David Van Den Berg

List of Publications by Year
in descending order

240 papers	55,078 citations	5248 83 h-index	1527 218 g-index
246 all docs	246 docs citations	246 times ranked	66831 citing authors

#	Article	IF	Citations
1	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
2	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
3	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
4	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
5	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	7.7	2,078
6	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
7	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
8	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
9	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
10	Integrated genomic characterization of oesophageal carcinoma. Nature, 2017, 541, 169-175.	13.7	1,448
11	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
12	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
13	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
14	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
15	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	13.9	1,040
16	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
17	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
18	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750

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19	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738
20	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	9.4	736
21	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
22	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. Nucleic Acids Research, 2013, 41, e90-e90.	6.5	647
23	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	7.7	623
24	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
25	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
26	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear laminaâ€“associated domains. Nature Genetics, 2012, 44, 40-46.	9.4	588
27	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. Genome Research, 2012, 22, 271-282.	2.4	527
28	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
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	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	9.4	493
31	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
32	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
33	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
34	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	7.7	422
35	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
36	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407

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37	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	7.7	400
38	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
39	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
40	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
41	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
42	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
43	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	2.9	329
44	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
45	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
46	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	7.7	309
47	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
48	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
49	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
50	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
51	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	9.4	276
52	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
53	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	7.7	270
54	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245

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55	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	9.4	235
56	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
57	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
58	Sun Exposure, Vitamin D Receptor Gene Polymorphisms, and Risk of Advanced Prostate Cancer. Cancer Research, 2005, 65, 5470-5479.	0.4	210
59	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205
60	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
61	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
62	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. Nature Genetics, 2011, 43, 570-573.	9.4	198
63	Dietary isothiocyanates, glutathione S-transferase polymorphisms and colorectal cancer risk in the Singapore Chinese Health Study. Carcinogenesis, 2002, 23, 2055-2061.	1.3	195
64	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
65	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
66	Roberts syndrome: A review of 100 cases and a new rating system for severity. American Journal of Medical Genetics Part A, 1993, 47, 1104-1123.	2.4	175
67	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
68	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	3.0	152
69	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
70	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	5.8	138
71	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	1.4	137
72	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	2.9	134

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73	Nicotinic acetylcholine receptor Î²2 subunit gene implicated in a systems-based candidate gene study of smoking cessation. Human Molecular Genetics, 2008, 17, 2834-2848.	1.4	129
74	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129
75	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
76	Characteristics of Triple-Negative Breast Cancer in Patients With a BRCA1 Mutation: Results From a Population-Based Study of Young Women. Journal of Clinical Oncology, 2011, 29, 4373-4380.	0.8	112
77	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
78	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
79	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
80	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
81	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
82	Common genetic determinants of breast-cancer risk in East Asian women: a collaborative study of 23 637 breast cancer cases and 25 579 controls. Human Molecular Genetics, 2013, 22, 2539-2550.	1.4	86
83	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
84	Green tea intake, MTHFR/TYMS genotype and breast cancer risk: the Singapore Chinese Health Study. Carcinogenesis, 2008, 29, 1967-1972.	1.3	84
85	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
86	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
87	A Genome Screen of Families with Multiple Cases of Prostate Cancer: Evidence of Genetic Heterogeneity. American Journal of Human Genetics, 2001, 69, 148-158.	2.6	80
88	Second-Generation Linkage Maps for the Pacific OysterCrassostrea gigasReveal Errors in Assembly of Genome Scaffolds. G3: Genes, Genomes, Genetics, 2015, 5, 2007-2019.	0.8	80
89	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
90	Genetic polymorphisms in themethylenetetrahydrofolate reductase andthymidylate synthase genes and risk of hepatocellular carcinoma. Hepatology, 2007, 46, 749-758.	3.6	75

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91	ESR1/SYNE1 Polymorphism and Invasive Epithelial Ovarian Cancer Risk: An Ovarian Cancer Association Consortium Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 245-250.	1.1	75
92	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388.	2.3	73
93	Effect of Reproductive Factors and Oral Contraceptives on Breast Cancer Risk inBRCA1/2Mutation Carriers and Noncarriers: Results from a Population-Based Study. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 3170-3178.	1.1	73
94	Tea and circulating estrogen levels in postmenopausal Chinese women in Singapore. Carcinogenesis, 2005, 26, 976-980.	1.3	72
95	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. Nature Communications, 2014, 5, 4613.	5.8	72
96	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	3.0	72
97	A genome-wide association study of breast cancer in women of African ancestry. Human Genetics, 2013, 132, 39-48.	1.8	70
98	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	1.4	70
99	Genome-Wide Testing of Putative Functional Exonic Variants in Relationship with Breast and Prostate Cancer Risk in a Multiethnic Population. PLoS Genetics, 2013, 9, e1003419.	1.5	67
100	A genome-wide meta-analysis of nodular sclerosing Hodgkin lymphoma identifies risk loci at 6p21.32. Blood, 2012, 119, 469-475.	0.6	66
101	Genetic determinants of mammographic density. Breast Cancer Research, 2002, 4, R5.	2.2	65
102	HSD17B1 andCYP17 polymorphisms and breast cancer risk among Chinese women in Singapore. International Journal of Cancer, 2003, 104, 450-457.	2.3	64
103	Single Nucleotide Polymorphisms in the TP53 Region and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2009, 69, 2349-2357.	0.4	63
104	Isothiocyanates, glutathione Sâ€transferase M1 and T1 polymorphisms and gastric cancer risk: A prospective study of men in Shanghai, China. International Journal of Cancer, 2009, 125, 2652-2659.	2.3	62
105	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. Human Molecular Genetics, 2013, 22, 2748-2753.	1.4	59
106	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
107	Interleukin-6-Related Genotypes, Body Mass Index, and Risk of Multiple Myeloma and Plasmacytoma. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2285-2291.	1.1	57
108	Double-Strand Break Damage and Associated DNA Repair Genes Predispose Smokers to Gene Methylation. Cancer Research, 2008, 68, 3049-3056.	0.4	57

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109	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	3.0	57
110	CrkL and CrkII participate in the generation of the growth inhibitory effects of interferons on primary hematopoietic progenitors. Experimental Hematology, 1999, 27, 1315-1321.	0.2	56
111	Polymorphisms in angiotensin II type 1 receptor and angiotensin I-converting enzyme genes and breast cancer risk among Chinese women in Singapore. Carcinogenesis, 2004, 26, 459-464.	1.3	55
112	Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. International Journal of Cancer, 2011, 128, 2063-2074.	2.3	54
113	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
114	Genetic variations on chromosomes 5p15 and 15q25 and bladder cancer risk: findings from the Los Angelesâ€“Shanghai bladder caseâ€“control study. Carcinogenesis, 2011, 32, 197-202.	1.3	52
115	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	1.3	50
116	The effect of cyclin D1 (CCND1) G870A-polymorphism on breast cancer risk is modified by oxidative stress among Chinese women in Singapore. Carcinogenesis, 2005, 26, 1457-1464.	1.3	49
117	Risk of Ovarian Cancer and the NF-Î^ºB Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.4	48
118	Marine n-3 fatty acid intake, glutathione S-transferase polymorphisms and breast cancer risk in post-menopausal Chinese women in Singapore. Carcinogenesis, 2004, 25, 2143-2147.	1.3	42
119	Comprehensive association testing of common genetic variation in DNA repair pathway genes in relationship with breast cancer risk in multiple populations. Human Molecular Genetics, 2008, 17, 825-834.	1.4	42
120	Association between invasive ovarian cancer susceptibility and 11 best candidate SNPs from breast cancer genome-wide association study. Human Molecular Genetics, 2009, 18, 2297-2304.	1.4	42
121	The effect of the cyclin D1 (CCND1) A870G polymorphism on colorectal cancer risk is modified by glutathione-S-transferase polymorphisms and isothiocyanate intake in the Singapore Chinese Health Study. Carcinogenesis, 2006, 27, 2475-2482.	1.3	41
122	Dopamine Genes and Nicotine Dependence in Treatment-Seeking and Community Smokers. Neuropsychopharmacology, 2009, 34, 2252-2264.	2.8	41
123	Snagger: A user-friendly program for incorporating additional information for tagSNP selection. BMC Bioinformatics, 2008, 9, 174.	1.2	40
124	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
125	Glutathione S-transferase (GST) gene polymorphisms, cigarette smoking and colorectal cancer risk among Chinese in Singapore. Carcinogenesis, 2011, 32, 1507-1511.	1.3	39
126	Interleukin-2, interleukin-12, and interferon-Î³ levels and risk of young adult Hodgkin lymphoma. Blood, 2008, 111, 3377-3382.	0.6	38

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127	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38
128	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
129	Peroxisome proliferator-activated receptor (PPAR) Â gene polymorphisms and colorectal cancer risk among Chinese in Singapore. Carcinogenesis, 2006, 27, 1797-1802.	1.3	36
130	Role of inducible nitric oxide synthase in asthma risk and lung function growth during adolescence. Thorax, 2010, 65, 139-145.	2.7	35
131	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
132	Genome-wide association study of colorectal cancer in Hispanics. Carcinogenesis, 2016, 37, 547-556.	1.3	34
133	Urinary Total Isothiocyanates and Colorectal Cancer: A Prospective Study of Men in Shanghai, China. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1354-1359.	1.1	33
134	Variation in the GST mu Locus and Tobacco Smoke Exposure as Determinants of Childhood Lung Function. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 601-607.	2.5	33
135	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
136	No association between the SRD5A2 gene A49T missense variant and prostate cancer risk: lessons learned. Human Molecular Genetics, 2008, 17, 2456-2461.	1.4	32
137	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
138	Large chromosome deletions, duplications, and gene conversion events accumulate with age in normal human colon crypts. Aging Cell, 2013, 12, 269-279.	3.0	31
139	Polymorphisms in genes involved in estrogen and progesterone metabolism and mammographic density changes in women randomized to postmenopausal hormone therapy: results from a pilot study. Breast Cancer Research, 2005, 7, R336-44.	2.2	30
140	Role of Members of the Wnt Gene Family in Human Hematopoiesis. Blood, 1998, 92, 3189-3202.	0.6	30
141	Genetic risk factors for orofacial clefts in Central Africans and Southeast Asians. American Journal of Medical Genetics, Part A, 2014, 164, 2572-2580.	0.7	28
142	Underlying genetic structure impacts the association between CYP2B6 polymorphisms and response to efavirenz and nevirapine. Aids, 2012, 26, 2097-2106.	1.0	26
143	Novel colon cancer susceptibility variants identified from a genomeâ€wide association study in African Americans. International Journal of Cancer, 2017, 140, 2728-2733.	2.3	26
144	Genetic Variation in TYMS in the One-Carbon Transfer Pathway Is Associated with Ovarian Carcinoma Types in the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1822-1830.	1.1	24

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145	Heterogenous effect of androgen receptor CAG tract length on testicular germ cell tumor risk: shorter repeats associated with seminoma but not other histologic types. Carcinogenesis, 2011, 32, 1238-1243.	1.3	24
146	Native American Ancestry Affects the Risk for Gene Methylation in the Lungs of Hispanic Smokers from New Mexico. American Journal of Respiratory and Critical Care Medicine, 2013, 188, 1110-1116.	2.5	24
147	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.4	24
148	Polymorphism in the GALNT1 Gene and Epithelial Ovarian Cancer in Non-Hispanic White Women: The Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 600-604.	1.1	23
149	Haplotypes of DNMT1 and DNMT3B are associated with mutagen sensitivity induced by benzo[a]pyrene diol epoxide among smokers. Carcinogenesis, 2008, 29, 1380-1385.	1.3	22
150	Genetic variation in insulin-like growth factor 2 may play a role in ovarian cancer risk. Human Molecular Genetics, 2011, 20, 2263-2272.	1.4	22
151	Genetic Determinants for Promoter Hypermethylation in the Lungs of Smokers: A Candidate Gene-Based Study. Cancer Research, 2012, 72, 707-715.	0.4	22
152	Comprehensive analyses of DNA repair pathways, smoking and bladder cancer risk in Los Angeles and Shanghai. International Journal of Cancer, 2014, 135, 335-347.	2.3	22
153	Improvements in the Epstein-Barr-based shuttle vector system for direct cloning in human tissue culture cells. Methods, 1992, 4, 133-142.	1.9	21
154	Large-Scale Evaluation of Common Variation in Regulatory T Cellâ€“Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	1.6	21
155	Evaluation of unclassified variants in the breast cancer susceptibility genes BRCA1 and BRCA2using five methods: results from a population-based study of young breast cancer patients. Breast Cancer Research, 2008, 10, R19.	2.2	20
156	Genetic variation in the progesterone receptor gene and risk of endometrial cancer: a haplotype-based approach. Carcinogenesis, 2010, 31, 1392-1399.	1.3	20
157	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. Fertility and Sterility, 2011, 95, 40-45.	0.5	20
158	Elevated 4-Aminobiphenyl and 2,6-Dimethylaniline Hemoglobin Adducts and Increased Risk of Bladder Cancer among Lifelong Nonsmokersâ€”The Shanghai Bladder Cancer Study. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 937-945.	1.1	20
159	A Genome-Wide Scan for Breast Cancer Risk Haplotypes among African American Women. PLoS ONE, 2013, 8, e57298.	1.1	20
160	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	3.6	20
161	Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. Circulation Research, 2022, 131, .	2.0	20
162	A Systematic Assessment of Common Genetic Variation in CYP11A and Risk of Breast Cancer. Cancer Research, 2006, 66, 12019-12025.	0.4	19

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163	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	1.4	19
164	A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1609-1618.	1.1	18
165	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	2.6	18
166	The Role of Established Breast Cancer Susceptibility Loci in Mammographic Density in Young Women. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 258-260.	1.1	17
167	Genetic Variation in the Base Excision Repair Pathway, Environmental Risk Factors, and Colorectal Adenoma Risk. PLoS ONE, 2013, 8, e71211.	1.1	17
168	Risk of Urinary Bladder Cancer Is Associated with 8q24 Variant rs9642880[T] in Multiple Racial/Ethnic Groups: Results from the Los Angelesâ€“Shanghai Caseâ€“Control Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 3150-3156.	1.1	16
169	Variation in folate pathway genes and distal colorectal adenoma risk: a sigmoidoscopy-based caseâ€“control study. Cancer Causes and Control, 2011, 22, 541-552.	0.8	16
170	Genetic Variation in Peroxisome Proliferatorâ€“Activated Receptor Gamma, Soy, and Mammographic Density in Singapore Chinese Women. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 635-644.	1.1	16
171	Polymorphisms in hormone metabolism and growth factor genes and mammographic density in Norwegian postmenopausal hormone therapy users and non-users. Breast Cancer Research, 2012, 14, R135.	2.2	16
172	15q12 Variants, Sputum Gene Promoter Hypermethylation, and Lung Cancer Risk: A GWAS in Smokers. Journal of the National Cancer Institute, 2015, 107, .	3.0	16
173	A meta-analysis of genome-wide association studies of multiple myeloma among men and women of African ancestry. Blood Advances, 2020, 4, 181-190.	2.5	16
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