David Van Den Berg

List of Publications by Year
in descending order

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240	55,078	5268	1536
papers	citations	83 h-index	218 g-index

246	246	246	66831
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. Circulation Research, 2022, 131, .	4.5	20
2	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	5.1	35
3	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
4	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	8.2	20
5	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.	6.2	18
6	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	6.7	72
7	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
8	Genome-Wide Association Analyses Identify Variants in IRF4 Associated With Acute Myeloid Leukemia and Myelodysplastic Syndrome Susceptibility. Frontiers in Genetics, 2021, 12, 554948.	2.3	8
9	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.	3.3	4
10	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	2.9	6
11	Novel genetic variants associated with mortality after unrelated donor allogeneic hematopoietic cell transplantation. EClinicalMedicine, 2021, 40, 101093.	7.1	8
12	Pre-HCT mosaicism increases relapse risk and lowers survival in acute lymphoblastic leukemia patients postâ€“unrelated HCT. Blood Advances, 2021, 5, 66-70.	5.2	6
13	Whole-Exome Sequencing in Multiplex Families to Identify Novel AYA Classical Hodgkin Lymphoma Predisposition Genes. Blood, 2021, 138, 3499-3499.	1.4	1
14	Associations between DNA methylation and BMI vary by metabolic health status: a potential link to disparate cardiovascular outcomes. Clinical Epigenetics, 2021, 13, 230.	4.1	11
15	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
16	Variability in Cytogenetic Testing for Multiple Myeloma: A Comprehensive Analysis From Across the United States. JCO Oncology Practice, 2020, 16, e1169-e1180.	2.9	8
17	A meta-analysis of genome-wide association studies of multiple myeloma among men and women of African ancestry. Blood Advances, 2020, 4, 181-190.	5.2	16
18	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.	1.4	0

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19	Population Distribution of GvL and GvH Minor Histocompatibility Antigens. Blood, 2020, 136, 23-25.	1.4	0
20	Associations of Clinical Outcomes after Allogeneic Hematopoietic Cell Transplantation with Number of Predicted Class II Restricted mHA. Blood, 2020, 136, 2-2.	1.4	0
21	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.	1.4	0
22	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
23	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.	1.3	11
24	Data-adaptive multi-locus association testing in subjects with arbitrary genealogical relationships. Statistical Applications in Genetics and Molecular Biology, 2019, 18, .	0.6	1
25	Validation of genetic associations with acute GVHD and nonrelapse mortality in DISCOVeRY-BMT. Blood Advances, 2019, 3, 2337-2341.	5.2	8
26	Multiple functional variants in the IL1RL1 region are pretransplant markers for risk of GVHD and infection deaths. Blood Advances, 2019, 3, 2512-2524.	5.2	7
27	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
28	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
29	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.	1.4	0
30	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
31	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
32	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
33	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
34	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
35	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
36	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111

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37	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
38	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
39	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
40	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
41	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
42	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
43	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
44	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
45	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
46	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
47	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
48	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
49	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
50	Ovarian cancer risk, <scp>ALDH</scp>2 polymorphism and alcohol drinking: Asian data from the Ovarian Cancer Association Consortium. Cancer Science, 2018, 109, 435-445.	3.9	10
51	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
52	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
53	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
54	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.	16.8	400

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55	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
56	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
57	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
58	Growth factor genes and change in mammographic density after stopping combined hormone therapy in the California Teachers Study. BMC Cancer, 2018, 18, 1072.	2.6	1
59	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.	6.2	134
60	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
61	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	6.4	329
62	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
63	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	6.4	324
64	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
65	Abstract 223: A meta-analysis of genome-wide association studies of multiple myeloma among African Americans. , 2018, , .		0
66	Genome Wide Association Analyses Identify Pleiotropic Variants Associated with Acute Myeloid Leukemia (AML) and Myelodysplastic Syndrome (MDS) Susceptibility. Blood, 2018, 132, 1500-1500.	1.4	0
67	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.	1.4	0
68	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
69	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
70	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
71	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
72	Novel colon cancer susceptibility variants identified from a genomeâ€wide association study in African Americans. International Journal of Cancer, 2017, 140, 2728-2733.	5.1	26

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73	Integrated genomic characterization of oesophageal carcinoma. Nature, 2017, 541, 169-175.	27.8	1,448
74	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
75	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
76	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
77	Genome-Wide Testing of Exonic Variants and Breast Cancer Risk in the California Teachers Study. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1462-1465.	2.5	0
78	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
79	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
80	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	2.5	278
81	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	6.3	57
82	Pharmacogenetic Associations with ADME Variants and Virologic Response to an Initial HAART Regimen in HIV-Infected Women. International Journal of HIV/AIDS and Research, 2017, 4, 149-155.	0.0	0
83	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
84	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.	2.5	18
85	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.	6.2	59
86	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.	2.9	33
87	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
88	Genome-wide association study of colorectal cancer in Hispanics. Carcinogenesis, 2016, 37, 547-556.	2.8	34
89	Assessment of Multifactor Geneâ€"Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 780-790.	2.5	10
90	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	2.9	19

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91	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.	2.9	38
92	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.	3.2	94
93	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	2.5	9
94	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040
95	HLA Haplotypes Are Associated with Multiple Myeloma Risk in the African American Multiple Myeloma Study (AAMMS). Blood, 2016, 128, 3250-3250.	1.4	1
96	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	1.8	7
97	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.	6.3	152
98	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.	2.5	2
99	Second-Generation Linkage Maps for the Pacific OysterCrassostrea gigasReveal Errors in Assembly of Genome Scaffolds. G3: Genes, Genomes, Genetics, 2015, 5, 2007-2019.	1.8	80
100	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
101	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.	6.2	76
102	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
103	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138
104	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
105	15q12 Variants, Sputum Gene Promoter Hypermethylation, and Lung Cancer Risk: A GWAS in Smokers. Journal of the National Cancer Institute, 2015, 107, .	6.3	16
106	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.	2.9	38
107	Abstract 4629: Multiple myeloma susceptibility loci examined in African and European ancestry populations. , 2015, , .		0
108	DNA Methylation Differences in Twins Discordant for Adolescent/Young Adult Hodgkin Lymphoma. Blood, 2015, 126, 179-179.	1.4	1

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109	Exome-Wide Association Study of Endometrial Cancer in a Multiethnic Population. PLoS ONE, 2014, 9, e97045.	2.5	12
110	Variation in NF-Î¹B Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1421-1427.	2.5	13
111	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.	2.9	90
112	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
113	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	2.9	70
114	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. Nature Communications, 2014, 5, 4613.	12.8	72
115	Genetic risk factors for orofacial clefts in Central Africans and Southeast Asians. American Journal of Medical Genetics, Part A, 2014, 164, 2572-2580.	1.2	28
116	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.	5.0	5
117	Breast Cancer Susceptibility Variants and Mammographic Density Phenotypes in Norwegian Postmenopausal Women. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1752-1763.	2.5	9
118	Antiretroviral therapy modifies the genetic effect of known type 2 diabetes-associated risk variants in HIV-infected women. Aids, 2014, 28, 1815-1823.	2.2	5
119	Risk of Ovarian Cancer and the NF-Î¹B Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.9	48
120	Large-Scale Evaluation of Common Variation in Regulatory T Cellâ€“Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	3.4	21
121	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	2.8	50
122	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	2.9	137
123	Comprehensive analyses of DNA repair pathways, smoking and bladder cancer risk in Los Angeles and Shanghai. International Journal of Cancer, 2014, 135, 335-347.	5.1	22
124	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.9	24
125	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
126	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14

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127	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;) Tj ETQq1 1 0.784314 rgBT /Overloc		
128	Abstract LB-294: Growth factor genes, interaction with hormone therapy use and breast cancer risk in the California Teachers Study. , 2014, , .		0
129	Abstract 3852: Obesity is associated with clinical characteristics in African American multiple myeloma patients. , 2014, , .		0
130	Abstract LB-282: Transethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. , 2014, , .		1
131	Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common variants in GATA3. Blood, 2014, 124, 135-135.	1.4	1
132	Large chromosome deletions, duplications, and gene conversion events accumulate with age in normal human colon crypts. Aging Cell, 2013, 12, 269-279.	6.7	31
133	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
134	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. Human Molecular Genetics, 2013, 22, 2748-2753.	2.9	59
135	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.	6.2	98
136	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
137	Reproducibility and reliability of SNP analysis using human cellular DNA at or near nanogram levels. BMC Research Notes, 2013, 6, 515.	1.4	3
138	A genome-wide association study of breast cancer in women of African ancestry. Human Genetics, 2013, 132, 39-48.	3.8	70
139	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
140	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
141	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
142	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.	2.9	86
143	Genetic polymorphisms of epidermal growth factor in relation to risk of hepatocellular carcinoma: two case-control studies. BMC Gastroenterology, 2013, 13, 32.	2.0	14
144	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	21.4	232

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145	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.	5.6	24
146	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.	2.5	20
147	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.	3.5	67
148	Hormone Metabolism Genes and Mammographic Density in Singapore Chinese Women. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 984-986.	2.5	3
149	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. Nucleic Acids Research, 2013, 41, e90-e90.	14.5	647
150	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
151	Genetic Variation in Transforming Growth Factor Beta 1 and Mammographic Density in Singapore Chinese Women. Cancer Research, 2013, 73, 1876-1882.	0.9	14
152	A Genome-Wide Scan for Breast Cancer Risk Haplotypes among African American Women. PLoS ONE, 2013, 8, e57298.	2.5	20
153	Genetic Variation in the Base Excision Repair Pathway, Environmental Risk Factors, and Colorectal Adenoma Risk. PLoS ONE, 2013, 8, e71211.	2.5	17
154	Polymorphisms In IRS1 and IL6R and Susceptibility To Multiple Myeloma. Blood, 2013, 122, 3154-3154.	1.4	0
155	Obesity In Young Adulthood Is Associated With Early Onset Multiple Myeloma In African Americans. Blood, 2013, 122, 1872-1872.	1.4	0
156	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.	1.4	2
157	A Meta-Analysis Of Hodgkin Lymphoma Reveals 19p13.3 (TCF3) As a Novel Susceptibility Loc. Blood, 2013, 122, 626-626.	1.4	0
158	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. Genome Research, 2012, 22, 271-282.	5.5	527
159	Genetic Determinants for Promoter Hypermethylation in the Lungs of Smokers: A Candidate Gene-Based Study. Cancer Research, 2012, 72, 707-715.	0.9	22
160	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.	2.5	16
161	Progestogen levels, progesterone receptor gene polymorphisms, and mammographic density changes. Menopause, 2012, 19, 302-310.	2.0	14
162	Underlying genetic structure impacts the association between CYP2B6 polymorphisms and response to efavirenz and nevirapine. Aids, 2012, 26, 2097-2106.	2.2	26

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163	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.	5.0	16
164	A genome-wide meta-analysis of nodular sclerosing Hodgkin lymphoma identifies risk loci at 6p21.32. Blood, 2012, 119, 469-475.	1.4	66
165	Genetic variation in insulin pathway genes and distal colorectal adenoma risk. International Journal of Colorectal Disease, 2012, 27, 1587-1595.	2.2	7
166	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	2.9	168
167	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear laminaâ€“associated domains. Nature Genetics, 2012, 44, 40-46.	21.4	588
168	Variations in sex hormone metabolism genes, postmenopausal hormone therapy and risk of endometrial cancer. International Journal of Cancer, 2012, 130, 1629-1638.	5.1	6
169	Abstract 2634: Polymorphisms in DNA repair genes and risk of multiple myeloma. , 2012, , .		1
170	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
171	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	21.4	736
172	Progesterone receptor gene polymorphisms and risk of endometriosis: results from an international collaborative effort. Fertility and Sterility, 2011, 95, 40-45.	1.0	20
173	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.	5.0	15
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