David Van Den Berg

List of Publications by Citations

229 papers	34,469 citations	80 h-index	185 g-index
246 ext. papers	46,430 ext. citations	12.8 avg, IF	5.34 L-index

#	Paper	IF	Citations
229	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
228	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
227	Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. *Cancer Cell*, **2010**, 17, 510-22	24.3	1754
226	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
225	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
224	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
223	Integrated genomic characterization of oesophageal carcinoma. *Nature*, **2017**, 541, 169-175	50.4	965
222	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell*, **2017**, 171, 540-556.e25	56.2	961
221	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.5	896
220	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
219	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
218	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
217	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *New England Journal of Medicine*, **2016**, 374, 135-45	59.2	753
216	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
215	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. *Nature Genetics*, **2011**, 43, 887-92	36.3	605
214	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
213	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. *Nature Genetics*, **2011**, 44, 40-6	36.3	474

212	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. *Genome Research*, **2012**, 22, 271-82	9.7	466
211	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
210	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
209	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. *Nature Genetics*, **2010**, 42, 978-84	36.3	408
208	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature Genetics*, **2015**, 47, 373-80	36.3	406
207	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
206	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. *Nucleic Acids Research*, **2013**, 41, e90	20.1	393
205	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
204	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
203	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
202	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. *Cancer Cell*, **2018**, 34, 211-224.e6	24.3	327
201	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
200	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
199	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
198	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
197	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
196	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	24.3	275
195	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268

194	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. *Nature Genetics*, **2013**, 45, 362-70, 370e1-2	36.3	267
193	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. *Cancer Discovery*, **2018**, 8, 1548-1565	24.4	258
192	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. *Nature Genetics*, **2011**, 43, 1210-4	36.3	253
191	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
190	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. *Nature Genetics*, **2009**, 41, 996-1000	36.3	240
189	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
188	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
187	Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **2017**, 31, 411-423	24.3	210
186	Common variants at 19p13 are associated with susceptibility to ovarian cancer. *Nature Genetics*, **2010**, 42, 880-4	36.3	210
185	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
184	Sun exposure, vitamin D receptor gene polymorphisms, and risk of advanced prostate cancer. *Cancer Research*, **2005**, 65, 5470-9	10.1	194
183	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. *Nature Genetics*, **2013**, 45, 690-6	36.3	192
182	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
181	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188
180	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
179	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
178	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
177	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. *Nature Genetics*, **2011**, 43, 570-3	36.3	171

176	Dietary isothiocyanates, glutathione S-transferase polymorphisms and colorectal cancer risk in the Singapore Chinese Health Study. *Carcinogenesis*, **2002**, 23, 2055-61	4.6	168
175	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	11	167
174	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
173	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. *Cell Systems*, **2018**, 6, 282-300.e2	10.6	159
172	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. *Cell Reports*, **2018**, 25, 1304-1317.e5	10.6	152
171	The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, **2018**, 33, 244-258.e10	24.3	150
170	Roberts syndrome: a review of 100 cases and a new rating system for severity. *American Journal of Medical Genetics Part A*, **1993**, 47, 1104-23		149
169	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. *Cell Reports*, **2018**, 23, 297-312.e12	10.6	147
168	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. *Cell Reports*, **2018**, 23, 194-212.e6	10.6	146
167	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, 5373-84	5.6	143
166	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e12	56.2	133
165	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. *Nature Communications*, **2013**, 4, 1628	17.4	124
164	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
163	Nicotinic acetylcholine receptor beta2 subunit gene implicated in a systems-based candidate gene study of smoking cessation. *Human Molecular Genetics*, **2008**, 17, 2834-48	5.6	118
162	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
161	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	9.7	107
160	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. *Nature Communications*, **2015**, 6, 7138	17.4	106
159	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101

158	Genome-wide association study identifies multiple loci associated with bladder cancer risk. *Human Molecular Genetics*, **2014**, 23, 1387-98	5.6	101
157	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
156	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, 4373-80	2.2	87
155	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-β Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85
154	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. *Journal of Medical Genetics*, **2016**, 53, 298-309	5.8	83
153	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, 1046-60	11	80
152	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, 6616-33	5.6	77
151	Green tea intake, MTHFR/TYMS genotype and breast cancer risk: the Singapore Chinese Health Study. *Carcinogenesis*, **2008**, 29, 1967-72	4.6	77
150	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, 2539-50	5.6	75
149	A genome screen of families with multiple cases of prostate cancer: evidence of genetic heterogeneity. *American Journal of Human Genetics*, **2001**, 69, 148-58	11	75
148	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 146-157	9.7	67
147	Genetic polymorphisms in the methylenetetrahydrofolate reductase and thymidylate synthase genes and risk of hepatocellular carcinoma. *Hepatology*, **2007**, 46, 749-58	11.2	67
146	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
145	Consortium analysis of 7 candidate SNPs for ovarian cancer. *International Journal of Cancer*, **2008**, 123, 380-388	7.5	66
144	ESR1/SYNE1 polymorphism and invasive epithelial ovarian cancer risk: an Ovarian Cancer Association Consortium study. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 245-50	4	64
143	A genome-wide association study of breast cancer in women of African ancestry. *Human Genetics*, **2013**, 132, 39-48	6.3	63
142	Tea and circulating estrogen levels in postmenopausal Chinese women in Singapore. *Carcinogenesis* , **2005**, 26, 976-80	4.6	63
141	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. *Nature Communications*, **2014**, 5, 4613	17.4	62

140	HSD17B1 and CYP17 polymorphisms and breast cancer risk among Chinese women in Singapore. *International Journal of Cancer*, **2003**, 104, 450-7	7.5	62
139	Effect of reproductive factors and oral contraceptives on breast cancer risk in BRCA1/2 mutation carriers and noncarriers: results from a population-based study. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 3170-8	4	61
138	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. *Nature Communications*, **2016**, 7, 11843	17.4	59
137	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	11	59
136	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226	26.3	56
135	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	6	55
134	Isothiocyanates, glutathione S-transferase M1 and T1 polymorphisms and gastric cancer risk: a prospective study of men in Shanghai, China. *International Journal of Cancer*, **2009**, 125, 2652-9	7.5	54
133	Double-strand break damage and associated DNA repair genes predispose smokers to gene methylation. *Cancer Research*, **2008**, 68, 3049-56	10.1	54
132	Interleukin-6-related genotypes, body mass index, and risk of multiple myeloma and plasmacytoma. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 2285-91	4	54
131	Genetic determinants of mammographic density. *Breast Cancer Research*, **2002**, 4, R5	8.3	54
130	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. *Human Molecular Genetics*, **2013**, 22, 2748-53	5.6	53
129	A genome-wide meta-analysis of nodular sclerosing Hodgkin lymphoma identifies risk loci at 6p21.32. *Blood*, **2012**, 119, 469-75	2.2	52
128	Single nucleotide polymorphisms in the TP53 region and susceptibility to invasive epithelial ovarian cancer. *Cancer Research*, **2009**, 69, 2349-57	10.1	52
127	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 795-806	7.8	52
126	Genome-wide interaction studies reveal sex-specific asthma risk alleles. *Human Molecular Genetics*, **2014**, 23, 5251-9	5.6	50
125	CrkL and CrkII participate in the generation of the growth inhibitory effects of interferons on primary hematopoietic progenitors. *Experimental Hematology*, **1999**, 27, 1315-21	3.1	50
124	Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. *International Journal of Cancer*, **2011**, 128, 2063-74	7.5	49
123	Polymorphisms in angiotensin II type 1 receptor and angiotensin I-converting enzyme genes and breast cancer risk among Chinese women in Singapore. *Carcinogenesis*, **2005**, 26, 459-64	4.6	49

122	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2014**, 23, 6096-111	5.6	48
121	Genetic variations on chromosomes 5p15 and 15q25 and bladder cancer risk: findings from the Los Angeles-Shanghai bladder case-control study. *Carcinogenesis*, **2011**, 32, 197-202	4.6	46
120	Second-Generation Linkage Maps for the Pacific Oyster Crassostrea gigas Reveal Errors in Assembly of Genome Scaffolds. *G3: Genes, Genomes, Genetics*, **2015**, 5, 2007-19	3.2	43
119	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	11	43
118	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, 1457-64	4.6	42
117	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	38
116	Dopamine genes and nicotine dependence in treatment-seeking and community smokers. *Neuropsychopharmacology*, **2009**, 34, 2252-64	8.7	38
115	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, 825-34	5.6	38
114	Association between invasive ovarian cancer susceptibility and 11 best candidate SNPs from breast cancer genome-wide association study. *Human Molecular Genetics*, **2009**, 18, 2297-304	5.6	37
113	Snagger: a user-friendly program for incorporating additional information for tagSNP selection. *BMC Bioinformatics*, **2008**, 9, 174	3.6	37
112	Marine n-3 fatty acid intake, glutathione S-transferase polymorphisms and breast cancer risk in post-menopausal Chinese women in Singapore. *Carcinogenesis*, **2004**, 25, 2143-7	4.6	37
111	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
110	Risk of ovarian cancer and the NF-B pathway: genetic association with IL1A and TNFSF10. *Cancer Research*, **2014**, 74, 852-61	10.1	36
109	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, 2475-82	4.6	36
108	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. *Human Molecular Genetics*, **2015**, 24, 285-98	5.6	35
107	Genome-wide interaction study of smoking and bladder cancer risk. *Carcinogenesis*, **2014**, 35, 1737-44	4.6	33
106	Glutathione S-transferase (GST) gene polymorphisms, cigarette smoking and colorectal cancer risk among Chinese in Singapore. *Carcinogenesis*, **2011**, 32, 1507-11	4.6	33
105	Role of inducible nitric oxide synthase in asthma risk and lung function growth during adolescence. *Thorax*, **2010**, 65, 139-45	7.3	32

104	Interleukin-2, interleukin-12, and interferon-gamma levels and risk of young adult Hodgkin lymphoma. *Blood*, **2008**, 111, 3377-82	2.2	32
103	Large chromosome deletions, duplications, and gene conversion events accumulate with age in normal human colon crypts. *Aging Cell*, **2013**, 12, 269-79	9.9	30
102	Role of Members of the Wnt Gene Family in Human Hematopoiesis. *Blood*, **1998**, 92, 3189-3202	2.2	30
101	Urinary total isothiocyanates and colorectal cancer: a prospective study of men in Shanghai, China. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 1354-9	4	29
100	Peroxisome proliferator-activated receptor (PPAR) gamma gene polymorphisms and colorectal cancer risk among Chinese in Singapore. *Carcinogenesis*, **2006**, 27, 1797-802	4.6	29
99	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, 601-7	10.2	28
98	No association between the SRD5A2 gene A49T missense variant and prostate cancer risk: lessons learned. *Human Molecular Genetics*, **2008**, 17, 2456-61	5.6	28
97	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	8.3	27
96	Genome-wide association study of colorectal cancer in Hispanics. *Carcinogenesis*, **2016**, 37, 547-556	4.6	26
95	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	5.6	24
94	Genetic risk factors for orofacial clefts in Central Africans and Southeast Asians. *American Journal of Medical Genetics, Part A*, **2014**, 164A, 2572-80	2.5	24
93	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, 1822-30	4	22
92	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, 1238-43	4.6	22
91	Underlying genetic structure impacts the association between CYP2B6 polymorphisms and response to efavirenz and nevirapine. *Aids*, **2012**, 26, 2097-106	3.5	22
90	Genetic determinants for promoter hypermethylation in the lungs of smokers: a candidate gene-based study. *Cancer Research*, **2012**, 72, 707-15	10.1	21
89	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, 1203-14	5.6	20
88	Comprehensive analyses of DNA repair pathways, smoking and bladder cancer risk in Los Angeles and Shanghai. *International Journal of Cancer*, **2014**, 135, 335-47	7.5	20
87	Large-scale evaluation of common variation in regulatory T cell-related genes and ovarian cancer outcome. *Cancer Immunology Research*, **2014**, 2, 332-40	12.5	20

86	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, 1110-6	10.2	20
85	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, 600-4	4	20
84	The 19q12 bladder cancer GWAS signal: association with cyclin E function and aggressive disease. *Cancer Research*, **2014**, 74, 5808-18	10.1	19
83	Genetic variation in the progesterone receptor gene and risk of endometrial cancer: a haplotype-based approach. *Carcinogenesis*, **2010**, 31, 1392-9	4.6	19
82	Haplotypes of DNMT1 and DNMT3B are associated with mutagen sensitivity induced by benzo[a]pyrene diol epoxide among smokers. *Carcinogenesis*, **2008**, 29, 1380-5	4.6	19
81	Improvements in the Epstein-Barr-based shuttle vector system for direct cloning in human tissue culture cells. *Methods*, **1992**, 4, 133-142	4.6	19
80	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. *Fertility and Sterility*, **2011**, 95, 40-5	4.8	18
79	Genetic variation in insulin-like growth factor 2 may play a role in ovarian cancer risk. *Human Molecular Genetics*, **2011**, 20, 2263-72	5.6	18
78	Novel colon cancer susceptibility variants identified from a genome-wide association study in African Americans. *International Journal of Cancer*, **2017**, 140, 2728-2733	7.5	17
77	A genome-wide scan for breast cancer risk haplotypes among African American women. *PLoS ONE*, **2013**, 8, e57298	3.7	17
76	Evaluation of unclassified variants in the breast cancer susceptibility genes BRCA1 and BRCA2 using five methods: results from a population-based study of young breast cancer patients. *Breast Cancer Research*, **2008**, 10, R19	8.3	17
75	A systematic assessment of common genetic variation in CYP11A and risk of breast cancer. *Cancer Research*, **2006**, 66, 12019-25	10.1	17
74	15q12 variants, sputum gene promoter hypermethylation, and lung cancer risk: a GWAS in smokers. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	16
73	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. *Human Molecular Genetics*, **2016**, 25, 2612-2620	5.6	15
72	Elevated 4-aminobiphenyl and 2,6-dimethylaniline hemoglobin adducts and increased risk of bladder cancer among lifelong nonsmokers--The Shanghai Bladder Cancer Study. *Cancer Epidemiology Biomarkers and Prevention*, **2013**, 22, 937-45	4	15
71	Genetic variation in the base excision repair pathway, environmental risk factors, and colorectal adenoma risk. *PLoS ONE*, **2013**, 8, e71211	3.7	15
70	Variation in folate pathway genes and distal colorectal adenoma risk: a sigmoidoscopy-based case-control study. *Cancer Causes and Control*, **2011**, 22, 541-52	2.8	15
69	Risk of urinary bladder cancer is associated with 8q24 variant rs9642880[T] in multiple racial/ethnic groups: results from the Los Angeles-Shanghai case-control study. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 3150-6	4	15

68	The role of established breast cancer susceptibility loci in mammographic density in young women. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 258-60	4	15
67	Genetic variation in peroxisome proliferator-activated receptor gamma, soy, and mammographic density in Singapore Chinese women. *Cancer Epidemiology Biomarkers and Prevention*, **2012**, 21, 635-44	4	14
66	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
65	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	8.3	13
64	Genetic polymorphisms of epidermal growth factor in relation to risk of hepatocellular carcinoma: two case-control studies. *BMC Gastroenterology*, **2013**, 13, 32	3	13
63	The association of polymorphisms in hormone metabolism pathway genes, menopausal hormone therapy, and breast cancer risk: a nested case-control study in the California Teachers Study cohort. *Breast Cancer Research*, **2011**, 13, R37	8.3	13
62	Progestogen levels, progesterone receptor gene polymorphisms, and mammographic density changes: results from the Postmenopausal Estrogen/Progestin Interventions Mammographic Density Study. *Menopause*, **2012**, 19, 302-10	2.5	13
61	Comprehensive evaluation of ESR2 variation and ovarian cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 393-6	4	13
60	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	4	13
59	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. *International Journal of Cancer*, **2021**, 148, 307-319	7.5	13
58	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. *Breast Cancer Research*, **2014**, 16, R51	8.3	12
57	Variation in NF-B signaling pathways and survival in invasive epithelial ovarian cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 1421-7	4	11
56	Combined effects of MDM2 SNP309 and TP53 R72P polymorphisms, and soy isoflavones on breast cancer risk among Chinese women in Singapore. *Breast Cancer Research and Treatment*, **2011**, 130, 1011-9	4.4	11
55	Sequence variant on 3q28 and urinary bladder cancer risk: findings from the Los Angeles-Shanghai bladder case-control study. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 3057-61	4	11
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