Jacques Simard

List of Publications by Year
in descending order

348 papers	28,075 citations	8172 76 h-index	7944 149 g-index
362 all docs	362 docs citations	362 times ranked	24379 citing authors

#	Article	IF	Citations
1	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. International Journal of Epidemiology, 2022, 50, 1897-1911.	0.9	43
2	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
3	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
4	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
5	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
6	Womenâ€™s perceptions of PERSPECTIVE: a breast cancer risk stratification e-platform. Hereditary Cancer in Clinical Practice, 2022, 20, 8.	0.6	4
7	Polygenic risk scores for prediction of breast cancer risk in Asian populations. Genetics in Medicine, 2022, 24, 586-600.	1.1	27
8	A Genome-Wide Gene-Based Geneâ€“Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	0.7	6
9	Gynecologic Cancer Risk and Genetics: Informing an Ideal Model of Gynecologic Cancer Prevention. Current Oncology, 2022, 29, 4632-4646.	0.9	1
10	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
11	PALB2 Variants: Protein Domains and Cancer Susceptibility. Trends in Cancer, 2021, 7, 188-197.	3.8	13
12	Personalizing Breast Cancer Screening Based on Polygenic Risk and Family History. Journal of the National Cancer Institute, 2021, 113, 434-442.	3.0	34
13	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
14	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
15	Womenâ€™s Views on Multifactorial Breast Cancer Risk Assessment and Risk-Stratified Screening: A Population-Based Survey from Four Provinces in Canada. Journal of Personalized Medicine, 2021, 11, 95.	1.1	28
16	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
17	A Collaborative Model to Implement Flexible, Accessible and Efficient Oncogenetic Services for Hereditary Breast and Ovarian Cancer: The C-MOnGene Study. Cancers, 2021, 13, 2729.	1.7	8
18	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. Npj Breast Cancer, 2021, 7, 52.	2.3	7

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19	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. Human Genetics and Genomics Advances, 2021, 2, 100042.	1.0	6
20	Toward a Population-Based Breast Cancer Risk Stratification Approach? The Needs and Concerns of Healthcare Providers. Journal of Personalized Medicine, 2021, 11, 540.	1.1	9
21	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
22	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
23	Risk-Stratified Approach to Breast Cancer Screening in Canada: Womenâ€™s Knowledge of the Legislative Context and Concerns about Discrimination from Genetic and Other Predictive Health Data. Journal of Personalized Medicine, 2021, 11, 726.	1.1	5
24	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
25	Potential of polygenic risk scores for improving population estimates of womenâ€™s breast cancer genetic risks. Genetics in Medicine, 2021, 23, 2114-2121.	1.1	9
26	Oral contraceptive use and ovarian cancer risk for BRCA1/2 mutation carriers: an international cohort study. American Journal of Obstetrics and Gynecology, 2021, 225, 51.e1-51.e17.	0.7	34
27	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.0	6
28	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
29	Should Age-Dependent Absolute Risk Thresholds Be Used for Risk Stratification in Risk-Stratified Breast Cancer Screening?. Journal of Personalized Medicine, 2021, 11, 916.	1.1	8
30	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
31	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228â€‰951 Women of European Descent. Journal of the National Cancer Institute, 2020, 112, 295-304.	3.0	35
32	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	2.3	13
33	Functional characterization of 84 PALB2 variants of uncertain significance. Genetics in Medicine, 2020, 22, 622-632.	1.1	40
34	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
35	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. International Journal of Epidemiology, 2020, 49, 1117-1131.	0.9	41
36	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

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37	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. Nature Communications, 2020, 11, 3833.	5.8	88
38	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44.	2.3	5
39	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
40	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	12.5	178
41	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
42	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. Nature Communications, 2020, 11, 1217.	5.8	46
43	Sequence kernel association test for survival outcomes in the presence of a non-susceptible fraction. Biostatistics, 2020, 21, 518-530.	0.9	3
44	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
45	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
46	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
47	Alcohol Consumption, Cigarette Smoking, and Risk of Breast Cancer for BRCA1 and BRCA2 Mutation Carriers: Results from The BRCA1 and BRCA2 Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 368-378.	1.1	24
48	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
49	Risk-reducing salpingo-oophorectomy, natural menopause, and breast cancer risk: an international prospective cohort of BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2020, 22, 8.	2.2	41
50	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
51	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. EBioMedicine, 2019, 48, 203-211.	2.7	14
52	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
53	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
54	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2019, 121, 180-192.	2.9	19

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55	Authorsâ€™ response: Associations of obesity and circulating insulin and glucose with breast cancer risk. International Journal of Epidemiology, 2019, 48, 1016-1017.	0.9	1
56	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
57	Functional Analysis of Promoter Variants in Genes Involved in Sex Steroid Action, DNA Repair and Cell Cycle Control. Genes, 2019, 10, 186.	1.0	6
58	Health professionalsâ€™ perspectives on breast cancer risk stratification: understanding evaluation of risk versus screening for disease. Public Health Reviews, 2019, 40, 2.	1.3	27
59	Body mass index and the association between low-density lipoprotein cholesterol as predicted by HMGCR genetic variants and breast cancer risk. International Journal of Epidemiology, 2019, 48, 1727-1730.	0.9	3
60	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
61	The association between weight at birth and breast cancer risk revisited using Mendelian randomisation. European Journal of Epidemiology, 2019, 34, 591-600.	2.5	16
62	A response to â€œPersonalised medicine and population health: breast and ovarian cancerâ€• Human Genetics, 2019, 138, 287-289.	1.8	14
63	A global functional analysis of missense mutations reveals two major hotspots in the PALB2 tumor suppressor. Nucleic Acids Research, 2019, 47, 10662-10677.	6.5	39
64	Functional analysis of genetic variants in the high-risk breast cancer susceptibility gene PALB2. Nature Communications, 2019, 10, 5296.	5.8	45
65	Prevalence of BRCA1 and BRCA2 pathogenic variants in a large, unselected breast cancer cohort. International Journal of Cancer, 2019, 144, 1195-1204.	2.3	31
66	The Tumor Suppressor PALB2: Inside Out. Trends in Biochemical Sciences, 2019, 44, 226-240.	3.7	83
67	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	1.1	415
68	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. Journal of the National Cancer Institute, 2019, 111, 350-364.	3.0	30
69	Organizational challenges to equity in the delivery of services within a new personalized risk-based approach to breast cancer screening. New Genetics and Society, 2019, 38, 38-59.	0.7	12
70	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	0.9	81
71	DSNetwork: An Integrative Approach to Visualize Predictions of Variantsâ€™ Deleteriousness. Frontiers in Genetics, 2019, 10, 1349.	1.1	5
72	Envisioning Implementation of a Personalized Approach in Breast Cancer Screening Programs: Stakeholder Perspectives. Healthcare Policy, 2019, 15, 39-54.	0.3	12

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73	Disentangling the determinants of interest and willingness-to-pay for breast cancer susceptibility testing in the general population: a cross-sectional Web-based survey among women of QuÃ©bec (Canada). BMJ Open, 2018, 8, e016662.	0.8	9
74	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
75	Inherited mutations in BRCA1 and BRCA2 in an unselected multiethnic cohort of Asian patients with breast cancer and healthy controls from Malaysia. Journal of Medical Genetics, 2018, 55, 97-103.	1.5	34
76	The Influence of Number and Timing of Pregnancies on Breast Cancer Risk for Women With BRCA1 or BRCA2 Mutations. JNCI Cancer Spectrum, 2018, 2, pky078.	1.4	21
77	Oral Contraceptive Use and Breast Cancer Risk: Retrospective and Prospective Analyses From a BRCA1 and BRCA2 Mutation Carrier Cohort Study. JNCI Cancer Spectrum, 2018, 2, pky023.	1.4	33
78	Differential Burden of Rare and Common Variants on Tumor Characteristics, Survival, and Mode of Detection in Breast Cancer. Cancer Research, 2018, 78, 6329-6338.	0.4	19
79	A <scp>RAD</scp> 51 assay feasible in routine tumor samples calls <scp>PARP</scp> inhibitor response beyond <scp>BRCA</scp> mutation. EMBO Molecular Medicine, 2018, 10, .	3.3	169
80	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.4	54
81	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
82	Risks of Breast, Ovarian, and Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. JAMA - Journal of the American Medical Association, 2017, 317, 2402.	3.8	1,898
83	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
84	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
85	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
86	Geneâ€“environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	2.3	20
87	Increased Use of BRCA Mutation Test in Unaffected Women Over the Period 2004â€“2014 in the U.S.: Further Evidence of the â€œAngelina Jolie Effectâ€?. American Journal of Preventive Medicine, 2017, 53, e195-e196.	1.6	7
88	VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis. Bioinformatics, 2017, 33, 1389-1391.	1.8	2
89	Inherited Chromosomally Integrated Human Herpesvirus 6 and Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 425-427.	1.1	5
90	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	1.1	18

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91	Do women change their breast cancer mammogram screening behaviour after BRCA1/2 testing?. Familial Cancer, 2017, 16, 35-40.	0.9	5
92	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278
93	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2017, 109, .	3.0	242
94	Breast Cancer Risk Estimation and Personal Insurance: A Qualitative Study Presenting Perspectives from Canadian Patients and Decision Makers. Frontiers in Genetics, 2017, 8, 128.	1.1	17
95	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
96	Transcriptional signature of lymphoblastoid cell lines ofBRCA1,BRCA2and non-BRCA1/2high risk breast cancer families. Oncotarget, 2017, 8, 78691-78712.	0.8	8
97	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
98	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
99	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
100	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	1.1	10
101	ABRAXAS (FAM175A) and Breast Cancer Susceptibility: No Evidence of Association in the Breast Cancer Family Registry. PLoS ONE, 2016, 11, e0156820.	1.1	5
102	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
103	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
104	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
105	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
106	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. Breast Cancer Research, 2016, 18, 124.	2.2	52
107	Clinical follow-up and breast and ovarian cancer screening of true BRCA1/2 noncarriers: a qualitative investigation. Genetics in Medicine, 2016, 18, 627-634.	1.1	6
108	Incorporating truncating variants in PALB2, CHEK2, and ATM into the BOADICEA breast cancer risk model. Genetics in Medicine, 2016, 18, 1190-1198.	1.1	80

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109	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
110	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
111	Usefulness of Canadian Public Health Insurance Administrative Databases to Assess Breast and Ovarian Cancer Screening Imaging Technologies for BRCA1/2 Mutation Carriers. Canadian Association of Radiologists Journal, 2016, 67, 308-312.	1.1	3
112	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
113	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
114	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
115	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
116	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	2.2	42
117	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
118	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
119	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
120	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
121	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
122	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
123	The knowledge value-chain of genetic counseling for breast cancer: an empirical assessment of prediction and communication processes. Familial Cancer, 2016, 15, 1-17.	0.9	10
124	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
125	SNP Set Association Testing for Survival Outcomes in the Presence of Intrafamilial Correlation. Genetic Epidemiology, 2015, 39, 406-414.	0.6	6
126	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

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127	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
128	SNP-SNP interaction analysis of NF-Î²B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
129	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
130	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
131	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
132	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
133	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
134	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
135	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
136	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
137	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.4	55
138	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
139	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	1.4	67
140	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
141	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
142	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
143	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	1.1	22
144	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49

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145	Medical Genetic Counseling for Breast Cancer in Primary Care: A Synthesis of Major Determinants of Physicians' Practices in Primary Care Settings. Public Health Genomics, 2014, 17, 190-208.	0.6	13
146	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
147	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
148	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
149	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	2.2	57
150	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
151	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	0.6	28
152	Life insurance: genomic stratification and risk classification. European Journal of Human Genetics, 2014, 22, 575-579.	1.4	41
153	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
154	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
155	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
156	COMPLEXO: identifying the missing heritability of breast cancer via next generation collaboration. Breast Cancer Research, 2013, 15, 402.	2.2	36
157	Family Communication Following BRCA1/2 Genetic Testing: A Close Look at the Process. Journal of Genetic Counseling, 2013, 22, 323-335.	0.9	32
158	Life Events may Contribute to Family Communication About Cancer Risk Following BRCA1/2 Testing. Journal of Genetic Counseling, 2013, 22, 249-257.	0.9	15
159	Genetic discrimination and life insurance: a systematic review of the evidence. BMC Medicine, 2013, 11, 25.	2.3	98
160	Exploring resources for intrafamilial communication of cancer genetic risk: we still need to talk. European Journal of Human Genetics, 2013, 21, 903-910.	1.4	13
161	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
162	Tamoxifen and Risk of Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. Journal of Clinical Oncology, 2013, 31, 3091-3099.	0.8	148

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163	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
164	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
165	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
166	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
167	A focus group study on breast cancer risk presentation: one format does not fit all. European Journal of Human Genetics, 2013, 21, 719-724.	1.4	17
168	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
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