Peter A Fasching

List of Publications by Year
in descending order

367 papers	42,326 citations	3731 89 h-index	2895 190 g-index
410 all docs	410 docs citations	410 times ranked	35902 citing authors

#	Article	IF	Citations
1	Pathological complete response and long-term clinical benefit in breast cancer: the CTNeoBC pooled analysis. Lancet, The, 2014, 384, 164-172.	13.7	3,224
2	Definition and Impact of Pathologic Complete Response on Prognosis After Neoadjuvant Chemotherapy in Various Intrinsic Breast Cancer Subtypes. Journal of Clinical Oncology, 2012, 30, 1796-1804.	1.6	2,062
3	Trastuzumab Emtansine for Residual Invasive HER2-Positive Breast Cancer. New England Journal of Medicine, 2019, 380, 617-628.	27.0	1,610
4	Pembrolizumab for Early Triple-Negative Breast Cancer. New England Journal of Medicine, 2020, 382, 810-821.	27.0	1,542
5	Tumour-infiltrating lymphocytes and prognosis in different subtypes of breast cancer: a pooled analysis of 3771 patients treated with neoadjuvant therapy. Lancet Oncology, The, 2018, 19, 40-50.	10.7	1,327
6	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
7	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
8	Neoadjuvant carboplatin in patients with triple-negative and HER2-positive early breast cancer (GeparSixto; GBG 66): a randomised phase 2 trial. Lancet Oncology, The, 2014, 15, 747-756.	10.7	810
9	Association between endometriosis and risk of histological subtypes of ovarian cancer: a pooled analysis of caseâ€“control studies. Lancet Oncology, The, 2012, 13, 385-394.	10.7	753
10	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
11	Phase III Randomized Study of Ribociclib and Fulvestrant in Hormone Receptorâ€“Positive, Human Epidermal Growth Factor Receptor 2â€“Negative Advanced Breast Cancer: MONALEESA-3. Journal of Clinical Oncology, 2018, 36, 2465-2472.	1.6	704
12	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
13	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
14	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
15	Inherited Mutations in 17 Breast Cancer Susceptibility Genes Among a Large Triple-Negative Breast Cancer Cohort Unselected for Family History of Breast Cancer. Journal of Clinical Oncology, 2015, 33, 304-311.	1.6	521
16	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
17	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
18	Neoadjuvant Treatment With Trastuzumab in HER2-Positive Breast Cancer: Results From the GeparQuattro Study. Journal of Clinical Oncology, 2010, 28, 2024-2031.	1.6	487

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19	Overall Survival with Ribociclib plus Fulvestrant in Advanced Breast Cancer. New England Journal of Medicine, 2020, 382, 514-524.	27.0	482
20	Neoadjuvant Chemotherapy and Bevacizumab for HER2-Negative Breast Cancer. New England Journal of Medicine, 2012, 366, 299-309.	27.0	473
21	Association Between CYP2D6 Polymorphisms and Outcomes Among Women With Early Stage Breast Cancer Treated With Tamoxifen. JAMA - Journal of the American Medical Association, 2009, 302, 1429.	7.4	468
22	Pathologic Complete Response After Neoadjuvant Chemotherapy Plus Trastuzumab Predicts Favorable Survival in Human Epidermal Growth Factor Receptor 2â€“Overexpressing Breast Cancer: Results From the TECHNO Trial of the AGO and GBG Study Groups. Journal of Clinical Oncology, 2011, 29, 3351-3357.	1.6	456
23	Event-free Survival with Pembrolizumab in Early Triple-Negative Breast Cancer. New England Journal of Medicine, 2022, 386, 556-567.	27.0	444
24	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
25	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
26	Lapatinib versus trastuzumab in combination with neoadjuvant anthracycline-taxane-based chemotherapy (GeparQuinto, GBG 44): a randomised phase 3 trial. Lancet Oncology, The, 2012, 13, 135-144.	10.7	425
27	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
28	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
29	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
30	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
31	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
32	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	21.4	309
33	Germline Mutation Status, Pathological Complete Response, and Disease-Free Survival in Triple-Negative Breast Cancer. JAMA Oncology, 2017, 3, 1378.	7.1	300
34	Pooled Analysis of the Prognostic Relevance of Circulating Tumor Cells in Primary Breast Cancer. Clinical Cancer Research, 2016, 22, 2583-2593.	7.0	289
35	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
36	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

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37	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
38	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
39	Ki67, chemotherapy response, and prognosis in breast cancer patients receiving neoadjuvant treatment. BMC Cancer, 2011, 11, 486.	2.6	260
40	Dose-Response Association of CD8⁺ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. JAMA Oncology, 2017, 3, e173290.	7.1	260
41	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
42	Clinical and molecular characteristics of HER2-low-positive breast cancer: pooled analysis of individual patient data from four prospective, neoadjuvant clinical trials. Lancet Oncology, The, 2021, 22, 1151-1161.	10.7	248
43	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
44	PIK3CA Mutations Are Associated With Lower Rates of Pathologic Complete Response to Antiâ€“Human Epidermal Growth Factor Receptor 2 (HER2) Therapy in Primary HER2-Overexpressing Breast Cancer. Journal of Clinical Oncology, 2014, 32, 3212-3220.	1.6	231
45	Standardized evaluation of tumor-infiltrating lymphocytes in breast cancer: results of the ring studies of the international immuno-oncology biomarker working group. Modern Pathology, 2016, 29, 1155-1164.	5.5	230
46	Impact of treatment characteristics on response of different breast cancer phenotypes: pooled analysis of the German neo-adjuvant chemotherapy trials. Breast Cancer Research and Treatment, 2011, 125, 145-156.	2.5	228
47	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. Journal of the National Cancer Institute, 2018, 110, 855-862.	6.3	225
48	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
49	Circulating Micro-RNAs as Potential Blood-Based Markers for Early Stage Breast Cancer Detection. PLoS ONE, 2012, 7, e29770.	2.5	219
50	Molecular profiling of single circulating tumor cells with diagnostic intention. EMBO Molecular Medicine, 2014, 6, 1371-1386.	6.9	218
51	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
52	Capecitabine in Addition to Anthracycline- and Taxane-Based Neoadjuvant Treatment in Patients With Primary Breast Cancer: Phase III GeparQuattro Study. Journal of Clinical Oncology, 2010, 28, 2015-2023.	1.6	194
53	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
54	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183

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55	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
56	The Contributions of Breast Density and Common Genetic Variation to Breast Cancer Risk. Journal of the National Cancer Institute, 2015, 107, .	6.3	174
57	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
58	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	2.9	168
59	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
60	Tumor-Infiltrating Lymphocytes: A Predictive and Prognostic Biomarker in Neoadjuvant-Treated HER2-Positive Breast Cancer. Clinical Cancer Research, 2016, 22, 5747-5754.	7.0	158
61	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
62	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
63	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
64	Neoadjuvant Trastuzumab Emtansine and Pertuzumab in Human Epidermal Growth Factor Receptor 2â€“Positive Breast Cancer: Three-Year Outcomes From the Phase III KRISTINE Study. Journal of Clinical Oncology, 2019, 37, 2206-2216.	1.6	152
65	Hereditary breast and ovarian cancer: review and future perspectives. Journal of Molecular Medicine, 2006, 84, 16-28.	3.9	149
66	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	2.8	145
67	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
68	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	21.4	141
69	Ki67 Measured after Neoadjuvant Chemotherapy for Primary Breast Cancer. Clinical Cancer Research, 2013, 19, 4521-4531.	7.0	137
70	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
71	Specific microRNA signatures in exosomes of triple-negative and HER2-positive breast cancer patients undergoing neoadjuvant therapy within the GeparSixto trial. BMC Medicine, 2018, 16, 179.	5.5	134
72	Proliferation and cellâ€“cell fusion of endometrial carcinoma are induced by the human endogenous retroviral Syncytin-1 and regulated by TGF-Î². Journal of Molecular Medicine, 2006, 85, 23-38.	3.9	132

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73	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
74	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
75	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
76	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	1.9	111
77	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
78	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	12.8	109
79	Changes in serum levels of miR-21, miR-210, and miR-373 in HER2-positive breast cancer patients undergoing neoadjuvant therapy: a translational research project within the Geparquinto trial. Breast Cancer Research and Treatment, 2014, 147, 61-68.	2.5	108
80	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
81	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
82	Common Breast Cancer Susceptibility Variants in LSP1 and RAD51L1 Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1156-1166.	2.5	101
83	Presence of Circulating Tumor Cells in High-Risk Early Breast Cancer During Follow-Up and Prognosis. Journal of the National Cancer Institute, 2019, 111, 380-387.	6.3	101
84	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
85	Risk of Estrogen Receptorâ€“Positive and â€“Negative Breast Cancer and Singleâ€“Nucleotide Polymorphism 2q35-rs13387042. Journal of the National Cancer Institute, 2009, 101, 1012-1018.	6.3	99
86	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
87	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
88	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
89	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
90	NAB-Paclitaxel Improves Disease-Free Survival in Early Breast Cancer: GBG 69â€“GeparSepto. Journal of Clinical Oncology, 2019, 37, 2226-2234.	1.6	95

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91	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
92	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
93	Response and prognosis after neoadjuvant chemotherapy in 1,051 patients with infiltrating lobular breast carcinoma. Breast Cancer Research and Treatment, 2014, 144, 153-162.	2.5	92
94	MicroRNA in diagnosis and therapy monitoring of early-stage triple-negative breast cancer. Scientific Reports, 2018, 8, 11584.	3.3	91
95	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
96	Going Digital: A Survey on Digitalization and Large-Scale Data Analytics in Healthcare. Proceedings of the IEEE, 2016, 104, 2180-2206.	21.3	89
97	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
98	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
99	BRCA1/2 Mutations and Bevacizumab in the Neoadjuvant Treatment of Breast Cancer: Response and Prognosis Results in Patients With Triple-Negative Breast Cancer From the GeparQuinto Study. Journal of Clinical Oncology, 2018, 36, 2281-2287.	1.6	86
100	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 2009, 18, 1131-1139.	2.9	84
101	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. Breast Cancer Research, 2010, 12, R110.	5.0	82
102	Population Distribution of Lifetime Risk of Ovarian Cancer in the United States. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 671-676.	2.5	82
103	CYP2D6 Polymorphisms as Predictors of Outcome in Breast Cancer Patients Treated with Tamoxifen: Expanded Polymorphism Coverage Improves Risk Stratification. Clinical Cancer Research, 2010, 16, 4468-4477.	7.0	81
104	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
105	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80
106	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
107	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
108	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

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109	Association of Pathologic Complete Response with Long-Term Survival Outcomes in Triple-Negative Breast Cancer: A Meta-Analysis. Cancer Research, 2020, 80, 5427-5434.	0.9	77
110	Ki-67 as a prognostic molecular marker in routine clinical use in breast cancer patients. Breast, 2009, 18, 135-141.	2.2	76
111	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
112	A Phase II Randomized Study of Neoadjuvant Letrozole Plus Alpelisib for Hormone Receptor-Positive, Human Epidermal Growth Factor Receptor 2-Negative Breast Cancer (NEO-ORB). Clinical Cancer Research, 2019, 25, 2975-2987.	7.0	76
113	Neoadjuvant chemotherapy with paclitaxel and everolimus in breast cancer patients with non-responsive tumours to epirubicin/cyclophosphamide (EC)Â±bevacizumab â€“ Results of the randomised GeparQuinto study (GBG 44). European Journal of Cancer, 2013, 49, 2284-2293.	2.8	75
114	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
115	Circulating miR-148b and miR-133a as biomarkers for breast cancer detection. Oncotarget, 2014, 5, 5284-5294.	1.8	74
116	AGO Recommendations for the Diagnosis and Treatment of Patients with Early Breast Cancer: Update 2019. Breast Care, 2019, 14, 224-245.	1.4	72
117	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
118	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	1.9	71
119	Association of p16 expression with prognosis varies across ovarian carcinoma histotypes: an Ovarian Tumor Tissue Analysis consortium study. Journal of Pathology: Clinical Research, 2018, 4, 250-261.	3.0	70
120	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
121	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
122	Lymphedema in breast cancer survivors: Assessment and information provision in a specialized breast unit. Patient Education and Counseling, 2007, 66, 311-318.	2.2	65
123	Characterizing mammographic images by using generic texture features. Breast Cancer Research, 2012, 14, R59.	5.0	65
124	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1503-1510.	2.5	64
125	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
126	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62

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127	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
128	HER2 and ESR1 mRNA expression levels and response to neoadjuvant trastuzumab plus chemotherapy in patients with primary breast cancer. Breast Cancer Research, 2013, 15, R11.	5.0	59
129	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
130	Prediction of pathological complete response and prognosis in patients with neoadjuvant treatment for triple-negative breast cancer. BMC Cancer, 2018, 18, 1051.	2.6	59
131	Interdisciplinary Screening, Diagnosis, Therapy and Follow-up of Breast Cancer. Guideline of the DGGG and the DKG (S3-Level, AWMF Registry Number 032/045OL, December 2017) â€“ Part 1 with Recommendations for the Screening, Diagnosis and Therapy of Breast Cancer. Geburtshilfe Und Frauenheilkunde, 2018, 78, 927-948.	1.8	59
132	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
133	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
134	BRCA mutations and their influence on pathological complete response and prognosis in a clinical cohort of neoadjuvantly treated breast cancer patients. Breast Cancer Research and Treatment, 2018, 171, 85-94.	2.5	56
135	ABCB1 (MDR1) polymorphisms and ovarian cancer progression and survival: A comprehensive analysis from the Ovarian Cancer Association Consortium and The Cancer Genome Atlas. Gynecologic Oncology, 2013, 131, 8-14.	1.4	55
136	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.9	55
137	Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. International Journal of Cancer, 2011, 128, 2063-2074.	5.1	54
138	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.9	54
139	Mammographic density as a risk factor for breast cancer in a German caseâ€“control study. European Journal of Cancer Prevention, 2011, 20, 1-8.	1.3	53
140	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
141	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
142	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
143	AGO Recommendations for the Diagnosis and Treatment of Patients with Early Breast Cancer: Update 2021. Breast Care, 2021, 16, 214-227.	1.4	51
144	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

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145	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
146	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
147	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
148	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.9	49
149	Association Between a Germline OCA2 Polymorphism at Chromosome 15q13.1 and Estrogen Receptorâ€"Negative Breast Cancer Survival. Journal of the National Cancer Institute, 2010, 102, 650-662.	6.3	48
150	Risk of Ovarian Cancer and the NF-Îºß Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.9	48
151	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	7.0	47
152	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
153	Association of mammographic density with hormone receptors in invasive breast cancers: Results from a caseâ€only study. International Journal of Cancer, 2012, 131, 2643-2649.	5.1	44
154	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
155	14th St. Gallen International Breast Cancer Conference 2015: Evidence, Controversies, Consensus - Primary Therapy of Early Breast Cancer: Opinions Expressed by German Experts. Breast Care, 2015, 10, 211-219.	1.4	43
156	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
157	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
158	Survival Analysis After Neoadjuvant Chemotherapy With Trastuzumab or Lapatinib in Patients With Human Epidermal Growth Factor Receptor 2â€"Positive Breast Cancer in the GeparQuinto (G5) Study (GBG 44). Journal of Clinical Oncology, 2018, 36, 1308-1316.	1.6	43
159	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	7.0	43
160	Association of Germline Variant Status With Therapy Response in High-risk Early-Stage Breast Cancer. JAMA Oncology, 2020, 6, 744.	7.1	42
161	Integrated Analysis of PTEN and p4EBP1 Protein Expression as Predictors for pCR in HER2-Positive Breast Cancer. Clinical Cancer Research, 2016, 22, 2675-2683.	7.0	41
162	Therapy response and prognosis of patients with early breast cancer with low positivity for hormone receptors â€" An analysis of 2765 patients from neoadjuvant clinical trials. European Journal of Cancer, 2021, 148, 159-170.	2.8	41

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163	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
164	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
165	Efficacy of neoadjuvant pertuzumab in addition to chemotherapy and trastuzumab in routine clinical treatment of patients with primary breast cancer: a multicentric analysis. Breast Cancer Research and Treatment, 2019, 173, 319-328.	2.5	40
166	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
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