Alison Margaret Dunning

List of Publications by Year
in descending order

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		2802	4015
368	38,197	94	176
papers	citations	h-index	g-index

392	392	392	36872
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
2	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
3	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
4	Subtyping of Breast Cancer by Immunohistochemistry to Investigate a Relationship between Subtype and Short and Long Term Survival: A Collaborative Analysis of Data for 10,159 Cases from 12 Studies. PLoS Medicine, 2010, 7, e1000279.	8.4	764
5	Beyond GWASs: Illuminating the Dark Road from Association to Function. American Journal of Human Genetics, 2013, 93, 779-797.	6.2	688
6	Genome-wide association study identifies five new breast cancer susceptibility loci. Nature Genetics, 2010, 42, 504-507.	21.4	653
7	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
8	Normal tissue reactions to radiotherapy: towards tailoring treatment dose by genotype. Nature Reviews Cancer, 2009, 9, 134-142.	28.4	593
9	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
10	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
11	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
12	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
13	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
14	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.	21.4	493
15	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492
16	Germline mutations of the BRCA1 gene in breast and ovarian cancer families provide evidence for a genotypeâ€"phenotype correlation. Nature Genetics, 1995, 11, 428-433.	21.4	484
17	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	21.4	434
18	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428

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19	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.	21.4	426
20	Association studies for finding cancer-susceptibility genetic variants. Nature Reviews Cancer, 2004, 4, 850-860.	28.4	417
21	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	27.8	413
22	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
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.	21.4	357
24	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	21.4	319
25	Germline BRCA mutation and outcome in young-onset breast cancer (POSH): a prospective cohort study. Lancet Oncology, The, 2018, 19, 169-180.	10.7	316
26	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	3.5	315
27	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.	21.4	309
28	Polymorphisms Associated With Circulating Sex Hormone Levels in Postmenopausal Women. Journal of the National Cancer Institute, 2004, 96, 936-945.	6.3	308
29	Multiple Loci With Different Cancer Specificities Within the 8q24 Gene Desert. Journal of the National Cancer Institute, 2008, 100, 962-966.	6.3	306
30	Shortened Telomere Length Is Associated with Increased Risk of Cancer: A Meta-Analysis. PLoS ONE, 2011, 6, e20466.	2.5	292
31	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
32	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
33	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
34	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	2.5	278
35	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	1.6	270
36	Differential Genetic Effects of <EMPH TYPE="ITAL">ESR1</EMPH> Gene Polymorphisms on Osteoporosis Outcomes. JAMA - Journal of the American Medical Association, 2004, 292, 2105.	7.4	265

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37	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
38	A transforming growth factorbeta1 signal peptide variant increases secretion in vitro and is associated with increased incidence of invasive breast cancer. Cancer Research, 2003, 63, 2610-5.	0.9	265
39	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	21.4	264
40	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
41	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	3.5	244
42	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
43	DNA repair polymorphisms and cancer risk in non-smokers in a cohort study. Carcinogenesis, 2006, 27, 997-1007.	2.8	227
44	The Association between Common Vitamin D Receptor Gene Variations and Osteoporosis: A Participant-Level Meta-Analysis. Annals of Internal Medicine, 2006, 145, 255.	3.9	219
45	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
46	Independent validation of genes and polymorphisms reported to be associated with radiation toxicity: a prospective analysis study. Lancet Oncology, The, 2012, 13, 65-77.	10.7	202
47	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.	6.2	201
48	The Extent of Linkage Disequilibrium in Four Populations with Distinct Demographic Histories. American Journal of Human Genetics, 2000, 67, 1544-1554.	6.2	192
49	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
50	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
51	IGF1 and IGFBP3 tagging polymorphisms are associated with circulating levels of IGF1, IGFBP3 and risk of breast cancer. Human Molecular Genetics, 2006, 15, 1-10.	2.9	181
52	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
53	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
54	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	2.9	168

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55	Familial defective apolipoprotein B-100: detection in the United Kingdom and Scandinavia, and clinical characteristics of ten cases. Atherosclerosis, 1990, 80, 235-242.	0.8	165
56	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.	1.6	162
57	Large-Scale Evidence for the Effect of the COLIA1 Sp1 Polymorphism on Osteoporosis Outcomes: The GENOMOS Study. PLoS Medicine, 2006, 3, e90.	8.4	160
58	Air pollution and risk of lung cancer in a prospective study in Europe. International Journal of Cancer, 2006, 119, 169-174.	5.1	158
59	TP53 and KRAS2 Mutations in Plasma DNA of Healthy Subjects and Subsequent Cancer Occurrence: A Prospective Study. Cancer Research, 2006, 66, 6871-6876.	0.9	158
60	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.	9.4	157
61	A polymorphic stop codon in BRCA2. Nature Genetics, 1996, 14, 253-254.	21.4	152
62	A common variant in BRCA2 is associated with both breast cancer risk and prenatal viability. Nature Genetics, 2000, 26, 362-364.	21.4	152
63	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.	2.9	152
64	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
65	Errors in the Polymerase Chain Reaction. Nucleic Acids Research, 1988, 16, 10393-10393.	14.5	150
66	Telomere Length in Prospective and Retrospective Cancer Case-Control Studies. Cancer Research, 2010, 70, 3170-3176.	0.9	142
67	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	21.4	141
68	Genetic Variation at the CYP19A1 Locus Predicts Circulating Estrogen Levels but not Breast Cancer Risk in Postmenopausal Women. Cancer Research, 2007, 67, 1893-1897.	0.9	140
69	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
70	A Common 8q24 Variant in Prostate and Breast Cancer from a Large Nested Case-Control Study. Cancer Research, 2007, 67, 2951-2956.	0.9	136
71	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
72	Association between Common Variation in 120 Candidate Genes and Breast Cancer Risk. PLoS Genetics, 2007, 3, e42.	3.5	134

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73	Reproducibility of telomere length assessment: an international collaborative study. International Journal of Epidemiology, 2015, 44, 1673-1683.	1.9	133
74	A genome-wide association scan (GWAS) for mean telomere length within the COGS project: identified loci show little association with hormone-related cancer risk. Human Molecular Genetics, 2013, 22, 5056-5064.	2.9	130
75	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2015, 107, .	6.3	129
76	Red clover-derived isoflavones and mammographic breast density: a double-blind, randomized, placebo-controlled trial [ISRCTN42940165]. Breast Cancer Research, 2004, 6, R170-9.	5.0	128
77	A genome wide association study (GWAS) providing evidence of an association between common genetic variants and late radiotherapy toxicity. Radiotherapy and Oncology, 2014, 111, 178-185.	0.6	128
78	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
79	Somatically acquired hypomethylation of IGF2 in breast and colorectal cancer. Human Molecular Genetics, 2008, 17, 2633-2643.	2.9	124
80	Polymorphisms in DNA repair genes and epithelial ovarian cancer risk. International Journal of Cancer, 2005, 117, 611-618.	5.1	123
81	Saliva samples are a viable alternative to blood samples as a source of DNA for high throughput genotyping. BMC Medical Genomics, 2012, 5, 19.	1.5	120
82	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. Nature Genetics, 2017, 49, 1133-1140.	21.4	120
83	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
84	A three-stage genome-wide association study identifies a susceptibility locus for late radiotherapy toxicity at 2q24.1. Nature Genetics, 2014, 46, 891-894.	21.4	114
85	Effect of germ-line genetic variation on breast cancer survival in a population-based study. Cancer Research, 2002, 62, 3052-7.	0.9	114
86	FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. Human Molecular Genetics, 2009, 18, 1692-1703.	2.9	110
87	DNA Adducts and Lung Cancer Risk: A Prospective Study. Cancer Research, 2005, 65, 8042-8048.	0.9	109
88	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
89	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
90	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105

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91	No association between androgen or vitamin D receptor gene polymorphisms and risk of breast cancer. Carcinogenesis, 1999, 20, 2131-2135.	2.8	103
92	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
93	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	2.9	100
94	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.	6.3	99
95	Life Stress, Emotional Health, and Mean Telomere Length in the European Prospective Investigation into Cancer (EPIC)-Norfolk Population Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2011, 66A, 1152-1162.	3.6	99
96	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. Nature Genetics, 2012, 44, 1182-1184.	21.4	99
97	Radiogenomics: Radiobiology Enters the Era of Big Data and Team Science. International Journal of Radiation Oncology Biology Physics, 2014, 89, 709-713.	0.8	99
98	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
99	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.	6.2	98
100	Individual patient data meta-analysis shows a significant association between the ATM rs1801516 SNP and toxicity after radiotherapy in 5456 breast and prostate cancer patients. Radiotherapy and Oncology, 2016, 121, 431-439.	0.6	98
101	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.	5.0	97
102	Amount of DNA in plasma and cancer risk: A prospective study. International Journal of Cancer, 2004, 111, 746-749.	5.1	95
103	Common variants in the ATM, BRCA1, BRCA2, CHEK2 and TP53 cancer susceptibility genes are unlikely to increase breast cancer risk. Breast Cancer Research, 2007, 9, R27.	5.0	94
104	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.	3.2	94
105	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
106	Large-scale analysis of association between polymorphisms in the transforming growth factor beta 1 gene (TGFB1) and osteoporosis: The GENOMOS study. Bone, 2008, 42, 969-981.	2.9	91
107	A combined analysis of genome-wide association studies in breast cancer. Breast Cancer Research and Treatment, 2011, 126, 717-727.	2.5	90
108	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90

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109	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
110	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536.	1.9	88
111	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
112	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
113	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. Nature Communications, 2020, 11, 3833.	12.8	88
114	Common genetic determinants of breast-cancer risk in East Asian women: a collaborative study of 23 637 breast cancer cases and 25 579 controls. Human Molecular Genetics, 2013, 22, 2539-2550.	2.9	86
115	Genetic variants in epigenetic genes and breast cancer risk. Carcinogenesis, 2006, 27, 1661-1669.	2.8	85
116	Most common â€˜sporadicâ€™ cancers have a significant germline genetic component. Human Molecular Genetics, 2014, 23, 6112-6118.	2.9	85
117	Prevalence of theHOXB13 G84E germline mutation in British men and correlation with prostate cancer risk, tumour characteristics and clinical outcomes. Annals of Oncology, 2015, 26, 756-761.	1.2	85
118	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 2009, 18, 1131-1139.	2.9	84
119	From candidate gene studies to GWAS and post-GWAS analyses in breast cancer. Current Opinion in Genetics and Development, 2015, 30, 32-41.	3.3	83
120	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
121	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. Breast Cancer Research, 2010, 12, R110.	5.0	82
122	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
123	Do MDM2 SNP309 and TP53 R72P Interact in Breast Cancer Susceptibility? A Large Pooled Series from the Breast Cancer Association Consortium. Cancer Research, 2007, 67, 9584-9590.	0.9	80
124	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80
125	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
126	A Genome-wide Association Study of Early-Onset Breast Cancer Identifies PFKM as a Novel Breast Cancer Gene and Supports a Common Genetic Spectrum for Breast Cancer at Any Age. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 658-669.	2.5	77

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127	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
128	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
129	Tagging Single-Nucleotide Polymorphisms in Antioxidant Defense Enzymes and Susceptibility to Breast Cancer. Cancer Research, 2006, 66, 1225-1233.	0.9	76
130	CYP2D6 gene variants: association with breast cancer specific survival in a cohort of breast cancer patients from the United Kingdom treated with adjuvant tamoxifen. Breast Cancer Research, 2010, 12, R64.	5.0	76
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.	6.2	76
132	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
133	Polymorphisms in the human aromatase cytochrome P450 gene (CYP19) and breast cancer risk. Carcinogenesis, 2000, 21, 189-193.	2.8	74
134	Polymorphisms in the Initiators of RET (Rearranged during Transfection) Signaling Pathway and Susceptibility to Sporadic Medullary Thyroid Carcinoma. Journal of Clinical Endocrinology and Metabolism, 2005, 90, 6268-6274.	3.6	74
135	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	2.9	71
136	Radiogenomics Consortium Genome-Wide Association Study Meta-Analysis of Late Toxicity After Prostate Cancer Radiotherapy. Journal of the National Cancer Institute, 2020, 112, 179-190.	6.3	71
137	Allelic association of the human homologue of the mouse modifier Ptprj with breast cancer. Human Molecular Genetics, 2005, 14, 2349-2356.	2.9	70
138	Multi-factor dimensionality reduction applied to a large prospective investigation on gene-gene and gene-environment interactions. Carcinogenesis, 2006, 28, 414-422.	2.8	70
139	Telomere length and common disease: study design and analytical challenges. Human Genetics, 2015, 134, 679-689.	3.8	70
140	Meta-analysis of Genome Wide Association Studies Identifies Genetic Markers of Late Toxicity Following Radiotherapy for Prostate Cancer. EBioMedicine, 2016, 10, 150-163.	6.1	69
141	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
142	Association of single-nucleotide polymorphisms in the cell cycle genes with breast cancer in the British population. Carcinogenesis, 2008, 29, 333-341.	2.8	68
143	Fine scale mapping of the breast cancer 16q12 locus. Human Molecular Genetics, 2010, 19, 2507-2515.	2.9	68
144	Rare, protein-truncating variants inATM,CHEK2andPALB2, but notXRCC2, are associated with increased breast cancer risks. Journal of Medical Genetics, 2017, 54, 732-741.	3.2	68

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145	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	2.9	67
146	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
147	Genetic Variation in the HSD17B1 Gene and Risk of Prostate Cancer. PLoS Genetics, 2005, 1, e68.	3.5	66
148	A replicated association between polymorphisms near TNFÎ± and risk for adverse reactions to radiotherapy. British Journal of Cancer, 2012, 107, 748-753.	6.4	66
149	Thepatched polymorphism Pro1315Leu (C3944T) may modulate the association between use of oral contraceptives and breast cancer risk. International Journal of Cancer, 2003, 103, 779-783.	5.1	65
150	Individual patient data meta-analysis shows no association between the SNP rs1800469 in TGFB and late radiotherapy toxicity. Radiotherapy and Oncology, 2012, 105, 289-295.	0.6	65
151	Rat Mcs5a is a compound quantitative trait locus with orthologous human loci that associate with breast cancer risk. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6299-6304.	7.1	64
152	XRCC1 Polymorphism Associated With Late Toxicity After Radiation Therapy in Breast Cancer Patients. International Journal of Radiation Oncology Biology Physics, 2015, 92, 1084-1092.	0.8	64
153	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1503-1510.	2.5	64
154	Prognostic Value of PAI1 in Invasive Breast Cancer: Evidence That Tumor-Specific Factors Are More Important Than Genetic Variation in Regulating PAI1 Expression. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2107-2114.	2.5	63
155	Standardized Total Average Toxicity Score: A Scale- and Grade-Independent Measure of Late Radiotherapy Toxicity to Facilitate Pooling of Data From Different Studies. International Journal of Radiation Oncology Biology Physics, 2012, 82, 1065-1074.	0.8	63
156	Radiogenomics: the search for genetic predictors of radiotherapy response. Future Oncology, 2014, 10, 2391-2406.	2.4	63
157	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
158	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
159	Common variants associated with breast cancer in genome-wide association studies are modifiers of breast cancer risk in BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2010, 19, 2886-2897.	2.9	60
160	Genetic susceptibility according to three metabolic pathways in cancers of the lung and bladder and in myeloid leukemias in nonsmokers. Annals of Oncology, 2007, 18, 1230-1242.	1.2	59
161	STROGAR â€“ STrengthening the Reporting Of Genetic Association studies in Radiogenomics. Radiotherapy and Oncology, 2014, 110, 182-188.	0.6	59
162	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.	6.2	59

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163	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340.	12.8	58
164	Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1610-1616.	2.5	57
165	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
166	Common ERBB2 polymorphisms and risk of breast cancer in a white British population: a caseâ€“control study. Breast Cancer Research, 2005, 7, R204-9.	5.0	55
167	Association of theProgesterone ReceptorGene with Breast Cancer Risk: A Single-Nucleotide Polymorphism Tagging Approach. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 675-682.	2.5	55
168	Phytoestrogen Exposure Is Associated with Circulating Sex Hormone Levels in Postmenopausal Women and Interact withESR1andNR1I2Gene Variants. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1009-1016.	2.5	55
169	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.9	55
170	Phytoestrogen Exposure, Polymorphisms in COMT, CYP19, ESR1, and SHBG Genes, and Their Associations With Prostate Cancer Risk. Nutrition and Cancer, 2006, 56, 31-39.	2.0	54
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