Peter Devilee

List of Publications by Year
in descending order

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208 papers	34,133 citations	9756 73 h-index	3903 177 g-index
226 all docs	226 docs citations	226 times ranked	28888 citing authors

#	Article	IF	Citations
1	Risk-Adjusted Cancer Screening and Prevention (RiskAP): Complementing Screening for Early Disease Detection by a Learning Screening Based on Risk Factors. Breast Care, 2022, 17, 208-223.	0.8	6
2	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
3	RNF12 is regulated by AKT phosphorylation and promotes TGF-Î² driven breast cancer metastasis. Cell Death and Disease, 2022, 13, 44.	2.7	6
4	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
5	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
6	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
7	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
8	Functional Analysis Identifies DamagingCHEK2Missense Variants Associated with Increased Cancer Risk. Cancer Research, 2022, 82, 615-631.	0.4	26
9	Assessment of psychosocial difficulties by genetic clinicians and distress in women at high risk of breast cancer: a prospective study. European Journal of Human Genetics, 2022, 30, 1067-1075.	1.4	2
10	Genetic clinicians' confidence in <scp>BOADICEA</scp> comprehensive breast cancer risk estimates and counselees' psychosocial outcomes: A prospective study. Clinical Genetics, 2022, 102, 30-39.	1.0	3
11	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
12	Minigeneâ€based splicing analysis and <scp>ACMG</scp>/<scp>AMP</scp>â€based tentative classification of 56 <scp>ATM</scp> variants. Journal of Pathology, 2022, 258, 83-101.	2.1	5
13	Hypothesis: Why Different Types of SDH Gene Variants Cause Divergent Tumor Phenotypes. Genes, 2022, 13, 1025.	1.0	3
14	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. Cancers, 2022, 14, 3363.	1.7	2
15	Germline DLST Variants Promote Epigenetic Modifications in Pheochromocytoma-Paraganglioma. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 459-471.	1.8	6
16	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
17	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
18	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

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19	RAD51D Aberrant Splicing in Breast Cancer: Identification of Splicing Regulatory Elements and Minigene-Based Evaluation of 53 DNA Variants. Cancers, 2021, 13, 2845.	1.7	10
20	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
21	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
22	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
23	Information needs on breast cancer genetic and non-genetic risk factors in relatives of women with a BRCA1/2 or PALB2 pathogenic variant. Breast, 2021, 60, 38-44.	0.9	6
24	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
25	SDHB variant type impacts phenotype and malignancy in pheochromocytoma-paraganglioma. Journal of Medical Genetics, 2021, , jmedgenet-2020-107656.	1.5	3
26	Survey on Physicians' Knowledge and Training Needs in Genetic Counseling in Germany. Breast Care, 2021, 16, 389-395.	0.8	0
27	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
28	The â€œPsychosocial Aspects in Hereditary Cancerâ€•questionnaire in women attending breast cancer genetic clinics: Psychometric validation across Frenchâ€, Germanâ€•and Spanishâ€language versions. European Journal of Cancer Care, 2020, 29, e13173.	0.7	2
29	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
30	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
31	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
32	Comprehensive Functional Characterization and Clinical Interpretation of 20 Splice-Site Variants of the RAD51C Gene. Cancers, 2020, 12, 3771.	1.7	10
33	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
34	Clustering of known low and moderate risk alleles rather than a novel recessive highâ€risk gene in nonâ€• BRCA1 /2 sib trios affected with breast cancer. International Journal of Cancer, 2020, 147, 2708-2716.	2.3	2
35	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
36	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	12.5	178

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37	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
38	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
39	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
40	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
41	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	1.1	14
42	Advances in paragangliomaâ€“pheochromocytoma cell lines and xenografts. Endocrine-Related Cancer, 2020, 27, R433-R450.	1.6	8
43	The functional impact of variants of uncertain significance in BRCA2. Genetics in Medicine, 2019, 21, 293-302.	1.1	58
44	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
45	Breast Cancer Susceptibilityâ€”Towards Individualised Risk Prediction. Current Genetic Medicine Reports, 2019, 7, 124-135.	1.9	4
46	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
47	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
48	Psychosocial problems in women attending French, German and Spanish genetics clinics before and after targeted or multigene testing results: an observational prospective study. BMJ Open, 2019, 9, e029926.	0.8	9
49	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
50	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
51	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
52	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
53	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
54	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	2.2	24

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55	Functional analysis of genetic variants in the high-risk breast cancer susceptibility gene PALB2. Nature Communications, 2019, 10, 5296.	5.8	45
56	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
57	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	0.6	29
58	Cliniciansâ€™ use of breast cancer risk assessment tools according to their perceived importance of breast cancer risk factors: an international survey. Journal of Community Genetics, 2019, 10, 61-71.	0.5	7
59	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
60	The association between cancer family history and ovarian cancer risk in BRCA1/2 mutation carriers: can it be explained by the mutation position?. European Journal of Human Genetics, 2018, 26, 848-857.	1.4	5
61	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
62	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
63	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
64	Use of the BOADICEA Web Application in clinical practice: appraisals by clinicians from various countries. Familial Cancer, 2018, 17, 31-41.	0.9	9
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	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
67	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
68	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
69	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
70	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
71	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
72	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

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73	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
74	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
75	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
76	Whole Gene Capture Analysis of 15 CRC Susceptibility Genes in Suspected Lynch Syndrome Patients. PLoS ONE, 2016, 11, e0157381.	1.1	12
77	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
78	Functional Analysis of Missense Variants in the Putative Breast Cancer Susceptibility GeneXRCC2. Human Mutation, 2016, 37, 914-925.	1.1	12
79	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
80	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
81	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
82	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
83	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
84	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
85	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
86	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
87	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
88	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
89	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
90	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

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91	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
92	Making sense of big data in health research: Towards an EU action plan. Genome Medicine, 2016, 8, 71.	3.6	190
93	Classification and Clinical Management of Variants of Uncertain Significance in High Penetrance Cancer Predisposition Genes. Human Mutation, 2016, 37, 331-336.	1.1	31
94	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
95	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
96	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
97	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
98	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
99	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
100	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
101	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
102	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
103	SNP-SNP interaction analysis of NF-ÎºB signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
104	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
105	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	13.9	764
106	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	2.7	56
107	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
108	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

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109	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.	1.3	14
110	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
111	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
112	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
113	Models of parent-of-origin tumorigenesis in hereditary paraganglioma. Seminars in Cell and Developmental Biology, 2015, 43, 117-124.	2.3	22
114	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
115	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
116	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
117	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
118	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
119	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
120	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
121	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
122	Nuclear receptor NR4A1 promotes breast cancer invasion and metastasis by activating TGF-Î² signalling. Nature Communications, 2014, 5, 3388.	5.8	156
123	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
124	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
125	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
126	Paraganglioma and pheochromocytoma upon maternal transmission of SDHDmutations. BMC Medical Genetics, 2014, 15, 111.	2.1	38

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127	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
128	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
129	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
130	Rare Mutations in RINT1 Predispose Carriers to Breast and Lynch Syndromeâ€“Spectrum Cancers. Cancer Discovery, 2014, 4, 804-815.	7.7	44
131	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
132	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
133	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
134	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	0.8	22
135	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
136	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
137	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
138	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
139	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
140	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
141	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
142	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.4	100
143	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
144	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	1.4	80

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145	The Warburg effect in 2012. Current Opinion in Oncology, 2012, 24, 62-67.	1.1	164
146	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
147	Rare variants in XRCC2 as breast cancer susceptibility alleles: TableÂ1. Journal of Medical Genetics, 2012, 49, 618-620.	1.5	49
148	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	1.1	35
149	Prediction of BRCA2-association in hereditary breast carcinomas using array-CGH. Breast Cancer Research and Treatment, 2012, 132, 379-389.	1.1	47
150	MUTYH gene variants and breast cancer in a Dutch caseâ€“control study. Breast Cancer Research and Treatment, 2012, 134, 219-227.	1.1	38
151	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
152	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
153	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
154	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
155	Leiden open variation database of the MUTYH gene. Human Mutation, 2010, 31, 1205-1215.	1.1	72
156	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
157	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
158	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
159	Mutation of SDHB is a Cause of Hypoxia-Related High-Altitude Paraganglioma. Clinical Cancer Research, 2010, 16, 4148-4154.	3.2	64
160	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
161	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
162	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

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163	Sdhd and Sdhd/H19 Knockout Mice Do Not Develop Paraganglioma or Pheochromocytoma. PLoS ONE, 2009, 4, e7987.	1.1	49
164	SDH5 , a Gene Required for Flavination of Succinate Dehydrogenase, Is Mutated in Paraganglioma. Science, 2009, 325, 1139-1142.	6.0	682
165	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
166	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
167	Deep sequencing to reveal new variants in pooled DNA samples. Human Mutation, 2009, 30, 1703-1712.	1.1	71
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