

Carl Blomqvist

List of Publications by Year in descending order

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Version: 2024-02-01

289
papers

23,980
citations

10351

72
h-index

9553

142
g-index

300
all docs

300
docs citations

300
times ranked

26225
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	9.4	960
3	53BP1 loss rescues BRCA1 deficiency and is associated with triple-negative and BRCA-mutated breast cancers. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 688-695.	3.6	846
4	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.	3.9	764
5	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
6	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, 250-263.	3.0	596
7	A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007, 39, 352-358.	9.4	591
8	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
9	Breast Cancer Risk Genes Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	13.9	532
10	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	9.4	513
11	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, 371-384.	9.4	493
12	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. <i>Nature Genetics</i> , 2009, 41, 585-590.	9.4	434
13	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	428
14	Tailored fluorouracil, epirubicin, and cyclophosphamide compared with marrow-supported high-dose chemotherapy as adjuvant treatment for high-risk breast cancer: a randomised trial. <i>Lancet</i> , The, 2000, 356, 1384-1391.	6.3	402
15	A CHEK2 Genetic Variant Contributing to a Substantial Fraction of Familial Breast Cancer. <i>American Journal of Human Genetics</i> , 2002, 71, 432-438.	2.6	402
16	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
17	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.	9.4	357
18	Distribution of Coronary Artery Stenosis After Radiation for Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 380-386.	0.8	319

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19	Adjuvant Clodronate Treatment Does Not Reduce the Frequency of Skeletal Metastases in Node-Positive Breast Cancer Patients: 5-Year Results of a Randomized Controlled Trial. <i>Journal of Clinical Oncology</i> , 2001, 19, 10-17.	0.8	318
20	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. <i>PLoS Genetics</i> , 2008, 4, e1000054.	1.5	315
21	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
22	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	9.4	279
23	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020, 38, 674-685.	0.8	270
24	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.	9.4	265
25	Prognostic impact of immunohistochemically defined germinal center phenotype in diffuse large B-cell lymphoma patients treated with immunochemotherapy. <i>Blood</i> , 2007, 109, 4930-4935.	0.6	260
26	The combined status of ATM and p53 link tumor development with therapeutic response. <i>Genes and Development</i> , 2009, 23, 1895-1909.	2.7	259
27	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	9.4	256
28	Cement is recommended in intralesional surgery of giant cell tumors: A Scandinavian Sarcoma Group study of 294 patients followed for a median time of 5 years. <i>Monthly Notices of the Royal Astronomical Society: Letters</i> , 2008, 79, 86-93.	1.2	210
29	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.	2.6	201
30	Ten-year follow-up of a randomized controlled trial of adjuvant clodronate treatment in node-positive breast cancer patients. <i>Acta Oncologica</i> , 2004, 43, 650-656.	0.8	189
31	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.	9.4	184
32	NAD(P)H:quinone oxidoreductase 1 NQO1*2 genotype (P187S) is a strong prognostic and predictive factor in breast cancer. <i>Nature Genetics</i> , 2008, 40, 844-853.	9.4	181
33	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
34	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	1.4	168
35	Genomic subtypes of breast cancer identified by array-comparative genomic hybridization display distinct molecular and clinical characteristics. <i>Breast Cancer Research</i> , 2010, 12, R42.	2.2	167
36	<i>CHEK2</i> *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, 4308-4316.	0.8	162

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37	Exome sequencing identifies FANCM as a susceptibility gene for triple-negative breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15172-15177.	3.3	162
38	Treatment-Related Factors Predisposing to Chronic Pain in Patients with Breast Cancer<i>A Multivariate Approach</i>. Acta Oncol ³ gica, 1997, 36, 625-630.	0.8	157
39	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.	7.7	157
40	Tamoxifen Treatment After Adjuvant Chemotherapy Has Opposite Effects on Bone Mineral Density in Premenopausal Patients Depending on Menstrual Status. Journal of Clinical Oncology, 2006, 24, 675-680.	0.8	155
41	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.	1.4	152
42	Aberrations of the MRE11â€“RAD50â€“NBS1 DNA damage sensor complex in human breast cancer: <i>MRE11</i> as a candidate familial cancerâ€“predisposing gene. Molecular Oncology, 2008, 2, 296-316.	2.1	147
43	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	1.3	145
44	Breast Cancer Patients with p53 Pro72 Homozygous Genotype Have a Poorer Survival. Clinical Cancer Research, 2005, 11, 5098-5103.	3.2	138
45	CHEK2 variant I157T may be associated with increased breast cancer risk. International Journal of Cancer, 2004, 111, 543-547.	2.3	134
46	DNA sequence copy number increase at 8q: A potential new prognostic marker in high-grade osteosarcoma. , 1999, 84, 114-121.		128
47	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
48	RAD51C is a susceptibility gene for ovarian cancer. Human Molecular Genetics, 2011, 20, 3278-3288.	1.4	124
49	Clinical course of nonvisceral soft tissue leiomyosarcoma in 225 patients from the Scandinavian Sarcoma Group. Cancer, 2007, 109, 282-291.	2.0	123
50	The Breast Cancer Susceptibility Mutation <i>PALB2 1592delT</i> Is Associated with an Aggressive Tumor Phenotype. Clinical Cancer Research, 2009, 15, 3214-3222.	3.2	122
51	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
52	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.4	109
53	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
54	The predictive value of bcl-2, bax, bcl-xL, bag-1, fas, and fasL for chemotherapy response in advanced breast cancer. Clinical Cancer Research, 2002, 8, 811-6.	3.2	104

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55	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.4	100
56	Risk of Estrogen Receptor-Positive and -Negative Breast Cancer and Single-Nucleotide Polymorphism 2q35-rs13387042. <i>Journal of the National Cancer Institute</i> , 2009, 101, 1012-1018.	3.0	99
57	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	3.0	99
58	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, 1046-1060.	2.6	98
59	Correlation of CHEK2 protein expression and c.1100delC mutation status with tumor characteristics among unselected breast cancer patients. <i>International Journal of Cancer</i> , 2005, 113, 575-580.	2.3	97
60	Prognostic Role of HuR in Hereditary Breast Cancer. <i>Clinical Cancer Research</i> , 2007, 13, 6959-6963.	3.2	97
61	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.	2.2	97
62	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
63	A combined analysis of genome-wide association studies in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 126, 717-727.	1.1	90
64	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90
65	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
66	Bisphosphonate Therapy in Metastatic Breast Cancer. <i>Acta Oncologica</i> , 1996, 35, 81-83.	0.8	87
67	Histopathological features of breast tumours in BRCA1, BRCA2 and mutation-negative breast cancer families. <i>Breast Cancer Research</i> , 2004, 7, R93-100.	2.2	86
68	A High Serum Matrix Metalloproteinase-2 Level Is Associated with an Adverse Prognosis in Node-Positive Breast Carcinoma. <i>Clinical Cancer Research</i> , 2004, 10, 1057-1063.	3.2	85
69	Gains and losses of DNA sequences in liposarcomas evaluated by comparative genomic hybridization. , 1996, 15, 89-94.		81
70	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.	0.9	81
71	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, 9584-9590.	0.4	80
72	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	1.4	80

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73	High expression of cyclin D1 is associated to high proliferation rate and increased risk of mortality in women with ER-positive but not in ER-negative breast cancers. <i>Breast Cancer Research and Treatment</i> , 2017, 164, 667-678.	1.1	79
74	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
75	A Genome-wide Association Study of Early-Onset Breast Cancer Identifies <i>PFKFB3</i> as a Novel Breast Cancer Gene and Supports a Common Genetic Spectrum for Breast Cancer at Any Age. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 658-669.	1.1	77
76	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	3.0	77
77	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.	2.6	76
78	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. <i>European Journal of Human Genetics</i> , 2000, 8, 757-763.	1.4	75
79	The relationship between radiation doses to coronary arteries and location of coronary stenosis requiring intervention in breast cancer survivors. <i>Radiation Oncology</i> , 2019, 14, 40.	1.2	74
80	Increased incidence of stroke in women with breast cancer. <i>European Journal of Cancer</i> , 2005, 41, 423-429.	1.3	73
81	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, 4693-4706.	1.4	71
82	MiR-34a Expression Has an Effect for Lower Risk of Metastasis and Associates with Expression Patterns Predicting Clinical Outcome in Breast Cancer. <i>PLoS ONE</i> , 2011, 6, e26122.	1.1	70
83	Mast cells and eosinophils in invasive breast carcinoma. <i>BMC Cancer</i> , 2007, 7, 165.	1.1	68
84	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67
85	Overrepresentation of 1q21q23 and 12q13q21 in lipoma-like liposarcomas but not in benign lipomas: A comparative genomic hybridization study. <i>Cancer Genetics and Cytogenetics</i> , 1997, 99, 14-18.	1.0	63
86	Molecular subtypes in ductal carcinoma in situ of the breast and their relation to prognosis: a population-based cohort study. <i>BMC Cancer</i> , 2013, 13, 512.	1.1	61
87	Effectiveness of a 12-month exercise program on physical performance and quality of life of breast cancer survivors. <i>Anticancer Research</i> , 2012, 32, 3875-84.	0.5	58
88	Relationship of patients' age to histopathological features of breast tumours in BRCA1 and BRCA2 and mutation-negative breast cancer families. <i>Breast Cancer Research</i> , 2005, 7, R465-9.	2.2	57
89	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	56
90	Cyclin D1 expression is associated with poor prognostic features in estrogen receptor positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2009, 113, 75-82.	1.1	55

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91	Breast tumors from CHEK2 1100delC- mutation carriers: genomic landscape and clinical implications. <i>Breast Cancer Research</i> , 2011, 13, R90.	2.2	55
92	Survival of breast cancer patients in BRCA1, BRCA2, and non-BRCA1/2 breast cancer families: A relative survival analysis from Finland. <i>International Journal of Cancer</i> , 2001, 93, 368-372.	2.3	54
93	Ten-Year Follow-Up of 3 Years of Oral Adjuvant Clodronate Therapy Shows Significant Prevention of Osteoporosis in Early-Stage Breast Cancer. <i>Journal of Clinical Oncology</i> , 2008, 26, 4289-4295.	0.8	53
94	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	1.4	53
95	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52
96	Evaluation of RAD50 in familial breast cancer predisposition. <i>International Journal of Cancer</i> , 2006, 118, 2911-2916.	2.3	51
97	TOP2A and HER2 gene amplification as predictors of response to anthracycline treatment in breast cancer. <i>Acta Oncologica</i> , 2006, 45, 590-596.	0.8	51
98	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , 2015, 13, 156.	2.3	51
99	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.	1.6	51
100	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.	1.1	51
101	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	3.4	51
102	The response evaluation of bone metastases in mammary carcinoma. The value of radiology, scintigraphy, and biochemical markers of bone metabolism. <i>Cancer</i> , 1987, 60, 2907-2912.	2.0	50
103	Free β -Subunit of Human Chorionic Gonadotropin in Serum Is a Diagnostically Sensitive Marker of Seminomatous Testicular Cancer. <i>Clinical Chemistry</i> , 2008, 54, 1840-1843.	1.5	50
104	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	1.1	49
105	Association Between a Germline OCA2 Polymorphism at Chromosome 15q13.1 and Estrogen Receptor- α Negative Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2010, 102, 650-662.	3.0	48
106	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, 230-234.	1.1	47
107	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
108	The prognostic role of HER2 expression in ductal breast carcinoma in situ (DCIS); a population-based cohort study. <i>BMC Cancer</i> , 2015, 15, 468.	1.1	44

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109	Variants on the promoter region of PTEN affect breast cancer progression and patient survival. <i>Breast Cancer Research</i> , 2011, 13, R130.	2.2	43
110	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
111	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017, 19, 119.	2.2	43
112	Effectiveness of a 12-month Exercise Intervention on Physical Activity and Quality of Life of Breast Cancer Survivors; Five-year Results of the BREX-study. <i>In Vivo</i> , 2019, 33, 881-888.	0.6	43
113	Clinical Importance of Genomic Imbalances in Synovial Sarcoma Evaluated by Comparative Genomic Hybridization. <i>Cancer Genetics and Cytogenetics</i> , 1999, 115, 39-46.	1.0	42
114	Identification of Inherited Genetic Variations Influencing Prognosis in Early-Onset Breast Cancer. <i>Cancer Research</i> , 2013, 73, 1883-1891.	0.4	42
115	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. <i>PLoS ONE</i> , 2014, 9, e101488.	1.1	42
116	Breast cancer on the Internet: the quality of Swedish breast cancer websites. <i>Breast</i> , 2004, 13, 376-382.	0.9	41
117	BARD1 variants Cys557Ser and Val507Met in breast cancer predisposition. <i>European Journal of Human Genetics</i> , 2006, 14, 167-172.	1.4	41
118	Multi-Variant Pathway Association Analysis Reveals the Importance of Genetic Determinants of Estrogen Metabolism in Breast and Endometrial Cancer Susceptibility. <i>PLoS Genetics</i> , 2010, 6, e1001012.	1.5	41
119	A Finnish founder mutation in <i>RAD51D</i> : analysis in breast, ovarian, prostate, and colorectal cancer: Table 1. <i>Journal of Medical Genetics</i> , 2012, 49, 429-432.	1.5	41
120	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	1.4	40
121	A cytogenetic study of malignant fibrous histiocytoma. <i>Cancer Genetics and Cytogenetics</i> , 1995, 85, 91-96.	1.0	39
122	Pulmonary toxicity after radiotherapy in primary breast cancer patients: results from a randomized chemotherapy study. <i>International Journal of Radiation Oncology Biology Physics</i> , 2002, 52, 128-136.	0.4	39
123	Soft-Tissue Sarcomas of the Upper Extremity: Surgical Treatment and Outcome. <i>Plastic and Reconstructive Surgery</i> , 2004, 113, 222-230.	0.7	39
124	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	1.5	39
125	Patient survival and tumor characteristics associated with CHEK2:p.1157T findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	2.2	39
126	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, 285-298.	1.4	38

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127	Long-term survival of women with basal-like ductal carcinoma in situ of the breast: a population-based cohort study. <i>BMC Cancer</i> , 2010, 10, 653.	1.1	37
128	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, 934-945.	1.1	37
129	Metaplastic carcinoma of the breast: Prognosis and response to systemic treatment in metastatic disease. <i>Breast Journal</i> , 2019, 25, 418-424.	0.4	36
130	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.	2.2	35
131	A genome-wide association scan on estrogen receptor-negative breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R93.	2.2	35
132	11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012, 33, 1123-1132.	1.1	35
133	Oral trofosfamide: an active drug in the treatment of soft-tissue sarcoma. <i>Cancer Chemotherapy and Pharmacology</i> , 1995, 36, 263-265.	1.1	34
134	Complexity of 12q13â€“22 amplicon in liposarcoma: Microsatellite repeat analysis. , 1997, 18, 66-79.		34
135	Post-mastectomy radiotherapy in pT3N0M0 breast cancer: is it needed?. <i>Radiotherapy and Oncology</i> , 1999, 52, 213-217.	0.3	34
136	Short-Term Intermittent Intravenous Clodronate in the Prevention of Bone Loss Related to Chemotherapy-Induced Ovarian Failure. <i>Breast Cancer Research and Treatment</i> , 2004, 87, 181-188.	1.1	34
137	Missense Variants in <i>ATM</i> in 26,101 Breast Cancer Cases and 29,842 Controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2143-2151.	1.1	33
138	Eukaryotic translation initiation factor 4E (eIF4E) expression is associated with breast cancer tumor phenotype and predicts survival after anthracycline chemotherapy treatment. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 79-88.	1.1	33
139	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, 1934-1946.	1.4	32
140	Transcriptome-wide association study of breast cancer risk by estrogenâ€“receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
141	Clinical significance of genetic imbalances revealed by comparative genomic hybridization in chondrosarcomas. <i>Human Pathology</i> , 1999, 30, 1247-1253.	1.1	31
142	Combined effect of CCND1 and COMT polymorphisms and increased breast cancer risk. <i>BMC Cancer</i> , 2008, 8, 6.	1.1	31
143	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.	0.8	31
144	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.	2.2	31

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145	Radiation dose distribution in coronary arteries in breast cancer radiotherapy. <i>Acta Oncologica</i> , 2016, 55, 959-963.	0.8	31
146	Prophylactic Filgrastim (G-CSF) During Mitomycin-C, Mitoxantrone, and Methotrexate (MMM) Treatment for Metastatic Breast Cancer. <i>American Journal of Clinical Oncology: Cancer Clinical Trials</i> , 1996, 19, 232-234.	0.6	31
147	Radiotherapy in desmoid tumors. <i>Strahlentherapie Und Onkologie</i> , 2017, 193, 269-275.	1.0	30
148	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
149	BACH1 Ser919Pro variant and breast cancer risk. <i>BMC Cancer</i> , 2006, 6, 19.	1.1	29
150	CHEK2 c.1100delC mutation is associated with an increased risk for male breast cancer in Finnish patient population. <i>BMC Cancer</i> , 2017, 17, 620.	1.1	29
151	Long-term risk of ischemic heart disease after adjuvant radiotherapy in breast cancer: results from a large population-based cohort. <i>Breast Cancer Research</i> , 2020, 22, 10.	2.2	29
152	Increased Human Chorionic Gonadotropin Due to Hypogonadism after Treatment of a Testicular Seminoma. <i>Clinical Chemistry</i> , 2007, 53, 1560-1561.	1.5	28
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