

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	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
3	A genome-wide association study identifies alleles in <i>FGFR2</i> associated with risk of sporadic postmenopausal breast cancer. <i>Nature Genetics</i> , 2007, 39, 870-874.	9.4	1,370
4	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
5	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. <i>Nature Genetics</i> , 2007, 39, 645-649.	9.4	1,059
6	Multiple loci identified in a genome-wide association study of prostate cancer. <i>Nature Genetics</i> , 2008, 40, 310-315.	9.4	871
7	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2017, 49, 1211-1218.	9.4	693
8	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. <i>Nature</i> , 2018, 555, 371-376.	13.7	649
9	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
10	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. <i>Nature Genetics</i> , 2010, 42, 224-228.	9.4	539
11	Detectable clonal mosaicism and its relationship to aging and cancer. <i>Nature Genetics</i> , 2012, 44, 651-658.	9.4	519
12	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 978-984.	9.4	493
13	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. <i>American Journal of Human Genetics</i> , 2009, 85, 679-691.	2.6	489
14	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (<i>RAD51L1</i>). <i>Nature Genetics</i> , 2009, 41, 579-584.	9.4	487
15	A shared susceptibility locus in <i>PLCE1</i> at 10q23 for gastric adenocarcinoma and esophageal squamous cell carcinoma. <i>Nature Genetics</i> , 2010, 42, 764-767.	9.4	453
16	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	9.4	408
17	Diverse and Targetable Kinase Alterations Drive Histiocytic Neoplasms. <i>Cancer Discovery</i> , 2016, 6, 154-165.	7.7	372
18	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371

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19	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. <i>Nature Genetics</i> , 2014, 46, 736-741.	9.4	360
20	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
21	The landscape of recombination in African Americans. <i>Nature</i> , 2011, 476, 170-175.	13.7	319
22	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. <i>Nature Genetics</i> , 2014, 46, 994-1000.	9.4	294
23	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
24	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. <i>Nature Genetics</i> , 2012, 44, 1330-1335.	9.4	286
25	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. <i>Nature Genetics</i> , 2014, 46, 482-486.	9.4	283
26	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 126-135.	1.1	278
27	Genome-wide association study of glioma subtypes identifies specific differences in genetic susceptibility to glioblastoma and non-glioblastoma tumors. <i>Nature Genetics</i> , 2017, 49, 789-794.	9.4	259
28	Distribution of allele frequencies and effect sizes and their interrelationships for common genetic susceptibility variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18026-18031.	3.3	249
29	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. <i>Nature Genetics</i> , 2012, 44, 1090-1097.	9.4	238
30	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , 2013, 45, 690-696.	9.4	232
31	Genome-wide association study of glioma and meta-analysis. <i>Human Genetics</i> , 2012, 131, 1877-1888.	1.8	222
32	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. <i>Nature Genetics</i> , 2011, 43, 60-65.	9.4	220
33	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. <i>Nature Genetics</i> , 2009, 41, 1055-1057.	9.4	218
34	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. <i>Nature Genetics</i> , 2011, 43, 570-573.	9.4	198
35	Analysis of error profiles in deep next-generation sequencing data. <i>Genome Biology</i> , 2019, 20, 50.	3.8	196
36	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , 2018, 9, 556.	5.8	188

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37	Genome-wide association study identifies two susceptibility loci for osteosarcoma. <i>Nature Genetics</i> , 2013, 45, 799-803.	9.4	181
38	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2013, 45, 868-876.	9.4	179
39	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	5.8	178
40	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
41	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	1.4	168
42	Genome-wide association study identifies new prostate cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2011, 20, 3867-3875.	1.4	160
43	Meta-analysis identifies four new loci associated with testicular germ cell tumor. <i>Nature Genetics</i> , 2013, 45, 680-685.	9.4	154
44	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv279.	3.0	152
45	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. <i>Nature Genetics</i> , 2014, 46, 1001-1006.	9.4	148
46	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 1233-1238.	9.4	147
47	Genome-wide association study identifies multiple loci associated with bladder cancer risk. <i>Human Molecular Genetics</i> , 2014, 23, 1387-1398.	1.4	137
48	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014, 5, 3365.	5.8	123
49	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. <i>Human Molecular Genetics</i> , 2013, 22, 3597-3607.	1.4	116
50	Population Substructure and Control Selection in Genome-Wide Association Studies. <i>PLoS ONE</i> , 2008, 3, e2551.	1.1	111
51	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. <i>Cancer Discovery</i> , 2015, 5, 878-891.	7.7	111
52	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv431.	3.0	111
53	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. <i>Cancer Discovery</i> , 2021, 11, 1082-1099.	7.7	109
54	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. <i>Cancer Research</i> , 2013, 73, 2211-2220.	0.4	107

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55	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. <i>Nature Communications</i> , 2017, 8, 15724.	5.8	106
56	Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor. <i>Nature Genetics</i> , 2017, 49, 1141-1147.	9.4	105
57	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. <i>Journal of Clinical Oncology</i> , 2018, 36, 2078-2087.	0.8	105
58	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	2.6	101
59	A genome-wide association study of bladder cancer identifies a new susceptibility locus within SLC14A1, a urea transporter gene on chromosome 18q12.3. <i>Human Molecular Genetics</i> , 2011, 20, 4282-4289.	1.4	100
60	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.4	100
61	Genome-wide association study of gastric adenocarcinoma in Asia: a comparison of associations between cardia and non-cardia tumours. <i>Gut</i> , 2016, 65, 1611-1618.	6.1	99
62	Premature Physiologic Aging as a Paradigm for Understanding Increased Risk of Adverse Health Across the Lifespan of Survivors of Childhood Cancer. <i>Journal of Clinical Oncology</i> , 2018, 36, 2206-2215.	0.8	99
63	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. <i>American Journal of Human Genetics</i> , 2014, 95, 462-471.	2.6	96
64	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , 2016, 7, 10933.	5.8	94
65	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
66	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	1.4	90
67	A Genome-Wide Scan Identifies Variants in <i>NFIB</i> Associated with Metastasis in Patients with Osteosarcoma. <i>Cancer Discovery</i> , 2015, 5, 920-931.	7.7	88
68	Two susceptibility loci identified for prostate cancer aggressiveness. <i>Nature Communications</i> , 2015, 6, 6889.	5.8	88
69	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. <i>Oncotarget</i> , 2016, 7, 66328-66343.	0.8	88
70	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	5.8	86
71	A genome-wide association study identifies a novel susceptibility locus for renal cell carcinoma on 12p11.23. <i>Human Molecular Genetics</i> , 2012, 21, 456-462.	1.4	81
72	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. <i>Nature Communications</i> , 2017, 8, 14175.	5.8	75

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73	A genome-wide association study of prostate cancer in West African men. <i>Human Genetics</i> , 2014, 133, 509-521.	1.8	72
74	Genetic variants associated with longer telomere length are associated with increased lung cancer risk among never-smoking women in Asia: a report from the female lung cancer consortium in Asia. <i>International Journal of Cancer</i> , 2015, 137, 311-319.	2.3	72
75	Cohort Profile: The St. Jude Lifetime Cohort Study (SJLIFE) for paediatric cancer survivors. <i>International Journal of Epidemiology</i> , 2021, 50, 39-49.	0.9	70
76	A comprehensive candidate gene approach identifies genetic variation associated with osteosarcoma. <i>BMC Cancer</i> , 2011, 11, 209.	1.1	69
77	Common genetic variation and risk of gallbladder cancer in India: a case-control genome-wide association study. <i>Lancet Oncology</i> , 2017, 18, 535-544.	5.1	69
78	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. <i>Gut</i> , 2017, 66, 581-587.	6.1	68
79	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. <i>Carcinogenesis</i> , 2014, 35, 2698-2705.	1.3	67
80	Genome-Wide Association Study to Identify Susceptibility Loci That Modify Radiation-Related Risk for Breast Cancer After Childhood Cancer. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	66
81	Common Variation in Genes Related to Innate Immunity and Risk of Adult Glioma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 1651-1658.	1.1	60
82	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248.	2.6	60
83	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. <i>Human Molecular Genetics</i> , 2013, 22, 2748-2753.	1.4	59
84	The influence of obesity-related factors in the etiology of renal cell carcinoma—A mendelian randomization study. <i>PLoS Medicine</i> , 2019, 16, e1002724.	3.9	59
85	Genotypic variants at 2q33 and risk of esophageal squamous cell carcinoma in China: a meta-analysis of genome-wide association studies. <i>Human Molecular Genetics</i> , 2012, 21, 2132-2141.	1.4	58
86	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. <i>Nature Communications</i> , 2015, 6, 5751.	5.8	58
87	Genome-wide association study of prostate-specific antigen levels identifies novel loci independent of prostate cancer. <i>Nature Communications</i> , 2017, 8, 14248.	5.8	58
88	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. <i>Gastroenterology</i> , 2017, 152, 2011-2021.	0.6	58
89	TERT gene harbors multiple variants associated with pancreatic cancer susceptibility. <i>International Journal of Cancer</i> , 2015, 137, 2175-2183.	2.3	57
90	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	57

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91	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. <i>Scientific Reports</i> , 2018, 8, 7352.	1.6	56
92	Inherited Variation at Chromosome 12p13.33, Including <i>RAD52</i> , Influences the Risk of Squamous Cell Lung Carcinoma. <i>Cancer Discovery</i> , 2012, 2, 131-139.	7.7	54
93	Common variation at 2q22.3 (<i>ZEB2</i>) influences the risk of renal cancer. <i>Human Molecular Genetics</i> , 2013, 22, 825-831.	1.4	54
94	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. <i>Human Molecular Genetics</i> , 2016, 25, 1663-1676.	1.4	52
95	Sex-specific gene and pathway modeling of inherited glioma risk. <i>Neuro-Oncology</i> , 2019, 21, 71-82.	0.6	52
96	Fine mapping the <i>KLK3</i> locus on chromosome 19q13.33 associated with prostate cancer susceptibility and PSA levels. <i>Human Genetics</i> , 2011, 129, 675-685.	1.8	50
97	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , 2014, 35, 1737-1744.	1.3	50
98	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. <i>Human Molecular Genetics</i> , 2015, 24, 5603-5618.	1.4	50
99	Association between GWAS-identified lung adenocarcinoma susceptibility loci and <i>EGFR</i> mutations in never-smoking Asian women, and comparison with findings from Western populations. <i>Human Molecular Genetics</i> , 2016, 26, ddw414.	1.4	50
100	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. <i>Human Molecular Genetics</i> , 2016, 25, 620-629.	1.4	50
101	Genome-wide association study confirms lung cancer susceptibility loci on chromosomes 5p15 and 15q25 in an African-American population. <i>Lung Cancer</i> , 2016, 98, 33-42.	0.9	49
102	Improved imputation of common and uncommon SNPs with a new reference set. <i>Nature Genetics</i> , 2012, 44, 6-7.	9.4	45
103	Using Principal Components of Genetic Variation for Robust and Powerful Detection of Gene-Gene Interactions in Case-Control and Case-Only Studies. <i>American Journal of Human Genetics</i> , 2010, 86, 331-342.	2.6	41
104	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of <i>TERT</i> by <i>ZNF148</i> . <i>Nature Communications</i> , 2017, 8, 15034.	5.8	40
105	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. <i>European Urology</i> , 2017, 72, 747-754.	0.9	39
106	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. <i>Human Molecular Genetics</i> , 2016, 25, 1203-1214.	1.4	38
107	Epigenetic Age Acceleration and Chronic Health Conditions Among Adult Survivors of Childhood Cancer. <i>Journal of the National Cancer Institute</i> , 2021, 113, 597-605.	3.0	37
108	Meta-analysis of genome-wide association studies and functional assays decipher susceptibility genes for gastric cancer in Chinese populations. <i>Gut</i> , 2020, 69, 641-651.	6.1	36

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109	Large-Scale Pathway-Based Analysis of Bladder Cancer Genome-Wide Association Data from Five Studies of European Background. <i>PLoS ONE</i> , 2012, 7, e29396.	1.1	36
110	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , 2021, 148, 307-319.	2.3	35
111	Interactions between household air pollution and GWAS-identified lung cancer susceptibility markers in the Female Lung Cancer Consortium in Asia (FLCCA). <i>Human Genetics</i> , 2015, 134, 333-341.	1.8	34
112	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. <i>Journal of Clinical Oncology</i> , 2020, 38, 2728-2740.	0.8	34
113	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. <i>Clinical Cancer Research</i> , 2020, 26, 2362-2371.	3.2	34
114	An integrated transcriptome and epigenome analysis identifies a novel candidate gene for pancreatic cancer. <i>BMC Medical Genomics</i> , 2013, 6, 33.	0.7	31
115	Personal History of Diabetes, Genetic Susceptibility to Diabetes, and Risk of Brain Glioma: A Pooled Analysis of Observational Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 47-54.	1.1	31
116	Subsequent Breast Cancer in Female Childhood Cancer Survivors in the St Jude Lifetime Cohort Study (SJLIFE). <i>Journal of Clinical Oncology</i> , 2019, 37, 1647-1656.	0.8	31
117	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. <i>Human Molecular Genetics</i> , 2011, 20, 3322-3329.	1.4	28
118	Pathway-based analysis of GWAs data identifies association of sex determination genes with susceptibility to testicular germ cell tumors. <i>Human Molecular Genetics</i> , 2014, 23, 6061-6068.	1.4	28
119	Pediatric Cancer Variant Pathogenicity Information Exchange (PeCanPIE): a cloud-based platform for curating and classifying germline variants. <i>Genome Research</i> , 2019, 29, 1555-1565.	2.4	28
120	Sex specific associations in genome wide association analysis of renal cell carcinoma. <i>European Journal of Human Genetics</i> , 2019, 27, 1589-1598.	1.4	27
121	Telomere length and variation in telomere biology genes in individuals with osteosarcoma. <i>International Journal of Molecular Epidemiology and Genetics</i> , 2011, 2, 19-29.	0.4	27
122	Association between adult height, genetic susceptibility and risk of glioma. <i>International Journal of Epidemiology</i> , 2012, 41, 1075-1085.	0.9	26
123	Genetic variants in fas signaling pathway genes and risk of gastric cancer. <i>International Journal of Cancer</i> , 2014, 134, 822-831.	2.3	26
124	Enrichment of heterozygous germline <i>RECQL4</i> loss-of-function variants in pediatric osteosarcoma. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004218.	0.5	26
125	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. <i>Cancer Research</i> , 2014, 74, 5808-5818.	0.4	24
126	Functional characterization of a chr13q22.1 pancreatic cancer risk locus reveals long-range interaction and allele-specific effects on <i>DIS3</i> expression. <i>Human Molecular Genetics</i> , 2016, 25, ddw300.	1.4	24

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127	Genetic Modifiers of Progression-Free Survival in Never-Smoking Lung Adenocarcinoma Patients Treated with First-Line Tyrosine Kinase Inhibitors. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 663-673.	2.5	24
128	Genetic Variants Associated with Therapy-Related Cardiomyopathy among Childhood Cancer Survivors of African Ancestry. <i>Cancer Research</i> , 2021, 81, 2556-2565.	0.4	24
129	Intraspinal rhabdoid meningioma metastasis to the liver. <i>Journal of Clinical Neuroscience</i> , 2011, 18, 714-716.	0.8	23
130	Clinical outcomes of Ex Vivo liver resection and liver autotransplantation for hepatic alveolar echinococcosis. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2012, 32, 598-600.	1.0	23
131	Morphological classification of intraductal papillary neoplasm of the bile duct. <i>European Radiology</i> , 2018, 28, 1568-1578.	2.3	23
132	Known glioma risk loci are associated with glioma with a family history of brain tumoursâ€”A caseâ€”control gene association study. <i>International Journal of Cancer</i> , 2013, 132, 2464-2468.	2.3	22
133	Ageâ€”specific genomeâ€”wide association study in glioblastoma identifies increased proportion of â€”lower grade gliomaâ€”like features associated with younger age. <i>International Journal of Cancer</i> , 2018, 143, 2359-2366.	2.3	21
134	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. <i>Clinical Cancer Research</i> , 2019, 25, 6700-6708.	3.2	21
135	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 557-567.	3.0	21
136	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. <i>PLoS ONE</i> , 2013, 8, e60083.	1.1	21
137	A Flexible Bayesian Model for Studying Geneâ€”Environment Interaction. <i>PLoS Genetics</i> , 2012, 8, e1002482.	1.5	20
138	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. <i>Human Genetics</i> , 2012, 131, 1507-1517.	1.8	20
139	Association between MDR1 C3435T polymorphism and risk of breast cancer. <i>Gene</i> , 2013, 532, 94-99.	1.0	20
140	A Genome-Wide Association Study of Renal Cell Carcinoma among African Americans. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 209-214.	1.1	20
141	Further Confirmation of Germline Glioma Risk Variant rs78378222 in <i>TP53</i> and Its Implication in Tumor Tissues via Integrative Analysis of TCGA Data. <i>Human Mutation</i> , 2015, 36, 684-688.	1.1	19
142	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. <i>Human Molecular Genetics</i> , 2016, 25, ddw092.	1.4	19
143	Pathway, <i>in silico</i> and tissue-specific expression quantitative analyses of oesophageal squamous cell carcinoma genome-wide association studies data. <i>International Journal of Epidemiology</i> , 2016, 45, 206-220.	0.9	19
144	A High-risk Haplotype for Premature Menopause in Childhood Cancer Survivors Exposed to Gonadotoxic Therapy. <i>Journal of the National Cancer Institute</i> , 2018, 110, 895-904.	3.0	19

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145	Association of Germline <i>BRCA2</i> Mutations With the Risk of Pediatric or Adolescent Non-Hodgkin Lymphoma. <i>JAMA Oncology</i> , 2019, 5, 1362.	3.4	19
146	Common Variation at 1q24.1 (ALDH9A1) Is a Potential Risk Factor for Renal Cancer. <i>PLoS ONE</i> , 2015, 10, e0122589.	1.1	19
147	Polygenic Determinants for Subsequent Breast Cancer Risk in Survivors of Childhood Cancer: The St Jude Lifetime Cohort Study (SJLIFE). <i>Clinical Cancer Research</i> , 2018, 24, 6230-6235.	3.2	18
148	Genome-Wide Association Study in Irradiated Childhood Cancer Survivors Identifies <i>HTR2A</i> for Subsequent Basal Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2019, 139, 2042-2045.e8.	0.3	18
149	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021, 108, 564-582.	2.6	18
150	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the <i>WNT4</i> 1p36.12 locus. <i>Human Genetics</i> , 2021, 140, 1353-1365.	1.8	18
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