Paul D P Pharoah

List of Publications by Year
in descending order

829	78,883	418	872
papers	citations	132 h-index	243 g-index

892	892	892	62856
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Average Risks of Breast and Ovarian Cancer Associated with BRCA1 or BRCA2 Mutations Detected in Case Series Unselected for Family History: A Combined Analysis of 22 Studies. American Journal of Human Genetics, 2003, 72, 1117-1130.	2.6	3,105
2	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
3	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	13.7	1,778
4	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. Nature Communications, 2016, 7, 11479.	5.8	1,221
5	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
6	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
7	Polygenic susceptibility to breast cancer and implications for prevention. Nature Genetics, 2002, 31, 33-36.	9.4	874
8	Rethinking ovarian cancer II: reducing mortality from high-grade serous ovarian cancer. Nature Reviews Cancer, 2015, 15, 668-679.	12.8	839
9	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
10	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	13.9	764
11	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
12	Genome-wide association study identifies five new breast cancer susceptibility loci. Nature Genetics, 2010, 42, 504-507.	9.4	653
13	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
14	Association between CD8+ T-cell infiltration and breast cancer survival in 12 439 patients. Annals of Oncology, 2014, 25, 1536-1543.	0.6	610
15	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
16	Normal tissue reactions to radiotherapy: towards tailoring treatment dose by genotype. Nature Reviews Cancer, 2009, 9, 134-142.	12.8	593
17	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	9.4	591
18	Incidence of gastric cancer and breast cancer in CDH1 (E-cadherin) mutation carriers from hereditary diffuse gastric cancer families. Gastroenterology, 2001, 121, 1348-1353.	0.6	579

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19	Prevalence and penetrance of BRCA1 and BRCA2 mutations in a population-based series of breast cancer cases. British Journal of Cancer, 2000, 83, 1301-1308.	2.9	573
20	p53 polymorphisms: cancer implications. Nature Reviews Cancer, 2009, 9, 95-107.	12.8	564
21	Helicobacter pylori and Interleukin 1 Genotyping: An Opportunity to Identify High-Risk Individuals for Gastric Carcinoma. Journal of the National Cancer Institute, 2002, 94, 1680-1687.	3.0	563
22	Polygenes, Risk Prediction, and Targeted Prevention of Breast Cancer. New England Journal of Medicine, 2008, 358, 2796-2803.	13.9	558
23	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
24	Association Between <emph type="ital">BRCA1</emph> and <emph type="ital">BRCA2</emph> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. JAMA - Journal of the American Medical Association, 2012, 307, 382.	3.8	546
25	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. Nature Genetics, 2008, 40, 631-637.	9.4	542
26	Hereditary Diffuse Gastric Cancer Syndrome. JAMA Oncology, 2015, 1, 23.	3.4	540
27	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
28	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
29	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
30	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	9.4	498
31	Family history and the risk of breast cancer: A systematic review and meta-analysis. , 1997, 71, 800-809.		494
32	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
33	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	492
34	Patterns of Immune Infiltration in Breast Cancer and Their Clinical Implications: A Gene-Expression-Based Retrospective Study. PLoS Medicine, 2016, 13, e1002194.	3.9	473
35	The BOADICEA model of genetic susceptibility to breast and ovarian cancers: updates and extensions. British Journal of Cancer, 2008, 98, 1457-1466.	2.9	461
36	A proinflammatory genetic profile increases the risk for chronic atrophic gastritis and gastric carcinoma. Gastroenterology, 2003, 125, 364-371.	0.6	450

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37	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	9.4	445
38	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434
39	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
40	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
41	A comprehensive model for familial breast cancer incorporating BRCA1, BRCA2 and other genes. British Journal of Cancer, 2002, 86, 76-83.	2.9	422
42	Association studies for finding cancer-susceptibility genetic variants. Nature Reviews Cancer, 2004, 4, 850-860.	12.8	417
43	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	1.1	415
44	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	13.7	413
45	The BOADICEA model of genetic susceptibility to breast and ovarian cancer. British Journal of Cancer, 2004, 91, 1580-1590.	2.9	411
46	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
47	Interleukin 1B and interleukin 1RN polymorphisms are associated with increased risk of gastric carcinoma. Gastroenterology, 2001, 121, 823-829.	0.6	402
48	Founder and Recurrent CDH1 Mutations in Families With Hereditary Diffuse Gastric Cancer. JAMA - Journal of the American Medical Association, 2007, 297, 2360.	3.8	394
49	Relative and absolute risk of colorectal cancer for individuals with a family history: A meta-analysis. European Journal of Cancer, 2006, 42, 216-227.	1.3	377
50	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
51	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
52	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 2020, 52, 1219-1226.	9.4	367
53	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
54	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356

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55	Proliferation markers and survival in early breast cancer: A systematic review and meta-analysis of 85 studies in 32,825 patients. Breast, 2008, 17, 323-334.	0.9	353
56	Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. Nature Genetics, 2010, 42, 973-977.	9.4	335
57	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	5.1	335
58	Common variants in WFS1 confer risk of type 2 diabetes. Nature Genetics, 2007, 39, 951-953.	9.4	333
59	Variants in DNA double-strand break repair genes and breast cancer susceptibility. Human Molecular Genetics, 2002, 11, 1399-1407.	1.4	331
60	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
61	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	9.4	321
62	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. Breast Cancer Research, 2013, 15, R92.	2.2	320
63	Germline BRCA mutation and outcome in young-onset breast cancer (POSH): a prospective cohort study. Lancet Oncology, The, 2018, 19, 169-180.	5.1	316
64	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
65	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. Journal of the National Cancer Institute, 2015, 107, .	3.0	311
66	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
67	Polymorphisms Associated With Circulating Sex Hormone Levels in Postmenopausal Women. Journal of the National Cancer Institute, 2004, 96, 936-945.	3.0	308
68	Multiple Loci With Different Cancer Specificities Within the 8q24 Gene Desert. Journal of the National Cancer Institute, 2008, 100, 962-966.	3.0	306
69	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
70	PREDICT: a new UK prognostic model that predicts survival following surgery for invasive breast cancer. Breast Cancer Research, 2010, 12, R1.	2.2	285
71	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
72	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

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73	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	9.4	276
74	Acceptability and accuracy of a non-endoscopic screening test for Barrett's oesophagus in primary care: cohort study. BMJ: British Medical Journal, 2010, 341, c4372-c4372.	2.4	271
75	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
76	Somatic mutations in the p53 gene and prognosis in breast cancer: a meta-analysis. British Journal of Cancer, 1999, 80, 1968-1973.	2.9	268
77	Contribution of Germline Mutations in the RAD51B, RAD51C, and RAD51D Genes to Ovarian Cancer in the Population. Journal of Clinical Oncology, 2015, 33, 2901-2907.	0.8	266
78	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	9.4	265
79	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
80	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.	0.4	265
81	Evidence for further breast cancer susceptibility genes in addition toBRCA1 andBRCA2 in a population-based study. Genetic Epidemiology, 2001, 21, 1-18.	0.6	263
82	Dose-Response Association of CD8⁺ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. JAMA Oncology, 2017, 3, e173290.	3.4	260
83	BCL2 in breast cancer: a favourable prognostic marker across molecular subtypes and independent of adjuvant therapy received. British Journal of Cancer, 2010, 103, 668-675.	2.9	259
84	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
85	Model of the early development of diffuse gastric cancer in E-cadherin mutation carriers and its implications for patient screening. Journal of Pathology, 2004, 203, 681-687.	2.1	242
86	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
87	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.	13.7	239
88	Commonly Studied Single-Nucleotide Polymorphisms and Breast Cancer: Results From the Breast Cancer Association Consortium. Journal of the National Cancer Institute, 2006, 98, 1382-1396.	3.0	238
89	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	9.4	235
90	PD-L1 protein expression in breast cancer is rare, enriched in basal-like tumours and associated with infiltrating lymphocytes. Annals of Oncology, 2015, 26, 1488-1493.	0.6	234

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91	Pathology of Ovarian Cancers in BRCA1 and BRCA2 Carriers. Clinical Cancer Research, 2004, 10, 2473-2481.	3.2	224
92	Cancer genetics of epigenetic genes. Human Molecular Genetics, 2007, 16, R28-R49.	1.4	223
93	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
94	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. Nature Genetics, 2011, 43, 60-65.	9.4	220
95	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
96	Cell type-specific DNA methylation patterns in the human breast. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14076-14081.	3.3	210
97	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	9.4	210
98	A systematic review and meta-analysis of family history and risk of ovarian cancer. BJOG: an International Journal of Obstetrics and Gynaecology, 1998, 105, 493-499.	1.1	209
99	The BRCA1-Î”11q Alternative Splice Isoform Bypasses Germline Mutations and Promotes Therapeutic Resistance to PARP Inhibition and Cisplatin. Cancer Research, 2016, 76, 2778-2790.	0.4	208
100	Independent validation of genes and polymorphisms reported to be associated with radiation toxicity: a prospective analysis study. Lancet Oncology, The, 2012, 13, 65-77.	5.1	202
101	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
102	Prediction of pathogenic mutations in patients with early-onset breast cancer by family history. Lancet, The, 2003, 361, 1101-1102.	6.3	200
103	Cost-effectiveness and Benefit-to-Harm Ratio of Risk-Stratified Screening for Breast Cancer. JAMA Oncology, 2018, 4, 1504.	3.4	199
104	The prognostic significance of lymphovascular invasion in invasive breast carcinoma. Cancer, 2012, 118, 3670-3680.	2.0	197
105	Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. Nature Communications, 2020, 11, 597.	5.8	193
106	Association of a Common Variant of the CASP8 Gene With Reduced Risk of Breast Cancer. Journal of the National Cancer Institute, 2004, 96, 1866-1869.	3.0	188
107	Bcl-2 Is a Prognostic Marker in Breast Cancer Independently of the Nottingham Prognostic Index. Clinical Cancer Research, 2006, 12, 2468-2475.	3.2	188
108	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	1.5	188

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109	Multi-omic machine learning predictor of breast cancer therapy response. Nature, 2022, 601, 623-629.	13.7	187
110	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
111	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
112	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.	1.4	181
113	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
114	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	12.5	178
115	Risk Factors for the Incidence of Breast Cancer: Do They Affect Survival From the Disease?. Journal of Clinical Oncology, 2008, 26, 3310-3316.	0.8	174
116	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. Nature Genetics, 2013, 45, 1487-1493.	9.4	174
117	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
118	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172
119	Sipa1 is a candidate for underlying the metastasis efficiency modifier locus Mtes1. Nature Genetics, 2005, 37, 1055-1062.	9.4	169
120	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
121	Predicting the likelihood of carrying a BRCA1 or BRCA2 mutation: validation of BOADICEA, BRCAPRO, IBIS, Myriad and the Manchester scoring system using data from UK genetics clinics. Journal of Medical Genetics, 2008, 45, 425-431.	1.5	167
122	PREDICT Plus: development and validation of a prognostic model for early breast cancer that includes HER2. British Journal of Cancer, 2012, 107, 800-807.	2.9	163
123	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
124	An updated PREDICT breast cancer prognostication and treatment benefit prediction model with independent validation. Breast Cancer Research, 2017, 19, 58.	2.2	161
125	Meta-analysis confirms BCL2 is an independent prognostic marker in breast cancer. BMC Cancer, 2008, 8, 153.	1.1	159
126	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

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127	Molecular Classification of Breast Carcinomas Using Tissue Microarrays. Diagnostic Molecular Pathology, 2003, 12, 27-34.	2.1	153
128	Polygenic susceptibility to prostate and breast cancer: implications for personalised screening. British Journal of Cancer, 2011, 104, 1656-1663.	2.9	153
129	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. BMJ: British Medical Journal, 2018, 360, j5757.	2.4	153
130	A common variant in BRCA2 is associated with both breast cancer risk and prenatal viability. Nature Genetics, 2000, 26, 362-364.	9.4	152
131	BRCA1 and BRCA2 mutations in a population-based study of male breast cancer. Breast Cancer Research, 2001, 4, R2.	2.2	152
132	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
133	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
134	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
135	Telomere Length in Prospective and Retrospective Cancer Case-Control Studies. Cancer Research, 2010, 70, 3170-3176.	0.4	142
136	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	9.4	141
137	BRCA1, BRCA2 and TP53 mutations in very early-onset breast cancer with associated risks to relatives. European Journal of Cancer, 2006, 42, 1143-1150.	1.3	139
138	Oral contraceptive use and ovarian cancer risk among carriers of BRCA1 or BRCA2 mutations. British Journal of Cancer, 2004, 91, 1911-1915.	2.9	138
139	Germline Mutation in BRCA1 or BRCA2 and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	3.2	138
140	Cost-effectiveness of Population-Based BRCA1, BRCA2, RAD51C, RAD51D, BRIP1, PALB2 Mutation Testing in Unselected General Population Women. Journal of the National Cancer Institute, 2018, 110, 714-725.	3.0	138
141	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.	9.4	138
142	Identification and validation of prognostic markers in breast cancer with the complementary use of array-CGH and tissue microarrays. Journal of Pathology, 2005, 205, 388-396.	2.1	137
143	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	1.5	136
144	The malignant phenotype in breast cancer is driven by eIF4A1-mediated changes in the translational landscape. Cell Death and Disease, 2015, 6, e1603-e1603.	2.7	136

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145	Opium use and mortality in Golestan Cohort Study: prospective cohort study of 50 000 adults in Iran. BMJ, The, 2012, 344, e2502-e2502.	3.0	135
146	Association between Common Variation in 120 Candidate Genes and Breast Cancer Risk. PLoS Genetics, 2007, 3, e42.	1.5	134
147	Genome-wide association studies in oesophageal adenocarcinoma and Barrett's oesophagus: a large-scale meta-analysis. Lancet Oncology, The, 2016, 17, 1363-1373.	5.1	133
148	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.	1.4	130
149	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2015, 107, .	3.0	129
150	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129
151	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.	0.3	128
152	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
153	Somatically acquired hypomethylation of IGF2 in breast and colorectal cancer. Human Molecular Genetics, 2008, 17, 2633-2643.	1.4	124
154	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	2.6	124
155	Five Glutathione S-Transferase Gene Variants in 23,452 Cases of Lung Cancer and 30,397 Controls: Meta-Analysis of 130 Studies. PLoS Medicine, 2006, 3, e91.	3.9	124
156	Polymorphisms in DNA repair genes and epithelial ovarian cancer risk. International Journal of Cancer, 2005, 117, 611-618.	2.3	123
157	Individual and Combined Effects of Environmental Risk Factors for Esophageal Cancer Based on Results From theÂGolestan Cohort Study. Gastroenterology, 2019, 156, 1416-1427.	0.6	123
158	Predictive markers of anthracycline benefit: a prospectively planned analysis of the UK National Epirubicin Adjuvant Trial (NEAT/BR9601). Lancet Oncology, The, 2010, 11, 266-274.	5.1	122
159	Breast and ovarian cancer risks to carriers of the BRCA1 5382insC and 185delAG and BRCA2 6174delT mutations: a combined analysis of 22 population based studies. Journal of Medical Genetics, 2005, 42, 602-603.	1.5	121
160	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
161	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
162	Cumulative impact of common genetic variants and other risk factors on colorectal cancer risk in 42â€ˆ103 individuals. Gut, 2013, 62, 871-881.	6.1	117

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163	The contribution of deleterious germline mutations in BRCA1, BRCA2 and the mismatch repair genes to ovarian cancer in the population. Human Molecular Genetics, 2014, 23, 4703-4709.	1.4	112
164	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	0.9	111
165	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.	1.4	110
166	Prevalence, awareness and risk factors of hypertension in a large cohort of Iranian adult population. Journal of Hypertension, 2013, 31, 1364-1371.	0.3	110
167	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
168	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.4	109
169	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	3.0	109
170	Public health implications from COGS and potential for risk stratification and screening. Nature Genetics, 2013, 45, 349-351.	9.4	108
171	A large-scale meta-analysis to refine colorectal cancer risk estimates associated with MUTYH variants. British Journal of Cancer, 2010, 103, 1875-1884.	2.9	107
172	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	5.8	106
173	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. Journal of the National Cancer Institute, 2020, 112, 1242-1250.	3.0	106
174	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
175	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
176	No association between androgen or vitamin D receptor gene polymorphisms and risk of breast cancer. Carcinogenesis, 1999, 20, 2131-2135.	1.3	103
177	Common Germline Genetic Variation in Antioxidant Defense Genes and Survival After Diagnosis of Breast Cancer. Journal of Clinical Oncology, 2007, 25, 3015-3023.	0.8	102
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