Melissa C. Southey

List of Publications by Year
in descending order

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		2426	3031
572	46,452	97	188
papers	citations	h-index	g-index

603	603	603	37269
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.	13.7	2,165
2	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
3	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
4	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
5	Multiple newly identified loci associated with prostate cancer susceptibility. Nature Genetics, 2008, 40, 316-321.	9.4	796
6	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.	3.9	764
7	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	13.9	764
8	Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506.	13.9	745
9	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
10	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
11	Iron-Overloadâ€“Related Disease inHFEHereditary Hemochromatosis. New England Journal of Medicine, 2008, 358, 221-230.	13.9	649
12	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263.	3.0	596
13	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	9.4	591
14	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
15	A genome-wide association study identifies colorectal cancer susceptibility loci on chromosomes 10p14 and 8q23.3. Nature Genetics, 2008, 40, 623-630.	9.4	514
16	Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 134-147.	1.1	513
17	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
18	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

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19	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	492
20	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434
21	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
22	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
23	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
24	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. Nature Genetics, 2009, 41, 1116-1121.	9.4	389
25	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
26	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
27	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
28	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
29	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
30	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
31	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
32	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
33	Colorectal and Other Cancer Risks for Carriers and Noncarriers From Families With a DNA Mismatch Repair Gene Mutation: A Prospective Cohort Study. Journal of Clinical Oncology, 2012, 30, 958-964.	0.8	286
34	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	3.4	285
35	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	9.4	279
36	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	9.4	276

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37	Multiple loci on 8q24 associated with prostate cancer susceptibility. Nature Genetics, 2009, 41, 1058-1060.	9.4	273
38	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	0.8	270
39	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	9.4	265
40	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
41	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.	9.4	264
42	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
43	The Breast Cancer Family Registry: an infrastructure for cooperative multinational, interdisciplinary and translational studies of the genetic epidemiology of breast cancer. Breast Cancer Research, 2004, 6, R375-89.	2.2	255
44	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
45	The histologic phenotypes of breast carcinoma occurring before age 40 years in women with and without BRCA1 or BRCA2 germline mutations. Cancer, 1998, 83, 2335-2345.	2.0	243
46	Metachronous colorectal cancer risk for mismatch repair gene mutation carriers: the advantage of more extensive colon surgery. Gut, 2011, 60, 950-957.	6.1	227
47	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
48	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
49	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
50	Hypomethylation of smoking-related genes is associated with future lung cancer in four prospective cohorts. Nature Communications, 2015, 6, 10192.	5.8	197
51	Use of Molecular Tumor Characteristics to Prioritize Mismatch Repair Gene Testing in Early-Onset Colorectal Cancer. Journal of Clinical Oncology, 2005, 23, 6524-6532.	0.8	194
52	Rare variants in the ATMgene and risk of breast cancer. Breast Cancer Research, 2011, 13, R73.	2.2	188
53	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
54	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183

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55	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
56	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
57	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.	1.4	168
58	Rare, Evolutionarily Unlikely Missense Substitutions in ATM Confer Increased Risk of Breast Cancer. American Journal of Human Genetics, 2009, 85, 427-446.	2.6	165
59	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
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.	7.7	157
61	BRCA2 Mutation-associated Breast Cancers Exhibit a Distinguishing Phenotype Based on Morphology and Molecular Profiles From Tissue Microarrays. American Journal of Surgical Pathology, 2007, 31, 121-128.	2.1	156
62	Adaptive evolution of the tumour suppressor BRCA1 in humans and chimpanzees. Nature Genetics, 2000, 25, 410-413.	9.4	153
63	Genetic and Histopathologic Evaluation of BRCA1 and BRCA2 DNA Sequence Variants of Unknown Clinical Significance. Cancer Research, 2006, 66, 2019-2027.	0.4	153
64	DNA methylationâ€based biological aging and cancer risk and survival: Pooled analysis of seven prospective studies. International Journal of Cancer, 2018, 142, 1611-1619.	2.3	153
65	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
66	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
67	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
68	Cancer Risks For Mismatch Repair Gene Mutation Carriers: A Population-Based Early Onset Case-Family Study. Clinical Gastroenterology and Hepatology, 2006, 4, 489-498.	2.4	151
69	Familial Risks, Early-Onset Breast Cancer, and BRCA1 and BRCA2 Germline Mutations. Journal of the National Cancer Institute, 2003, 95, 448-457.	3.0	150
70	Multiple Novel Prostate Cancer Predisposition Loci Confirmed by an International Study: The PRACTICAL Consortium. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2052-2061.	1.1	148
71	Tamoxifen and Risk of Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. Journal of Clinical Oncology, 2013, 31, 3091-3099.	0.8	148
72	Constitutional Methylation of the BRCA1 Promoter Is Specifically Associated with BRCA1 Mutation-Associated Pathology in Early-Onset Breast Cancer. Cancer Prevention Research, 2011, 4, 23-33.	0.7	147

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73	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
74	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	1.3	145
75	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
76	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	9.4	142
77	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. Aging, 2019, 11, 2045-2070.	1.4	137
78	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	1.5	136
79	Breast Cancer Prognosis in BRCA1 and BRCA2 Mutation Carriers: An International Prospective Breast Cancer Family Registry Population-Based Cohort Study. Journal of Clinical Oncology, 2012, 30, 19-26.	0.8	134
80	Oral Contraceptive Use and Risk of Early-Onset Breast Cancer in Carriers and Noncarriers of BRCA1 and BRCA2 Mutations. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 350-356.	1.1	133
81	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129
82	Colorectal carcinomas with KRAS mutation are associated with distinctive morphological and molecular features. Modern Pathology, 2013, 26, 825-834.	2.9	126
83	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
84	HFE C282Y homozygotes are at increased risk of breast and colorectal cancer. Hepatology, 2010, 51, 1311-1318.	3.6	123
85	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
86	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. Human Molecular Genetics, 2013, 22, 408-415.	1.4	118
87	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
88	PIK3CA Activating Mutation in Colorectal Carcinoma: Associations with Molecular Features and Survival. PLoS ONE, 2013, 8, e65479.	1.1	117
89	10-year performance of four models of breast cancer risk: a validation study. Lancet Oncology, The, 2019, 20, 504-517.	5.1	116
90	BRCA1 and BRCA2 Mutation Carriers, Oral Contraceptive Use, and Breast Cancer Before Age 50. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 1863-1870.	1.1	115

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91	DNA methylation changes measured in preâ€diagnostic peripheral blood samples are associated with smoking and lung cancer risk. International Journal of Cancer, 2017, 140, 50-61.	2.3	115
92	A genome wide linkage search for breast cancer susceptibility genes. Genes Chromosomes and Cancer, 2006, 45, 646-655.	1.5	111
93	Cumulative Burden of Colorectal Cancerâ€"Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	0.6	110
94	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. Nature Genetics, 2011, 43, 185-187.	9.4	109
95	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	5.8	109
96	Risk of extracolonic cancers for people with biallelic and monoallelic mutations in MUTYH. International Journal of Cancer, 2016, 139, 1557-1563.	2.3	107
97	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. Human Molecular Genetics, 2016, 25, 2256-2268.	1.4	106
98	Association of DNA Methylation-Based Biological Age With Health Risk Factors and Overall and Cause-Specific Mortality. American Journal of Epidemiology, 2018, 187, 529-538.	1.6	106
99	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
100	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
101	A PALB2 mutation associated with high risk of breast cancer. Breast Cancer Research, 2010, 12, R109.	2.2	102
102	HFEC282Y/H63D compound heterozygotes are at low risk of hemochromatosis-related morbidity. Hepatology, 2009, 50, 94-101.	3.6	101
103	Common Breast Cancer Susceptibility Variants in LSP1 and RAD51L1 Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1156-1166.	1.1	101
104	19p13.1 Is a Triple-Negativeâ€"Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.4	100
105	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
106	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
107	Rare key functional domain missense substitutions in MRE11A, RAD50, and NBNcontribute to breast cancer susceptibility: results from a Breast Cancer Family Registry case-control mutation-screening study. Breast Cancer Research, 2014, 16, R58.	2.2	99
108	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99

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109	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
110	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	5.8	98
111	After BRCA1 and BRCA2â€"What Next? Multifactorial Segregation Analyses of Three-Generation, Population-Based Australian Families Affected by Female Breast Cancer. American Journal of Human Genetics, 2001, 68, 420-431.	2.6	97
112	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
113	Ethnicity and Risk for Colorectal Cancers Showing Somatic BRAF V600E Mutation or CpG Island Methylator Phenotype. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1774-1780.	1.1	96
114	Breast Cancer Risk Prediction Using Clinical Models and 77 Independent Risk-Associated SNPs for Women Aged Under 50 Years: Australian Breast Cancer Family Registry. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 359-365.	1.1	96
115	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
116	Comparison of mRNA Splicing Assay Protocols across Multiple Laboratories: Recommendations for Best Practice in Standardized Clinical Testing. Clinical Chemistry, 2014, 60, 341-352.	1.5	95
117	Causal effect of smoking on DNA methylation in peripheral blood: a twin and family study. Clinical Epigenetics, 2018, 10, 18.	1.8	95
118	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94
119	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
120	Cancer risks for monoallelic MUTYH mutation carriers with a family history of colorectal cancer. International Journal of Cancer, 2011, 129, 2256-2262.	2.3	93
121	Epigenome-wide methylation in DNA from peripheral blood as a marker of risk for breast cancer. Breast Cancer Research and Treatment, 2014, 148, 665-673.	1.1	93
122	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
123	Interplay between BRCA1 and RHAMM Regulates Epithelial Apicobasal Polarization and May Influence Risk of Breast Cancer. PLoS Biology, 2011, 9, e1001199.	2.6	91
124	A Cost-effectiveness Analysis of Multigene Testing for All Patients With Breast Cancer. JAMA Oncology, 2019, 5, 1718.	3.4	91
125	Penetrance Analysis of the PALB2 c.1592delT Founder Mutation. Clinical Cancer Research, 2008, 14, 4667-4671.	3.2	90
126	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90

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127	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
128	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	0.8	90
129	Epigenetic supersimilarity of monozygotic twin pairs. Genome Biology, 2018, 19, 2.	3.8	89
130	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	2.2	88
131	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.	0.9	88
132	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
133	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
134	The Natural History of Serum Iron Indices for HFE C282Y Homozygosity Associated With Hereditary Hemochromatosis. Gastroenterology, 2008, 135, 1945-1952.	0.6	86
135	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	1.5	85
136	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 2009, 18, 1131-1139.	1.4	84
137	Population-Based Estimate of the Contribution of TP53 Mutations to Subgroups of Early-Onset Breast Cancer: Australian Breast Cancer Family Study. Cancer Research, 2010, 70, 4795-4800.	0.4	84
138	Associations of alcohol intake, smoking, physical activity and obesity with survival following colorectal cancer diagnosis by stage, anatomic site and tumor molecular subtype. International Journal of Cancer, 2018, 142, 238-250.	2.3	83
139	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.	2.2	82
140	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
141	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
142	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	1.4	80
143	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	2.2	78
144	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78

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145	Double-Strand Break Repair Gene Polymorphisms and Risk of Breast or Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 319-323.	1.1	77
146	The E211 G>A Androgen Receptor Polymorphism Is Associated with a Decreased Risk of Metastatic Prostate Cancer and Androgenetic Alopecia. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 993-996.	1.1	77
147	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.	1.1	77
148	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
149	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
150	Heritable DNA methylation marks associated with susceptibility to breast cancer. Nature Communications, 2018, 9, 867.	5.8	76
151	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
152	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
153	Comparison of DNA- and RNA-Based Methods for Detection of TruncatingBRCA1 Mutations. Human Mutation, 2002, 20, 65-73.	1.1	74
154	Common Genetic Variants Associated with Breast Cancer and Mammographic Density Measures That Predict Disease. Cancer Research, 2010, 70, 1449-1458.	0.4	74
155	Rare, evolutionarily unlikely missense substitutions in CHEK2contribute to breast cancer susceptibility: results from a breast cancer family registry case-control mutation-screening study. Breast Cancer Research, 2011, 13, R6.	2.2	74
156	Common breast cancer susceptibility alleles are associated with tumour subtypes in BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2011, 13, R110.	2.2	71
157	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.	1.4	71
158	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	0.9	71
159	Are the so-called low penetrance breast cancer genes, ATM, BRIP1, PALB2 and CHEK2, high risk for women with strong family histories?. Breast Cancer Research, 2008, 10, 208.	2.2	70
160	Evaluation of a 5-Tier Scheme Proposed for Classification of Sequence Variants Using Bioinformatic and Splicing Assay Data: Inter-Reviewer Variability and Promotion of Minimum Reporting Guidelines. Human Mutation, 2013, 34, 1424-1431.	1.1	67
161	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
162	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67

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163	Uncommon CHEK2 mis-sense variant and reduced risk of tobacco-related cancers: caseâ€“control study. Human Molecular Genetics, 2007, 16, 1794-1801.	1.4	66
164	Body size and risk for colorectal cancers showing BRAF mutations or microsatellite instability: a pooled analysis. International Journal of Epidemiology, 2012, 41, 1060-1072.	0.9	65
165	The Common Variant rs1447295 on Chromosome 8q24 and Prostate Cancer Risk: Results from an Australian Population-Based Case-Control Study. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 610-612.	1.1	64
166	Mutation analysis of BRCA1 and BRCA2 cancer predisposition genes in radiation hypersensitive cancer patients. International Journal of Radiation Oncology Biology Physics, 2000, 48, 959-965.	0.4	63
167	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
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