David Van Den Berg

List of Publications by Year in Descending Order

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	Whole-Exome Sequencing in Multiplex Families to Identify Novel AYA Classical Hodgkin Lymphoma Predisposition Genes. *Blood*, **2021**, 138, 3499-3499	2.2	0
228	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. *Genome Medicine*, **2021**, 13, 74	14.4	3
227	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	11	7
226	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. *Aging Cell*, **2021**, 20, e13366	9.9	9
225	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
224	Genome-Wide Association Analyses Identify Variants in Associated With Acute Myeloid Leukemia and Myelodysplastic Syndrome Susceptibility. *Frontiers in Genetics*, **2021**, 12, 554948	4.5	3
223	Prognostic impact of pre-transplant chromosomal aberrations in peripheral blood of patients undergoing unrelated donor hematopoietic cell transplant for acute myeloid leukemia. *Scientific Reports*, **2021**, 11, 15004	4.9	1
222	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
221	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
220	Novel genetic variants associated with mortality after unrelated donor allogeneic hematopoietic cell transplantation. *EClinicalMedicine*, **2021**, 40, 101093	11.3	0
219	Pre-HCT mosaicism increases relapse risk and lowers survival in acute lymphoblastic leukemia patients post-unrelated HCT. *Blood Advances*, **2021**, 5, 66-70	7.8	2
218	Associations between DNA methylation and BMI vary by metabolic health status: a potential link to disparate cardiovascular outcomes.. *Clinical Epigenetics*, **2021**, 13, 230	7.7	0
217	Variability in Cytogenetic Testing for Multiple Myeloma: A Comprehensive Analysis From Across the United States. *JCO Oncology Practice*, **2020**, 16, e1169-e1180	2.3	2
216	Meta-Analysis of Genome-Wide Association Studies of Acute Myeloid Leukemia (AML) Patients Identifies Variants Associated with Risk of 11q23/KMT2A-Translocated and Core-Binding Factor (CBF) AML and Suggests a Role for Transcription Elongation in Leukemogenesis. *Blood*, **2020**, 136, 29-30	2.2	
215	Population Distribution of GvL and GvH Minor Histocompatibility Antigens. *Blood*, **2020**, 136, 23-25	2.2	
214	Associations of Clinical Outcomes after Allogeneic Hematopoietic Cell Transplantation with Number of Predicted Class II Restricted mHA. *Blood*, **2020**, 136, 2-2	2.2	
213	Pre-Transplant Clonal Mosaicism Is Associated with Increased Relapse and Lower Survival in Acute Lymphoblastic Leukemia Patients Undergoing Allogeneic Hematopoietic Cell Transplant. *Blood*, **2020**, 136, 9-10	2.2	

212	A meta-analysis of genome-wide association studies of multiple myeloma among men and women of African ancestry. *Blood Advances*, **2020**, 4, 181-190	7.8	5
211	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. *Nature Communications*, **2020**, 11, 5182	17.4	6
210	DNA methylation patterns of adult survivors of adolescent/young adult Hodgkin lymphoma compared to their unaffected monozygotic twin. *Leukemia and Lymphoma*, **2019**, 60, 1429-1437	1.9	7
209	Data-adaptive multi-locus association testing in subjects with arbitrary genealogical relationships. *Statistical Applications in Genetics and Molecular Biology*, **2019**, 18,	1.2	1
208	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 146-157	9.7	67
207	Genome Wide Interaction Analysis Identifies Expression Quantitative Trait Loci Associated with Reduced Survival after Reduced Intensity Conditioning HLA-Matched Unrelated Donor Allogeneic Hematopoietic Cell Transplant. *Blood*, **2019**, 134, 4595-4595	2.2	
206	Validation of genetic associations with acute GVHD and nonrelapse mortality in DISCOVeRY-BMT. *Blood Advances*, **2019**, 3, 2337-2341	7.8	4
205	Multiple functional variants in the region are pretransplant markers for risk of GVHD and infection deaths. *Blood Advances*, **2019**, 3, 2512-2524	7.8	4
204	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
203	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
202	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
201	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
200	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
199	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e12	56.2	133
198	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
197	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
196	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
195	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342

194	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
193	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
192	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. *Cell Reports*, **2018**, 23, 194-212.e6	10.6	146
191	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
190	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
189	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
188	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
187	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
186	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226.e3	10.6	56
185	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
184	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
183	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
182	Ovarian cancer risk, ALDH2 polymorphism and alcohol drinking: Asian data from the Ovarian Cancer Association Consortium. *Cancer Science*, **2018**, 109, 435-445	6.9	9
181	The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, **2018**, 33, 244-258.e10	24.3	150
180	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
179	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
178	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
177	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377

176	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
175	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
174	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. *Cancer Cell*, **2018**, 34, 211-224.e6	24.3	327
173	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
172	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
171	Genome Wide Association Analyses Identify Pleiotropic Variants Associated with Acute Myeloid Leukemia (AML) and Myelodysplastic Syndrome (MDS) Susceptibility. *Blood*, **2018**, 132, 1500-1500	2.2	
170	Multiple Functional Donor Polymorphisms in IL1RL1 region Associate with Death Due to GvHD or Infection after Unrelated Donor Allogeneic Hematopoietic Stem Cell Transplantation (HCT) for AML and MDS. *Blood*, **2018**, 132, 312-312	2.2	
169	Growth factor genes and change in mammographic density after stopping combined hormone therapy in the California Teachers Study. *BMC Cancer*, **2018**, 18, 1072	4.8	1
168	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85
167	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. *Cancer Discovery*, **2018**, 8, 1548-1565	24.4	258
166	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. *Cell Reports*, **2018**, 25, 1304-1317.e5	10.6	152
165	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
164	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
163	Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **2017**, 31, 411-423	24.3	210
162	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
161	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
160	Integrated genomic characterization of oesophageal carcinoma. *Nature*, **2017**, 541, 169-175	50.4	965
159	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell*, **2017**, 171, 540-556.e25	36.2	961

158	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
157	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
156	Genome-Wide Testing of Exonic Variants and Breast Cancer Risk in the California Teachers Study. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1462-1465	4	
155	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.5	896
154	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
153	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
152	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	38
151	Pharmacogenetic Associations with ADME Variants and Virologic Response to an Initial HAART Regimen in HIV-Infected Women **2017**, 4, 154-160		
150	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
149	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. *Nature Communications*, **2016**, 7, 11843	17.4	59
148	Genome-wide association study of colorectal cancer in Hispanics. *Carcinogenesis*, **2016**, 37, 547-556	4.6	26
147	Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 780-90	4	8
146	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. *Human Molecular Genetics*, **2016**, 25, 2612-2620	5.6	15
145	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
144	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
143	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 446-54	4	6
142	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *New England Journal of Medicine*, **2016**, 374, 135-45	59.2	753
141	HLA Haplotypes Are Associated with Multiple Myeloma Risk in the African American Multiple Myeloma Study (AAMMS). *Blood*, **2016**, 128, 3250-3250	2.2	1

140	A targeted genetic association study of epithelial ovarian cancer susceptibility. *Oncotarget*, **2016**, 7, 7381-9	5.9	7
139	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
138	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
137	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
136	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
135	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. *Nature Communications*, **2015**, 6, 7138	17.4	106
134	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
133	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
132	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
131	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
130	Methodological Considerations in Estimation of Phenotype Heritability Using Genome-Wide SNP Data, Illustrated by an Analysis of the Heritability of Height in a Large Sample of African Ancestry Adults. *PLoS ONE*, **2015**, 10, e0131106	3.7	2
129	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
128	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
127	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
126	DNA Methylation Differences in Twins Discordant for Adolescent/Young Adult Hodgkin Lymphoma. *Blood*, **2015**, 126, 179-179	2.2	
125	Genome-wide interaction study of smoking and bladder cancer risk. *Carcinogenesis*, **2014**, 35, 1737-44	4.6	33
124	Genome-wide association study identifies multiple loci associated with bladder cancer risk. *Human Molecular Genetics*, **2014**, 23, 1387-98	5.6	101
123	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

122	The 19q12 bladder cancer GWAS signal: association with cyclin E function and aggressive disease. *Cancer Research*, **2014**, 74, 5808-18	10.1	19
121	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
120	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
119	Exome-wide association study of endometrial cancer in a multiethnic population. *PLoS ONE*, **2014**, 9, e97045	3.7	8
118	Variation in NF-Β signaling pathways and survival in invasive epithelial ovarian cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 1421-7	4	11
117	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
116	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
115	Genome-wide interaction studies reveal sex-specific asthma risk alleles. *Human Molecular Genetics*, **2014**, 23, 5251-9	5.6	50
114	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. *Nature Communications*, **2014**, 5, 4613	17.4	62
113	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
112	Hormone metabolism pathway genes and mammographic density change after quitting estrogen and progestin combined hormone therapy in the California Teachers Study. *Breast Cancer Research*, **2014**, 16, 477	8.3	4
111	Breast cancer susceptibility variants and mammographic density phenotypes in norwegian postmenopausal women. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 1752-63	4	6
110	Antiretroviral therapy modifies the genetic effect of known type 2 diabetes-associated risk variants in HIV-infected women. *Aids*, **2014**, 28, 1815-23	3.5	3
109	Risk of ovarian cancer and the NF-Β pathway: genetic association with IL1A and TNFSF10. *Cancer Research*, **2014**, 74, 852-61	10.1	36
108	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
107	High-throughput exome array for identification of novel polymorphisms associated with clinical outcome in mCRC patients treated with first-line FOLFOXIRI/BEV versus FOLFIRI/BEV (TRIBE trial; NCT00719797).. *Journal of Clinical Oncology*, **2014**, 32, 3632-3632	2.2	
106	Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common variants in GATA3. *Blood*, **2014**, 124, 135-135	2.2	
105	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

104	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. *Nature Genetics*, **2013**, 45, 362-70, 370e1-2	36.3	267
103	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. *Human Molecular Genetics*, **2013**, 22, 2748-53	5.6	53
102	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
101	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
100	Reproducibility and reliability of SNP analysis using human cellular DNA at or near nanogram levels. *BMC Research Notes*, **2013**, 6, 515	2.3	2
99	A genome-wide association study of breast cancer in women of African ancestry. *Human Genetics*, **2013**, 132, 39-48	6.3	63
98	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
97	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
96	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
95	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
94	Genetic polymorphisms of epidermal growth factor in relation to risk of hepatocellular carcinoma: two case-control studies. *BMC Gastroenterology*, **2013**, 13, 32	3	13
93	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
92	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
91	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
90	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
89	Hormone metabolism genes and mammographic density in Singapore Chinese women. *Cancer Epidemiology Biomarkers and Prevention*, **2013**, 22, 984-6	4	1
88	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. *Nucleic Acids Research*, **2013**, 41, e90	20.1	393
87	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. *Nature Communications*, **2013**, 4, 1628	17.4	124

86	Genetic variation in transforming growth factor beta 1 and mammographic density in Singapore Chinese women. *Cancer Research*, **2013**, 73, 1876-82	10.1	10
85	A genome-wide scan for breast cancer risk haplotypes among African American women. *PLoS ONE*, **2013**, 8, e57298	3.7	17
84	Genetic variation in the base excision repair pathway, environmental risk factors, and colorectal adenoma risk. *PLoS ONE*, **2013**, 8, e71211	3.7	15
83	Polymorphisms In IRS1 and IL6R and Susceptibility To Multiple Myeloma. *Blood*, **2013**, 122, 3154-3154	2.2	
82	Obesity In Young Adulthood Is Associated With Early Onset Multiple Myeloma In African Americans. *Blood*, **2013**, 122, 1872-1872	2.2	
81	A Meta-Analysis Of Genome-Wide Association Studies Of Multiple Myeloma In Cases and Controls Of European Origin Identifies a Risk Locus In 12q23.1. *Blood*, **2013**, 122, 3111-3111	2.2	
80	A Meta-Analysis Of Hodgkin Lymphoma Reveals 19p13.3 (TCF3) As a Novel Susceptibility Loc. *Blood* , **2013**, 122, 626-626	2.2	
79	Variations in sex hormone metabolism genes, postmenopausal hormone therapy and risk of endometrial cancer. *International Journal of Cancer*, **2012**, 130, 1629-38	7.5	5
78	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
77	A genome-wide meta-analysis of nodular sclerosing Hodgkin lymphoma identifies risk loci at 6p21.32. *Blood*, **2012**, 119, 469-75	2.2	52
76	Genetic variation in insulin pathway genes and distal colorectal adenoma risk. *International Journal of Colorectal Disease*, **2012**, 27, 1587-95	3	5
75	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
74	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. *Genome Research*, **2012**, 22, 271-82	9.7	466
73	Genetic determinants for promoter hypermethylation in the lungs of smokers: a candidate gene-based study. *Cancer Research*, **2012**, 72, 707-15	10.1	21
72	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
71	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
70	Underlying genetic structure impacts the association between CYP2B6 polymorphisms and response to efavirenz and nevirapine. *Aids*, **2012**, 26, 2097-106	3.5	22
69	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

68	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. *Nature Genetics*, **2011**, 43, 887-92	36.3	605
67	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. *Fertility and Sterility*, **2011**, 95, 40-5	4.8	18
66	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
65	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
64	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
63	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
62	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
61	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
60	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
59	Association of the calcyon neuron-specific vesicular protein gene (CALY) with adolescent smoking initiation in China and California. *American Journal of Epidemiology*, **2011**, 173, 1039-48	3.8	6
58	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
57	Glutathione S-transferase (GST) gene polymorphisms, cigarette smoking and colorectal cancer risk among Chinese in Singapore. *Carcinogenesis*, **2011**, 32, 1507-11	4.6	33
56	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
55	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
54	Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer **2011**,		4
53	Common variants at 19p13 are associated with susceptibility to ovarian cancer. *Nature Genetics*, **2010**, 42, 880-4	36.3	210
52	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. *Nature Genetics*, **2010**, 42, 978-84	36.3	408
51	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

50	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
49	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
48	Genetic variation in the progesterone receptor gene and risk of endometrial cancer: a haplotype-based approach. *Carcinogenesis*, **2010**, 31, 1392-9	4.6	19
47	Role of inducible nitric oxide synthase in asthma risk and lung function growth during adolescence. *Thorax*, **2010**, 65, 139-45	7.3	32
46	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
45	Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. *Cancer Cell*, **2010**, 17, 510-22	24.3	1754
44	Genome wide mapping of histone methylation reveals a distinct epigenomic signature in human pluripotent stem cells. *FASEB Journal*, **2010**, 24, 833.11	0.9	
43	Polymorphisms in the FGF2 gene and risk of serous ovarian cancer: results from the ovarian cancer association consortium. *Twin Research and Human Genetics*, **2009**, 12, 269-75	2.2	5
42	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
41	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
40	Dopamine genes and nicotine dependence in treatment-seeking and community smokers. *Neuropsychopharmacology*, **2009**, 34, 2252-64	8.7	38
39	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
38	Single nucleotide polymorphisms in the TP53 region and susceptibility to invasive epithelial ovarian cancer. *Cancer Research*, **2009**, 69, 2349-57	10.1	52
37	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
36	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. *Nature Genetics*, **2009**, 41, 996-1000	36.3	240
35	Snagger: a user-friendly program for incorporating additional information for tagSNP selection. *BMC Bioinformatics*, **2008**, 9, 174	3.6	37
34	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
33	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

32	Comprehensive evaluation of ESR2 variation and ovarian cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 393-6	4	13
31	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
30	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
29	Green tea intake, MTHFR/TYMS genotype and breast cancer risk: the Singapore Chinese Health Study. *Carcinogenesis*, **2008**, 29, 1967-72	4.6	77
28	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
27	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
26	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
25	Double-strand break damage and associated DNA repair genes predispose smokers to gene methylation. *Cancer Research*, **2008**, 68, 3049-56	10.1	54
24	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
23	Association between common genetic variation in Cockayne syndrome A and B genes and nucleotide excision repair capacity among smokers. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 2062-9	4	5
22	Interleukin-2, interleukin-12, and interferon-gamma levels and risk of young adult Hodgkin lymphoma. *Blood*, **2008**, 111, 3377-82	2.2	32
21	Consortium analysis of 7 candidate SNPs for ovarian cancer. *International Journal of Cancer*, **2008**, 123, 380-388	7.5	66
20	Genetic polymorphisms in the methylenetetrahydrofolate reductase and thymidylate synthase genes and risk of hepatocellular carcinoma. *Hepatology*, **2007**, 46, 749-58	11.2	67
19	Germ line variation at 8q24 and endometrial cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2007**, 16, 2166-8	4	4
18	Peroxisome proliferator-activated receptor (PPAR) gamma gene polymorphisms and colorectal cancer risk among Chinese in Singapore. *Carcinogenesis*, **2006**, 27, 1797-802	4.6	29
17	A systematic assessment of common genetic variation in CYP11A and risk of breast cancer. *Cancer Research*, **2006**, 66, 12019-25	10.1	17
16	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
15	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

14	Tea and circulating estrogen levels in postmenopausal Chinese women in Singapore. *Carcinogenesis* , **2005**, 26, 976-80	4.6	63
13	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
12	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
11	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
10	Sun exposure, vitamin D receptor gene polymorphisms, and risk of advanced prostate cancer. *Cancer Research*, **2005**, 65, 5470-9	10.1	194
9	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
8	HSD17B1 and CYP17 polymorphisms and breast cancer risk among Chinese women in Singapore. *International Journal of Cancer*, **2003**, 104, 450-7	7.5	62
7	Dietary isothiocyanates, glutathione S-transferase polymorphisms and colorectal cancer risk in the Singapore Chinese Health Study. *Carcinogenesis*, **2002**, 23, 2055-61	4.6	168
6	Genetic determinants of mammographic density. *Breast Cancer Research*, **2002**, 4, R5	8.3	54
5	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
4	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
3	Role of Members of the Wnt Gene Family in Human Hematopoiesis. *Blood*, **1998**, 92, 3189-3202	2.2	30
2	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
1	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