Peter Kraft

List of Publications by Year in descending order

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Version: 2024-02-01

310 papers	26,003 citations	9234 74 h-index	10708 138 g-index
319 all docs	319 docs citations	319 times ranked	35896 citing authors

#	Article	IF	Citations
1	Reassessing the causal role of obesity in breast cancer susceptibility: a comprehensive multivariable Mendelian randomization investigating the distribution and timing of exposure. International Journal of Epidemiology, 2023, 52, 58-70.	0.9	9
2	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
3	Obesity, Adiposity, and Risk of Symptomatic Gallstone Disease According to Genetic Susceptibility. Clinical Gastroenterology and Hepatology, 2022, 20, e1083-e1120.	2.4	5
4	A Metabolomics Analysis of Circulating Carotenoids and Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 85-96.	1.1	6
5	Mendelian Randomization With Repeated Measures of a Time-varying Exposure. Epidemiology, 2022, 33, 84-94.	1.2	9
6	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
7	Genome-wide association study meta-analysis identifies three novel loci for circulating anti-MÃ¼llerian hormone levels in women. Human Reproduction, 2022, 37, 1069-1082.	0.4	13
8	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
9	Genomic correlation, shared loci, and causal relationship between obesity and polycystic ovary syndrome: a large-scale genome-wide cross-trait analysis. BMC Medicine, 2022, 20, 66.	2.3	22
10	Somatic mutational profiles and germline polygenic risk scores in human cancer. Genome Medicine, 2022, 14, 14.	3.6	14
11	Breast Cancer Screening Strategies for Women With ATM, CHEK2, and PALB2 Pathogenic Variants. JAMA Oncology, 2022, 8, 587.	3.4	36
12	Abstract P3-13-02: A genome-wide association study of mammographic texture variation. Cancer Research, 2022, 82, P3-13-02-P3-13-02.	0.4	0
13	Polygenic risk scores for prediction of breast cancer risk in Asian populations. Genetics in Medicine, 2022, 24, 586-600.	1.1	27
14	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
15	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	1.6	2
16	Development of a clinical polygenic risk score assay and reporting workflow. Nature Medicine, 2022, 28, 1006-1013.	15.2	74
17	A novel DPH5-related diphthamide-deficiency syndrome causing embryonic lethality or profound neurodevelopmental disorder. Genetics in Medicine, 2022, 24, 1567-1582.	1.1	5
18	Polygenic scores, diet quality, and type 2 diabetes risk: An observational study among 35,759 adults from 3 US cohorts. PLoS Medicine, 2022, 19, e1003972.	3.9	17

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19	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. Journal of the National Cancer Institute, 2022, 114, 1706-1719.	3.0	14
20	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	1.1	12
21	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	3.0	45
22	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	2.3	35
23	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
24	Circulating carotenoids and breast cancer among high-risk individuals. American Journal of Clinical Nutrition, 2021, 113, 525-533.	2.2	13
25	Personalizing Breast Cancer Screening Based on Polygenic Risk and Family History. Journal of the National Cancer Institute, 2021, 113, 434-442.	3.0	34
26	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
27	A Genomeâ€Wide Association Study of Childhood Body Fatness. Obesity, 2021, 29, 446-453.	1.5	8
28	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
29	A Population-Based Study of Genes Previously Implicated in Breast Cancer. New England Journal of Medicine, 2021, 384, 440-451.	13.9	414
30	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. Cancer Research, 2021, 81, 3134-3143.	0.4	8
31	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science Advances, 2021, 7, .	4.7	36
32	Estimating the effective sample size in association studies of quantitative traits. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	12
33	Prediagnostic Inflammation and Pancreatic Cancer Survival. Journal of the National Cancer Institute, 2021, 113, 1186-1193.	3.0	9
34	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
35	Leveraging expression from multiple tissues using sparse canonical correlation analysis and aggregate tests improves the power of transcriptome-wide association studies. PLoS Genetics, 2021, 17, e1008973.	1.5	35
36	Germline pathogenic variants in cancer predisposition genes among women with invasive lobular cancer of breast.. Journal of Clinical Oncology, 2021, 39, 10581-10581.	0.8	0

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37	Breast cancer screening for carriers of ATM, CHEK2, and PALB2 pathogenic variants: A comparative modeling analysis.. Journal of Clinical Oncology, 2021, 39, 10500-10500.	0.8	0
38	Multitrait transcriptomeâ€wide association study (TWAS) tests. Genetic Epidemiology, 2021, 45, 563-576.	0.6	9
39	Heterozygous loss-of-function variants significantly expand the phenotypes associated with loss of GDF11. Genetics in Medicine, 2021, 23, 1889-1900.	1.1	13
40	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
41	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. American Journal of Clinical Nutrition, 2021, 114, 1408-1417.	2.2	9
42	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
43	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	2.2	7
44	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. Journal of Clinical Oncology, 2021, 39, 2564-2573.	0.8	47
45	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
46	Multitrait GWAS to connect disease variants and biological mechanisms. PLoS Genetics, 2021, 17, e1009713.	1.5	16
47	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
48	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	1.1	19
49	Simplified Breast Risk Tool Integrating Questionnaire Risk Factors, Mammographic Density, and Polygenic Risk Score: Development and Validation. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 600-607.	1.1	14
50	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
51	Returning actionable genomic results in a research biobank: Analytic validity, clinical implementation, and resource utilization. American Journal of Human Genetics, 2021, 108, 2224-2237.	2.6	34
52	Instrumental variable estimation for a time-varying treatment and a time-to-event outcome via structural nested cumulative failure time models. BMC Medical Research Methodology, 2021, 21, 258.	1.4	11
53	Colorectal cancer susceptibility variants and risk of conventional adenomas and serrated polyps: results from three cohort studies. International Journal of Epidemiology, 2020, 49, 259-269.	0.9	13
54	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. Human Molecular Genetics, 2020, 29, 70-79.	1.4	17

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55	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	2.3	13
56	Circulating Lysophosphatidylcholines, Phosphatidylcholines, Ceramides, and Sphingomyelins and Ovarian Cancer Risk: A 23-Year Prospective Study. Journal of the National Cancer Institute, 2020, 112, 628-636.	3.0	34
57	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	3.0	59
58	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
59	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. International Journal of Epidemiology, 2020, 49, 1117-1131.	0.9	41
60	Sex-Stratified Polygenic Risk Score Identifies Individuals at Increased Risk of Basal Cell Carcinoma. Journal of Investigative Dermatology, 2020, 140, 971-975.	0.3	12
61	Mixed-model admixture mapping identifies smoking-dependent loci of lung function in African Americans. European Journal of Human Genetics, 2020, 28, 656-668.	1.4	7
62	Involvement of fine particulate matter exposure with gene expression pathways in breast tumor and adjacent-normal breast tissue. Environmental Research, 2020, 186, 109535.	3.7	0
63	De Novo Variants in the ATPase Module of MORC2 Cause a Neurodevelopmental Disorder with Growth Retardation and Variable Craniofacial Dysmorphism. American Journal of Human Genetics, 2020, 107, 352-363.	2.6	64
64	Diabetes, Weight Change, and Pancreatic Cancer Risk. JAMA Oncology, 2020, 6, e202948.	3.4	72
65	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2735-2739.	1.1	6
66	Identification of an Identical de Novo SCAMP5 Missense Variant in Four Unrelated Patients With Seizures and Severe Neurodevelopmental Delay. Frontiers in Pharmacology, 2020, 11, 599191.	1.6	2
67	De novo mutations in TOMM70, a receptor of the mitochondrial import translocase, cause neurological impairment. Human Molecular Genetics, 2020, 29, 1568-1579.	1.4	29
68	Genetic and Circulating Biomarker Data Improve Risk Prediction for Pancreatic Cancer in the General Population. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 999-1008.	1.1	19
69	Height, nevus count, and risk of cutaneous malignant melanoma: Results from 2 large cohorts of US women. Journal of the American Academy of Dermatology, 2020, 83, 1049-1056.	0.6	1
70	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
71	The Use of Genetic Correlation and Mendelian Randomization Studies to Increase Our Understanding of Relationships between Complex Traits. Current Epidemiology Reports, 2020, 7, 104-112.	1.1	21
72	Genome-Wide Geneâ€“Diabetes and Geneâ€“Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1784-1791.	1.1	5

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73	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
74	PPARA Polymorphism Influences the Cardiovascular Benefit of Fenofibrate in Type 2 Diabetes: Findings From ACCORD-Lipid. Diabetes, 2020, 69, 771-783.	0.3	28
75	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
76	The Association of Modifiable Breast Cancer Risk Factors and Somatic Genomic Alterations in Breast Tumors: The Cancer Genome Atlas Network. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 599-605.	1.1	7
77	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
78	A Prospective Analysis of Circulating Plasma Metabolites Associated with Ovarian Cancer Risk. Cancer Research, 2020, 80, 1357-1367.	0.4	54
79	Allergy, asthma, and the risk of breast and prostate cancer: a Mendelian randomization study. Cancer Causes and Control, 2020, 31, 273-282.	0.8	14
80	Validating Breast Cancer Risk Prediction Models in the Korean Cancer Prevention Study-II Biobank. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1271-1277.	1.1	6
81	Prediagnostic 25-Hydroxyvitamin D Concentrations in Relation to Tumor Molecular Alterations and Risk of Breast Cancer Recurrence. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1253-1263.	1.1	4
82	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2020, 11, 820.	5.8	30
83	Genome-Wide Association Study for Urinary and Fecal Incontinence in Women. Journal of Urology, 2020, 203, 978-983.	0.2	8
84	Rare Inherited Defects of the Complement System in Purpura Fulminans. Blood, 2020, 136, 35-36.	0.6	1
85	Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863.	0.6	28
86	Metabolome-Wide Association Study of the Relationship Between Habitual Physical Activity and Plasma Metabolite Levels. American Journal of Epidemiology, 2019, 188, 1932-1943.	1.6	26
87	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
88	Association of a Primary Open-Angle Glaucoma Genetic Risk Score With Earlier Age at Diagnosis. JAMA Ophthalmology, 2019, 137, 1190.	1.4	32
89	Noncirrhotic hyperammonemia after deceased donor kidney transplantation: A case report. American Journal of Transplantation, 2019, 19, 3197-3201.	2.6	13
90	A Pathway Analysis of Hereditary Hemochromatosis-related Genes and Pancreatic Ductal Adenocarcinoma Risk (FS11-05-19). Current Developments in Nutrition, 2019, 3, nzz037.FS11-05-19.	0.1	0

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91	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	1.4	27
92	Yield of whole exome sequencing in undiagnosed patients facing insurance coverage barriers to genetic testing. Journal of Genetic Counseling, 2019, 28, 1107-1118.	0.9	42
93	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
94	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
95	De Novo Pathogenic Variants in N-cadherin Cause a Syndromic Neurodevelopmental Disorder with Corpus Callosum, Axon, Cardiac, Ocular, and Genital Defects. American Journal of Human Genetics, 2019, 105, 854-868.	2.6	29
96	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
97	Particulate Matter and Traffic-Related Exposures in Relation to Breast Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 751-759.	1.1	24
98	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
99	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. American Journal of Ophthalmology, 2019, 206, 245-255.	1.7	12
100	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. Breast Cancer Research, 2019, 21, 68.	2.2	31
101	Integration of Metabolomic and Other Omics Data in Population-Based Study Designs: An Epidemiological Perspective. Metabolites, 2019, 9, 117.	1.3	47
102	Homozygous TRPV4 mutation causes congenital distal spinal muscular atrophy and arthrogryposis. Neurology: Genetics, 2019, 5, e312.	0.9	15
103	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
104	Family history of cancer, Ashkenazi Jewish ancestry, and pancreatic cancer risk. British Journal of Cancer, 2019, 120, 848-854.	2.9	11
105	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. PLoS Genetics, 2019, 15, e1007530.	1.5	35
106	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
107	Efficient cross-trait penalized regression increases prediction accuracy in large cohorts using secondary phenotypes. Nature Communications, 2019, 10, 569.	5.8	50
108	Prediagnostic Leukocyte Telomere Length and Pancreatic Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1868-1875.	1.1	17

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109	Associations of dairy intake with risk of mortality in women and men: three prospective cohort studies. BMJ: British Medical Journal, 2019, 367, l6204.	2.4	54
110	Joint Analysis of Multiple Interaction Parameters in Genetic Association Studies. Genetics, 2019, 211, 483-494.	1.2	12
111	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. Journal of the National Cancer Institute, 2019, 111, 557-567.	3.0	21
112	Circulating vitamin D concentrations and risk of breast and prostate cancer: a Mendelian randomization study. International Journal of Epidemiology, 2019, 48, 1416-1424.	0.9	51
113	Genome-wide association study of anti-MÃ¼llerian hormone levels in pre-menopausal women of late reproductive age and relationship with genetic determinants of reproductive lifespan. Human Molecular Genetics, 2019, 28, 1392-1401.	1.4	22
114	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
115	The genetics of vitamin D. Bone, 2019, 126, 59-77.	1.4	47
116	Genetic predisposition to breast cancer among African American women.. Journal of Clinical Oncology, 2019, 37, 104-104.	0.8	0
117	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
118	Statin use and pancreatic cancer risk in two prospective cohort studies. Journal of Gastroenterology, 2018, 53, 959-966.	2.3	33
119	Use of deep whole-genome sequencing data to identify structure risk variants in breast cancer susceptibility genes. Human Molecular Genetics, 2018, 27, 853-859.	1.4	20
120	Quantifying the Polygenic Contribution to Cutaneous Squamous Cell Carcinoma Risk. Journal of Investigative Dermatology, 2018, 138, 1507-1510.	0.3	25
121	Interaction of a genetic risk score with physical activity, physical inactivity, and body mass index in relation to venous thromboembolism risk. Genetic Epidemiology, 2018, 42, 354-365.	0.6	16
122	Modulation of GLP-1 Levels by a Genetic Variant That Regulates the Cardiovascular Effects of Intensive Glycemic Control in ACCORD. Diabetes Care, 2018, 41, 348-355.	4.3	16
123	A comprehensive analysis of polymorphic variants in steroid hormone and insulinâ€like growth factorâ€1 metabolism and risk of in situ breast cancer: Results from the Breast and Prostate Cancer Cohort Consortium. International Journal of Cancer, 2018, 142, 1182-1188.	2.3	0
124	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
125	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	5.8	43
126	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341

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127	Genetic Tools for Coronary Risk Assessment in Type 2 Diabetes: A Cohort Study From the ACCORD Clinical Trial. Diabetes Care, 2018, 41, 2404-2413.	4.3	32
128	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for WaldenstrÃ¶m macroglobulinemia. Nature Communications, 2018, 9, 4182.	5.8	15
129	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
130	Addition of a polygenic risk score, mammographic density, and endogenous hormones to existing breast cancer risk prediction models: A nested caseâ€“control study. PLoS Medicine, 2018, 15, e1002644.	3.9	91
131	Polygenic risk score of shorter telomere length and risk of depression and anxiety in women. Journal of Psychiatric Research, 2018, 103, 182-188.	1.5	9
132	Transcriptomeâ€wide association studies accounting for colocalization using Egger regression. Genetic Epidemiology, 2018, 42, 418-433.	0.6	59
133	Hierarchical modeling of melanocortin 1 receptor variants with skin cancer risk. Genetic Epidemiology, 2018, 42, 571-586.	0.6	5
134	A genome-wide association study of energy intake and expenditure. PLoS ONE, 2018, 13, e0201555.	1.1	14
135	HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. Cancer Research, 2018, 78, 4086-4096.	0.4	34
136	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
137	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
138	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
139	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
140	Precision Prevention and Early Detection of Cancer: Fundamental Principles. Cancer Discovery, 2018, 8, 803-811.	7.7	62
141	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
142	Breast cancer risk prediction using a polygenic risk score in the familial setting: a prospective study from the Breast Cancer Family Registry and kConFab. Genetics in Medicine, 2017, 19, 30-35.	1.1	53
143	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	0.9	36
144	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75

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145	Leucocyte telomere length, genetic variants at theTERTgene region and risk of pancreatic cancer. Gut, 2017, 66, 1116-1122.	6.1	39
146	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
147	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	3.5	90
148	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	5.8	40
149	Biomarker correlation network in colorectal carcinoma by tumor anatomic location. BMC Bioinformatics, 2017, 18, 304.	1.2	18
150	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	5.8	106
151	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	9.4	114
152	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
153	Covariate selection for association screening in multiphenotype genetic studies. Nature Genetics, 2017, 49, 1789-1795.	9.4	27
154	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
155	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. European Journal of Human Genetics, 2017, 25, 1261-1267.	1.4	18
156	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	1.6	16
157	Inherited variation in circadian rhythm genes and risks of prostate cancer and three other cancer sites in combined cancer consortia. International Journal of Cancer, 2017, 141, 1794-1802.	2.3	28
158	Investigating the genetic relationship between Alzheimerâ€™s disease and cancer using GWAS summary statistics. Human Genetics, 2017, 136, 1341-1351.	1.8	46
159	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. European Urology, 2017, 72, 747-754.	0.9	39
160	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	1.1	15
161	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	1.1	48
162	VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis. Bioinformatics, 2017, 33, 1389-1391.	1.8	2

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163	Prescription medication changes following direct-to-consumer personal genomic testing: findings from the Impact of Personal Genomics (PGen) Study. Genetics in Medicine, 2017, 19, 537-545.	1.1	39
164	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
165	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
166	Residential particulate matter and distance to roadways in relation to mammographic density: results from the Nursesâ€™ Health Studies. Breast Cancer Research, 2017, 19, 124.	2.2	19
167	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. BMJ: British Medical Journal, 2017, 359, j4761.	2.4	126
168	Joint Effects of PON1 Polymorphisms and Vegetable Intake on Ischemic Stroke: A Family-Based Case Control Study. International Journal of Molecular Sciences, 2017, 18, 2652.	1.8	12
169	Genome-Wide Association Studies of Multiple Keratinocyte Cancers. PLoS ONE, 2017, 12, e0169873.	1.1	10
170	Cigarette Smoking and Pancreatic Cancer Survival. Journal of Clinical Oncology, 2017, 35, 1822-1828.	0.8	78
171	Fine Tuning the Risk of Hereditary Cancer Using Genome-Wide Association Studies. Journal of Clinical Oncology, 2017, 35, 2224-2225.	0.8	1
172	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts. PLoS ONE, 2017, 12, e0173997.	1.1	52
173	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	1.1	79
174	Prostate cancer meta-analysis from more than 145,000 men to identify 65 novel prostate cancer susceptibility loci.. Journal of Clinical Oncology, 2017, 35, 1-1.	0.8	0
175	Prostate cancer meta-analysis from more than 145,000 men to identify 65 novel prostate cancer susceptibility loci.. Journal of Clinical Oncology, 2017, 2017, 1-1.	0.8	5
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