2 mutation carriers. British Journal of Cancer, 2005, 93, 287-292.	6.4	307

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19	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
20	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
21	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
22	Somatic mutations in the chromatin remodeling gene ARID1A occur in several tumor types. Human Mutation, 2012, 33, 100-103.	2.5	263
23	The 70-gene prognosis-signature predicts disease outcome in breast cancer patients with 1â€“3 positive lymph nodes in an independent validation study. Breast Cancer Research and Treatment, 2009, 116, 295-302.	2.5	260
24	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
25	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
26	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
27	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
28	Annexin A1 regulates TGF-Î² signaling and promotes metastasis formation of basal-like breast cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6340-6345.	7.1	182
29	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	27.6	178
30	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
31	PREDICT Plus: development and validation of a prognostic model for early breast cancer that includes HER2. British Journal of Cancer, 2012, 107, 800-807.	6.4	163
32	CHEK2*1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancerâ€“Specific Death, and Increased Risk of a Second Breast Cancer. Journal of Clinical Oncology, 2012, 30, 4308-4316.	1.6	162
33	An updated PREDICT breast cancer prognostication and treatment benefit prediction model with independent validation. Breast Cancer Research, 2017, 19, 58.	5.0	161
34	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
35	Calibration and discriminatory accuracy of prognosis calculation for breast cancer with the online Adjuvant! program: a hospital-based retrospective cohort study. Lancet Oncology, The, 2009, 10, 1070-1076.	10.7	154
36	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, 3289-3303.	2.9	152

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37	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
38	An aCGH classifier derived from BRCA1-mutated breast cancer and benefit of high-dose platinum-based chemotherapy in HER2-negative breast cancer patients. Annals of Oncology, 2011, 22, 1561-1570.	1.2	150
39	Geneâ€“environment interaction and risk of breast cancer. British Journal of Cancer, 2016, 114, 125-133.	6.4	147
40	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
41	The 70-gene prognosis signature predicts early metastasis in breast cancer patients between 55 and 70 years of age. Annals of Oncology, 2010, 21, 717-722.	1.2	129
42	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
43	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
44	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	8.4	118
45	Breast Cancer Survival and Tumor Characteristics in Premenopausal Women Carrying the CHEK2*1100delC Germline Mutation. Journal of Clinical Oncology, 2007, 26, 64-69.	1.6	110
46	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
47	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
48	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
49	Independent Prognostic Value of Screen Detection in Invasive Breast Cancer. Journal of the National Cancer Institute, 2011, 103, 585-597.	6.3	100
50	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
51	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
52	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
53	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
54	Use of Insulin and Insulin Analogs and Risk of Cancer â€” Systematic Review and Meta-Analysis of Observational Studies. Current Drug Safety, 2013, 8, 333-348.	0.6	95

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55	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
56	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
57	The single-nucleotide polymorphism 309 in the MDM2 gene contributes to the Liâ€“Fraumeni syndrome and related phenotypes. European Journal of Human Genetics, 2007, 15, 110-114.	2.8	91
58	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
59	Worse Breast Cancer Prognosis of BRCA1/BRCA2 Mutation Carriers: What's the Evidence? A Systematic Review with Meta-Analysis. PLoS ONE, 2015, 10, e0120189.	2.5	88
60	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536.	1.9	88
61	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
62	Weekly Supplementation with Iron and Vitamin A during Pregnancy Increases Hemoglobin Concentration but Decreases Serum Ferritin Concentration in Indonesian Pregnant Women. Journal of Nutrition, 2001, 131, 85-90.	2.9	84
63	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 2009, 18, 1131-1139.	2.9	84
64	Impact of Age at Primary Breast Cancer on Contralateral Breast Cancer Risk in BRCA1/2 Mutation Carriers. Journal of Clinical Oncology, 2016, 34, 409-418.	1.6	84
65	Cancer-immune interactions in ER-positive breast cancers: PI3K pathway alterations and tumor-infiltrating lymphocytes. Breast Cancer Research, 2019, 21, 90.	5.0	81
66	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
67	Do MDM2 SNP309 and TP53 R72P Interact in Breast Cancer Susceptibility? A Large Pooled Series from the Breast Cancer Association Consortium. Cancer Research, 2007, 67, 9584-9590.	0.9	80
68	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80
69	Assessment of PD-L1 expression across breast cancer molecular subtypes, in relation to mutation rate, BRCA1-like status, tumor-infiltrating immune cells and survival. OncoImmunology, 2018, 7, e1509820.	4.6	80
70	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
71	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
72	Identification of women with an increased risk of developing radiation-induced breast cancer: a case only study. Breast Cancer Research, 2007, 9, R26.	5.0	76

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73	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.	6.2	76
74	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
75	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
76	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 Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	2.9	71
77	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
78	CHEK2*1100delC homozygosity is associated with a high breast cancer risk in women. Journal of Medical Genetics, 2011, 48, 860-863.	3.2	66
79	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	6.2	59
80	Nutritional Status and Linear Growth of Indonesian Infants in West Java Are Determined More by Prenatal Environment than by Postnatal Factors. Journal of Nutrition, 2002, 132, 2202-2207.	2.9	57
81	Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1610-1616.	2.5	57
82	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	5.0	57
83	Cancer risk among insulin users: comparing analogues with human insulin in the CARING five-country cohort study. Diabetologia, 2017, 60, 1691-1703.	6.3	57
84	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
85	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	6.1	56
86	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
87	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.	5.0	56
88	Breast Cancer Survival of BRCA1/BRCA2 Mutation Carriers in a Hospital-Based Cohort of Young Women. Journal of the National Cancer Institute, 2017, 109, .	6.3	55
89	Long-term impact of the 70-gene signature on breast cancer outcome. Breast Cancer Research and Treatment, 2014, 143, 587-592.	2.5	54
90	Cause-specific Mortality in a Population-based Cohort of 9799 Women Treated for Ductal Carcinoma In Situ. Annals of Surgery, 2018, 267, 952-958.	4.2	54

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91	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
92	Mammographic screening detects low-risk tumor biology breast cancers. Breast Cancer Research and Treatment, 2014, 144, 103-111.	2.5	53
93	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
94	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	5.5	51
95	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
96	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. Breast Cancer Research and Treatment, 2016, 159, 553-563.	2.5	51
97	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. Scientific Reports, 2018, 8, 6574.	3.3	51
98	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	2.5	51
99	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
100	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
101	Validation of the BOADICEA model and a 313-variant polygenic risk score for breast cancer risk prediction in a Dutch prospective cohort. Genetics in Medicine, 2020, 22, 1803-1811.	2.4	49
102	Family History, Genetic Testing, and Clinical Risk Prediction: Pooled Analysis of CHEK2*1100delC in 1,828 Bilateral Breast Cancers and 7,030 Controls. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 230-234.	2.5	47
103	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. Journal of Medical Genetics, 2011, 48, 477-484.	3.2	47
104	Diabetes and Breast Cancer Subtypes. PLoS ONE, 2017, 12, e0170084.	2.5	47
105	Weekly Vitamin A and Iron Supplementation during Pregnancy Increases Vitamin A Concentration of Breast Milk but Not Iron Status in Indonesian Lactating Women. Journal of Nutrition, 2001, 131, 2664-2669.	2.9	46
106	Treatment with insulin (analogues) and breast cancer risk in diabetics; a systematic review and meta-analysis of in vitro, animal and human evidence. Breast Cancer Research, 2015, 17, 100.	5.0	45
107	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
108	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	6.3	45

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109	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, 40, 2361-2374.	1.6	45
110	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
111	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
112	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. International Journal of Epidemiology, 2022, 50, 1897-1911.	1.9	43
113	Exceptions to the rule of informed consent for research with an intervention. BMC Medical Ethics, 2016, 17, 9.	2.4	42
114	Risk factors for metachronous contralateral breast cancer: A systematic review and meta-analysis. Breast, 2019, 44, 1-14.	2.2	42
115	The prognostic value of the tumour-stroma ratio in primary operable invasive cancer of the breast: a validation study. Breast Cancer Research and Treatment, 2017, 166, 435-445.	2.5	41
116	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. Annals of Surgery, 2019, 270, 364-372.	4.2	41
117	Predictors of an Invasive Breast Cancer Recurrence after DCIS: A Systematic Review and Meta-analyses. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 835-845.	2.5	41
118	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. International Journal of Epidemiology, 2020, 49, 1117-1131.	1.9	41
119	The prognostic value of the tumorâ€“stroma ratio is most discriminative in patients with grade III or tripleâ€negative breast cancer. International Journal of Cancer, 2020, 146, 2296-2304.	5.1	41
120	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
121	The Influence of Adjuvant Systemic Regimens on Contralateral Breast Cancer Risk and Receptor Subtype. Journal of the National Cancer Institute, 2019, 111, 709-718.	6.3	40
122	Breast cancer risk factors and their effects on survival: a Mendelian randomisation study. BMC Medicine, 2020, 18, 327.	5.5	40
123	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
124	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	5.0	39
125	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
126	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38

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127	Accuracy of the online prognostication tools PREDICT and Adjuvant! for early-stage breast cancer patients younger than 50 years. European Journal of Cancer, 2017, 78, 37-44.	2.8	38
128	Alcohol Consumption and Survival after a Breast Cancer Diagnosis: A Literature-Based Meta-analysis and Collaborative Analysis of Data for 29,239 Cases. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 934-945.	2.5	37
129	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	6.2	37
130	Combined effects of single nucleotide polymorphisms TP53 R72P and MDM2 SNP309, and p53 expression on survival of breast cancer patients. Breast Cancer Research, 2009, 11, R89.	5.0	35
131	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35
132	Use of Metformin and Survival of Diabetic Women with Breast Cancer. Current Drug Safety, 2013, 8, 357-363.	0.6	35
133	Vitamin A and iron supplementation of Indonesian pregnant women benefits vitamin A status of their infants. British Journal of Nutrition, 2001, 86, 607-615.	2.3	34
134	Mental and psychomotor development in Indonesian infants of mothers supplemented with vitamin A in addition to iron during pregnancy. British Journal of Nutrition, 2004, 91, 279-285.	2.3	34
135	A trial of consent procedures for future research with clinically derived biological samples. British Journal of Cancer, 2009, 101, 1505-1512.	6.4	34
136	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	5.1	34
137	Comprehensive trends in incidence, treatment, survival and mortality of first primary invasive breast cancer stratified by age, stage and receptor subtype in the Netherlands between 1989 and 2017. International Journal of Cancer, 2021, 148, 2289-2303.	5.1	34
138	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. Nature Genetics, 2022, 54, 850-860.	21.4	34
139	Missense Variants in ATM in 26,101 Breast Cancer Cases and 29,842 Controls. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2143-2151.	2.5	33
140	Association between polymorphisms of the reninâ€“angiotensin system genes and breast cancer risk: a meta-analysis. Breast Cancer Research and Treatment, 2011, 130, 561-568.	2.5	33
141	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	2.9	33
142	Variants of uncertain clinical significance in hereditary breast and ovarian cancer genes: best practices in functional analysis for clinical annotation. Journal of Medical Genetics, 2020, 57, 509-518.	3.2	33
143	The spectrum of ATM missense variants and their contribution to contralateral breast cancer. Breast Cancer Research and Treatment, 2008, 107, 243-248.	2.5	32
144	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, 1934-1946.	2.9	32

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145	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
146	Obtaining â€˜freshâ€™ consent for genetic research with biological samples archived 10 years ago. European Journal of Cancer, 2009, 45, 1168-1174.	2.8	31
147	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	1.8	31
148	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.	5.0	31
149	Clinicopathological Risk Factors for an Invasive Breast Cancer Recurrence after Ductal Carcinoma In Situâ€”A Nested Caseâ€“Control Study. Clinical Cancer Research, 2018, 24, 3593-3601.	7.0	30
150	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
151	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. European Journal of Clinical Nutrition, 2002, 56, 338-346.	2.9	29
152	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. Journal of Clinical Pathology, 2009, 62, 275-278.	2.0	29
153	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	1.4	29
154	Genetic variants in TGFÎ²-1 and PAI-1 as possible risk factors for cardiovascular disease after radiotherapy for breast cancer. Radiotherapy and Oncology, 2012, 102, 115-121.	0.6	28
155	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
156	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
157	Outcome of Patients With an Ultralow-Risk 70-Gene Signature in the MINDACT Trial. Journal of Clinical Oncology, 2022, 40, 1335-1345.	1.6	28
158	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptorâ€“Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	2.5	27
159	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
160	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
161	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.	3.0	24
162	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24

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163	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
164	Inferior survival for young patients with contralateral compared to unilateral breast cancer: a nationwide population-based study in the Netherlands. Breast Cancer Research and Treatment, 2013, 139, 811-819.	2.5	23
165	Optimized outcome prediction in breast cancer by combining the 70-gene signature with clinical risk prediction algorithms. Breast Cancer Research and Treatment, 2014, 145, 697-705.	2.5	22
166	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	2.5	22
167	Determinants of weight and length of Indonesian neonates. European Journal of Clinical Nutrition, 2002, 56, 947-951.	2.9	21
168	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	6.4	21
169	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	1.8	21
170	Assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk, in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2020, 49, 216-232.	1.9	21
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172	Excess breast cancer risk in first degree relatives of CHEK2âˆ—1100delC positive familial breast cancer cases. European Journal of Cancer, 2013, 49, 1993-1999.	2.8	20
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