Peter Devilee

List of Publications by Year
in descending order

208 papers	34,133 citations	11235 73 h-index	4511 177 g-index
226 all docs	226 docs citations	226 times ranked	31464 citing authors

#	Article	IF	Citations
1	Identification of the breast cancer susceptibility gene BRCA2. Nature, 1995, 378, 789-792.	13.7	3,230
2	Mutations in the p53 gene occur in diverse human tumour types. Nature, 1989, 342, 705-708.	13.7	2,702
3	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
4	Localization of a breast cancer susceptibility gene, BRCA2, to chromosome 13q12-13. Science, 1994, 265, 2088-2090.	6.0	1,725
5	Mutations in SDHD, a Mitochondrial Complex II Gene, in Hereditary Paraganglioma. Science, 2000, 287, 848-851.	6.0	1,554
6	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
7	Low-penetrance susceptibility to breast cancer due to CHEK2*1100delC in noncarriers of BRCA1 or BRCA2 mutations. Nature Genetics, 2002, 31, 55-59.	9.4	1,001
8	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
9	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	13.9	764
10	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
11	SDH5 , a Gene Required for Flavination of Succinate Dehydrogenase, Is Mutated in Paraganglioma. Science, 2009, 325, 1139-1142.	6.0	682
12	Multifactorial Analysis of Differences Between Sporadic Breast Cancers and Cancers Involving BRCA1 and BRCA2 Mutations. Journal of the National Cancer Institute, 1998, 90, 1138-1145.	3.0	652
13	Prediction of BRCA1 Status in Patients with Breast Cancer Using Estrogen Receptor and Basal Phenotype. Clinical Cancer Research, 2005, 11, 5175-5180.	3.2	577
14	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
15	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
16	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
17	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	9.4	493
18	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434

#	Article	IF	Citations
19	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
20	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	9.4	426
21	BRCA1 genomic deletions are major founder mutations in Dutch breast cancer patients. Nature Genetics, 1997, 17, 341-345.	9.4	414
22	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
23	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
24	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
25	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	9.4	309
26	Rapid detection of BRCA1 mutations by the protein truncation test. Nature Genetics, 1995, 10, 208-212.	9.4	307
27	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
28	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
29	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
30	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244
31	RAD51 135Gâ†’C Modifies Breast Cancer Risk among BRCA2 Mutation Carriers: Results from a Combined Analysis of 19 Studies. American Journal of Human Genetics, 2007, 81, 1186-1200.	2.6	217
32	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.	2.6	201
33	Making sense of big data in health research: Towards an EU action plan. Genome Medicine, 2016, 8, 71.	3.6	190
34	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
35	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	12.5	178
36	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174

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37	Common Breast Cancer Susceptibility Alleles and the Risk of Breast Cancer for BRCA1 and BRCA2 Mutation Carriers: Implications for Risk Prediction. Cancer Research, 2010, 70, 9742-9754.	0.4	169
38	The Warburg effect in 2012. Current Opinion in Oncology, 2012, 24, 62-67.	1.1	164
39	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.	0.8	162
40	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
41	Nuclear receptor NR4A1 promotes breast cancer invasion and metastasis by activating TGF-Î² signalling. Nature Communications, 2014, 5, 3388.	5.8	156
42	TP53 mutations and breast cancer prognosis: Particularly poor survival rates for cases with mutations in the zinc-binding domains. Genes Chromosomes and Cancer, 1995, 14, 71-75.	1.5	154
43	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2011, 20, 3289-3303.	1.4	152
44	Nearly all hereditary paragangliomas in The Netherlands are caused by two founder mutations in theSDHDgene. Genes Chromosomes and Cancer, 2001, 31, 274-281.	1.5	149
45	Familial male breast cancer is not linked to the BRCA1 locus on chromosome 17q. Nature Genetics, 1994, 7, 103-107.	9.4	146
46	Somatic loss of maternal chromosome 11 causes parent-of-origin-dependent inheritance in SDHD-linked paraganglioma and phaeochromocytoma families. Oncogene, 2004, 23, 4076-4083.	2.6	146
47	Inhibition of succinate dehydrogenase dysregulates histone modification in mammalian cells. Molecular Cancer, 2009, 8, 89.	7.9	127
48	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
49	At least two different regions are involved in allelic imbalance on chromosome arm 16q in breast cancer. Genes Chromosomes and Cancer, 1994, 9, 101-107.	1.5	123
50	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
51	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
52	A genome wide linkage search for breast cancer susceptibility genes. Genes Chromosomes and Cancer, 2006, 45, 646-655.	1.5	111
53	Warburg tumours and the mechanisms of mitochondrial tumour suppressor genes. Barking up the right tree?. Current Opinion in Genetics and Development, 2010, 20, 324-329.	1.5	111
54	Survival after bilateral risk-reducing mastectomy in healthy BRCA1 and BRCA2 mutation carriers. Breast Cancer Research and Treatment, 2019, 177, 723-733.	1.1	111

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55	Combined mismatch repair and POLE/POLD1 defects explain unresolved suspected Lynch syndrome cancers. European Journal of Human Genetics, 2016, 24, 1089-1092.	1.4	110
56	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
57	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.4	100
58	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.	3.0	99
59	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2009, 18, 4442-4456.	1.4	99
60	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
61	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
62	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.	2.2	97
63	Comparative genomic hybridization profiles in human BRCA1 and BRCA2 breast tumors highlight differential sets of genomic aberrations. Cancer Research, 2005, 65, 822-7.	0.4	97
64	Whole Exome Sequencing Suggests Much of Non-BRCA1/BRCA2 Familial Breast Cancer Is Due to Moderate and Low Penetrance Susceptibility Alleles. PLoS ONE, 2013, 8, e55681.	1.1	95
65	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
66	Ever since Knudson. Trends in Genetics, 2001, 17, 569-573.	2.9	93
67	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
68	FANCMc.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. Human Molecular Genetics, 2015, 24, 5345-5355.	1.4	91
69	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
70	Inactivation of SDH and FH cause loss of 5hmC and increased H3K9me3 in paraganglioma/pheochromocytoma and smooth muscle tumors. Oncotarget, 2015, 6, 38777-38788.	0.8	90
71	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
72	The CHEK2*1100delC variant acts as a breast cancer risk modifier in non-BRCA1/BRCA2 multiple-case families. Cancer Research, 2003, 63, 8153-7.	0.4	86

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73	Prevalence of founderBRCA1 andBRCA2 mutations among breast and ovarian cancer patients in hungary. , 2000, 86, 737-740.		85
74	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	1.1	82
75	BRCA1-related breast cancer in Austrian breast and ovarian cancer families: SpecificBRCA1 mutations and pathological characteristics. , 1998, 77, 354-360.		81
76	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	1.4	80
77	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
78	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77
79	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
80	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
81	Breast and ovarian cancer risks in a large series of clinically ascertained families with a high proportion of BRCA1 and BRCA2 Dutch founder mutations. Journal of Medical Genetics, 2014, 51, 98-107.	1.5	74
82	Leiden open variation database of the MUTYH gene. Human Mutation, 2010, 31, 1205-1215.	1.1	72
83	Deep sequencing to reveal new variants in pooled DNA samples. Human Mutation, 2009, 30, 1703-1712.	1.1	71
84	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2011, 20, 3304-3321.	1.4	68
85	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
86	Clinical correlates of low-risk variants in FGFR2, TNRC9, MAP3K1, LSP1 and 8q24 in a Dutch cohort of incident breast cancer cases. Breast Cancer Research, 2007, 9, R78.	2.2	64
87	Mutation of SDHB is a Cause of Hypoxia-Related High-Altitude Paraganglioma. Clinical Cancer Research, 2010, 16, 4148-4154.	3.2	64
88	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
89	Personalized Risk Assessment for Prevention and Early Detection of Breast Cancer: Integration and Implementation (PERSPECTIVE I&I). Journal of Personalized Medicine, 2021, 11, 511.	1.1	59
90	The functional impact of variants of uncertain significance in BRCA2. Genetics in Medicine, 2019, 21, 293-302.	1.1	58

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91	Allelotype of head and neck paragangliomas: Allelic imbalance is confined to the long arm of chromosome 11, the site of the predisposing locusPGL. Genes Chromosomes and Cancer, 1994, 11, 71-78.	1.5	56
92	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	2.7	56
93	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
94	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. Breast Cancer Research, 2016, 18, 104.	2.2	56
95	A targeted mouse Brca1 mutation removing the last BRCT repeat results in apoptosis and embryonic lethality at the headfold stage. Oncogene, 2001, 20, 2544-2550.	2.6	55
96	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
97	Repositioning the hereditary paraganglioma critical region on chromosome band 11q23. Human Genetics, 1999, 104, 219-225.	1.8	52
98	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
99	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
100	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.	1.6	51
101	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
102	Comprehensive Mutation Analysis ofPMS2in a Large Cohort of Probands Suspected of Lynch Syndrome or Constitutional Mismatch Repair Deficiency Syndrome. Human Mutation, 2016, 37, 1162-1179.	1.1	50
103	The BRCA1 c. 5096G>A p.Arg1699Gln (R1699Q) intermediate risk variant: breast and ovarian cancer risk estimation and recommendations for clinical management from the ENIGMA consortium. Journal of Medical Genetics, 2018, 55, 15-20.	1.5	50
104	Sdhd and Sdhd/H19 Knockout Mice Do Not Develop Paraganglioma or Pheochromocytoma. PLoS ONE, 2009, 4, e7987.	1.1	49
105	Rare variants in XRCC2 as breast cancer susceptibility alleles: TableÂ1. Journal of Medical Genetics, 2012, 49, 618-620.	1.5	49
106	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
107	Validation of the BOADICEA model and a 313-variant polygenic risk score for breast cancer risk prediction in a Dutch prospective cohort. Genetics in Medicine, 2020, 22, 1803-1811.	1.1	49
108	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.	3.0	48

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109	Men at risk of being a mutation carrier for hereditary breast/ovarian cancer: an exploration of attitudes and psychological functioning during genetic testing. European Journal of Human Genetics, 2001, 9, 492-500.	1.4	47
110	Prediction of BRCA2-association in hereditary breast carcinomas using array-CGH. Breast Cancer Research and Treatment, 2012, 132, 379-389.	1.1	47
111	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	1.5	47
112	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
113	Functional analysis of genetic variants in the high-risk breast cancer susceptibility gene PALB2. Nature Communications, 2019, 10, 5296.	5.8	45
114	Rare Mutations in RINT1 Predispose Carriers to Breast and Lynch Syndromeâ€“Spectrum Cancers. Cancer Discovery, 2014, 4, 804-815.	7.7	44
115	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
116	Fractional allelic imbalance in human breast cancer increases with tetraploidization and chromosome loss. International Journal of Cancer, 1992, 50, 544-548.	2.3	42
117	Increased MUTYH mutation frequency among Dutch families with breast cancer and colorectal cancer. Breast Cancer Research and Treatment, 2010, 124, 635-641.	1.1	40
118	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
119	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
120	Allelotype analysis of flow-sorted breast cancer cells demonstrates genetically related diploid and aneuploid subpopulations in primary tumors and lymph node metastases. , 2000, 28, 173-183.		38
121	MUTYH gene variants and breast cancer in a Dutch caseâ€“control study. Breast Cancer Research and Treatment, 2012, 134, 219-227.	1.1	38
122	Paraganglioma and pheochromocytoma upon maternal transmission of SDHDmutations. BMC Medical Genetics, 2014, 15, 111.	2.1	38
123	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
124	Coding polymorphisms in Casp5, Casp8 and DR4 genes may play a role in predisposition to lung cancer. Cancer Letters, 2009, 278, 183-191.	3.2	37
125	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
126	Absence of evidence for a familial breast cancer susceptibility gene at chromosome 8p12-p22. Oncogene, 2000, 19, 4170-4173.	2.6	35

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127	Allele-specific regulation of FGFR2 expression is cell type-dependent and may increase breast cancer risk through a paracrine stimulus involving FGF10. Breast Cancer Research, 2011, 13, R72.	2.2	35
128	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	1.1	35
129	Addition of a 161-SNP polygenic risk score to family history-based risk prediction: impact on clinical management in non-BRCA1/2breast cancer families. Journal of Medical Genetics, 2019, 56, 581-589.	1.5	35
130	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
131	Missense Variants in ATM in 26,101 Breast Cancer Cases and 29,842 Controls. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2143-2151.	1.1	33
132	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
133	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.	1.4	32
134	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
135	Characterization of Familial Non-BRCA1/2 Breast Tumors by Loss of Heterozygosity and Immunophenotyping. Clinical Cancer Research, 2006, 12, 1693-1700.	3.2	31
136	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
137	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.	2.2	31
138	Classification and Clinical Management of Variants of Uncertain Significance in High Penetrance Cancer Predisposition Genes. Human Mutation, 2016, 37, 331-336.	1.1	31
139	The Dutch founder mutation SDHD.D92Y shows a reduced penetrance for the development of paragangliomas in a large multigenerational family. European Journal of Human Genetics, 2010, 18, 62-66.	1.4	30
140	Alternative splicing and ACMG-AMP-2015-based classification of PALB2 genetic variants: an ENIGMA report. Journal of Medical Genetics, 2019, 56, 453-460.	1.5	30
141	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
142	CHEK2*1100delC homozygosity in the Netherlandsâ€”prevalence and risk of breast and lung cancer. European Journal of Human Genetics, 2014, 22, 46-51.	1.4	29
143	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	0.6	29
144	Exome Sequencing of Germline DNA from Non-BRCA1/2 Familial Breast Cancer Cases Selected on the Basis of aCGH Tumor Profiling. PLoS ONE, 2013, 8, e55734.	1.1	29

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145	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
146	A sporadic breast tumor with a somatically acquired complex genomic rearrangement inBRCA1. , 2000, 27, 295-302.		26
147	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	2.2	26
148	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
149	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
150	Functional Analysis Identifies DamagingCHEK2Missense Variants Associated with Increased Cancer Risk. Cancer Research, 2022, 82, 615-631.	0.4	26
151	Mutations in exons 5-8 of thep53 gene, independent of their type and location, are associated with increased apoptosis and mitosis in invasive breast carcinoma. , 1999, 189, 504-513.		25
152	Homozygosity for aCHEK2*1100delC mutation identified in familial colorectal cancer does not lead to a severe clinical phenotype. Journal of Pathology, 2005, 206, 198-204.	2.1	24
153	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	1.1	24
154	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	2.2	24
155	Alternative mRNA splicing can attenuate the pathogenicity of presumed loss-of-function variants in BRCA2. Genetics in Medicine, 2020, 22, 1355-1365.	1.1	23
156	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
157	Models of parent-of-origin tumorigenesis in hereditary paraganglioma. Seminars in Cell and Developmental Biology, 2015, 43, 117-124.	2.3	22
158	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	0.8	22
159	Loss of maternal chromosome 11 is a signature event in SDHAF2, SDHD, and VHL-related paragangliomas, but less significant in SDHB-related paragangliomas. Oncotarget, 2017, 8, 14525-14536.	0.8	21
160	SNP-SNP interaction analysis of NF-ÎºB signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
161	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
162	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19

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163	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. International Journal of Cancer, 2018, 143, 746-757.	2.3	19
164	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
165	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
166	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
167	Genomeâ€wide linkage scan in Dutch hereditary nonâ€BRCA1/2 breast cancer families identifies 9q21â€22 as a putative breast cancer susceptibility locus. Genes Chromosomes and Cancer, 2008, 47, 947-956.	1.5	16
168	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
169	Variant type is associated with disease characteristics in SDHB, SDHC and SDHD-linked phaeochromocytomaâ€“paraganglioma. Journal of Medical Genetics, 2020, 57, 96-103.	1.5	16
170	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	1.1	16
171	Splicing predictions, minigene analyses, and <scp>ACMG</scp>â€<scp>AMP</scp> clinical classification of 42 germline <scp>PALB2</scp> spliceâ€site variants. Journal of Pathology, 2022, 256, 321-334.	2.1	16
172	Parent-of-origin tumourigenesis is mediated by an essential imprinted modifier inSDHD-linked paragangliomas:SLC22A18andCDKN1Care candidate tumour modifiers. Human Molecular Genetics, 2016, 25, 3715-3728.	1.4	15
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