Carl Blomqvist

List of Publications by Year
in descending order

289 papers	23,980 citations	10389 72 h-index	9589 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. 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	53BP1 loss rescues BRCA1 deficiency and is associated with triple-negative and BRCA-mutated breast cancers. Nature Structural and Molecular Biology, 2010, 17, 688-695.	8.2	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. PLoS Medicine, 2010, 7, e1000279.	8.4	764
5	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
6	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
7	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
8	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
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	Tailored fluorouracil, epirubicin, and cyclophosphamide compared with marrow-supported high-dose chemotherapy as adjuvant treatment for high-risk breast cancer: a randomised trial. Lancet, The, 2000, 356, 1384-1391.	13.7	402
15	A CHEK2 Genetic Variant Contributing to a Substantial Fraction of Familial Breast Cancer. American Journal of Human Genetics, 2002, 71, 432-438.	6.2	402
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	Distribution of Coronary Artery Stenosis After Radiation for Breast Cancer. Journal of Clinical Oncology, 2012, 30, 380-386.	1.6	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. Journal of Clinical Oncology, 2001, 19, 10-17.	1.6	318
20	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	3.5	315
21	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
22	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
23	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	1.6	270
24	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
25	Prognostic impact of immunohistochemically defined germinal center phenotype in diffuse large B-cell lymphoma patients treated with immunochemotherapy. Blood, 2007, 109, 4930-4935.	1.4	260
26	The combined status of ATM and p53 link tumor development with therapeutic response. Genes and Development, 2009, 23, 1895-1909.	5.9	259
27	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	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. Monthly Notices of the Royal Astronomical Society: Letters, 2008, 79, 86-93.	3.3	210
29	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
30	Ten-year follow-up of a randomized controlled trial of adjuvant clodronate treatment in node-positive breast cancer patients. Acta OncolÃ³gica, 2004, 43, 650-656.	1.8	189
31	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
32	NAD(P)H:quinone oxidoreductase 1 NQO1*2 genotype (P187S) is a strong prognostic and predictive factor in breast cancer. Nature Genetics, 2008, 40, 844-853.	21.4	181
33	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
34	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
35	Genomic subtypes of breast cancer identified by array-comparative genomic hybridization display distinct molecular and clinical characteristics. Breast Cancer Research, 2010, 12, R42.	5.0	167
36	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

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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.	7.1	162
38	Treatment-Related Factors Predisposing to Chronic Pain in Patients with Breast CancerA Multivariate Approach. Acta OncolÃ³gica, 1997, 36, 625-630.	1.8	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.	9.4	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.	1.6	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.	2.9	152
42	Aberrations of the MRE11â€“RAD50â€“NBS1 DNA damage sensor complex in human breast cancer: MRE11 as a candidate familial cancerâ€predisposing gene. Molecular Oncology, 2008, 2, 296-316.	4.6	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.	2.8	145
44	Breast Cancer Patients with p53 Pro72 Homozygous Genotype Have a Poorer Survival. Clinical Cancer Research, 2005, 11, 5098-5103.	7.0	138
45	CHEK2 variant I157T may be associated with increased breast cancer risk. International Journal of Cancer, 2004, 111, 543-547.	5.1	134
46	DNA sequence copy number increase at 8q: A potential new prognostic marker in high-grade osteosarcoma. International Journal of Cancer, 1999, 84, 114-121.	5.1	128
47	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
48	RAD51C is a susceptibility gene for ovarian cancer. Human Molecular Genetics, 2011, 20, 3278-3288.	2.9	124
49	Clinical course of nonvisceral soft tissue leiomyosarcoma in 225 patients from the Scandinavian Sarcoma Group. Cancer, 2007, 109, 282-291.	4.1	123
50	The Breast Cancer Susceptibility Mutation PALB2 1592delT Is Associated with an Aggressive Tumor Phenotype. Clinical Cancer Research, 2009, 15, 3214-3222.	7.0	122
51	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
52	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
53	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	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.	7.0	104

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55	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
56	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
57	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
58	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
59	Correlation of CHEK2 protein expression and c.1100delC mutation status with tumor characteristics among unselected breast cancer patients. International Journal of Cancer, 2005, 113, 575-580.	5.1	97
60	Prognostic Role of HuR in Hereditary Breast Cancer. Clinical Cancer Research, 2007, 13, 6959-6963.	7.0	97
61	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
62	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
63	A combined analysis of genome-wide association studies in breast cancer. Breast Cancer Research and Treatment, 2011, 126, 717-727.	2.5	90
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	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
66	Bisphosphonate Therapy in Metastatic Breast Cancer. Acta OncolÃ³gica, 1996, 35, 81-83.	1.8	87
67	Histopathological features of breast tumours in BRCA1, BRCA2 and mutation-negative breast cancer families. Breast Cancer Research, 2004, 7, R93-100.	5.0	86
68	A High Serum Matrix Metalloproteinase-2 Level Is Associated with an Adverse Prognosis in Node-Positive Breast Carcinoma. Clinical Cancer Research, 2004, 10, 1057-1063.	7.0	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. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
71	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
72	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	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. Breast Cancer Research and Treatment, 2017, 164, 667-678.	2.5	79
74	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
75	A Genome-wide Association Study of Early-Onset Breast Cancer Identifies PFKM as a Novel Breast Cancer Gene and Supports a Common Genetic Spectrum for Breast Cancer at Any Age. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 658-669.	2.5	77
76	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
77	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
78	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. European Journal of Human Genetics, 2000, 8, 757-763.	2.8	75
79	The relationship between radiation doses to coronary arteries and location of coronary stenosis requiring intervention in breast cancer survivors. Radiation Oncology, 2019, 14, 40.	2.7	74
80	Increased incidence of stroke in women with breast cancer. European Journal of Cancer, 2005, 41, 423-429.	2.8	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 Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	2.9	71
82	MiR-34a Expression Has an Effect for Lower Risk of Metastasis and Associates with Expression Patterns Predicting Clinical Outcome in Breast Cancer. PLoS ONE, 2011, 6, e26122.	2.5	70
83	Mast cells and eosinophils in invasive breast carcinoma. BMC Cancer, 2007, 7, 165.	2.6	68
84	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
85	Overrepresentation of 1q21â€“23 and 12q13â€“21 in lipoma-like liposarcomas but not in benign lipomas: A comparative genomic hybridization study. Cancer Genetics and Cytogenetics, 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. BMC Cancer, 2013, 13, 512.	2.6	61
87	Effectiveness of a 12-month exercise program on physical performance and quality of life of breast cancer survivors. Anticancer Research, 2012, 32, 3875-84.	1.1	58
88	Relationship of patients' age to histopathological features of breast tumours in BRCA1 and BRCA2and mutation-negative breast cancer families. Breast Cancer Research, 2005, 7, R465-9.	5.0	57
89	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
90	Cyclin D1 expression is associated with poor prognostic features in estrogen receptor positive breast cancer. Breast Cancer Research and Treatment, 2009, 113, 75-82.	2.5	55

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91	Breast tumors from CHEK2 1100delC- mutation carriers: genomic landscape and clinical implications. Breast Cancer Research, 2011, 13, R90.	5.0	55
92	Survival of breast cancer patients in BRCA1, BRCA2, and non-BRCA1/2 breast cancer families: A relative survival analysis from Finland. International Journal of Cancer, 2001, 93, 368-372.	5.1	54
93	Ten-Year Follow-Up of 3 Years of Oral Adjuvant Clodronate Therapy Shows Significant Prevention of Osteoporosis in Early-Stage Breast Cancer. Journal of Clinical Oncology, 2008, 26, 4289-4295.	1.6	53
94	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
95	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
96	Evaluation ofRAD50 in familial breast cancer predisposition. International Journal of Cancer, 2006, 118, 2911-2916.	5.1	51
97	TOP2A and HER2 gene amplification as predictors of response to anthracycline treatment in breast cancer. Acta OncolÃ³gica, 2006, 45, 590-596.	1.8	51
98	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	5.5	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. Scientific Reports, 2018, 8, 6574.	3.3	51
100	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
101	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
102	The response evaluation of bone metastases in mammary carcinoma. The value of radiology, scintigraphy, and biochemical markers of bone metabolism. Cancer, 1987, 60, 2907-2912.	4.1	50
103	Free Î²-Subunit of Human Chorionic Gonadotropin in Serum Is a Diagnostically Sensitive Marker of Seminomatous Testicular Cancer. Clinical Chemistry, 2008, 54, 1840-1843.	3.2	50
104	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
105	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
106	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
107	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
108	The prognostic role of HER2 expression in ductal breast carcinoma in situ (DCIS); a population-based cohort study. BMC Cancer, 2015, 15, 468.	2.6	44

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109	Variants on the promoter region of PTEN affect breast cancer progression and patient survival. Breast Cancer Research, 2011, 13, R130.	5.0	43
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	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. In Vivo, 2019, 33, 881-888.	1.3	43
113	Clinical Importance of Genomic Imbalances in Synovial Sarcoma Evaluated by Comparative Genomic Hybridization. Cancer Genetics and Cytogenetics, 1999, 115, 39-46.	1.0	42
114	Identification of Inherited Genetic Variations Influencing Prognosis in Early-Onset Breast Cancer. Cancer Research, 2013, 73, 1883-1891.	0.9	42
115	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. PLoS ONE, 2014, 9, e101488.	2.5	42
116	Breast cancer on the Internet: the quality of Swedish breast cancer websites. Breast, 2004, 13, 376-382.	2.2	41
117	BARD1 variants Cys557Ser and Val507Met in breast cancer predisposition. European Journal of Human Genetics, 2006, 14, 167-172.	2.8	41
118	Multi-Variant Pathway Association Analysis Reveals the Importance of Genetic Determinants of Estrogen Metabolism in Breast and Endometrial Cancer Susceptibility. PLoS Genetics, 2010, 6, e1001012.	3.5	41
119	A Finnish founder mutation inRAD51D: analysis in breast, ovarian, prostate, and colorectal cancer: Table 1. Journal of Medical Genetics, 2012, 49, 429-432.	3.2	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	A cytogenetic study of malignant fibrous histiocytoma. Cancer Genetics and Cytogenetics, 1995, 85, 91-96.	1.0	39
122	Pulmonary toxicity after radiotherapy in primary breast cancer patients: results from a randomized chemotherapy study. International Journal of Radiation Oncology Biology Physics, 2002, 52, 128-136.	0.8	39
123	Soft-Tissue Sarcomas of the Upper Extremity: Surgical Treatment and Outcome. Plastic and Reconstructive Surgery, 2004, 113, 222-230.	1.4	39
124	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
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 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	Long-term survival of women with basal-like ductal carcinoma in situ of the breast: a population-based cohort study. BMC Cancer, 2010, 10, 653.	2.6	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. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 934-945.	2.5	37
129	Metaplastic carcinoma of the breast: Prognosis and response to systemic treatment in metastatic disease. Breast Journal, 2019, 25, 418-424.	1.0	36
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	A genome-wide association scan on estrogen receptor-negative breast cancer. Breast Cancer Research, 2010, 12, R93.	5.0	35
132	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35
133	Oral trofosfamide: an active drug in the treatment of soft-tissue sarcoma. Cancer Chemotherapy and Pharmacology, 1995, 36, 263-265.	2.3	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?. Radiotherapy and Oncology, 1999, 52, 213-217.	0.6	34
136	Short-Term Intermittent Intravenous Clodronate in the Prevention of Bone Loss Related to Chemotherapy-Induced Ovarian Failure. Breast Cancer Research and Treatment, 2004, 87, 181-188.	2.5	34
137	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
138	Eukaryotic translation initiation factor 4E (eIF4E) expression is associated with breast cancer tumor phenotype and predicts survival after anthracycline chemotherapy treatment. Breast Cancer Research and Treatment, 2013, 141, 79-88.	2.5	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. Human Molecular Genetics, 2014, 23, 1934-1946.	2.9	32
140	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
141	Clinical significance of genetic imbalances revealed by comparative genomic hybridization in chondrosarcomas. Human Pathology, 1999, 30, 1247-1253.	2.0	31
142	Combined effect of CCND1 and COMT polymorphisms and increased breast cancer risk. BMC Cancer, 2008, 8, 6.	2.6	31
143	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
144	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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145	Radiation dose distribution in coronary arteries in breast cancer radiotherapy. Acta OncolÃ³gica, 2016, 55, 959-963.	1.8	31
146	Prophylactic Filgrastim (G-CSF) During Mitomycin-C, Mitoxantrone, and Methotrexate (MMM) Treatment for Metastatic Breast Cancer. American Journal of Clinical Oncology: Cancer Clinical Trials, 1996, 19, 232-234.	1.3	31
147	Radiotherapy in desmoid tumors. Strahlentherapie Und Onkologie, 2017, 193, 269-275.	2.0	30
148	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
149	BACH1 Ser919Pro variant and breast cancer risk. BMC Cancer, 2006, 6, 19.	2.6	29
150	CHEK2 c.1100delC mutation is associated with an increased risk for male breast cancer in Finnish patient population. BMC Cancer, 2017, 17, 620.	2.6	29
151	Long-term risk of ischemic heart disease after adjuvant radiotherapy in breast cancer: results from a large population-based cohort. Breast Cancer Research, 2020, 22, 10.	5.0	29
152	Increased Human Chorionic Gonadotropin Due to Hypogonadism after Treatment of a Testicular Seminoma. Clinical Chemistry, 2007, 53, 1560-1561.	3.2	28
153	Application of the multicellular tumour spheroid model to screen PET tracers for analysis of early response of chemotherapy in breast cancer. Breast Cancer Research, 2007, 9, R45.	5.0	28
154	Functional Outcome Measurement in Patients with Lower-Extremity Soft Tissue Sarcoma: A Systematic Literature Review. Annals of Surgical Oncology, 2019, 26, 4707-4722.	1.5	28
155	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
156	Multidisciplinary Oncovascular Surgery is Safe and Effective in the Treatment of Intra-abdominal and Retroperitoneal Sarcomas: A Retrospective Single Centre Cohort Study and a Comprehensive Literature Review. European Journal of Vascular and Endovascular Surgery, 2020, 60, 752-763.	1.5	28
157	Genome-wide scanning for linkage in Finnish breast cancer families. European Journal of Human Genetics, 2004, 12, 98-104.	2.8	27
158	Inter-observer variation in delineating the coronary arteries as organs at risk. Radiotherapy and Oncology, 2017, 122, 72-78.	0.6	27
159	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
160	FANCM mutation c.5791C>T is a risk factor for triple-negative breast cancer in the Finnish population. Breast Cancer Research and Treatment, 2017, 166, 217-226.	2.5	26
161	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
162	Comparative effects of clodronate and calcitonin on bone in metastatic breast cancer: A histomorphometric study. European Journal of Cancer, 1993, 29, 1677-1681.	2.8	25

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163	Risk of cancer in BRCA1 and BRCA2 mutation-positive and -negative breast cancer families (Finland). Cancer Causes and Control, 2001, 12, 739-746.	1.8	25
164	Familial Breast Cancers without Mutations in BRCA1 or BRCA2 Have Low Cyclin E and High Cyclin D1 in Contrast to Cancers in BRCA Mutation Carriers. Clinical Cancer Research, 2008, 14, 1976-1983.	7.0	25
165	Basal cytokeratins in breast tumours among BRCA1, BRCA2and mutation-negative breast cancer families. Breast Cancer Research, 2008, 10, R17.	5.0	24
166	Hyperglycosylated Human Chorionic Gonadotropin in Serum of Testicular Cancer Patients. Clinical Chemistry, 2012, 58, 1123-1129.	3.2	24
167	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
168	Polygenic risk score is associated with increased disease risk in 52 Finnish breast cancer families. Breast Cancer Research and Treatment, 2016, 158, 463-469.	2.5	24
169	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
170	ATM variants and cancer risk in breast cancer patients from Southern Finland. BMC Cancer, 2006, 6, 209.	2.6	23
171	Cyclin A Is a Proliferative Marker with Good Prognostic Value in Node-Negative Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2501-2506.	2.5	23
172	NQO1 expression correlates inversely with NFÎºB activation in human breast cancer. Breast Cancer Research and Treatment, 2012, 132, 955-968.	2.5	23
173	The expression of p53, bcl-2, bax, fas and fasL in the primary tumour and lymph node metastases of breast cancer. Acta OncolÃ³gica, 2009, 48, 1137-1143.	1.8	22
174	Recruitment of breast cancer survivors into a 12-month supervised exercise intervention is feasible. Contemporary Clinical Trials, 2009, 30, 457-463.	1.8	22
175	Evaluation of the role of Finnish ataxia-telangiectasia mutations in hereditary predisposition to breast cancer. Carcinogenesis, 2006, 28, 1040-1045.	2.8	21
176	A phase II study of epirubicin, cisplatin and capecitabine as neoadjuvant chemotherapy in locally advanced or inflammatory breast cancer. European Journal of Cancer, 2007, 43, 1153-1160.	2.8	21
177	Effect of image compression and scaling on automated scoring of immunohistochemical stainings and segmentation of tumor epithelium. Diagnostic Pathology, 2012, 7, 29.	2.0	21
178	RAD51, XRCC3, and XRCC2 mutation screening in Finnish breast cancer families. SpringerPlus, 2015, 4, 92.	1.2	21
179	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
180	Evaluation of the Hsp90 inhibitor NVP-AUY922 in multicellular tumour spheroids with respect to effects on growth and PET tracer uptake. Nuclear Medicine and Biology, 2009, 36, 335-342.	0.6	20

#	Article	IF	Citations
181	Breast Cancer with Neoductgenesis: Histopathological Criteria and Its Correlation with Mammographic and Tumour Features. International Journal of Breast Cancer, 2014, 2014, 1-10.	1.2	20
182	SNP-SNP interaction analysis of NF-Î²B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
183	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. Breast Cancer Research, 2015, 17, 18.	5.0	20
184	Case-control analysis of truncating mutations in DNA damage response genes connects TEX15 and FANCD2 with hereditary breast cancer susceptibility. Scientific Reports, 2017, 7, 681.	3.3	20
185	Expression of human chorionic gonadotropin in testicular germ cell tumors. Urologic Oncology: Seminars and Original Investigations, 2014, 32, 727-734.	1.6	19
186	Recurrent moderateâ€risk mutations in Finnish breast and ovarian cancer patients. International Journal of Cancer, 2019, 145, 2692-2700.	5.1	19
187	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
188	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
189	Genome-wide search for breast cancer linkage in large Icelandic non-BRCA1/2 families. Breast Cancer Research, 2010, 12, R50.	5.0	18
190	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131.	2.5	18
191	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
192	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. Nature Communications, 2017, 8, 1632.	12.8	18
193	Longâ€term results of surgical resection of lung metastases from soft tissue sarcoma: A single center experience. Journal of Surgical Oncology, 2019, 120, 168-175.	1.7	18
194	Glycodelin expression associates with differential tumour phenotype and outcome in sporadic and familial non-BRCA1/2 breast cancer patients. Breast Cancer Research and Treatment, 2011, 128, 85-95.	2.5	17
195	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1783-1791.	2.5	17
196	A Comparison of Tumor Biology in Primary Ductal CarcinomaIn SituRecurring as Invasive Carcinoma versus a NewIn Situ. International Journal of Breast Cancer, 2013, 2013, 1-8.	1.2	17
197	Long-term health-related quality of life of breast cancer survivors remains impaired compared to the age-matched general population especially in young women. Results from the prospective controlled BREX exercise study. Breast, 2021, 59, 110-116.	2.2	17
198	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16

#	Article	IF	Citations
199	Omitting radiotherapy in women â‰¥ 65 years with low-risk early breast cancer after breast-conserving surgery and adjuvant endocrine therapy is safe. European Journal of Surgical Oncology, 2018, 44, 951-956.	1.0	16
200	Estrogen receptor beta expression correlates with proliferation in desmoid tumors. Journal of Surgical Oncology, 2019, 119, 873-879.	1.7	16
201	Comparison between CT and MRI in detection of metastasis of the retroperitoneum in testicular germ cell tumors: a prospective trial. Acta OncolÃ³gica, 2020, 59, 660-665.	1.8	16
202	Genetic variation of ESR1 and its co-activator PPARGC1B is synergistic in augmenting the risk of estrogen receptor-positive breast cancer. Breast Cancer Research, 2011, 13, R10.	5.0	15
203	Cyclin E1 is a strong prognostic marker for death from lymph node negative breast cancer. A population-based case-control study. Acta OncolÃ³gica, 2015, 54, 543-549.	1.8	15
204	Health-related Quality of Life of Breast Cancer Survivors Attending an Exercise Intervention Study: A Five-year Follow-up. In Vivo, 2020, 34, 667-674.	1.3	15
205	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	1.8	15
206	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
207	Physical Performance, Toxicity, and Quality of Life as Assessed by the Physician and the Patient. Acta OncolÃ³gica, 2002, 41, 44-49.	1.8	14
208	Autobiographical memories in patients treated for breast cancer. Journal of Psychosomatic Research, 2004, 57, 363-366.	2.6	14
209	Predictive value of in vitro assessment of cytotoxic drug activity in advanced breast cancer. Anti-Cancer Drugs, 2005, 16, 609-615.	1.4	14
210	Multicellular tumour spheroid as a model for evaluation of [18F]FDG as biomarker for breast cancer treatment monitoring. Cancer Cell International, 2006, 6, 6.	4.1	14
211	Do DNA copy number changes differentiate uterine from non-uterine leiomyosarcomas and predict metastasis?. Modern Pathology, 2006, 19, 1068-1082.	5.5	14
212	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
213	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
214	SNPs in lncRNA Regions and Breast Cancer Risk. Frontiers in Genetics, 2020, 11, 550.	2.3	14
215	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
216	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

#	Article	IF	Citations
217	Chemoradiotherapy of anal cancer is feasible in elderly patients: Treatment results of mitomycinâ€“5-FU combined with radiotherapy at Helsinki University Central Hospital 1992â€“2003. Acta OncolÃ³gica, 2006, 45, 736-742.	1.8	13
218	FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2016, 139, 2760-2770.	5.1	13
219	ARLTS1 germline variants and the risk for breast, prostate, and colorectal cancer. European Journal of Human Genetics, 2008, 16, 983-991.	2.8	12
220	No evidence that GATA3 rs570613 SNP modifies breast cancer risk. Breast Cancer Research and Treatment, 2009, 117, 371-379.	2.5	12
221	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
222	Polymorphism at 19q13.41 Predicts Breast Cancer Survival Specifically after Endocrine Therapy. Clinical Cancer Research, 2015, 21, 4086-4096.	7.0	12
223	Risk of ischemic heart disease after radiotherapy for ductal carcinoma in situ. Breast Cancer Research and Treatment, 2018, 171, 95-101.	2.5	12
224	FEC (5-Fluorouracil-Epirubicin-Cyclophosphamide) Monthly Versus FEC Weekly in Metastatic Breast Cancer: First results of a randomized trial. Acta OncolÃ³gica, 1992, 31, 231-236.	1.8	11
225	Clodronate and Other Bisphosphonates as Supportive Therapy in Osteolysis Due to Malignancy. Acta OncolÃ³gica, 1995, 34, 629-636.	1.8	11
226	Cytogenetic study of extraskeletal mesenchymal chondrosarcoma. Cancer Genetics and Cytogenetics, 1996, 86, 170-173.	1.0	11
227	Germline variation in TP53 regulatory network genes associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2013, 132, 2044-2055.	5.1	11
228	Chemotherapy in Ewing's sarcoma. Acta Orthopaedica, 1999, 70, 69-73.	1.4	10
229	Dose-tailoring of FEC adjuvant chemotherapy based on leukopenia is feasible and well tolerated. Toxicity and dose intensity in the Scandinavian Breast Group phase 3 adjuvant Trial SBG 2000-1. Acta OncolÃ³gica, 2011, 50, 329-337.	1.8	10
230	Risk of primary lung cancer after adjuvant radiotherapy in breast cancerâ€”a large population-based study. Npj Breast Cancer, 2021, 7, 71.	5.2	10
231	Individually tailored toxicity-based 5-fluorouracil, epirubicin and cyclophosphamide (FEC) therapy of metastatic breast cancer. Acta OncolÃ³gica, 2007, 46, 165-171.	1.8	9
232	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
233	Effect of dichloromethylene diphosphonate (Cl2MDP) on immune function in breast cancer patients with bone metastases. Cancer Immunology, Immunotherapy, 1983, 15, 159-61.	4.2	8
234	Skin toxicity as a risk factor for major infections in breast cancer patients treated with docetaxel. Acta OncolÃ³gica, 2004, 43, 190-195.	1.8	8

#	Article	IF	Citations
235	No germline FH mutations in familial breast cancer patients. European Journal of Human Genetics, 2005, 13, 506-509.	2.8	8
236	INPP4B and RAD50 have an interactive effect on survival after breast cancer. Breast Cancer Research and Treatment, 2015, 149, 363-371.	2.5	8
237	Ghrelin expression is associated with a favorable outcome in male breast cancer. Scientific Reports, 2018, 8, 13586.	3.3	8
238	En bloc resection of visceral aorta and right kidney due to aortic sarcoma using temporary extracorporeal bypass grafting. Journal of Vascular Surgery Cases and Innovative Techniques, 2019, 5, 589-592.	0.6	8
239	Meta-analysis of three genome-wide association studies identifies two loci that predict survival and treatment outcome in breast cancer. Oncotarget, 2018, 9, 4249-4257.	1.8	8
240	The prognosis of stage III breast cancer treated with postoperative radiotherapy and adriamycin-based chemotherapy with and without tamoxifen. European Journal of Surgical Oncology, 1995, 21, 146-150.	1.0	7
241	Biweekly dose escalation in curative accelerated hyperfractionation for advanced head and neck cancer: A feasibility study. International Journal of Radiation Oncology Biology Physics, 1997, 39, 837-840.	0.8	7
242	Vinorelbine, Epirubicin and Fluorouracil as First-Line Therapy in Metastatic Breast Cancer. Acta OncolÃ³gica, 2003, 42, 309-314.	1.8	7
243	Health-related Quality of Life in Breast Cancer Patients after Adjuvant Treatments. Breast Journal, 2016, 22, 473-475.	1.0	7
244	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	6.4	7
245	Screening of HELQ in breast and ovarian cancer families. Familial Cancer, 2016, 15, 19-23.	1.9	7
246	High frequency of osteonecrosis of the jaw among denosumab-treated prostate cancer patients. Acta OncolÃ³gica, 2017, 56, 104-106.	1.8	7
247	Ductal Breast Carcinoma In Situ: Mammographic Features and Its Relation to Prognosis and Tumour Biology in a Population Based Cohort. International Journal of Breast Cancer, 2017, 2017, 1-9.	1.2	7
248	Predictive Factors for Response to Cytotoxic Treatment in Advanced Breast Cancer a Review. Acta OncolÃ³gica, 1996, 35, 84-90.	1.8	6
249	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
250	Expression of markers of stem cell characteristics, epithelial-mesenchymal transition, basal-like phenotype, proliferation, and androgen receptor in metaplastic breast cancer and their prognostic impact. Acta OncolÃ³gica, 2021, 60, 1233-1239.	1.8	6
251	Long-term Prognostic Impact of Immunohistochemical Estrogen Receptor Determinations Compared with Biochemical Receptor Determination in Primary Breast Cancer. Acta OncolÃ³gica, 1997, 36, 530-532.	1.8	5
252	Comprehensive analysis of NuMAvariation in breast cancer. BMC Cancer, 2008, 8, 71.	2.6	5

#	Article	IF	Citations
253	Germ-line variation at a functional p53 binding site increases susceptibility to breast cancer development. The HUGO Journal, 2009, 3, 31-40.	4.1	5
254	7q21-rs6964587 and breast cancer risk: an extended case-control study by the Breast Cancer Association Consortium. Journal of Medical Genetics, 2011, 48, 698-702.	3.2	5
255	High cyclin A expression, but not Ki67, is associated with early recurrence in desmoid tumors. Journal of Surgical Oncology, 2018, 118, 192-198.	1.7	5
256	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
257	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
258	Leukocyte nadir as a predictive factor for efficacy of adjuvant chemotherapy in breast cancer. Results from the prospective trial SBG 2000â€“1. Acta OncolÃ³gica, 2020, 59, 825-832.	1.8	5
259	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
260	Soft Tissue Sarcoma of Lower Extremity: Functional Outcome and Quality of Life. Annals of Surgical Oncology, 2021, 28, 6892-6905.	1.5	5
261	Monitoring serum estradiol levels in breast cancer patients during extended adjuvant letrozole treatment after five years of tamoxifen: a prospective trial. Breast Cancer Research and Treatment, 2021, 187, 769-775.	2.5	5
262	Quality of life of recently treated patients with breast cancer. Anticancer Research, 2014, 34, 1201-6.	1.1	5
263	Family history influences the tumor characteristics and prognosis of breast cancers developing during postmenopausal hormone therapy. Familial Cancer, 2018, 17, 321-331.	1.9	4
264	Further validation of the Toronto extremity salvage score for lower extremity soft tissue sarcoma based on Finnish patients. Journal of Plastic, Reconstructive and Aesthetic Surgery, 2021, 74, 71-78.	1.0	4
265	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
266	A graphical LASSO analysis of global quality of life, sub scales of the EORTC QLQ-C30 instrument and depression in early breast cancer. Scientific Reports, 2022, 12, 2112.	3.3	4
267	Kaposi sarcoma in Southern Finland (2006â€“2018). International Journal of Dermatology, 2019, 58, 1258-1263.	1.0	3
268	(Neo)adjuvant chemotherapy and interdigitated split-course hyperfractionated radiation in high risk soft tissue sarcoma â€“ Results from a large single-institution series. Scientific Reports, 2019, 9, 7304.	3.3	3
269	Single centre 30â€year experience in treating retroperitoneal liposarcomas. Journal of Surgical Oncology, 2020, 122, 1163-1172.	1.7	3
270	High miR-30 Expression Associates with Improved Breast Cancer Patient Survival and Treatment Outcome. Cancers, 2021, 13, 2907.	3.7	3

#	Article	IF	Citations
271	A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. Scientific Reports, 2021, 11, 14763.	3.3	3
272	Sense of Coherence as Predictor of Quality of Life in Early Breast Cancer Patients. Anticancer Research, 2021, 41, 5045-5052.	1.1	3
273	Data Resource Profile: Breast Cancer Data Base Sweden (BCBaSe 2.0). International Journal of Epidemiology, 2021, , .	1.9	3
274	Utilization of fluorescence in situ hybridization with cytokeratin discriminators in TOP2A assessment of chemotherapy-treated patients with breast cancer. Human Pathology, 2012, 43, 1363-1375.	2.0	2
275	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
276	The CDK 4/6 inhibitor ribociclib has activity in the treatment of inoperable desmoid tumor. A case report. Acta OncolÃ³gica, 2019, 58, 897-900.	1.8	2
277	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. The Clinical Journal of Pathology, 2014, , n/a-n/a.	0.0	2
278	Identification of genetic markers with synergistic survival effect in cancer. BMC Systems Biology, 2013, 7, S2.	3.0	1
279	Evaluation of the RHINO gene for breast cancer predisposition in Finnish breast cancer families. Breast Cancer Research and Treatment, 2014, 144, 437-441.	2.5	1
280	Does Rituximab Influence the Prognostic Effect of Germinal Centre Phenotype in Diffuse Large B-Cell Lymphoma?.. Blood, 2006, 108, 2743-2743.	1.4	1
281	Results of Treatment in Testicular Nonseminoma. Annals of Medicine, 1996, 28, 311-314.	3.8	0
282	Familial Breast Cancer in Southern Finland. Disease Markers, 1999, 15, 105-105.	1.3	0
283	Breast cancer radiotherapy and coronary artery disease: hazards and protection of organs at risk. Breast Cancer Management, 2012, 1, 13-16.	0.2	0
284	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
285	Replyâ€”Letter to the editor. Breast Journal, 2019, 25, 1332-1332.	1.0	0
286	Abstract 758: The clinical utility of BRCA1/2 pathogenic variants in breast cancer patient prognosis. , 2021, , .		0
287	Measuring functional outcome in upper extremity soft tissue sarcoma: Validation of the Toronto Extremity Salvage Score and the QuickDASH patient-reported outcome instruments. Journal of Plastic, Reconstructive and Aesthetic Surgery, 2021, , .	1.0	0
288	Abstract P3-20-02: The association of clinicopathological variables and patientÂ´s preference with surgical decision-making for early breast cancer. Cancer Research, 2022, 82, P3-20-02-P3-20-02.	0.9	0

#	Article	IF	Citations
289	Serum Concentration of Thymidine Kinase 1 (TK1) as a Tumor Marker in Soft Tissue Sarcomas. Anticancer Research, 2022, 42, 1509-1515.	1.1	0