

# Peter Devilee

## List of Publications by Year in descending order

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Version: 2024-02-01

208  
papers

34,133  
citations

9264

74  
h-index

3830

178  
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. <i>Breast Care</i> , 2022, 17, 208-223.	1.4	6
2	Splicing predictions, minigene analyses, and <scp>ACMG</scp>â€<scp>AMP</scp> clinical classification of 42 germline <scp><i>PALB2</i></scp> spliceâ€site variants. <i>Journal of Pathology</i> , 2022, 256, 321-334.	4.5	16
3	RNF12 is regulated by AKT phosphorylation and promotes TGF-Î² driven breast cancer metastasis. <i>Cell Death and Disease</i> , 2022, 13, 44.	6.3	6
4	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	4.4	6
5	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	2.8	23
6	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
7	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	7.1	51
8	Functional Analysis Identifies Damaging<i>CHEK2</i>Missense Variants Associated with Increased Cancer Risk. <i>Cancer Research</i> , 2022, 82, 615-631.	0.9	26
9	Assessment of psychosocial difficulties by genetic clinicians and distress in women at high risk of breast cancer: a prospective study. <i>European Journal of Human Genetics</i> , 2022, 30, 1067-1075.	2.8	2
10	Genetic clinicians' confidence in <scp>BOADICEA</scp> comprehensive breast cancer risk estimates and counselees' psychosocial outcomes: A prospective study. <i>Clinical Genetics</i> , 2022, 102, 30-39.	2.0	3
11	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	8.2	19
12	Minigeneâ€based splicing analysis and <scp>ACMG</scp>/<scp>AMP</scp>â€based tentative classification of 56 <scp><i>ATM</i></scp> variants. <i>Journal of Pathology</i> , 2022, 258, 83-101.	4.5	5
13	Hypothesis: Why Different Types of SDH Gene Variants Cause Divergent Tumor Phenotypes. <i>Genes</i> , 2022, 13, 1025.	2.4	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. <i>Cancers</i> , 2022, 14, 3363.	3.7	2
15	Germline <i>DLST</i> Variants Promote Epigenetic Modifications in Pheochromocytoma-Paraganglioma. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 459-471.	3.6	6
16	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	12.8	19
17	Breast Cancer Risk Genes â€ Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	27.0	532
18	Personalized Risk Assessment for Prevention and Early Detection of Breast Cancer: Integration and Implementation (PERSPECTIVE I&P). <i>Journal of Personalized Medicine</i> , 2021, 11, 511.	2.5	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. <i>Cancers</i> , 2021, 13, 2845.	3.7	10
20	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. <i>Genetics in Medicine</i> , 2021, 23, 1726-1737.	2.4	16
21	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
22	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
23	Information needs on breast cancer genetic and non-genetic risk factors in relatives of women with a BRCA1/2 or PALB2 pathogenic variant. <i>Breast</i> , 2021, 60, 38-44.	2.2	6
24	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , 2021, 11, 19787.	3.3	2
25	SDHB variant type impacts phenotype and malignancy in pheochromocytoma-paranglioma. <i>Journal of Medical Genetics</i> , 2021, , jmedgenet-2020-107656.	3.2	3
26	Survey on Physicians' Knowledge and Training Needs in Genetic Counseling in Germany. <i>Breast Care</i> , 2021, 16, 389-395.	1.4	0
27	Variant type is associated with disease characteristics in SDHB, SDHC and SDHD-linked phaeochromocytoma-paranglioma. <i>Journal of Medical Genetics</i> , 2020, 57, 96-103.	3.2	16
28	The Psychosocial Aspects in Hereditary Cancer questionnaire in women attending breast cancer genetic clinics: Psychometric validation across French, German and Spanish language versions. <i>European Journal of Cancer Care</i> , 2020, 29, e13173.	1.5	2
29	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
30	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	2.4	82
31	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	6.2	39
32	Comprehensive Functional Characterization and Clinical Interpretation of 20 Splice-Site Variants of the RAD51C Gene. <i>Cancers</i> , 2020, 12, 3771.	3.7	10
33	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
34	Clustering of known low and moderate risk alleles rather than a novel recessive high-risk gene in non-BRCA1 /2 sib trios affected with breast cancer. <i>International Journal of Cancer</i> , 2020, 147, 2708-2716.	5.1	2
35	Alternative mRNA splicing can attenuate the pathogenicity of presumed loss-of-function variants in BRCA2. <i>Genetics in Medicine</i> , 2020, 22, 1355-1365.	2.4	23
36	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 687-705.	27.6	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.	3.3	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.	2.4	49
39	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
40	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	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.	2.5	14
42	Advances in paraganglioma-pheochromocytoma cell lines and xenografts. Endocrine-Related Cancer, 2020, 27, R433-R450.	3.1	8
43	The functional impact of variants of uncertain significance in BRCA2. Genetics in Medicine, 2019, 21, 293-302.	2.4	58
44	Survival after bilateral risk-reducing mastectomy in healthy BRCA1 and BRCA2 mutation carriers. Breast Cancer Research and Treatment, 2019, 177, 723-733.	2.5	111
45	Breast Cancer Susceptibility-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.	5.2	28
47	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	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.	1.9	9
49	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
50	Addition of a 161-SNP polygenic risk score to family history-based risk prediction: impact on clinical management in non-BRCA1/2 breast cancer families. Journal of Medical Genetics, 2019, 56, 581-589.	3.2	35
51	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	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.	3.2	30
53	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
54	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24

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55	Functional analysis of genetic variants in the high-risk breast cancer susceptibility gene PALB2. <i>Nature Communications</i> , 2019, 10, 5296.	12.8	45
56	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
57	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. <i>Blood</i> , 2019, 133, 1130-1139.	1.4	29
58	Clinicians' use of breast cancer risk assessment tools according to their perceived importance of breast cancer risk factors: an international survey. <i>Journal of Community Genetics</i> , 2019, 10, 61-71.	1.2	7
59	The <i>BRCA2</i> c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018, 39, 729-741.	2.5	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?. <i>European Journal of Human Genetics</i> , 2018, 26, 848-857.	2.8	5
61	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. <i>International Journal of Cancer</i> , 2018, 143, 746-757.	5.1	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. <i>Scientific Reports</i> , 2018, 8, 6574.	3.3	51
63	The <i>BRCA1</i> c. 5096G>A p.Arg1699Gln (R1699Q) intermediate risk variant: breast and ovarian cancer risk estimation and recommendations for clinical management from the ENIGMA consortium. <i>Journal of Medical Genetics</i> , 2018, 55, 15-20.	3.2	50
64	Use of the BOADICEA Web Application in clinical practice: appraisals by clinicians from various countries. <i>Familial Cancer</i> , 2018, 17, 31-41.	1.9	9
65	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
66	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.9	75
67	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
68	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
69	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
70	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	2.4	67
71	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	1.9	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. <i>Oncotarget</i> , 2017, 8, 14525-14536.	1.8	21

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73	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	1.8	9
74	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016, 7, 80140-80163.	1.8	31
75	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
76	Whole Gene Capture Analysis of 15 CRC Susceptibility Genes in Suspected Lynch Syndrome Patients. <i>PLoS ONE</i> , 2016, 11, e0157381.	2.5	12
77	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	2.5	12
78	Functional Analysis of Missense Variants in the Putative Breast Cancer Susceptibility Gene <i>XRCC2</i> . <i>Human Mutation</i> , 2016, 37, 914-925.	2.5	12
79	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
80	<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
81	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	5.0	31
82	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	5.0	43
83	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
84	Parent-of-origin tumorigenesis is mediated by an essential imprinted modifier in <i>SDHD</i> -linked paragangliomas: <i>SLC22A18</i> and <i>CDKN1C</i> are candidate tumour modifiers. <i>Human Molecular Genetics</i> , 2016, 25, 3715-3728.	2.9	15
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	Comprehensive Mutation Analysis of <i>PMS2</i> in a Large Cohort of Probands Suspected of Lynch Syndrome or Constitutional Mismatch Repair Deficiency Syndrome. <i>Human Mutation</i> , 2016, 37, 1162-1179.	2.5	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. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	9.4	157
88	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
89	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
90	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

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91	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , 2016, 18, 104.	5.0	56
92	Making sense of big data in health research: Towards an EU action plan. <i>Genome Medicine</i> , 2016, 8, 71.	8.2	190
93	Classification and Clinical Management of Variants of Uncertain Significance in High Penetrance Cancer Predisposition Genes. <i>Human Mutation</i> , 2016, 37, 331-336.	2.5	31
94	Combined mismatch repair and POLE/POLD1 defects explain unresolved suspected Lynch syndrome cancers. <i>European Journal of Human Genetics</i> , 2016, 24, 1089-1092.	2.8	110
95	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
96	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
97	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	6.3	77
98	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	1.4	18
99	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	2.5	26
100	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2015, 17, 61.	5.0	26
101	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	5.0	26
102	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	2.5	34
103	SNP-SNP interaction analysis of NF- $\kappa$ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015, 6, 37979-37994.	1.8	20
104	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
105	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. <i>New England Journal of Medicine</i> , 2015, 372, 2243-2257.	27.0	764
106	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. <i>EBioMedicine</i> , 2015, 2, 681-689.	6.1	56
107	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	2.9	40
108	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



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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. <i>Carcinogenesis</i> , 2015, 36, 256-271.	2.8	14
110	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
111	<i>FANCM</i> c.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. <i>Human Molecular Genetics</i> , 2015, 24, 5345-5355.	2.9	91
112	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
113	Models of parent-of-origin tumorigenesis in hereditary paraganglioma. <i>Seminars in Cell and Developmental Biology</i> , 2015, 43, 117-124.	5.0	22
114	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	56
115	Association of Type and Location of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Risk of Breast and Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1347.	7.4	390
116	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
117	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
118	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	2.5	24
119	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
120	Inactivation of <i>SDH</i> and <i>FH</i> cause loss of 5hmC and increased H3K9me3 in paraganglioma/pheochromocytoma and smooth muscle tumors. <i>Oncotarget</i> , 2015, 6, 38777-38788.	1.8	90
121	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	2.5	49
122	Nuclear receptor NR4A1 promotes breast cancer invasion and metastasis by activating TGF- $\beta$ signalling. <i>Nature Communications</i> , 2014, 5, 3388.	12.8	156
123	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. <i>PLoS Genetics</i> , 2014, 10, e1004256.	3.5	47
124	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
125	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	2.9	53
126	Paraganglioma and pheochromocytoma upon maternal transmission of SDHD mutations. <i>BMC Medical Genetics</i> , 2014, 15, 111.	2.1	38



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127	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419.	5.0	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. <i>Journal of Medical Genetics</i> , 2014, 51, 98-107.	3.2	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. <i>Human Molecular Genetics</i> , 2014, 23, 1934-1946.	2.9	32
130	Rare Mutations in <i>RINT1</i> Predispose Carriers to Breast and Lynch Syndrome—“Spectrum Cancers. <i>Cancer Discovery</i> , 2014, 4, 804-815.	9.4	44
131	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
132	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
133	CHEK2*1100delC homozygosity in the Netherlands—prevalence and risk of breast and lung cancer. <i>European Journal of Human Genetics</i> , 2014, 22, 46-51.	2.8	29
134	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). <i>Oncotarget</i> , 2014, 5, 8223-8234.	1.8	22
135	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
136	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	21.4	493
137	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	6.2	201
138	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
139	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003212.	3.5	244
140	Whole Exome Sequencing Suggests Much of Non-BRCA1/BRCA2 Familial Breast Cancer Is Due to Moderate and Low Penetrance Susceptibility Alleles. <i>PLoS ONE</i> , 2013, 8, e55681.	2.5	95
141	Exome Sequencing of Germline DNA from Non-BRCA1/2 Familial Breast Cancer Cases Selected on the Basis of aCGH Tumor Profiling. <i>PLoS ONE</i> , 2013, 8, e55734.	2.5	29
142	19p13.1 Is a Triple-Negative—Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.9	100
143	<i>CHEK2</i> *1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancer—Specific Death, and Increased Risk of a Second Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 4308-4316.	1.6	162
144	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	2.9	80

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145	The Warburg effect in 2012. <i>Current Opinion in Oncology</i> , 2012, 24, 62-67.	2.4	164
146	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	21.4	256
147	Rare variants in XRCC2 as breast cancer susceptibility alleles: Table A1. <i>Journal of Medical Genetics</i> , 2012, 49, 618-620.	3.2	49
148	11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012, 33, 1123-1132.	2.5	35
149	Prediction of BRCA2-association in hereditary breast carcinomas using array-CGH. <i>Breast Cancer Research and Treatment</i> , 2012, 132, 379-389.	2.5	47
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