Meredith Yeager

List of Publications by Year
in descending order

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146 papers	10,623 citations	38742 50 h-index	36028 97 g-index
156 all docs	156 docs citations	156 times ranked	16199 citing authors

#	Article	IF	Citations
1	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nature Genetics, 2007, 39, 645-649.	21.4	1,059
2	Multiple loci identified in a genome-wide association study of prostate cancer. Nature Genetics, 2008, 40, 310-315.	21.4	871
3	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	21.4	493
4	Genetic variation in TNF and IL10 and risk of non-Hodgkin lymphoma: a report from the InterLymph Consortium. Lancet Oncology, The, 2006, 7, 27-38.	10.7	345
5	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	21.4	283
6	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
7	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.	21.4	259
8	SNP500Cancer: a public resource for sequence validation, assay development, and frequency analysis for genetic variation in candidate genes. Nucleic Acids Research, 2006, 34, D617-D621.	14.5	242
9	HPV16 E7 Genetic Conservation Is Critical to Carcinogenesis. Cell, 2017, 170, 1164-1174.e6.	28.9	221
10	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. Nature Genetics, 2011, 43, 60-65.	21.4	220
11	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2009, 41, 1055-1057.	21.4	218
12	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2016, 44, D869-D876.	14.5	184
13	Cytokine polymorphisms in the Th1/Th2 pathway and susceptibility to non-Hodgkin lymphoma. Blood, 2006, 107, 4101-4108.	1.4	166
14	Genome-wide association study identifies new prostate cancer susceptibility loci. Human Molecular Genetics, 2011, 20, 3867-3875.	2.9	160
15	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
16	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	21.4	148
17	Oxidative damage-related genes AKR1C3 and OGG1 modulate risks for lung cancer due to exposure to PAH-rich coal combustion emissions. Carcinogenesis, 2004, 25, 2177-2181.	2.8	147
18	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	21.4	147

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19	HPV16 Sublineage Associations With Histology-Specific Cancer Risk Using HPV Whole-Genome Sequences in 3200 Women. Journal of the National Cancer Institute, 2016, 108, djw100.	6.3	147
20	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	7.1	139
21	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	21.4	134
22	Common Genetic Variants in Proinflammatory and Other Immunoregulatory Genes and Risk for Non-Hodgkin Lymphoma. Cancer Research, 2006, 66, 9771-9780.	0.9	124
23	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. Human Molecular Genetics, 2013, 22, 408-415.	2.9	118
24	Germline TP53 Variants and Susceptibility to Osteosarcoma. Journal of the National Cancer Institute, 2015, 107, .	6.3	109
25	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	12.8	106
26	Predictors of mosaic chromosome Y loss and associations with mortality in the UK Biobank. Scientific Reports, 2018, 8, 12316.	3.3	105
27	Comprehensive resequence analysis of a 136Âkb region of human chromosome 8q24 associated with prostate and colon cancers. Human Genetics, 2008, 124, 161-170.	3.8	104
28	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
29	Genome-wide association study of gastric adenocarcinoma in Asia: a comparison of associations between cardia and non-cardia tumours. Gut, 2016, 65, 1611-1618.	12.1	99
30	Fine mapping and functional analysis of a common variant in MSMB on chromosome 10q11.2 associated with prostate cancer susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7933-7938.	7.1	96
31	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	6.2	96
32	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	12.8	94
33	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
34	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	12.8	88
35	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
36	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85

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37	Colorectal cancer susceptibility loci as predictive markers of rectal cancer prognosis after surgery. Genes Chromosomes and Cancer, 2018, 57, 140-149.	2.8	81
38	Prostate Cancer (PCa) Risk Variants and Risk of Fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. European Urology, 2014, 65, 1069-1075.	1.9	75
39	Deep sequencing of HPV16 genomes: A new high-throughput tool for exploring the carcinogenicity and natural history of HPV16 infection. Papillomavirus Research (Amsterdam, Netherlands), 2015, 1, 3-11.	4.5	75
40	<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.	5.1	72
41	Novel and known ribosomal causes of Diamond-Blackfan anaemia identified through comprehensive genomic characterisation. Journal of Medical Genetics, 2017, 54, 417-425.	3.2	71
42	Pooled analysis of genetic variation at chromosome 8q24 and colorectal neoplasia risk. Human Molecular Genetics, 2008, 17, 2665-2672.	2.9	70
43	Genome Analysis of Latin American Cervical Cancer: Frequent Activation of the PIK3CA Pathway. Clinical Cancer Research, 2015, 21, 5360-5370.	7.0	68
44	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705.	2.8	67
45	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, .	6.3	66
46	Lack of transgenerational effects of ionizing radiation exposure from the Chernobyl accident. Science, 2021, 372, 725-729.	12.6	60
47	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€”A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	8.4	59
48	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	12.8	58
49	Human papillomavirus 16 sub-lineage dispersal and cervical cancer risk worldwide: Whole viral genome sequences from 7116 HPV16-positive women. Papillomavirus Research (Amsterdam,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	4.5	58
50	Characterizing Associations and SNP-Environment Interactions for GWAS-Identified Prostate Cancer Risk Markersâ€”Results from BPC3. PLoS ONE, 2011, 6, e17142.	2.5	57
51	Polymorphisms in Cytokine and Cellular Adhesion Molecule Genes and Susceptibility to Hematotoxicity among Workers Exposed to Benzene. Cancer Research, 2005, 65, 9574-9581.	0.9	56
52	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.	3.3	56
53	Characterization of T gene sequence variants and germline duplications in familial and sporadic chordoma. Human Genetics, 2014, 133, 1289-1297.	3.8	54
54	Genetic regulation of OAS1 nonsense-mediated decay underlies association with COVID-19 hospitalization in patients of European and African ancestries. Nature Genetics, 2022, 54, 1103-1116.	21.4	54

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55	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	2.9	52
56	Sex-specific gene and pathway modeling of inherited glioma risk. Neuro-Oncology, 2019, 21, 71-82.	1.2	52
57	Mutations in the HPV16 genome induced by APOBEC3 are associated with viral clearance. Nature Communications, 2020, 11, 886.	12.8	52
58	Fine mapping the KLK3 locus on chromosome 19q13.33 associated with prostate cancer susceptibility and PSA levels. Human Genetics, 2011, 129, 675-685.	3.8	50
59	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.	2.9	50
60	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
61	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.	2.9	50
62	Genome-wide association study identifies multiple new loci associated with Ewing sarcoma susceptibility. Nature Communications, 2018, 9, 3184.	12.8	50
63	High level of functional polymorphism indicates a unique role of natural selection at human immune system loci. Immunogenetics, 2005, 57, 821-827.	2.4	44
64	Association of <scp>HPV35</scp> with cervical carcinogenesis among women of African ancestry: Evidence of viralâ€host interaction with implications for disease intervention. International Journal of Cancer, 2020, 147, 2677-2686.	5.1	44
65	Fine mapping of a region of chromosome 11q13 reveals multiple independent loci associated with risk of prostate cancer. Human Molecular Genetics, 2011, 20, 2869-2878.	2.9	43
66	Whole exome sequencing reveals a C-terminal germline variant in CEBPA-associated acute myeloid leukemia: 45-year follow up of a large family. Haematologica, 2016, 101, 846-852.	3.5	42
67	Pesticide Use Modifies the Association Between Genetic Variants on Chromosome 8q24 and Prostate Cancer. Cancer Research, 2010, 70, 9224-9233.	0.9	41
68	Addressing health disparities in Hispanic breast cancer: accurate and inexpensive sequencing of BRCA1 and BRCA2. GigaScience, 2015, 4, 50.	6.4	41
69	Whole exome sequencing in families at high risk for Hodgkin lymphoma: identification of a predisposing mutation in the KDR gene. Haematologica, 2016, 101, 853-860.	3.5	40
70	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. European Urology, 2017, 72, 747-754.	1.9	39
71	Evaluating the Causal Link Between Malaria Infection and Endemic Burkitt Lymphoma in Northern Uganda: A Mendelian Randomization Study. EBioMedicine, 2017, 25, 58-65.	6.1	37
72	Rare germline variants in known melanoma susceptibility genes in familial melanoma. Human Molecular Genetics, 2017, 26, 4886-4895.	2.9	37

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73	Whole-Exome Sequencing of Nasopharyngeal Carcinoma Families Reveals Novel Variants Potentially Involved in Nasopharyngeal Carcinoma. Scientific Reports, 2019, 9, 9916.	3.3	32
74	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. European Urology, 2020, 78, 316-320.	1.9	32
75	Genetic Susceptibility Loci, Pesticide Exposure and Prostate Cancer Risk. PLoS ONE, 2013, 8, e58195.	2.5	31
76	Genomeâ€wide association study identifies the GLDC/IL33 locus associated with survival of osteosarcoma patients. International Journal of Cancer, 2018, 142, 1594-1601.	5.1	31
77	Mosaic chromosome Y loss is associated with alterations in blood cell counts in UK Biobank men. Scientific Reports, 2020, 10, 3655.	3.3	31
78	Genetic susceptibility to diffuse large Bâ€cell lymphoma in a pooled study of three Eastern Asian populations. European Journal of Haematology, 2015, 95, 442-448.	2.2	30
79	Dubowitz Syndrome Is a Complex Comprised of Multiple, Genetically Distinct and Phenotypically Overlapping Disorders. PLoS ONE, 2014, 9, e98686.	2.5	29
80	Evolution of multiple cell clones over a 29-year period of a CLL patient. Nature Communications, 2016, 7, 13765.	12.8	29
81	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. Human Molecular Genetics, 2011, 20, 3322-3329.	2.9	28
82	Large-scale Exploration of Geneâ€“Gene Interactions in Prostate Cancer Using a Multistage Genome-wide Association Study. Cancer Research, 2011, 71, 3287-3295.	0.9	28
83	The genetic structure and adaptation of Andean highlanders and Amazonians are influenced by the interplay between geography and culture. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32557-32565.	7.1	28
84	Genotype frequency and F ST analysis of polymorphisms in immunoregulatory genes in Chinese and Caucasian populations. Immunogenetics, 2007, 59, 839-852.	2.4	27
85	Joint Associations Between Genetic Variants and Reproductive Factors in Glioma Risk Among Women. American Journal of Epidemiology, 2011, 174, 901-908.	3.4	27
86	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	2.8	27
87	Development of the TypeSeq Assay for Detection of 51 Human Papillomavirus Genotypes by Next-Generation Sequencing. Journal of Clinical Microbiology, 2019, 57, .	3.9	27
88	Refining the Prostate Cancer Genetic Association within the JAZF1 Gene on Chromosome 7p15.2. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1349-1355.	2.5	26
89	Characterising cis-regulatory variation in the transcriptome of histologically normal and tumour-derived pancreatic tissues. Gut, 2018, 67, 521-533.	12.1	26
90	Genome-wide Association Study Identifies HLA-DPB1 as a Significant Risk Factor for Severe Aplastic Anemia. American Journal of Human Genetics, 2020, 106, 264-271.	6.2	25

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91	Polymorphisms of an Innate Immune Gene, Toll-Like Receptor 4, and Aggressive Prostate Cancer Risk: A Systematic Review and Meta-Analysis. PLoS ONE, 2014, 9, e110569.	2.5	24
92	Rare inactivating PDE11A variants associated with testicular germ cell tumors. Endocrine-Related Cancer, 2015, 22, 909-917.	3.1	24
93	Multiple rare variants in high-risk pancreatic cancer-related genes may increase risk for pancreatic cancer in a subset of patients with and without germline CDKN2A mutations. Human Genetics, 2016, 135, 1241-1249.	3.8	24
94	Genetic signatures of gene flow and malaria-driven natural selection in sub-Saharan populations of the "endemic Burkitt Lymphoma belt". PLoS Genetics, 2019, 15, e1008027.	3.5	23
95	Genetic variation at chromosome 8q24 in osteosarcoma cases and controls. Carcinogenesis, 2010, 31, 1400-1404.	2.8	22
96	Comprehensive resequence analysis of a 97Âkb region of chromosome 10q11.2 containing the MSMB gene associated with prostate cancer. Human Genetics, 2009, 126, 743-750.	3.8	21
97	Juvenile myelomonocytic leukemia due to a germline CBL Y371C mutation: 35-year follow-up of a large family. Human Genetics, 2015, 134, 775-787.	3.8	21
98	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.	5.1	21
99	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.	2.5	19
100	SomaticCombiner: improving the performance of somatic variant calling based on evaluation tests and a consensus approach. Scientific Reports, 2020, 10, 12898.	3.3	19
101	Evaluation of TypeSeq, a Novel High-Throughput, Low-Cost, Next-Generation Sequencing-Based Assay for Detection of 51 Human Papillomavirus Genotypes. Journal of Infectious Diseases, 2019, 220, 1609-1619.	4.0	17
102	Successful use of whole genome amplified DNA from multiple source types for high-density Illumina SNP microarrays. BMC Genomics, 2018, 19, 182.	2.8	16
103	APOBEC Mutagenesis Is Concordant between Tumor and Viral Genomes in HPV-Positive Head and Neck Squamous Cell Carcinoma. Viruses, 2021, 13, 1666.	3.3	16
104	Whole exome sequencing in families with CLL detects a variant in Integrin Î² 2 associated with disease susceptibility. Blood, 2016, 128, 2261-2263.	1.4	15
105	Prospective study of DNA methylation at chromosome 8q24 in peripheral blood and prostate cancer risk. British Journal of Cancer, 2017, 116, 1470-1479.	6.4	15
106	Mosaic chromosome 20q deletions are more frequent in the aging population. Blood Advances, 2017, 1, 380-385.	5.2	15
107	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.	2.9	15
108	Patterns of Human Leukocyte Antigen Class I and Class II Associations and Cancer. Cancer Research, 2021, 81, 1148-1152.	0.9	15

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109	Y chromosome haplogroups and prostate cancer in populations of European and Ashkenazi Jewish ancestry. Human Genetics, 2012, 131, 1173-1185.	3.8	14
110	Mosaic 13q14 deletions in peripheral leukocytes of non-hematologic cancer cases and healthy controls. Journal of Human Genetics, 2016, 61, 411-418.	2.3	13
111	Detectable chromosome X mosaicism in males is rarely tolerated in peripheral leukocytes. Scientific Reports, 2021, 11, 1193.	3.3	13
112	Field Study of the Possible Effect of Parental Irradiation on the Germline of Children Born to Cleanup Workers and Evacuees of the Chornobyl Nuclear Accident. American Journal of Epidemiology, 2020, 189, 1451-1460.	3.4	12
113	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.	10.0	12
114	Oropharyngeal Squamous Cell Carcinoma Morphology and Subtypes by Human Papillomavirus Type and by 16 Lineages and Sublineages. Head and Neck Pathology, 2021, 15, 1089-1098.	2.6	12
115	Whole exome sequencing in 75 high-risk families with validation and replication in independent case-control studies identifies TANGO2, OR5H14, and CHAD as new prostate cancer susceptibility genes. Oncotarget, 2017, 8, 1495-1507.	1.8	11
116	Genomic diversity and phylogenetic relationships of human papillomavirus 16 (HPV16) in Nepal. Infection, Genetics and Evolution, 2016, 46, 7-11.	2.3	9
117	Chromosomal Aberrations and Survival after Unrelated Donor Hematopoietic Stem Cell Transplant in Patients with Fanconi Anemia. Biology of Blood and Marrow Transplantation, 2018, 24, 2003-2008.	2.0	9
118	Genome diversity in Ukraine. GigaScience, 2021, 10, .	6.4	9
119	Using whole-exome sequencing and protein interaction networks to prioritize candidate genes for germline cutaneous melanoma susceptibility. Scientific Reports, 2020, 10, 17198.	3.3	8
120	The D2 and D3 Sublineages of Human Papilloma Virus 16â€“Positive Cervical Cancer in Guatemala Differ in Integration Rate and Age of Diagnosis. Cancer Research, 2020, 80, 3803-3809.	0.9	8
121	HPV+ oropharyngeal squamous cell carcinomas from patients with two tumors display synchrony of viral genomes yet discordant mutational profiles and signatures. Carcinogenesis, 2021, 42, 14-20.	2.8	8
122	Reply to â€˜Mosaic loss of chromosome Y in leukocytes mattersâ€™. Nature Genetics, 2019, 51, 7-9.	21.4	7
123	Phylogenomic Analysis of Human Papillomavirus Type 31 and Cervical Carcinogenesis: A Study of 2093 Viral Genomes. Viruses, 2021, 13, 1948.	3.3	7
124	Low-frequency variation near common germline susceptibility loci are associated with risk of Ewing sarcoma. PLoS ONE, 2020, 15, e0237792.	2.5	6
125	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
126	Application of a Novel Score Test for Genetic Association Incorporating Gene-Gene Interaction Suggests Functionality for Prostate Cancer Susceptibility Regions. Human Heredity, 2011, 72, 182-193.	0.8	5

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127	Comprehensive resequence analysis of a 123â€kb region of chromosome 11q13 associated with prostate cancer. Prostate, 2012, 72, 476-486.	2.3	5
128	Evaluation of Rare and Common Variants from Suspected Familial or Sporadic Nasopharyngeal Carcinoma (NPC) Susceptibility Genes in Sporadic NPC. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1682-1686.	2.5	5
129	Genetics and geography of leukocyte telomere length in sub-Saharan Africans. Human Molecular Genetics, 2020, 29, 3014-3020.	2.9	5
130	Endemic Burkitt Lymphoma in second-degree relatives in Northern Uganda: in-depth genome-wide analysis suggests clues about genetic susceptibility. Leukemia, 2021, 35, 1209-1213.	7.2	5
131	Rare Germline Variants in Chordoma-Related Genes and Chordoma Susceptibility. Cancers, 2021, 13, 2704.	3.7	5
132	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
133	Integrated Analysis of Coexpression and Exome Sequencing to Prioritize Susceptibility Genes for Familial Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 2464-2475.e5.	0.7	4
134	Validation of the performance of a comprehensive genotyping assay panel of single nucleotide polymorphisms in drug metabolism enzyme genes. Human Mutation, 2008, 29, 750-756.	2.5	3
135	In search of genetic factors predisposing to familial hairy cell leukemia (HCL): exome-sequencing of four multiplex HCL pedigrees. Leukemia, 2020, 34, 1934-1938.	7.2	3
136	Rare germline variants in PALB2 and BRCA2 in familial and sporadic chordoma. Human Mutation, 2022, 43, 1396-1407.	2.5	3
137	Invited Commentary: More Surprises From a Gene Desert. American Journal of Epidemiology, 2012, 175, 488-491.	3.4	2
138	Characterization of breakpoint regions of large structural autosomal mosaic events. Human Molecular Genetics, 2017, 26, 4388-4394.	2.9	2
139	Improved Imputation of Common and Uncommon Single Nucleotide Polymorphisms (SNPs) with a New Reference Set. Nature Precedings, 2011, , .	0.1	0
140	Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217.		0
141	Characterization of population-based variation and putative functional elements for the multiple-cancer susceptibility loci at 5p15.33. F1000Research, 2014, 3, 231.	1.6	0
142	Germline Mutations in Patients Receiving Unrelated Donor Hematopoietic Cell Transplant for Severe Aplastic Anemia. Blood, 2016, 128, 68-68.	1.4	0
143	Title is missing!. , 2020, 15, e0237792.		0
144	Title is missing!. , 2020, 15, e0237792.		0

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145	Title is missing!. , 2020, 15, e0237792.		0
146	Title is missing!. , 2020, 15, e0237792.		0