Vessela N Kristensen

List of Publications by Year
in descending order

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168 papers	14,560 citations	36691 53 h-index	27587 110 g-index
178 all docs	178 docs citations	178 times ranked	24824 citing authors

#	Article	IF	Citations
1	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
2	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
3	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
4	Epigenetic alterations at distal enhancers are linked to proliferation in human breast cancer. NAR Cancer, 2022, 4, zcac008.	1.6	6
5	Abstract OT2-19-01: Presurgical treatment with ribociclib and letrozole in patients with locally advanced breast cancer: The NEOLETRIB study. Cancer Research, 2022, 82, OT2-19-01-OT2-19-01.	0.4	0
6	Quantification of Tumor Hypoxia through Unsupervised Modelling of Consumption and Supply Hypoxia MR Imaging in Breast Cancer. Cancers, 2022, 14, 1326.	1.7	3
7	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. Breast Cancer Research, 2022, 24, 27.	2.2	15
8	Pioneer transcription factors are associated with the modulation of DNA methylation patterns across cancers. Epigenetics and Chromatin, 2022, 15, 13.	1.8	13
9	miR-101-5p Acts as a Tumor Suppressor in HER2-Positive Breast Cancer Cells and Improves Targeted Therapy. Breast Cancer: Targets and Therapy, 2022, Volume 14, 25-39.	1.0	3
10	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
11	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.	2.9	5
12	miRNA normalization enables joint analysis of several datasets to increase sensitivity and to reveal novel miRNAs differentially expressed in breast cancer. PLoS Computational Biology, 2021, 17, e1008608.	1.5	1
13	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
14	Crosstalk between microRNA expression and DNA methylation drives the hormone-dependent phenotype of breast cancer. Genome Medicine, 2021, 13, 72.	3.6	27
15	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.	1.7	4
16	MicroRNA in combination with HER2-targeting drugs reduces breast cancer cell viability in vitro. Scientific Reports, 2021, 11, 10893.	1.6	18
17	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6
18	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	2.2	7

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19	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
20	Circadian PERformance in breast cancer: a germline and somatic genetic study of PER3VNTR polymorphisms and gene co-expression. Npj Breast Cancer, 2021, 7, 118.	2.3	3
21	Lack of cross-resistance between non-steroidal and steroidal aromatase inhibitors in breast cancer patients: the potential role of the adipokine leptin. Breast Cancer Research and Treatment, 2021, 190, 435-449.	1.1	8
22	Efficient gene expression signature for a breast cancer immuno-subtype. PLoS ONE, 2021, 16, e0245215.	1.1	2
23	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
24	Modeling molecular development of breast cancer in canine mammary tumors. Genome Research, 2021, 31, 337-347.	2.4	12
25	Subtype-specific transcriptional regulators in breast tumors subjected to genetic and epigenetic alterations. Bioinformatics, 2020, 36, 994-999.	1.8	6
26	Serum levels of inflammationâ€related markers and metabolites predict response to neoadjuvant chemotherapy with and without bevacizumab in breast cancers. International Journal of Cancer, 2020, 146, 223-235.	2.3	13
27	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
28	Loss of progesterone receptor is associated with distinct tyrosine kinase profiles in breast cancer. Breast Cancer Research and Treatment, 2020, 183, 585-598.	1.1	10
29	Spatial transcriptomics inferred from pathology whole-slide images links tumor heterogeneity to survival in breast and lung cancer. Scientific Reports, 2020, 10, 18802.	1.6	78
30	Coagulation factor V is a marker of tumor-infiltrating immune cells in breast cancer. OncoImmunology, 2020, 9, 1824644.	2.1	17
31	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
32	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
33	MiR-18a and miR-18b are expressed in the stroma of oestrogen receptor alpha negative breast cancers. BMC Cancer, 2020, 20, 377.	1.1	12
34	Immune phenotype of tumor microenvironment predicts response to bevacizumab in neoadjuvant treatment of <scp>ER</scp>â€positive breast cancer. International Journal of Cancer, 2020, 147, 2515-2525.	2.3	13
35	Comparable cancerâ€relevant mutation profiles in synchronous ductal carcinoma in situ and invasive breast cancer. Cancer Reports, 2020, 3, e1248.	0.6	5
36	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2

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37	Molecularly matched therapy in the context of sensitivity, resistance, and safety; patient outcomes in end-stage cancer â€“ the MetAction study. Acta OncolÃ³gica, 2020, 59, 733-740.	0.8	8
38	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
39	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
40	DNA copy number motifs are strong and independent predictors of survival in breast cancer. Communications Biology, 2020, 3, 153.	2.0	9
41	miRNA expression changes during the course of neoadjuvant bevacizumab and chemotherapy treatment in breast cancer. Molecular Oncology, 2019, 13, 2278-2296.	2.1	30
42	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
43	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
44	A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. Cell Systems, 2019, 8, 152-162.e6.	2.9	19
45	Toward Personalized Computer Simulation of Breast Cancer Treatment: A Multiscale Pharmacokinetic and Pharmacodynamic Model Informed by Multitype Patient Data. Cancer Research, 2019, 79, 4293-4304.	0.4	15
46	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
47	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749.	5.8	46
48	Breast cancer quantitative proteome and proteogenomic landscape. Nature Communications, 2019, 10, 1600.	5.8	152
49	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
50	Development of highâ€resolution melting analysis for ABCB1 promoter methylation: Clinical consequences in breast and ovarian carcinoma. Oncology Reports, 2019, 42, 763-774.	1.2	9
51	miRNA551b-3p Activates an Oncostatin Signaling Module for the Progression of Triple-Negative Breast Cancer. Cell Reports, 2019, 29, 4389-4406.e10.	2.9	55
52	An independent poor-prognosis subtype of breast cancer defined by a distinct tumor immune microenvironment. Nature Communications, 2019, 10, 5499.	5.8	132
53	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
54	Noninvasive profiling of serum cytokines in breast cancer patients and clinicopathological characteristics. OncoImmunology, 2019, 8, e1537691.	2.1	27

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55	Associations between clinical symptoms, plasma norepinephrine and deregulated immune gene networks in subgroups of adolescent with Chronic Fatigue Syndrome. Brain, Behavior, and Immunity, 2019, 76, 82-96.	2.0	9
56	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	1.3	62
57	MicroRNA Networks in Breast Cancer Cells. Methods in Molecular Biology, 2018, 1711, 55-81.	0.4	15
58	Enrichment of methylated molecules using enhanced-ice-co-amplification at lower denaturation temperature-PCR (E-ice-COLD-PCR)Âfor the sensitive detection of disease-related hypermethylation. Epigenomics, 2018, 10, 525-537.	1.0	9
59	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. Genome Medicine, 2018, 10, 92.	3.6	17
60	Somatic EP300-G211S mutations are associated with overall somatic mutational patterns and breast cancer specific survival in triple-negative breast cancer. Breast Cancer Research and Treatment, 2018, 172, 339-351.	1.1	11
61	Epigenetics of Breast Cancer. , 2018, , 141-168.		0
62	Basalâ€like breast cancer engages tumorâ€supportive macrophages via secreted factors induced by extracellular S100A4. Molecular Oncology, 2018, 12, 1540-1558.	2.1	30
63	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
64	Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. OncoImmunology, 2018, 7, e1457598.	2.1	18
65	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
66	The Antigenicity of the Tumor Cell â€" Context Matters. New England Journal of Medicine, 2017, 376, 491-493.	13.9	22
67	The Longitudinal Transcriptional Response to Neoadjuvant Chemotherapy with and without Bevacizumab in Breast Cancer. Clinical Cancer Research, 2017, 23, 4662-4670.	3.2	31
68	Integrative clustering reveals a novel split in the luminal A subtype of breast cancer with impact on outcome. Breast Cancer Research, 2017, 19, 44.	2.2	85
69	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. Nature Communications, 2017, 8, 1221.	5.8	75
70	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
71	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
72	Age, estrogen, and immune response in breast adenocarcinoma and adjacent normal tissue. OncoImmunology, 2017, 6, e1356142.	2.1	34

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73	DNA methylation at enhancers identifies distinct breast cancer lineages. Nature Communications, 2017, 8, 1379.	5.8	103
74	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
75	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
76	Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. Current Pharmaceutical Design, 2017, 23, 4716-4725.	0.9	11
77	Prognostic value of PAM50 and risk of recurrence score in patients with early-stage breast cancer with long-term follow-up. Breast Cancer Research, 2017, 19, 120.	2.2	93
78	Serum concentrations of active tamoxifen metabolites predict long-term survival in adjuvantly treated breast cancer patients. Breast Cancer Research, 2017, 19, 125.	2.2	58
79	DNA methylation signature (SAM40) identifies subgroups of the Luminal A breast cancer samples with distinct survival. Oncotarget, 2017, 8, 1074-1082.	0.8	16
80	Data-driven analysis of immune infiltrate in a large cohort of breast cancer and its association with disease progression, ER activity, and genomic complexity. Oncotarget, 2017, 8, 57121-57133.	0.8	31
81	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
82	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.	0.8	31
83	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	3.9	118
84	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
85	Molecular Features of Subtype-Specific Progression from Ductal Carcinoma In Situ to Invasive Breast Cancer. Cell Reports, 2016, 16, 1166-1179.	2.9	85
86	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
87	Subtypeâ€specific microâ€RNA expression signatures in breast cancer progression. International Journal of Cancer, 2016, 139, 1117-1128.	2.3	53
88	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
89	<scp>LIMT</scp> is a novel metastasis inhibiting lnc<scp>RNA</scp> suppressed by <scp>EGF</scp> and downregulated in aggressive breast cancer. EMBO Molecular Medicine, 2016, 8, 1052-1064.	3.3	77
90	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. Genome Biology, 2016, 17, 250.	3.8	68

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91	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
92	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.	0.8	21
93	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
94	Determinants of acquired activated protein C resistance and D-dimer in breast cancer. Thrombosis Research, 2016, 145, 78-83.	0.8	8
95	Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. International Journal of Cancer, 2016, 138, 87-97.	2.3	136
96	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
97	Tumour hypoxia causes DNA hypermethylation by reducing TET activity. Nature, 2016, 537, 63-68.	13.7	521
98	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.	1.6	2
99	Identification of a Natural Killer Cell Receptor Allele That Prolongs Survival of Cytomegalovirus-Positive Glioblastoma Patients. Cancer Research, 2016, 76, 5326-5336.	0.4	26
100	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
101	Cytokine profiling of tumor interstitial fluid of the breast and its relationship with lymphocyte infiltration and clinicopathological characteristics. OncoImmunology, 2016, 5, e1248015.	2.1	48
102	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
103	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
104	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	1.6	19
105	A systematic comparison of copy number alterations in four types of female cancer. BMC Cancer, 2016, 16, 913.	1.1	13
106	Women at high risk of breast cancer: Molecular characteristics, clinical presentation and management. Breast, 2016, 28, 136-144.	0.9	101
107	GFRA3 promoter methylation may be associated with decreased postoperative survival in gastric cancer. BMC Cancer, 2016, 16, 225.	1.1	13
108	Gene expression analysis supports tumor threshold over 2.0Âcm for T-category breast cancer. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 6.	1.4	2

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109	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
110	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
111	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
112	Genomeâ€wide DNA methylation analyses in lung adenocarcinomas: Association with EGFR, KRAS and TP53 mutation status, gene expression and prognosis. Molecular Oncology, 2016, 10, 330-343.	2.1	81
113	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. Human Genetics, 2016, 135, 137-154.	1.8	8
114	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
115	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
116	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	1.6	35
117	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.	1.1	6
118	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. Breast Cancer Research, 2015, 17, 44.	2.2	24
119	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
120	DNA methylation in ductal carcinoma in situ related with future development of invasive breast cancer. Clinical Epigenetics, 2015, 7, 75.	1.8	49
121	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. Genes, 2015, 6, 878-900.	1.0	19
122	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
123	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
124	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.	2.6	76
125	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. Molecular Oncology, 2015, 9, 115-127.	2.1	38
126	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. Nature Methods, 2015, 12, 211-214.	9.0	137

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127	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
128	Interaction between p53 Mutation and a Somatic HDMX Biomarker Better Defines Metastatic Potential in Breast Cancer. Cancer Research, 2015, 75, 698-708.	0.4	13
129	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	2.6	37
130	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
131	Integrated analysis reveals microRNA networks coordinately expressed with key proteins in breast cancer. Genome Medicine, 2015, 7, 21.	3.6	34
132	Glycanâ€related gene expression signatures in breast cancer subtypes; relation to survival. Molecular Oncology, 2015, 9, 861-876.	2.1	47
133	Copy number variations alter methylation and parallel IGF2 overexpression in adrenal tumors. Endocrine-Related Cancer, 2015, 22, 953-967.	1.6	21
134	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
135	Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type TP53. Molecular Cancer Research, 2015, 13, 493-501.	1.5	53
136	Expression of an estrogen-regulated variant transcript of the peroxisomal branched chain fatty acid oxidase ACOX2 in breast carcinomas. BMC Cancer, 2015, 15, 524.	1.1	20
137	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
138	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	1.6	25
139	Predicting prognosis and therapeutic response from interactions between lymphocytes and tumor cells. Molecular Oncology, 2015, 9, 2054-2062.	2.1	85
140	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.	1.4	38
141	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50
142	Canine Mammary Tumours Are Affected by Frequent Copy Number Aberrations, including Amplification of MYC and Loss of PTEN. PLoS ONE, 2015, 10, e0126371.	1.1	28
143	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
144	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39

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145	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
146	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. Clinical Cancer Research, 2014, 20, 6357-6366.	3.2	47
147	Copy Number Gain of hsa-miR-569 at 3q26.2 Leads to Loss of TP53INP1 and Aggressiveness of Epithelial Cancers. Cancer Cell, 2014, 26, 863-879.	7.7	46
148	TP53 Mutation Spectrum in Breast Cancer Is Subtype Specific and Has Distinct Prognostic Relevance. Clinical Cancer Research, 2014, 20, 3569-3580.	3.2	240
149	The 5p12 breast cancer susceptibility locus affects MRPS30 expression in estrogenâ€receptor positive tumors. Molecular Oncology, 2014, 8, 273-284.	2.1	26
150	Principles and methods of integrative genomic analyses in cancer. Nature Reviews Cancer, 2014, 14, 299-313.	12.8	337
151	Deregulation of cancer-related miRNAs is a common event in both benign and malignant human breast tumors. Carcinogenesis, 2014, 35, 76-85.	1.3	119
152	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
153	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
154	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
155	Long Non-Coding RNAs Differentially Expressed between Normal versus Primary Breast Tumor Tissues Disclose Converse Changes to Breast Cancer-Related Protein-Coding Genes. PLoS ONE, 2014, 9, e106076.	1.1	35
156	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.	2.6	98
157	Quantitative DNA methylation analyses reveal stage dependent DNA methylation and association to clinico-pathological factors in breast tumors. BMC Cancer, 2013, 13, 456.	1.1	62
158	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
159	Next-Generation Sequencing of Disseminated Tumor Cells. Frontiers in Oncology, 2013, 3, 320.	1.3	32
160	Integrated molecular profiles of invasive breast tumors and ductal carcinoma in situ (DCIS) reveal differential vascular and interleukin signaling. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2802-2807.	3.3	149
161	Methylation profiling with a panel of cancer related genes: Association with estrogen receptor, TP53 mutation status and expression subtypes in sporadic breast cancer. Molecular Oncology, 2011, 5, 61-76.	2.1	110
162	miRNA-mRNA Integrated Analysis Reveals Roles for miRNAs in Primary Breast Tumors. PLoS ONE, 2011, 6, e16915.	1.1	278

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163	Allele-specific copy number analysis of tumors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16910-16915.	3.3	979
164	The epigenetics of breast cancer. Molecular Oncology, 2010, 4, 242-254.	2.1	242
165	On the molecular biology of breast cancer. Molecular Oncology, 2010, 4, 171-173.	2.1	8
166	DNA methylation profiling in doxorubicin treated primary locally advanced breast tumours identifies novel genes associated with survival and treatment response. Molecular Cancer, 2010, 9, 68.	7.9	118
167	Frequent aberrant DNA methylation of ABCB1, FOXC1, PPP2R2B and PTEN in ductal carcinoma in situ and early invasive breast cancer. Breast Cancer Research, 2010, 12, R3.	2.2	128
168	Gene expression profiling of breast cancer in relation to estrogen receptor status and estrogen-metabolizing enzymes: clinical implications. Clinical Cancer Research, 2005, 11, 878s-83s.	3.2	24