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	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
2	Effects of chemotherapy on contralateral breast cancer risk in BRCA1 and BRCA2 mutation carriers: A nationwide cohort study. Breast, 2022, 61, 98-107.	2.2	6
3	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
4	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
5	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
6	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
7	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
8	Survival of BRCA1/BRCA2-associated pT1 breast cancer patients, a cohort study. Breast Cancer Research and Treatment, 2022, , .	2.5	1
9	Towards implementation of comprehensive breast cancer risk prediction tools in health care for personalised prevention. Preventive Medicine, 2022, 159, 107075.	3.4	3
10	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
11	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. Nature Genetics, 2022, 54, 850-860.	21.4	34
12	Prediction Models and Decision Aids for Women with Ductal Carcinoma In Situ: A Systematic Literature Review. Cancers, 2022, 14, 3259.	3.7	5
13	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. Cancers, 2022, 14, 3363.	3.7	2
14	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
15	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
16	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	6.4	5
17	Browser-based Data Annotation, Active Learning, and Real-Time Distribution of Artificial Intelligence Models: From Tumor Tissue Microarrays to COVID-19 Radiology. Journal of Pathology Informatics, 2021, 12, 38.	1.7	2
18	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19

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19	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
20	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. Npj Breast Cancer, 2021, 7, 52.	5.2	7
21	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	3.7	4
22	Letter to the editor regarding: â€˜Association between BRCA mutational status and survival in patients with breast cancer: a systematic review and meta-analysisâ€™. Breast Cancer Research and Treatment, 2021, 188, 821-823.	2.5	2
23	Combining method of detection and 70-gene signature for enhanced prognostication of breast cancer. Breast Cancer Research and Treatment, 2021, 189, 399-410.	2.5	5
24	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	2.4	16
25	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
26	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. Breast Cancer Research, 2021, 23, 86.	5.0	7
27	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
28	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
29	Long-term risk of subsequent ipsilateral lesions after surgery with or without radiotherapy for ductal carcinoma in situ of the breast. British Journal of Cancer, 2021, 125, 1443-1449.	6.4	6
30	Barriers and Facilitators for Implementing a National Guideline to Foster the Responsible Use of Residual Biospecimens and Data in Health Research. Biopreservation and Biobanking, 2021, , .	1.0	1
31	Circadian PERformance in breast cancer: a germline and somatic genetic study of PER3VNTR polymorphisms and gene co-expression. Npj Breast Cancer, 2021, 7, 118.	5.2	3
32	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	2.5	19
33	Performance of Breast Cancer Polygenic Risk Scores in 760 FemaleCHEK2Germline Mutation Carriers. Journal of the National Cancer Institute, 2021, 113, 893-899.	6.3	21
34	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2
35	Germline breast cancer susceptibility genes, tumor characteristics, and survival. Genome Medicine, 2021, 13, 185.	8.2	3
36	Outcome without any adjuvant systemic treatment in stage I ER+/HER2- breast cancer patients included in the MINDACT trial. Annals of Oncology, 2021, , .	1.2	9

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37	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
38	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
39	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. International Journal of Epidemiology, 2020, 49, 1117-1131.	1.9	41
40	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
41	Breast cancer risk factors and their effects on survival: a Mendelian randomisation study. BMC Medicine, 2020, 18, 327.	5.5	40
42	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
43	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44.	5.2	5
44	Contralateral breast cancer risk in patients with ductal carcinoma in situ and invasive breast cancer. Npj Breast Cancer, 2020, 6, 60.	5.2	9
45	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
46	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	27.6	178
47	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
48	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
49	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
50	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
51	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
52	The impact of patient characteristics and lifestyle factors on the risk of an ipsilateral event after a primary DCIS: A systematic review. Breast, 2020, 50, 95-103.	2.2	7
53	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
54	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	2.5	14

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55	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
56	Cancer-immune interactions in ER-positive breast cancers: PI3K pathway alterations and tumor-infiltrating lymphocytes. Breast Cancer Research, 2019, 21, 90.	5.0	81
57	Breast Cancer Susceptibilityâ€"Towards Individualised Risk Prediction. Current Genetic Medicine Reports, 2019, 7, 124-135.	1.9	4
58	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
59	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. EBioMedicine, 2019, 48, 203-211.	6.1	14
60	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
61	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
62	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
63	Type 2 Diabetes, but Not Insulin (Analog) Treatment, Is Associated With More Advanced Stages of Breast Cancer: A National Linkage of Cancer and Pharmacy Registries. Diabetes Care, 2019, 42, 434-442.	8.6	19
64	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
65	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
66	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
67	A response to â€œPersonalised medicine and population health: breast and ovarian cancerâ€• Human Genetics, 2019, 138, 287-289.	3.8	14
68	Discordant Marker Expression Between Invasive Breast Carcinoma and Corresponding Synchronous and Preceding DCIS. American Journal of Surgical Pathology, 2019, 43, 1574-1582.	3.7	17
69	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
70	Risk factors for metachronous contralateral breast cancer: A systematic review and meta-analysis. Breast, 2019, 44, 1-14.	2.2	42
71	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
72	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	1.4	29

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73	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	2.4	415
74	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
75	Cliniciansâ€™ use of breast cancer risk assessment tools according to their perceived importance of breast cancer risk factors: an international survey. Journal of Community Genetics, 2019, 10, 61-71.	1.2	7
76	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19
77	Patients' Attitudes Towards the Return of Incidental Findings After Research with Residual Tissue: A Mixed Methods Study. Genetic Testing and Molecular Biomarkers, 2018, 22, 178-186.	0.7	5
78	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. International Journal of Cancer, 2018, 143, 746-757.	5.1	19
79	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
80	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
81	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
82	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
83	Recall and Retention of Consent Procedure Contents and Decisions: Results of a Randomized Controlled Trial. Public Health Genomics, 2018, 21, 27-36.	1.0	1
84	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
85	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. Drug and Alcohol Dependence, 2018, 188, 94-101.	3.2	10
86	Breast cancerâ€“related deaths according to grade in ductal carcinoma in situ: A Dutch populationâ€“based study on patients diagnosed between 1999 and 2012. European Journal of Cancer, 2018, 101, 134-142.	2.8	14
87	The association of diabetes mellitus and insulin treatment with expression of insulin-related proteins in breast tumors. BMC Cancer, 2018, 18, 224.	2.6	11
88	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
89	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
90	An association study of established breast cancer reproductive and lifestyle risk factors with tumour subtype defined by the prognostic 70-gene expression signature (MammaPrint Â®). European Journal of Cancer, 2017, 75, 5-13.	2.8	13

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91	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
92	Trends in breast cancer incidence among women with type-2 diabetes in British general practice. Primary Care Diabetes, 2017, 11, 373-382.	1.8	10
93	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
94	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
95	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
96	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
97	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
98	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
99	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
100	Geneâ€“environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20
101	Long-term prognosis of young breast cancer patients (â‰¤40 years) who did not receive adjuvant systemic treatment: protocol for the PARADIGM initiative cohort study. BMJ Open, 2017, 7, e017842.	1.9	11
102	The role of Indonesian patientsâ€™ health behaviors in delaying the diagnosis of nasopharyngeal carcinoma. BMC Public Health, 2017, 17, 510.	2.9	18
103	The method of detection of ductal carcinoma in situ has no therapeutic implications: results of a population-based cohort study. Breast Cancer Research, 2017, 19, 26.	5.0	12
104	An updated PREDICT breast cancer prognostication and treatment benefit prediction model with independent validation. Breast Cancer Research, 2017, 19, 58.	5.0	161
105	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
106	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
107	Diabetes and Breast Cancer Subtypes. PLoS ONE, 2017, 12, e0170084.	2.5	47
108	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43

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109	Abstract P2-07-05: Risk of metachronous contralateral breast cancer: Systematic review and meta-analysis. , 2017, , .		1
110	Evaluation of the EGFR polymorphism R497K in two cohorts of neoadjuvantly treated breast cancer patients. PLoS ONE, 2017, 12, e0189750.	2.5	8
111	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	1.8	14
112	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
113	Independent replication of polymorphisms predicting toxicity in breast cancer patients randomized between dose-dense and docetaxel-containing adjuvant chemotherapy. Oncotarget, 2017, 8, 113531-113542.	1.8	8
114	Abstract 4738: Risk of ipsilateral invasive breast cancer after DCIS: a comparison of primary DCIS and subsequent invasive disease by morphological and immunohistochemical analysis. , 2017, , .		0
115	Abstract 5612: Cancer-immune interactions in luminal breast cancers:PI3KCAmutations, PI3K/AKT/mTOR activation and tumor-infiltrating lymphocytes. , 2017, , .		0
116	Abstract 575: PD-L1 positive tumor-infiltrating lymphocytes and mutational load in breast cancer. , 2017, , .		0
117	Abstract 2258: Genome-wide association studies of breast cancer prognosis. , 2017, , .		0
118	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
119	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
120	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
121	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
122	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
123	Recurrent HOXB13 mutations in the Dutch population do not associate with increased breast cancer risk. Scientific Reports, 2016, 6, 30026.	3.3	3
124	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
125	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
126	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

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127	Association Between Insulin Treatment and Breast Cancer Characteristics. Value in Health, 2016, 19, A715.	0.3	0
128	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
129	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
130	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
131	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
132	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
133	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
134	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
135	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
136	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	3.3	19
137	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
138	Effectiveness of a multicentre nasopharyngeal carcinoma awareness programme in Indonesia. BMJ Open, 2016, 6, e008571.	1.9	6
139	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
140	Exceptions to the rule of informed consent for research with an intervention. BMC Medical Ethics, 2016, 17, 9.	2.4	42
141	Geneâ€“environment interaction and risk of breast cancer. British Journal of Cancer, 2016, 114, 125-133.	6.4	147
142	Highâ€throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2016, 2, 138-153.	3.0	19
143	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
144	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

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145	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	6.4	7
146	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
147	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. Human Genetics, 2016, 135, 137-154.	3.8	8
148	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
149	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
150	Abstract 2030: The role of genetic variation in calcium-activated potassium channels in breast cancer patients treated with tamoxifen. Cancer Research, 2016, 76, 2030-2030.	0.9	2
151	The Impact of the Overall Radiotherapy Time on Clinical Outcome of Patients with Nasopharyngeal Carcinoma; A Retrospective Study. PLoS ONE, 2016, 11, e0151899.	2.5	10
152	A Randomised Controlled Trial of Consent Procedures for the Use of Residual Tissues for Medical Research: Preferences of and Implications for Patients, Research and Clinical Practice. PLoS ONE, 2016, 11, e0152509.	2.5	5
153	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
154	Abstract 3451: Breast cancer risk factor associations by loss of E-cadherin tumor tissue expression: A pooled analysis of 5,896 cases in 12 studies from the Breast Cancer Association Consortium (BCAC). , 2016, , .		0
155	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
156	Data management and data analysis techniques in pharmacoepidemiological studies using a preâ€planned multiâ€database approach: a systematic literature review. Pharmacoepidemiology and Drug Safety, 2015, 24, 897-905.	1.9	18
157	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. BMC Cancer, 2015, 15, 978.	2.6	6
158	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
159	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
160	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
161	SNP-SNP interaction analysis of NF-Î¹B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
162	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428

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163	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
164	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
165	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	6.1	56
166	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
167	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
168	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	2.8	14
169	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
170	Timing of risk reducing mastectomy in breast cancer patients carrying a BRCA1/2 mutation: retrospective data from the Dutch HEBON study. Familial Cancer, 2015, 14, 355-363.	1.9	12
171	Evaluation of the Dutch BRCA1/2 clinical genetic center referral criteria in an unselected early breast cancer population. European Journal of Human Genetics, 2015, 23, 588-595.	2.8	13
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