Stephen J Chanock

List of Publications by Year
in descending order

955	101,643	281	443
papers	citations	140 h-index	274 g-index

991	991	991	83947
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
3	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
4	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
5	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
6	Genome-wide association study reveals genetic risk underlying Parkinson's disease. Nature Genetics, 2009, 41, 1308-1312.	21.4	1,745
7	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572
8	Assessing the Probability That a Positive Report is False: An Approach for Molecular Epidemiology Studies. Journal of the National Cancer Institute, 2004, 96, 434-442.	6.3	1,553
9	Replicating genotypeâ€“phenotype associations. Nature, 2007, 447, 655-660.	27.8	1,509
10	LDlink: a web-based application for exploring population-specific haplotype structure and linking correlated alleles of possible functional variants. Bioinformatics, 2015, 31, 3555-3557.	4.1	1,473
11	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nature Genetics, 2007, 39, 870-874.	21.4	1,370
12	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	21.4	1,179
13	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
14	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nature Genetics, 2007, 39, 645-649.	21.4	1,059
15	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
16	Multiple loci identified in a genome-wide association study of prostate cancer. Nature Genetics, 2008, 40, 310-315.	21.4	871
17	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
18	Genome-wide association study of circulating vitamin D levels. Human Molecular Genetics, 2010, 19, 2739-2745.	2.9	700

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19	Genome-wide association scan identifies a colorectal cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2007, 39, 989-994.	21.4	676
20	Mutations inTERT,the Gene for Telomerase Reverse Transcriptase, in Aplastic Anemia. New England Journal of Medicine, 2005, 352, 1413-1424.	27.0	665
21	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
22	Estimation of effect size distribution from genome-wide association studies and implications for future discoveries. Nature Genetics, 2010, 42, 570-575.	21.4	609
23	Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. Nature Genetics, 2009, 41, 986-990.	21.4	597
24	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.	6.3	596
25	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
26	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
27	NAT2 slow acetylation, GSTM1 null genotype, and risk of bladder cancer: results from the Spanish Bladder Cancer Study and meta-analyses. Lancet, The, 2005, 366, 649-659.	13.7	558
28	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
29	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.	7.4	546
30	Powerful SNP-Set Analysis for Case-Control Genome-wide Association Studies. American Journal of Human Genetics, 2010, 86, 929-942.	6.2	541
31	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. Nature Genetics, 2010, 42, 224-228.	21.4	539
32	Identification of ten loci associated with height highlights new biological pathways in human growth. Nature Genetics, 2008, 40, 584-591.	21.4	537
33	Hematotoxicity in Workers Exposed to Low Levels of Benzene. Science, 2004, 306, 1774-1776.	12.6	533
34	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
35	Detectable clonal mosaicism and its relationship to aging and cancer. Nature Genetics, 2012, 44, 651-658.	21.4	519
36	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

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37	Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics, 2012, 44, 642-650.	21.4	511
38	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	21.4	493
39	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
40	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492
41	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	6.2	489
42	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). Nature Genetics, 2009, 41, 579-584.	21.4	487
43	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	21.4	472
44	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
45	A shared susceptibility locus in PLCE1 at 10q23 for gastric adenocarcinoma and esophageal squamous cell carcinoma. Nature Genetics, 2010, 42, 764-767.	21.4	453
46	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	21.4	445
47	A Genome-Wide Association Study Identifies Novel Alleles Associated with Hair Color and Skin Pigmentation. PLoS Genetics, 2008, 4, e1000074.	3.5	439
48	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	21.4	434
49	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
50	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. Nature Genetics, 2017, 49, 1476-1486.	21.4	427
51	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
52	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
53	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
54	A Double-Blind Comparison of Empirical Oral and Intravenous Antibiotic Therapy for Low-Risk Febrile Patients with Neutropenia during Cancer Chemotherapy. New England Journal of Medicine, 1999, 341, 305-311.	27.0	382

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55	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
56	Performance of Common Genetic Variants in Breast-Cancer Risk Models. New England Journal of Medicine, 2010, 362, 986-993.	27.0	376
57	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
58	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
59	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	21.4	360
60	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
61	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
62	Projecting the performance of risk prediction based on polygenic analyses of genome-wide association studies. Nature Genetics, 2013, 45, 400-405.	21.4	350
63	Genome-wide association studies identify loci associated with age at menarche and age at natural menopause. Nature Genetics, 2009, 41, 724-728.	21.4	348
64	Genetic variation in TNF and IL10 and risk of non-Hodgkin lymphoma: a report from the InterLymph Consortium. Lancet Oncology, The, 2006, 7, 27-38.	10.7	345
65	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
66	ABO Blood Group and the Risk of Pancreatic Cancer. Journal of the National Cancer Institute, 2009, 101, 424-431.	6.3	321
67	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	27.8	319
68	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	3.5	315
69	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
70	Cigarette Smoking and Pancreatic Cancer: A Pooled Analysis From the Pancreatic Cancer Cohort Consortium. American Journal of Epidemiology, 2009, 170, 403-413.	3.4	298
71	Cancer Survivorshipâ€”Genetic Susceptibility and Second Primary Cancers: Research Strategies and Recommendations. Journal of the National Cancer Institute, 2006, 98, 15-25.	6.3	295
72	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	21.4	294

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73	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	1.3	292
74	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
75	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. Nature Genetics, 2012, 44, 1330-1335.	21.4	286
76	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	7.1	285
77	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	21.4	283
78	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
79	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
80	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
81	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
82	Mutations of the human telomerase RNA gene (TERC) in aplastic anemia and myelodysplastic syndrome. Blood, 2003, 102, 916-918.	1.4	274
83	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	21.4	265
84	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
85	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
86	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
87	Genome-wide association study of glioma subtypes identifies specific differences in genetic susceptibility to glioblastoma and non-glioblastoma tumors. Nature Genetics, 2017, 49, 789-794.	21.4	259
88	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
89	Mutation of GATA3 in human breast tumors. Oncogene, 2004, 23, 7669-7678.	5.9	250
90	Distribution of allele frequencies and effect sizes and their interrelationships for common genetic susceptibility variants. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18026-18031.	7.1	249

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91	SNP500Cancer: a public resource for sequence validation, assay development, and frequency analysis for genetic variation in candidate genes. Nucleic Acids Research, 2006, 34, D617-D621.	14.5	242
92	A Subset-Based Approach Improves Power and Interpretation for the Combined Analysis of Genetic Association Studies of Heterogeneous Traits. American Journal of Human Genetics, 2012, 90, 821-835.	6.2	242
93	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. Nature Genetics, 2012, 44, 1090-1097.	21.4	238
94	Identification of FGFR4-activating mutations in human rhabdomyosarcomas that promote metastasis in xenotransplanted models. Journal of Clinical Investigation, 2009, 119, 3395-407.	8.2	237
95	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
96	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	21.4	232
97	Genome-Wide and Candidate Gene Association Study of Cigarette Smoking Behaviors. PLoS ONE, 2009, 4, e4653.	2.5	226
98	Single nucleotide polymorphic discrimination by an electronic dot blot assay on semiconductor microchips. Nature Biotechnology, 1999, 17, 365-370.	17.5	225
99	Novel Breast Cancer Susceptibility Locus at 9q31.2: Results of a Genome-Wide Association Study. Journal of the National Cancer Institute, 2011, 103, 425-435.	6.3	225
100	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. Nature Genetics, 2013, 45, 1464-1469.	21.4	224
101	Common variation at 2p13.3, 3q29, 7p13 and 17q25.1 associated with susceptibility to pancreatic cancer. Nature Genetics, 2015, 47, 911-916.	21.4	224
102	Genome-wide association study of glioma and meta-analysis. Human Genetics, 2012, 131, 1877-1888.	3.8	222
103	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. Nature Genetics, 2011, 43, 60-65.	21.4	220
104	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2009, 41, 1055-1057.	21.4	218
105	Angiotensin II Induces p67 ^{phox} mRNA Expression and NADPH Oxidase Superoxide Generation in Rabbit Aortic Adventitial Fibroblasts. Hypertension, 1998, 32, 331-337.	2.7	212
106	Genomic DNA hypomethylation as a biomarker for bladder cancer susceptibility in the Spanish Bladder Cancer Study: a caseâ€“control study. Lancet Oncology, The, 2008, 9, 359-366.	10.7	211
107	The Scientific Foundation for Personal Genomics: Recommendations from a National Institutes of Healthâ€“Centers for Disease Control and Prevention Multidisciplinary Workshop. Genetics in Medicine, 2009, 11, 559-567.	2.4	207
108	GWASdb: a database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2012, 40, D1047-D1054.	14.5	204

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109	Pancreatic Cancer Risk and ABO Blood Group Alleles: Results from the Pancreatic Cancer Cohort Consortium. Cancer Research, 2010, 70, 1015-1023.	0.9	203
110	A Spectrum of Severe Familial Liver Disorders Associate with Telomerase Mutations. PLoS ONE, 2009, 4, e7926.	2.5	201
111	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
112	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. Nature Genetics, 2011, 43, 570-573.	21.4	198
113	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	27.8	198
114	Polymorphisms in GSTT1 , GSTZ1 , and CYP2E1 , Disinfection By-products, and Risk of Bladder Cancer in Spain. Environmental Health Perspectives, 2010, 118, 1545-1550.	6.0	194
115	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	12.8	188
116	Genome-Wide Meta-Analysis Identifies Regions on 7p21 (AHR) and 15q24 (CYP1A2) As Determinants of Habitual Caffeine Consumption. PLoS Genetics, 2011, 7, e1002033.	3.5	187
117	LDlinkR: An R Package for Rapidly Calculating Linkage Disequilibrium Statistics in Diverse Populations. Frontiers in Genetics, 2020, 11, 157.	2.3	185
118	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2016, 44, D869-D876.	14.5	184
119	Meta-analysis of new genome-wide association studies of colorectal cancer risk. Human Genetics, 2012, 131, 217-234.	3.8	183
120	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
121	Genome-wide association study identifies two susceptibility loci for osteosarcoma. Nature Genetics, 2013, 45, 799-803.	21.4	181
122	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	21.4	179
123	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
124	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. Nature Genetics, 2013, 45, 1487-1493.	21.4	174
125	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
126	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173

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127	Safety, Tolerance, and Pharmacokinetics of a Small Unilamellar Liposomal Formulation of Amphotericin B (AmBisome) in Neutropenic Patients. Antimicrobial Agents and Chemotherapy, 1998, 42, 2391-2398.	3.2	172
128	Association of Aspirin and NSAID Use With Risk of Colorectal Cancer According to Genetic Variants. JAMA - Journal of the American Medical Association, 2015, 313, 1133.	7.4	171
129	Constitutional hypomorphic telomerase mutations in patients with acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1187-1192.	7.1	168
130	The 5p15.33 Locus Is Associated with Risk of Lung Adenocarcinoma in Never-Smoking Females in Asia. PLoS Genetics, 2010, 6, e1001051.	3.5	168
131	Von Hippel-Lindau (VHL) Inactivation in Sporadic Clear Cell Renal Cancer: Associations with Germline VHL Polymorphisms and Etiologic Risk Factors. PLoS Genetics, 2011, 7, e1002312.	3.5	168
132	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
133	Amphotericin B lipid complex in pediatric patients with invasive fungal infections. Pediatric Infectious Disease Journal, 1999, 18, 702-708.	2.0	167
134	Cytokine polymorphisms in the Th1/Th2 pathway and susceptibility to non-Hodgkin lymphoma. Blood, 2006, 107, 4101-4108.	1.4	166
135	Association of germline variants in the APOBEC3 region with cancer risk and enrichment with APOBEC-signature mutations in tumors. Nature Genetics, 2016, 48, 1330-1338.	21.4	161
136	Current status of genome-wide association studies in cancer. Human Genetics, 2011, 130, 59-78.	3.8	160
137	Genome-wide association study identifies new prostate cancer susceptibility loci. Human Molecular Genetics, 2011, 20, 3867-3875.	2.9	160
138	Common variants near TARDBP and EGR2 are associated with susceptibility to Ewing sarcoma. Nature Genetics, 2012, 44, 323-327.	21.4	160
139	Genome-wide significant predictors of metabolites in the one-carbon metabolism pathway. Human Molecular Genetics, 2009, 18, 4677-4687.	2.9	157
140	Chimeric EWSR1-FLI1 regulates the Ewing sarcoma susceptibility gene EGR2 via a GGAA microsatellite. Nature Genetics, 2015, 47, 1073-1078.	21.4	157
141	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
142	Meta-analysis identifies four new loci associated with testicular germ cell tumor. Nature Genetics, 2013, 45, 680-685.	21.4	154
143	Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. Nature Genetics, 2010, 42, 661-664.	21.4	152
144	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

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145	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormoneâ€“Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	3.5	151
146	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	21.4	148
147	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. PLoS Genetics, 2018, 14, e1007752.	3.5	148
148	Somatic Genomics and Clinical Features of Lung Adenocarcinoma: A Retrospective Study. PLoS Medicine, 2016, 13, e1002162.	8.4	148
149	Oxidative damage-related genes AKR1C3 and OGG1 modulate risks for lung cancer due to exposure to PAH-rich coal combustion emissions. Carcinogenesis, 2004, 25, 2177-2181.	2.8	147
150	Interactions Between Genetic Variants and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. Journal of the National Cancer Institute, 2011, 103, 1252-1263.	6.3	147
151	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	21.4	147
152	Constitutional telomerase mutations are genetic risk factors for cirrhosis. Hepatology, 2011, 53, 1600-1607.	7.3	145
153	Polymorphisms in DNA double-strand break repair genes and risk of breast cancer: two population-based studies in USA and Poland, and meta-analyses. Human Genetics, 2006, 119, 376-388.	3.8	144
154	Association of Breast Cancer Outcome With Status of p53 and MDM2 SNP309. Journal of the National Cancer Institute, 2006, 98, 911-919.	6.3	143
155	Common variants of FUT2 are associated with plasma vitamin B12 levels. Nature Genetics, 2008, 40, 1160-1162.	21.4	142
156	Vitamin D-related genes, serum vitamin D concentrations and prostate cancer risk. Carcinogenesis, 2009, 30, 769-776.	2.8	142
157	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	21.4	141
158	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
159	Characterization of Geneâ€“Environment Interactions for Colorectal Cancer Susceptibility Loci. Cancer Research, 2012, 72, 2036-2044.	0.9	140
160	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	7.1	139
161	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138
162	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

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163	DNA fingerprinting of the NCI-60 cell line panel. Molecular Cancer Therapeutics, 2009, 8, 713-724.	4.1	137
164	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	2.9	137
165	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
166	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
167	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	21.4	134
168	Rapid Extraction of Genomic DNA from Medically Important Yeasts and Filamentous Fungi by High-Speed Cell Disruption. Journal of Clinical Microbiology, 1998, 36, 1625-1629.	3.9	133
169	Beyond odds ratios â€" communicating disease risk based on genetic profiles. Nature Reviews Genetics, 2009, 10, 264-269.	16.3	131
170	Cardiovascular manifestations of human immunodeficiency virus infection in infants and children. American Journal of Cardiology, 1989, 63, 1489-1497.	1.6	129
171	Functional Variant of Manganese Superoxide Dismutase (SOD2 V16A) Polymorphism Is Associated with Prostate Cancer Risk in the Prostate, Lung, Colorectal, and Ovarian Cancer Study. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1581-1586.	2.5	129
172	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
173	Family history of cancer and risk of pancreatic cancer: A pooled analysis from the Pancreatic Cancer Cohort Consortium (PanScan). International Journal of Cancer, 2010, 127, 1421-1428.	5.1	128
174	Tumor Necrosis Factor (TNF) and Lymphotoxin-Â (LTA) Polymorphisms and Risk of Non-Hodgkin Lymphoma in the InterLymph Consortium. American Journal of Epidemiology, 2010, 171, 267-276.	3.4	128
175	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
176	Common Genetic Variants in Proinflammatory and Other Immunoregulatory Genes and Risk for Non-Hodgkin Lymphoma. Cancer Research, 2006, 66, 9771-9780.	0.9	124
177	Burden of Nonsynonymous Mutations among TCGA Cancers and Candidate Immune Checkpoint Inhibitor Responses. Cancer Research, 2016, 76, 3767-3772.	0.9	124
178	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. Nature Communications, 2014, 5, 3365.	12.8	123
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