Zhaoming Wang

List of Publications by Year
in descending order

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Version: 2024-02-01

216 papers	28,539 citations	12597 71 h-index	7234 158 g-index
230 all docs	230 docs citations	230 times ranked	42381 citing authors

#	Article	IF	Citations
1	Association between CEP72 genotype and persistent neuropathy in survivors of childhood acute lymphoblastic leukemia. Leukemia, 2022, 36, 1160-1163.	3.3	4
2	Blood DNA methylation signatures are associated with social determinants of health among survivors of childhood cancer. Epigenetics, 2022, , 1-15.	1.3	5
3	Genome-wide association studies identify novel genetic loci for epigenetic age acceleration among survivors of childhood cancer. Genome Medicine, 2022, 14, 32.	3.6	12
4	Contribution of Genome-Wide Polygenic Score to Risk of Coronary Artery Disease in Childhood Cancer Survivors. JACC: CardioOncology, 2022, 4, 258-267.	1.7	3
5	A Novel Locus on 6p21.2 for Cancer Treatmentâ€“Induced Cardiac Dysfunction Among Childhood Cancer Survivors. Journal of the National Cancer Institute, 2022, 114, 1109-1116.	3.0	4
6	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	1.1	12
7	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	2.3	35
8	Epigenetic Age Acceleration and Chronic Health Conditions Among Adult Survivors of Childhood Cancer. Journal of the National Cancer Institute, 2021, 113, 597-605.	3.0	37
9	The Role of Gallstones in Gallbladder Cancer in India: A Mendelian Randomization Study. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 396-403.	1.1	11
10	Genetic Variants Associated with Therapy-Related Cardiomyopathy among Childhood Cancer Survivors of African Ancestry. Cancer Research, 2021, 81, 2556-2565.	0.4	24
11	The clinicopathological and molecular features of sinusoidal large B-cell lymphoma. Modern Pathology, 2021, 34, 922-933.	2.9	5
12	SequencErr: measuring and suppressing sequencer errors in next-generation sequencing data. Genome Biology, 2021, 22, 37.	3.8	15
13	Sub-multiplicative interaction between polygenic risk score and household coal use in relation to lung adenocarcinoma among never-smoking women in Asia. Environment International, 2021, 147, 105975.	4.8	12
14	Progression of Frailty in Survivors of Childhood Cancer: A St. Jude Lifetime Cohort Report. Journal of the National Cancer Institute, 2021, 113, 1415-1421.	3.0	16
15	Short sleep duration and physical and psychological health outcomes among adult survivors of childhood cancer. Pediatric Blood and Cancer, 2021, 68, e28988.	0.8	5
16	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	2.6	18
17	Persistent variations of blood DNA methylation associated with treatment exposures and risk for cardiometabolic outcomes in long-term survivors of childhood cancer in the St. Jude Lifetime Cohort. Genome Medicine, 2021, 13, 53.	3.6	16
18	The Association of Mitochondrial Copy Number With Sarcopenia in Adult Survivors of Childhood Cancer. Journal of the National Cancer Institute, 2021, 113, 1570-1580.	3.0	7

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19	A Pedigree Analysis and Clonal Correlations of the Coexistence of B-Cell Lymphoma and Histiocytic/Dendritic Cell Tumor. International Journal of Surgical Pathology, 2021, 29, 106689692110134.	0.4	0
20	Accelerated aging and mortality in long-term survivors of childhood cancer: A report from the St. Jude Lifetime Cohort (SJLIFE).. Journal of Clinical Oncology, 2021, 39, 10045-10045.	0.8	1
21	Inflammation-related genes S100s, RNASE3, and CYBB and risk of leukemic transformation in patients with myelodysplastic syndrome with myelofibrosis. Biomarker Research, 2021, 9, 53.	2.8	3
22	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
23	Abstract 685: A social epigenomic investigation of racial disparity in pulmonary impairment among aging survivors of childhood cancer. , 2021, , .		0
24	Abstract 904: Epigenome-wide association study of dyslipidemia in survivors of childhood cancer: A report from the St. Jude lifetime cohort. , 2021, , .		0
25	Polygenic Risk Score Improves Risk Stratification and Prediction of Subsequent Thyroid Cancer after Childhood Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2096-2104.	1.1	11
26	Online Platform to Assess Complex Social Relationships and Patient-Reported Outcomes Among Adolescent and Young Adult Cancer Survivors. JCO Clinical Cancer Informatics, 2021, 5, 859-871.	1.0	8
27	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. Cancer Discovery, 2021, 11, 1082-1099.	7.7	109
28	Cohort Profile: The St. Jude Lifetime Cohort Study (SJLIFE) for paediatric cancer survivors. International Journal of Epidemiology, 2021, 50, 39-49.	0.9	70
29	Racial and Ethnic Disparities in Health Outcomes Among Long-Term Survivors of Childhood Cancer: A Scoping Review. Frontiers in Public Health, 2021, 9, 741334.	1.3	12
30	Molecular Mechanism of Telomere Length Dynamics and Its Prognostic Value in Pediatric Cancers. Journal of the National Cancer Institute, 2020, 112, 756-764.	3.0	11
31	Meta-analysis of genome-wide association studies and functional assays decipher susceptibility genes for gastric cancer in Chinese populations. Gut, 2020, 69, 641-651.	6.1	36
32	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	1.3	15
33	Estimated number of adult survivors of childhood cancer in United States with cancerâ€predisposing germline variants. Pediatric Blood and Cancer, 2020, 67, e28047.	0.8	13
34	Generalizability of â€œGWAS Hitsâ€•in Clinical Populations: Lessons from Childhood Cancer Survivors. American Journal of Human Genetics, 2020, 107, 636-653.	2.6	12
35	Pathogenic Germline Mutations in DNA Repair Genes in Combination With Cancer Treatment Exposures and Risk of Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2020, 38, 2728-2740.	0.8	34
36	A Novel Locus Predicts Spermatogenic Recovery among Childhood Cancer Survivors Exposed to Alkylating Agents. Cancer Research, 2020, 80, 3755-3764.	0.4	11

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37	Shortened Leukocyte Telomere Length Associates with an Increased Prevalence of Chronic Health Conditions among Survivors of Childhood Cancer: A Report from the St. Jude Lifetime Cohort. Clinical Cancer Research, 2020, 26, 2362-2371.	3.2	34
38	Genome-wide Association Studies Reveal Novel Locus With Sex-/Therapy-Specific Fracture Risk Effects in Childhood Cancer Survivors. Journal of Bone and Mineral Research, 2020, 36, 685-695.	3.1	7
39	Cardiomyopathy risk among childhood cancer survivors of African ancestry and its molecular mechanisms.. Journal of Clinical Oncology, 2020, 38, 10514-10514.	0.8	3
40	Sex-specific gene and pathway modeling of inherited glioma risk. Neuro-Oncology, 2019, 21, 71-82.	0.6	52
41	Association of Germline BRCA2 Mutations With the Risk of Pediatric or Adolescent Nonâ€“Hodgkin Lymphoma. JAMA Oncology, 2019, 5, 1362.	3.4	19
42	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	1.4	27
43	Enrichment of heterozygous germline RECQL4 loss-of-function variants in pediatric osteosarcoma. Journal of Physical Education and Sports Management, 2019, 5, a004218.	0.5	26
44	Pediatric Cancer Variant Pathogenicity Information Exchange (PeCanPIE): a cloud-based platform for curating and classifying germline variants. Genome Research, 2019, 29, 1555-1565.	2.4	28
45	Genome-Wide Association Study in Irradiated Childhood Cancer Survivors Identifies HTR2A forÂSubsequent Basal Cell Carcinoma. Journal of Investigative Dermatology, 2019, 139, 2042-2045.e8.	0.3	18
46	Subsequent Breast Cancer in Female Childhood Cancer Survivors in the St Jude Lifetime Cohort Study (SJLIFE). Journal of Clinical Oncology, 2019, 37, 1647-1656.	0.8	31
47	Analysis of error profiles in deep next-generation sequencing data. Genome Biology, 2019, 20, 50.	3.8	196
48	Wholeâ€“Genome Sequencing of Childhood Cancer Survivors Treated with Cranial Radiation Therapy Identifies 5p15.33 Locus for Stroke: A Report from the St. Jude Lifetime Cohort Study. Clinical Cancer Research, 2019, 25, 6700-6708.	3.2	21
49	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. Journal of the National Cancer Institute, 2019, 111, 557-567.	3.0	21
50	Clinical Significance of Prognostic Nutritional Index for Patients with Diffuse Large B-cell Lymphoma. Nutrition and Cancer, 2019, 71, 569-574.	0.9	11
51	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€”A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	3.9	59
52	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539.	1.3	6
53	Genome-wide association study using whole-genome sequencing to identify a novel locus associated with cardiomyopathy risk in adult survivors of childhood cancer: Utility of a two-stage analytic approach.. Journal of Clinical Oncology, 2019, 37, 1516-1516.	0.8	0
54	Polygenic risk of subsequent thyroid cancer after childhood cancer: A report from St. Jude lifetime cohort (SJLIFE) and Childhood Cancer Survivor Study (CCSS).. Journal of Clinical Oncology, 2019, 37, 10060-10060.	0.8	0

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55	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	13.7	649
56	Subphenotype meta-analysis of testicular cancer genome-wide association study data suggests a role for RBFOX family genes in cryptorchidism susceptibility. Human Reproduction, 2018, 33, 967-977.	0.4	10
57	A High-risk Haplotype for Premature Menopause in Childhood Cancer Survivors Exposed to Gonadotoxic Therapy. Journal of the National Cancer Institute, 2018, 110, 895-904.	3.0	19
58	BOLD MRI to evaluate early development of renal injury in a rat model of diabetes. Journal of International Medical Research, 2018, 46, 1391-1403.	0.4	8
59	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
60	Morphological classification of intraductal papillary neoplasm of the bile duct. European Radiology, 2018, 28, 1568-1578.	2.3	23
61	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	0.8	105
62	Premature Physiologic Aging as a Paradigm for Understanding Increased Risk of Adverse Health Across the Lifespan of Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2206-2215.	0.8	99
63	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for WaldenstrÃ¶m macroglobulinemia. Nature Communications, 2018, 9, 4182.	5.8	15
64	Polygenic Determinants for Subsequent Breast Cancer Risk in Survivors of Childhood Cancer: The St Jude Lifetime Cohort Study (SJLIFE). Clinical Cancer Research, 2018, 24, 6230-6235.	3.2	18
65	Ageâ€specific genomeâ€wide association study in glioblastoma identifies increased proportion of â€˜lower grade gliomaâ€™â€like features associated with younger age. International Journal of Cancer, 2018, 143, 2359-2366.	2.3	21
66	Atypical presentation of blastic plasmacytoid dendritic cell neoplasm: A potential diagnostic pitfall in nasal cavity. Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology, 2018, 126, e212-e214.	0.2	2
67	Sex-specific glioma genome-wide association study identifies new risk locus at 3p21.31 in females, and finds sex-differences in risk at 8q24.21. Scientific Reports, 2018, 8, 7352.	1.6	56
68	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
69	Hepatic carcinoma with indolent T-lymphoblastic proliferation (iT-LBP). International Journal of Clinical and Experimental Pathology, 2018, 11, 1674-1678.	0.5	1
70	Expression of hypoxia-inducible factor-1a predicts benefit from rituximab plus cyclophosphamide, doxorubicin, vincristine, and prednisone in diffuse large B-cell lymphoma. International Journal of Clinical and Experimental Pathology, 2018, 11, 4472-4482.	0.5	0
71	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. Gut, 2017, 66, 581-587.	6.1	68
72	Genome-wide association study of prostate-specific antigen levels identifies novel loci independent of prostate cancer. Nature Communications, 2017, 8, 14248.	5.8	58

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73	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. Gastroenterology, 2017, 152, 2011-2021.	0.6	58
74	A functional SNP rs1892901 in FOSL1 is associated with gastric cancer in Chinese population. Scientific Reports, 2017, 7, 41737.	1.6	6
75	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
76	Common genetic variation and risk of gallbladder cancer in India: a case-control genome-wide association study. Lancet Oncology, The, 2017, 18, 535-544.	5.1	69
77	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	5.8	40
78	Genome-Wide Association Study to Identify Susceptibility Loci That Modify Radiation-Related Risk for Breast Cancer After Childhood Cancer. Journal of the National Cancer Institute, 2017, 109, .	3.0	66
79	Potential Susceptibility Loci Identified for Renal Cell Carcinoma by Targeting Obesity-Related Genes. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1436-1442.	1.1	2
80	ICT1 predicts a poor survival and correlated with cell proliferation in diffuse large B-cell lymphoma. Gene, 2017, 627, 255-262.	1.0	7
81	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	5.8	106
82	Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor. Nature Genetics, 2017, 49, 1141-1147.	9.4	105
83	Genome-wide association study of glioma subtypes identifies specific differences in genetic susceptibility to glioblastoma and non-glioblastoma tumors. Nature Genetics, 2017, 49, 789-794.	9.4	259
84	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
85	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
86	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. European Urology, 2017, 72, 747-754.	0.9	39
87	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	1.1	15
88	GWAS follow-up study of esophageal squamous cell carcinoma identifies potential genetic loci associated with family history of upper gastrointestinal cancer. Scientific Reports, 2017, 7, 4642.	1.6	11
89	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1211-1218.	9.4	693
90	Increasing mapping precision of genome-wide association studies: to genotype and impute, sequence, or both?. Genome Biology, 2017, 18, 118.	3.8	16

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91	Genetic Modifiers of Progression-Free Survival in Never-Smoking Lung Adenocarcinoma Patients Treated with First-Line Tyrosine Kinase Inhibitors. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 663-673.	2.5	24
92	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278
93	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	3.0	57
94	A high-risk genetic profile for premature menopause (PM) in childhood cancer survivors (CCS) exposed to gonadotoxic therapy: A report from the St. Jude Lifetime Cohort (SJLIFE) and Childhood Cancer Survivor Study (CCSS).. Journal of Clinical Oncology, 2017, 35, 10502-10502.	0.8	1
95	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	0.8	88
96	Association between GWAS-identified lung adenocarcinoma susceptibility loci andEGFRmutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	1.4	50
97	Genome-wide association study confirms lung cancer susceptibility loci on chromosomes 5p15 and 15q25 in an African-American population. Lung Cancer, 2016, 98, 33-42.	0.9	49
98	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
99	Functional characterization of a chr13q22.1 pancreatic cancer risk locus reveals long-range interaction and allele-specific effects onDIS3expression. Human Molecular Genetics, 2016, 25, ddw300.	1.4	24
100	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
101	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
102	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94
103	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	1.4	50
104	Diverse and Targetable Kinase Alterations Drive Histiocytic Neoplasms. Cancer Discovery, 2016, 6, 154-165.	7.7	372
105	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	1.4	52
106	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	1.4	19
107	Pathway,in silicoand tissue-specific expression quantitative analyses of oesophageal squamous cell carcinoma genome-wide association studies data. International Journal of Epidemiology, 2016, 45, 206-220.	0.9	19
108	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. Journal of the National Cancer Institute, 2016, 108, djv431.	3.0	111

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109	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
110	Genome-wide association study of gastric adenocarcinoma in Asia: a comparison of associations between cardia and non-cardia tumours. Gut, 2016, 65, 1611-1618.	6.1	99
111	Further Confirmation of Germline Glioma Risk Variant rs78378222 inTP53and Its Implication in Tumor Tissues via Integrative Analysis of TCGA Data. Human Mutation, 2015, 36, 684-688.	1.1	19
112	<scp>G</scp>enetic variants associated with longer telomere length are associated with increased lung cancer risk among neverâ€smoking women in Asia: a report from the female lung cancer consortium in Asia. International Journal of Cancer, 2015, 137, 311-319.	2.3	72
113	<scp>TERT</scp> gene harbors multiple variants associated with pancreatic cancer susceptibility. International Journal of Cancer, 2015, 137, 2175-2183.	2.3	57
114	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	3.0	152
115	Multilevel-analysis identify a cis-expression quantitative trait locus associated with risk of renal cell carcinoma. Oncotarget, 2015, 6, 4097-4109.	0.8	1
116	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
117	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.	1.1	2
118	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	5.8	58
119	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
120	Noninvasive evaluation of renal oxygenation in primary nephrotic syndrome with blood oxygen level dependent magnetic resonance imaging: Initial experience. Journal of International Medical Research, 2015, 43, 356-363.	0.4	4
121	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. Cancer Discovery, 2015, 5, 878-891.	7.7	111
122	Distinct Genomic Alterations in Prostate Tumors from African American Men. EBioMedicine, 2015, 2, 1850-1851.	2.7	1
123	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
124	Interactions between household air pollution and GWAS-identified lung cancer susceptibility markers in the Female Lung Cancer Consortium in Asia (FLCCA). Human Genetics, 2015, 134, 333-341.	1.8	34
125	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
126	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	1.4	50

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127	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	7.7	88
128	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	5.8	88
129	Common genetic variants in epigenetic machinery genes and risk of upper gastrointestinal cancers. International Journal of Epidemiology, 2015, 44, 1341-1352.	0.9	13
130	Common Variation at 1q24.1 (ALDH9A1) Is a Potential Risk Factor for Renal Cancer. PLoS ONE, 2015, 10, e0122589.	1.1	19
131	Nodular pulmonary amyloidosis and obvious ossification due to primary pulmonary MALT lymphoma with extensive plasmacytic differentiation: Report of a rare case and review of the literature. International Journal of Clinical and Experimental Pathology, 2015, 8, 7482-7.	0.5	12
132	Gastric cancer following a liver transplantation for glycogen storage disease type Ia (von Gierke) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	0.8	6
133	A fast and powerful tree-based association test for detecting complex joint effects in caseâ€“control studies. Bioinformatics, 2014, 30, 2171-2178.	1.8	4
134	DNA Methylation Levels at Chromosome 8q24 in Peripheral Blood Are Associated with 8q24 Cancer Susceptibility Loci. Cancer Prevention Research, 2014, 7, 1282-1292.	0.7	13
135	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
136	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	1.3	50
137	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	1.4	137
138	A genome-wide association study of prostate cancer in West African men. Human Genetics, 2014, 133, 509-521.	1.8	72
139	Personal History of Diabetes, Genetic Susceptibility to Diabetes, and Risk of Brain Glioma: A Pooled Analysis of Observational Studies. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 47-54.	1.1	31
140	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	9.4	283
141	A Genome-Wide Association Study of Renal Cell Carcinoma among African Americans. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 209-214.	1.1	20
142	Genetic variants in fas signaling pathway genes and risk of gastric cancer. International Journal of Cancer, 2014, 134, 822-831.	2.3	26
143	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.4	24
144	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705.	1.3	67

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145	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	9.4	148
146	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
147	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. Nature Communications, 2014, 5, 3365.	5.8	123
148	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	2.6	96
149	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294
150	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
151	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
152	Pathway-based analysis of GWAs data identifies association of sex determination genes with susceptibility to testicular germ cell tumors. Human Molecular Genetics, 2014, 23, 6061-6068.	1.4	28
153	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	9.4	360
154	HHV-6-associated acute lymphadenitis in immunocompetent patients: a case report and review of literature. International Journal of Clinical and Experimental Pathology, 2014, 7, 3413-7.	0.5	7
155	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
156	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. Human Molecular Genetics, 2013, 22, 2748-2753.	1.4	59
157	Association between MDR1 C3435T polymorphism and risk of breast cancer. Gene, 2013, 532, 94-99.	1.0	20
158	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. Cancer Research, 2013, 73, 2211-2220.	0.4	107
159	Known glioma risk loci are associated with glioma with a family history of brain tumoursâ€"A caseâ€"control gene association study. International Journal of Cancer, 2013, 132, 2464-2468.	2.3	22
160	An integrated transcriptome and epigenome analysis identifies a novel candidate gene for pancreatic cancer. BMC Medical Genomics, 2013, 6, 33.	0.7	31
161	Genome-wide association study identifies two susceptibility loci for osteosarcoma. Nature Genetics, 2013, 45, 799-803.	9.4	181
162	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578

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163	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	9.4	179
164	Meta-analysis identifies four new loci associated with testicular germ cell tumor. Nature Genetics, 2013, 45, 680-685.	9.4	154
165	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
166	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. Human Molecular Genetics, 2013, 22, 3597-3607.	1.4	116
167	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
168	Common variation at 2q22.3 (ZEB2) influences the risk of renal cancer. Human Molecular Genetics, 2013, 22, 825-831.	1.4	54
169	Genetic Variants in Epidermal Growth Factor Receptor Pathway Genes and Risk of Esophageal Squamous Cell Carcinoma and Gastric Cancer in a Chinese Population. PLoS ONE, 2013, 8, e68999.	1.1	17
170	Characterization of SNPs Associated with Prostate Cancer in Men of Ashkenazic Descent from the Set of GWAS Identified SNPs: Impact of Cancer Family History and Cumulative SNP Risk Prediction. PLoS ONE, 2013, 8, e60083.	1.1	21
171	Medical simulation-based education improves medicos' clinical skills. Journal of Biomedical Research, 2013, 27, 81-4.	0.7	12
172	Uterine leiomyoma with indolent B-lymphoblastic proliferation. International Journal of Clinical and Experimental Pathology, 2013, 6, 1422-6.	0.5	1
173	A Flexible Bayesian Model for Studying Geneâ€“Environment Interaction. PLoS Genetics, 2012, 8, e1002482.	1.5	20
174	Genotypic variants at 2q33 and risk of esophageal squamous cell carcinoma in China: a meta-analysis of genome-wide association studies. Human Molecular Genetics, 2012, 21, 2132-2141.	1.4	58
175	Assessing Disease Risk in Genome-wide Association Studies Using Family History. Epidemiology, 2012, 23, 616-622.	1.2	8
176	Association between adult height, genetic susceptibility and risk of glioma. International Journal of Epidemiology, 2012, 41, 1075-1085.	0.9	26
177	Inherited Variation at Chromosome 12p13.33, Including RAD52, Influences the Risk of Squamous Cell Lung Carcinoma. Cancer Discovery, 2012, 2, 131-139.	7.7	54
178	Improved imputation of common and uncommon SNPs with a new reference set. Nature Genetics, 2012, 44, 6-7.	9.4	45
179	Insight in glioma susceptibility through an analysis of 6p22.3, 12p13.33-12.1, 17q22-23.2 and 18q23 SNP genotypes in familial and non-familial glioma. Human Genetics, 2012, 131, 1507-1517.	1.8	20
180	Genome-wide association study of glioma and meta-analysis. Human Genetics, 2012, 131, 1877-1888.	1.8	222

#	Article	IF	Citations
181	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. Nature Genetics, 2012, 44, 1330-1335.	9.4	286
182	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. Nature Genetics, 2012, 44, 1090-1097.	9.4	238
183	Clinical outcomes of Ex Vivo liver resection and liver autotransplantation for hepatic alveolar echinococcosis. Journal of Huazhong University of Science and Technology [Medical Sciences], 2012, 32, 598-600.	1.0	23
184	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	1.4	168
185	A genome-wide association study identifies a novel susceptibility locus for renal cell carcinoma on 12p11.23. Human Molecular Genetics, 2012, 21, 456-462.	1.4	81
186	Detectable clonal mosaicism and its relationship to aging and cancer. Nature Genetics, 2012, 44, 651-658.	9.4	519
187	A Twoâ€Platform Design for Next Generation Genomeâ€Wide Association Studies. Genetic Epidemiology, 2012, 36, 401-409.	0.6	14
188	Y chromosome haplogroups and prostate cancer in populations of European and Ashkenazi Jewish ancestry. Human Genetics, 2012, 131, 1173-1185.	1.8	14
189	Fine mapping of 14q24.1 breast cancer susceptibility locus. Human Genetics, 2012, 131, 479-490.	1.8	5
190	Large-Scale Pathway-Based Analysis of Bladder Cancer Genome-Wide Association Data from Five Studies of European Background. PLoS ONE, 2012, 7, e29396.	1.1	36
191	Intraspinal rhabdoid meningioma metastasis to the liver. Journal of Clinical Neuroscience, 2011, 18, 714-716.	0.8	23
192	Improved Imputation of Common and Uncommon Single Nucleotide Polymorphisms (SNPs) with a New Reference Set. Nature Precedings, 2011, , .	0.1	0
193	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. Nature Genetics, 2011, 43, 60-65.	9.4	220
194	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. Nature Genetics, 2011, 43, 570-573.	9.4	198
195	Fine mapping the KLK3 locus on chromosome 19q13.33 associated with prostate cancer susceptibility and PSA levels. Human Genetics, 2011, 129, 675-685.	1.8	50
196	A comprehensive candidate gene approach identifies genetic variation associated with osteosarcoma. BMC Cancer, 2011, 11, 209.	1.1	69
197	Genome-wide association study identifies new prostate cancer susceptibility loci. Human Molecular Genetics, 2011, 20, 3867-3875.	1.4	160
198	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. Human Molecular Genetics, 2011, 20, 3322-3329.	1.4	28

#	Article	IF	Citations
199	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	13.7	319
200	Distribution of allele frequencies and effect sizes and their interrelationships for common genetic susceptibility variants. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18026-18031.	3.3	249
201	A genome-wide association study of bladder cancer identifies a new susceptibility locus within SLC14A1, a urea transporter gene on chromosome 18q12.3. Human Molecular Genetics, 2011, 20, 4282-4289.	1.4	100
202	Telomere length and variation in telomere biology genes in individuals with osteosarcoma. International Journal of Molecular Epidemiology and Genetics, 2011, 2, 19-29.	0.4	27
203	Using Principal Components of Genetic Variation for Robust and Powerful Detection of Gene-Gene Interactions in Case-Control and Case-Only Studies. American Journal of Human Genetics, 2010, 86, 331-342.	2.6	41
204	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. Nature Genetics, 2010, 42, 224-228.	9.4	539
205	A shared susceptibility locus in PLCE1 at 10q23 for gastric adenocarcinoma and esophageal squamous cell carcinoma. Nature Genetics, 2010, 42, 764-767.	9.4	453
206	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	9.4	493
207	Genetic Admixture and Population Substructure in Guanacaste Costa Rica. PLoS ONE, 2010, 5, e13336.	1.1	16
208	Common Variation in Genes Related to Innate Immunity and Risk of Adult Glioma. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1651-1658.	1.1	60
209	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). Nature Genetics, 2009, 41, 579-584.	9.4	487
210	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2009, 41, 1055-1057.	9.4	218
211	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	2.6	489
212	Multiple loci identified in a genome-wide association study of prostate cancer. Nature Genetics, 2008, 40, 310-315.	9.4	871
213	Population Substructure and Control Selection in Genome-Wide Association Studies. PLoS ONE, 2008, 3, e2551.	1.1	111
214	Bone Marrow Metastasis of Desmoplastic Small round Cell Tumor. Tumori, 2007, 93, 511-513.	0.6	3
215	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nature Genetics, 2007, 39, 645-649.	9.4	1,059
216	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nature Genetics, 2007, 39, 870-874.	9.4	1,370