

Vessela N Kristensen

List of Publications by Year in descending order

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Version: 2024-02-01

168
papers

14,560
citations

31976

53
h-index

24258

110
g-index

178
all docs

178
docs citations

178
times ranked

22759
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
2	Allele-specific copy number analysis of tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16910-16915.	7.1	979
3	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
4	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	6.2	711
5	Breast Cancer Risk Genes Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	27.0	532
6	Tumour hypoxia causes DNA hypermethylation by reducing TET activity. <i>Nature</i> , 2016, 537, 63-68.	27.8	521
7	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.	21.4	513
8	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	428
9	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.	21.4	357
10	Principles and methods of integrative genomic analyses in cancer. <i>Nature Reviews Cancer</i> , 2014, 14, 299-313.	28.4	337
11	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
12	miRNA-mRNA Integrated Analysis Reveals Roles for miRNAs in Primary Breast Tumors. <i>PLoS ONE</i> , 2011, 6, e16915.	2.5	278
13	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.	21.4	265
14	The epigenetics of breast cancer. <i>Molecular Oncology</i> , 2010, 4, 242-254.	4.6	242
15	<i>TP53</i> Mutation Spectrum in Breast Cancer Is Subtype Specific and Has Distinct Prognostic Relevance. <i>Clinical Cancer Research</i> , 2014, 20, 3569-3580.	7.0	240
16	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.	21.4	184
17	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	12.8	178
18	<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.	3.2	174

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19	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	9.4	157
20	Breast cancer quantitative proteome and proteogenomic landscape. <i>Nature Communications</i> , 2019, 10, 1600.	12.8	152
21	Integrated molecular profiles of invasive breast tumors and ductal carcinoma in situ (DCIS) reveal differential vascular and interleukin signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2802-2807.	7.1	149
22	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. <i>Nature Methods</i> , 2015, 12, 211-214.	19.0	137
23	Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. <i>International Journal of Cancer</i> , 2016, 138, 87-97.	5.1	136
24	An independent poor-prognosis subtype of breast cancer defined by a distinct tumor immune microenvironment. <i>Nature Communications</i> , 2019, 10, 5499.	12.8	132
25	Frequent aberrant DNA methylation of ABCB1, FOXC1, PPP2R2B and PTEN in ductal carcinoma in situ and early invasive breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R3.	5.0	128
26	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	21.4	125
27	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
28	Deregulation of cancer-related miRNAs is a common event in both benign and malignant human breast tumors. <i>Carcinogenesis</i> , 2014, 35, 76-85.	2.8	119
29	DNA methylation profiling in doxorubicin treated primary locally advanced breast tumours identifies novel genes associated with survival and treatment response. <i>Molecular Cancer</i> , 2010, 9, 68.	19.2	118
30	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016, 13, e1002105.	8.4	118
31	Methylation profiling with a panel of cancer related genes: Association with estrogen receptor, TP53 mutation status and expression subtypes in sporadic breast cancer. <i>Molecular Oncology</i> , 2011, 5, 61-76.	4.6	110
32	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
33	DNA methylation at enhancers identifies distinct breast cancer lineages. <i>Nature Communications</i> , 2017, 8, 1379.	12.8	103
34	Women at high risk of breast cancer: Molecular characteristics, clinical presentation and management. <i>Breast</i> , 2016, 28, 136-144.	2.2	101
35	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	6.3	99
36	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.	6.2	98

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37	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	3.2	94
38	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
39	Prognostic value of PAM50 and risk of recurrence score in patients with early-stage breast cancer with long-term follow-up. <i>Breast Cancer Research</i> , 2017, 19, 120.	5.0	93
40	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	12.8	90
41	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
42	Predicting prognosis and therapeutic response from interactions between lymphocytes and tumor cells. <i>Molecular Oncology</i> , 2015, 9, 2054-2062.	4.6	85
43	Molecular Features of Subtype-Specific Progression from Ductal Carcinoma In Situ to Invasive Breast Cancer. <i>Cell Reports</i> , 2016, 16, 1166-1179.	6.4	85
44	Integrative clustering reveals a novel split in the luminal A subtype of breast cancer with impact on outcome. <i>Breast Cancer Research</i> , 2017, 19, 44.	5.0	85
45	Genome-wide DNA methylation analyses in lung adenocarcinomas: Association with EGFR, KRAS and TP53 mutation status, gene expression and prognosis. <i>Molecular Oncology</i> , 2016, 10, 330-343.	4.6	81
46	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
47	Spatial transcriptomics inferred from pathology whole-slide images links tumor heterogeneity to survival in breast and lung cancer. <i>Scientific Reports</i> , 2020, 10, 18802.	3.3	78
48	<i>LIMIT</i> is a novel metastasis inhibiting lncRNA suppressed by <i>EGF</i> and downregulated in aggressive breast cancer. <i>EMBO Molecular Medicine</i> , 2016, 8, 1052-1064.	6.9	77
49	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.	6.2	76
50	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , 2017, 8, 1221.	12.8	75
51	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. <i>Genome Biology</i> , 2016, 17, 250.	8.8	68
52	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	2.4	67
53	Quantitative DNA methylation analyses reveal stage dependent DNA methylation and association to clinico-pathological factors in breast tumors. <i>BMC Cancer</i> , 2013, 13, 456.	2.6	62
54	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2016, 23, 77-91.	3.1	62

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55	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. <i>Cancer Medicine</i> , 2018, 7, 1978-1987.	2.8	62
56	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016, 99, 903-911.	6.2	59
57	Serum concentrations of active tamoxifen metabolites predict long-term survival in adjuvantly treated breast cancer patients. <i>Breast Cancer Research</i> , 2017, 19, 125.	5.0	58
58	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	56
59	miRNA551b-3p Activates an Oncostatin Signaling Module for the Progression of Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2019, 29, 4389-4406.e10.	6.4	55
60	Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type TP53.	3.4	53
61	Subtype-specific microRNA expression signatures in breast cancer progression. <i>International Journal of Cancer</i> , 2016, 139, 1117-1128.	5.1	53
62	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	6.4	52
63	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	5.1	51
64	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	7.1	51
65	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 1478-1492.	2.9	50
66	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	2.5	49
67	DNA methylation in ductal carcinoma in situ related with future development of invasive breast cancer. <i>Clinical Epigenetics</i> , 2015, 7, 75.	4.1	49
68	Cytokine profiling of tumor interstitial fluid of the breast and its relationship with lymphocyte infiltration and clinicopathological characteristics. <i>Oncolmmunology</i> , 2016, 5, e1248015.	4.6	48
69	DNA Methylation Status of Key Cell-Cycle Regulators Such as CDKNA2/p16 and CCNA1 Correlates with Treatment Response to Doxorubicin and 5-Fluorouracil in Locally Advanced Breast Tumors. <i>Clinical Cancer Research</i> , 2014, 20, 6357-6366.	7.0	47
70	Glycan-related gene expression signatures in breast cancer subtypes; relation to survival. <i>Molecular Oncology</i> , 2015, 9, 861-876.	4.6	47
71	Copy Number Gain of hsa-miR-569 at 3q26.2 Leads to Loss of TP53INP1 and Aggressiveness of Epithelial Cancers. <i>Cancer Cell</i> , 2014, 26, 863-879.	16.8	46
72	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	12.8	46

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73	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	1.9	45
74	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	5.0	43
75	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	2.9	40
76	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	3.5	39
77	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	6.2	39
78	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015, 9, 115-127.	4.6	38
79	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.	2.9	38
80	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015, 97, 22-34.	6.2	37
81	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015, 5, 17369.	3.3	35
82	Long Non-Coding RNAs Differentially Expressed between Normal versus Primary Breast Tumor Tissues Disclose Converse Changes to Breast Cancer-Related Protein-Coding Genes. <i>PLoS ONE</i> , 2014, 9, e106076.	2.5	35
83	Integrated analysis reveals microRNA networks coordinately expressed with key proteins in breast cancer. <i>Genome Medicine</i> , 2015, 7, 21.	8.2	34
84	Age, estrogen, and immune response in breast adenocarcinoma and adjacent normal tissue. <i>Oncolmmunology</i> , 2017, 6, e1356142.	4.6	34
85	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	2.9	33
86	Next-Generation Sequencing of Disseminated Tumor Cells. <i>Frontiers in Oncology</i> , 2013, 3, 320.	2.8	32
87	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32
88	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.	1.8	31
89	The Longitudinal Transcriptional Response to Neoadjuvant Chemotherapy with and without Bevacizumab in Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 4662-4670.	7.0	31
90	Data-driven analysis of immune infiltrate in a large cohort of breast cancer and its association with disease progression, ER activity, and genomic complexity. <i>Oncotarget</i> , 2017, 8, 57121-57133.	1.8	31

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91	Basal-like breast cancer engages tumor-supportive macrophages via secreted factors induced by extracellular S100A4. <i>Molecular Oncology</i> , 2018, 12, 1540-1558.	4.6	30
92	miRNA expression changes during the course of neoadjuvant bevacizumab and chemotherapy treatment in breast cancer. <i>Molecular Oncology</i> , 2019, 13, 2278-2296.	4.6	30
93	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	12.8	30
94	Canine Mammary Tumours Are Affected by Frequent Copy Number Aberrations, including Amplification of MYC and Loss of PTEN. <i>PLoS ONE</i> , 2015, 10, e0126371.	2.5	28
95	Noninvasive profiling of serum cytokines in breast cancer patients and clinicopathological characteristics. <i>Oncolmunology</i> , 2019, 8, e1537691.	4.6	27
96	Crosstalk between microRNA expression and DNA methylation drives the hormone-dependent phenotype of breast cancer. <i>Genome Medicine</i> , 2021, 13, 72.	8.2	27
97	The 5p12 breast cancer susceptibility locus affects <i>MRPS30</i> expression in estrogen-receptor positive tumors. <i>Molecular Oncology</i> , 2014, 8, 273-284.	4.6	26
98	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	5.0	26
99	Identification of a Natural Killer Cell Receptor Allele That Prolongs Survival of Cytomegalovirus-Positive Glioblastoma Patients. <i>Cancer Research</i> , 2016, 76, 5326-5336.	0.9	26
100	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	2.5	26
101	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2015, 22, 851-861.	3.1	25
102	Tumor expression, plasma levels and genetic polymorphisms of the coagulation inhibitor TFPI are associated with clinicopathological parameters and survival in breast cancer, in contrast to the coagulation initiator TF. <i>Breast Cancer Research</i> , 2015, 17, 44.	5.0	24
103	Gene expression profiling of breast cancer in relation to estrogen receptor status and estrogen-metabolizing enzymes: clinical implications. <i>Clinical Cancer Research</i> , 2005, 11, 878s-83s.	7.0	24
104	The Antigenicity of the Tumor Cell " Context Matters. <i>New England Journal of Medicine</i> , 2017, 376, 491-493.	27.0	22
105	Copy number variations alter methylation and parallel IGF2 overexpression in adrenal tumors. <i>Endocrine-Related Cancer</i> , 2015, 22, 953-967.	3.1	21
106	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. <i>Cancer Causes and Control</i> , 2016, 27, 679-693.	1.8	21
107	Expression of an estrogen-regulated variant transcript of the peroxisomal branched chain fatty acid oxidase ACOX2 in breast carcinomas. <i>BMC Cancer</i> , 2015, 15, 524.	2.6	20
108	Heterogeneous DNA Methylation Patterns in the GSTP1 Promoter Lead to Discordant Results between Assay Technologies and Impede Its Implementation as Epigenetic Biomarkers in Breast Cancer. <i>Genes</i> , 2015, 6, 878-900.	2.4	19

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109	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , 2016, 6, 32512.	3.3	19
110	A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. <i>Cell Systems</i> , 2019, 8, 152-162.e6.	6.2	19
111	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	8.2	19
112	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	1.4	18
113	Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. <i>Oncolmmunology</i> , 2018, 7, e1457598.	4.6	18
114	MicroRNA in combination with HER2-targeting drugs reduces breast cancer cell viability in vitro. <i>Scientific Reports</i> , 2021, 11, 10893.	3.3	18
115	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. <i>Genome Medicine</i> , 2018, 10, 92.	8.2	17
116	Coagulation factor V is a marker of tumor-infiltrating immune cells in breast cancer. <i>Oncolmmunology</i> , 2020, 9, 1824644.	4.6	17
117	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, 4051.	12.8	16
118	DNA methylation signature (SAM40) identifies subgroups of the Luminal A breast cancer samples with distinct survival. <i>Oncotarget</i> , 2017, 8, 1074-1082.	1.8	16
119	MicroRNA Networks in Breast Cancer Cells. <i>Methods in Molecular Biology</i> , 2018, 1711, 55-81.	0.9	15
120	Toward Personalized Computer Simulation of Breast Cancer Treatment: A Multiscale Pharmacokinetic and Pharmacodynamic Model Informed by Multitype Patient Data. <i>Cancer Research</i> , 2019, 79, 4293-4304.	0.9	15
121	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
122	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. <i>Breast Cancer Research</i> , 2022, 24, 27.	5.0	15
123	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014, 16, R51.	5.0	14
124	Interaction between p53 Mutation and a Somatic HDMX Biomarker Better Defines Metastatic Potential in Breast Cancer. <i>Cancer Research</i> , 2015, 75, 698-708.	0.9	13
125	A systematic comparison of copy number alterations in four types of female cancer. <i>BMC Cancer</i> , 2016, 16, 913.	2.6	13
126	GFRA3 promoter methylation may be associated with decreased postoperative survival in gastric cancer. <i>BMC Cancer</i> , 2016, 16, 225.	2.6	13

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127	Serum levels of inflammation-related markers and metabolites predict response to neoadjuvant chemotherapy with and without bevacizumab in breast cancers. <i>International Journal of Cancer</i> , 2020, 146, 223-235.	5.1	13
128	Immune phenotype of tumor microenvironment predicts response to bevacizumab in neoadjuvant treatment of ER-positive breast cancer. <i>International Journal of Cancer</i> , 2020, 147, 2515-2525.	5.1	13
129	Pioneer transcription factors are associated with the modulation of DNA methylation patterns across cancers. <i>Epigenetics and Chromatin</i> , 2022, 15, 13.	3.9	13
130	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014, 23, 6034-6046.	2.9	12
131	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	2.5	12
132	MiR-18a and miR-18b are expressed in the stroma of oestrogen receptor alpha negative breast cancers. <i>BMC Cancer</i> , 2020, 20, 377.	2.6	12
133	Modeling molecular development of breast cancer in canine mammary tumors. <i>Genome Research</i> , 2021, 31, 337-347.	5.5	12
134	Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. <i>Current Pharmaceutical Design</i> , 2017, 23, 4716-4725.	1.9	11
135	Somatic EP300-G211S mutations are associated with overall somatic mutational patterns and breast cancer specific survival in triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2018, 172, 339-351.	2.5	11
136	Loss of progesterone receptor is associated with distinct tyrosine kinase profiles in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2020, 183, 585-598.	2.5	10
137	Enrichment of methylated molecules using enhanced-ice-co-amplification at lower denaturation temperature-PCR (E-ice-COLD-PCR) for the sensitive detection of disease-related hypermethylation. <i>Epigenomics</i> , 2018, 10, 525-537.	2.1	9
138	Development of high-resolution melting analysis for ABCB1 promoter methylation: Clinical consequences in breast and ovarian carcinoma. <i>Oncology Reports</i> , 2019, 42, 763-774.	2.6	9
139	Associations between clinical symptoms, plasma norepinephrine and deregulated immune gene networks in subgroups of adolescent with Chronic Fatigue Syndrome. <i>Brain, Behavior, and Immunity</i> , 2019, 76, 82-96.	4.1	9
140	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	6.4	9
141	DNA copy number motifs are strong and independent predictors of survival in breast cancer. <i>Communications Biology</i> , 2020, 3, 153.	4.4	9
142	PHIP - a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	1.8	9
143	On the molecular biology of breast cancer. <i>Molecular Oncology</i> , 2010, 4, 171-173.	4.6	8
144	Determinants of acquired activated protein C resistance and D-dimer in breast cancer. <i>Thrombosis Research</i> , 2016, 145, 78-83.	1.7	8

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145	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. <i>Human Genetics</i> , 2016, 135, 137-154.	3.8	8
146	Molecularly matched therapy in the context of sensitivity, resistance, and safety; patient outcomes in end-stage cancer – the MetAction study. <i>Acta Oncologica</i> , 2020, 59, 733-740.	1.8	8
147	Lack of cross-resistance between non-steroidal and steroidal aromatase inhibitors in breast cancer patients: the potential role of the adipokine leptin. <i>Breast Cancer Research and Treatment</i> , 2021, 190, 435-449.	2.5	8
148	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. <i>Breast Cancer Research</i> , 2021, 23, 86.	5.0	7
149	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. <i>BMC Cancer</i> , 2015, 15, 978.	2.6	6
150	Subtype-specific transcriptional regulators in breast tumors subjected to genetic and epigenetic alterations. <i>Bioinformatics</i> , 2020, 36, 994-999.	4.1	6
151	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	6.2	6
152	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	4.4	6
153	Epigenetic alterations at distal enhancers are linked to proliferation in human breast cancer. <i>NAR Cancer</i> , 2022, 4, zcac008.	3.1	6
154	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	3.3	5
155	Comparable cancer-relevant mutation profiles in synchronous ductal carcinoma in situ and invasive breast cancer. <i>Cancer Reports</i> , 2020, 3, e1248.	1.4	5
156	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	6.4	5
157	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?. <i>Cancers</i> , 2021, 13, 2370.	3.7	4
158	Circadian PERFORMANCE in breast cancer: a germline and somatic genetic study of PER3VNTR polymorphisms and gene co-expression. <i>Npj Breast Cancer</i> , 2021, 7, 118.	5.2	3
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161	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 36874.	3.3	2
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