David V Conti

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68 5,063 143 37 h-index g-index citations papers 6,798 4.68 171 7.2 avg, IF L-index ext. citations ext. papers

#	Paper	IF	Citations
143	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018 , 50, 928-936	36.3	340
142	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014 , 46, 1103-9	36.3	331
141	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. <i>Gastroenterology</i> , 2013 , 144, 799-807.e24	13.3	250
140	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. Journal of the National Cancer Institute, 2015 , 107,	9.7	239
139	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. <i>PLoS Genetics</i> , 2013 , 9, e1003864	6	189
138	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 126-135	4	183
137	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019 , 51, 76-	-83 6.3	177
136	Meta-analysis of new genome-wide association studies of colorectal cancer risk. <i>Human Genetics</i> , 2012 , 131, 217-34	6.3	173
135	A testing framework for identifying susceptibility genes in the presence of epistasis. <i>American Journal of Human Genetics</i> , 2006 , 78, 15-27	11	154
134	Nicotinic acetylcholine receptor beta2 subunit gene implicated in a systems-based candidate gene study of smoking cessation. <i>Human Molecular Genetics</i> , 2008 , 17, 2834-48	5.6	118
133	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. <i>Human Molecular Genetics</i> , 2014 , 23, 4729-37	5.6	107
132	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. <i>Nature Communications</i> , 2015 , 6, 7138	17.4	106
131	The contribution of rare variation to prostate cancer heritability. <i>Nature Genetics</i> , 2016 , 48, 30-5	36.3	106
130	Cross-disorder genome-wide analyses suggest a complex genetic relationship between Touretteß syndrome and OCD. <i>American Journal of Psychiatry</i> , 2015 , 172, 82-93	11.9	101
129	A new GWAS and meta-analysis with 1000Genomes imputation identifies novel risk variants for colorectal cancer. <i>Scientific Reports</i> , 2015 , 5, 10442	4.9	94
128	Genetic ancestry influences asthma susceptibility and lung function among Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 135, 228-35	11.5	85
127	Bayesian modeling of complex metabolic pathways. <i>Human Heredity</i> , 2003 , 56, 83-93	1.1	78

(2017-2016)

Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	72
Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 146-157	9.7	67
Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016 , 76, 5103-14	10.1	66
Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , 2021 , 53, 65-75	36.3	62
Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. <i>PLoS Genetics</i> , 2017 , 13, e1006719	6	60
Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. <i>Nature Communications</i> , 2018 , 9, 2256	17.4	57
Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. <i>European Journal of Cancer</i> , 2017 , 84, 228-238	7.5	56
Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. <i>Gastroenterology</i> , 2019 , 156, 1455-1466	13.3	55
Perfluoroalkyl substances, metabolomic profiling, and alterations in glucose homeostasis among overweight and obese Hispanic children: A proof-of-concept analysis. <i>Environment International</i> , 2019 , 126, 445-453	12.9	54
Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. <i>Human Molecular Genetics</i> , 2015 , 24, 5589-602	5.6	54
Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. <i>International Journal of Cancer</i> , 2017 , 140, 2701-2708	7.5	50
Perfluoroalkyl substances and severity of nonalcoholic fatty liver in Children: An untargeted metabolomics approach. <i>Environment International</i> , 2020 , 134, 105220	12.9	48
Genotype-environment interactions in microsatellite stable/microsatellite instability-low colorectal cancer: results from a genome-wide association study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011 , 20, 758-66	4	47
Cumulative Burden of Colorectal Cancer-Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. <i>Gastroenterology</i> , 2020 , 158, 1274-1286.e12	13.3	47
Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45
JAM: A Scalable Bayesian Framework for Joint Analysis of Marginal SNP Effects. <i>Genetic Epidemiology</i> , 2016 , 40, 188-201	2.6	41
Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. <i>British Journal of Cancer</i> , 2016 , 115, 266-72	8.7	39
Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2017 , 109,	9.7	38
	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157 Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-14 Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75 Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719 Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256 Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238 Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. Gastroenterology, 2019, 156, 1455-1466 Perfluoroalkyl substances, metabolomic profiling, and alterations in glucose homeostasis among overweight and obese Hispanic children: A proof-of-concept analysis. Environment International, 2019, 126, 445-453 Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-602 Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708 Perfluoroalkyl substances and severity of nonalcoholic fatty liver in Children: An untargeted metabolomics approach. Environment International, 2020, 134, 105220 Genotype-environment interactions in microsatellite stable/microsatellite instability-low colorectal cancer: results from a genome-wide association study. Cancer Epidemiology Biomarkers and Prevention, 2	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157 Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-14 Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75 Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719 Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256 Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238 Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. Castroenterology, 2019, 156, 1455-1466 Perfluoroalkyl substances, metabolomic profiling, and alterations in glucose homeostasis among overweight and obese Hispanic children: A proof-of-concept analysis. Environment International, 2019, 126, 445-453 Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-602 Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708 Perfluoroalkyl substances and severity of nonalcoholic fatty liver in Children: An untargeted metabolomics approach. Environment International, 2020, 134, 105220 Genotype-environment interactions in microsatellite stable/microsatellite instability-low colorectal cancer: results from a genome-wide association study. Cancer Epidemiology Biomarkers and Prevention, 2

108	Use of pathway information in molecular epidemiology. Human Genomics, 2009, 4, 21-42	6.8	38
107	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016 , 7, 10979	17.4	37
106	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, 5603-18	5.6	35
105	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , 2014 , 35, 1737-44	4.6	33
104	SNPs, haplotypes, and model selection in a candidate gene region: the SIMPle analysis for multilocus data. <i>Genetic Epidemiology</i> , 2004 , 27, 429-41	2.6	33
103	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. <i>Human Molecular Genetics</i> , 2014 , 23, 2198-209	5.6	31
102	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. <i>Nature Communications</i> , 2018 , 9, 4616	17.4	30
101	Genome-wide search for gene-gene interactions in colorectal cancer. <i>PLoS ONE</i> , 2012 , 7, e52535	3.7	29
100	Breast Cancer Family History and Contralateral Breast Cancer Risk in Young Women: An Update From the Womenß Environmental Cancer and Radiation Epidemiology Study. <i>Journal of Clinical Oncology</i> , 2018 , 36, 1513-1520	2.2	29
99	Germline DNA Repair Gene Mutations in Young-onset Prostate Cancer Cases in the UK: Evidence for a More Extensive Genetic Panel. <i>European Urology</i> , 2019 , 76, 329-337	10.2	28
98	Variation at 2q35 (PNKD and TMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. <i>Human Molecular Genetics</i> , 2016 , 25, 2349-2359	5.6	27
97	Rare germline variants in DNA repair genes and the angiogenesis pathway predispose prostate cancer patients to develop metastatic disease. <i>British Journal of Cancer</i> , 2018 , 119, 96-104	8.7	27
96	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015 , 5, 17369	4.9	27
95	Pleiotropic effects of genetic risk variants for other cancers on colorectal cancer risk: PAGE, GECCO and CCFR consortia. <i>Gut</i> , 2014 , 63, 800-7	19.2	27
94	Prenatal Exposure to Perfluoroalkyl Substances Associated With Increased Susceptibility to Liver Injury in Children. <i>Hepatology</i> , 2020 , 72, 1758-1770	11.2	27
93	Genome-wide association study of colorectal cancer in Hispanics. <i>Carcinogenesis</i> , 2016 , 37, 547-556	4.6	26
92	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1427-1435	4	25
91	A novel colorectal cancer risk locus at 4q32.2 identified from an international genome-wide association study. <i>Carcinogenesis</i> , 2014 , 35, 2512-9	4.6	25

(2020-2010)

90	Discovery of complex pathways from observational data. Statistics in Medicine, 2010, 29, 1998-2011	2.3	25
89	UGT1A and UGT2B genetic variation alters nicotine and nitrosamine glucuronidation in european and african american smokers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 94-104	4	24
88	Sneaker "jack" males outcompete dominant "hooknose" males under sperm competition in Chinook salmon (Oncorhynchus tshawytscha). <i>Ecology and Evolution</i> , 2013 , 3, 4987-97	2.8	24
87	Elucidation of causal direction between asthma and obesity: a bi-directional Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2019 , 48, 899-907	7.8	23
86	Identification of a Novel Mucin Gene HCG22 Associated With Steroid-Induced Ocular Hypertension 2015 , 56, 2737-48		22
85	Identification of a common variant with potential pleiotropic effect on risk of inflammatory bowel disease and colorectal cancer. <i>Carcinogenesis</i> , 2015 , 36, 999-1007	4.6	21
84	Genome-wide association study and meta-analysis in Northern European populations replicate multiple colorectal cancer risk loci. <i>International Journal of Cancer</i> , 2018 , 142, 540-546	7.5	21
83	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 143, 957-969	11.5	20
82	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. <i>Human Molecular Genetics</i> , 2016 , 25, 371-81	5.6	19
81	The 19q12 bladder cancer GWAS signal: association with cyclin E function and aggressive disease. <i>Cancer Research</i> , 2014 , 74, 5808-18	10.1	19
80	Inherited variation in circadian rhythm genes and risks of prostate cancer and three other cancer sites in combined cancer consortia. <i>International Journal of Cancer</i> , 2017 , 141, 1794-1802	7.5	19
79	Organic cation transporter variation and response to smoking cessation therapies. <i>Nicotine and Tobacco Research</i> , 2014 , 16, 1638-46	4.9	18
78	Novel colon cancer susceptibility variants identified from a genome-wide association study in African Americans. <i>International Journal of Cancer</i> , 2017 , 140, 2728-2733	7.5	17
77	Enlight: web-based integration of GWAS results with biological annotations. <i>Bioinformatics</i> , 2015 , 31, 275-6	7.2	17
76	Genetic risk of prostate cancer in Ugandan men. <i>Prostate</i> , 2018 , 78, 370-376	4.2	17
75	The Four-Kallikrein Panel Is Effective in Identifying Aggressive Prostate Cancer in a Multiethnic Population. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 1381-1388	4	15
74	Genetic overlap between autoimmune diseases and non-Hodgkin lymphoma subtypes. <i>Genetic Epidemiology</i> , 2019 , 43, 844-863	2.6	15
73	A Cross-Sectional Study Examining the Seroprevalence of Severe Acute Respiratory Syndrome Coronavirus 2 Antibodies in a University Student Population. <i>Journal of Adolescent Health</i> , 2020 , 67, 763	3 <i>-</i> 788	15

72	Detecting Gene-Environment Interactions for a Quantitative Trait in a Genome-Wide Association Study. <i>Genetic Epidemiology</i> , 2016 , 40, 394-403	2.6	15
71	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. <i>Gastroenterology</i> , 2021 , 160, 1164-1178.e6	13.3	15
70	Drug Metabolizing Enzyme and Transporter Gene Variation, Nicotine Metabolism, Prospective Abstinence, and Cigarette Consumption. <i>PLoS ONE</i> , 2015 , 10, e0126113	3.7	14
69	Germline Sequencing DNA Repair Genes in 5545 Men With Aggressive and Nonaggressive Prostate Cancer. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 616-625	9.7	14
68	Prenatal metal mixtures and child blood pressure in the Rhea mother-child cohort in Greece. <i>Environmental Health</i> , 2021 , 20, 1	6	14
67	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. <i>European Urology</i> , 2020 , 78, 316-320	10.2	13
66	Pathogenic Variants in Cancer Predisposition Genes and Prostate Cancer Risk in Men of African Ancestry. <i>JCO Precision Oncology</i> , 2020 , 4, 32-43	3.6	13
65	A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 1609-16	18	13
64	A genome-wide association study of prostate cancer in Latinos. <i>International Journal of Cancer</i> , 2020 , 146, 1819-1826	7.5	13
63	Characterizing Genetic Susceptibility to Breast Cancer in Women of African Ancestry. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1016-1026	4	12
62	Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 860-870	4	12
61	Elevated numbers of PD-L1 expressing B cells are associated with the development of AIDS-NHL. <i>Scientific Reports</i> , 2019 , 9, 9371	4.9	12
60	Nicotine dependence as a moderator of genetic influences on smoking cessation treatment outcome. <i>Drug and Alcohol Dependence</i> , 2014 , 138, 109-17	4.9	12
59	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. <i>Nature Communications</i> , 2020 , 11, 3905	17.4	12
58	Environmental chemical burden in metabolic tissues and systemic biological pathways in adolescent bariatric surgery patients: A pilot untargeted metabolomic approach. <i>Environment International</i> , 2020 , 143, 105957	12.9	11
57	Association of Fish Consumption and Mercury Exposure During Pregnancy With Metabolic Health and Inflammatory Biomarkers in Children. <i>JAMA Network Open</i> , 2020 , 3, e201007	10.4	10
56	Common variants in the obesity-associated genes FTO and MC4R are not associated with risk of colorectal cancer. <i>Cancer Epidemiology</i> , 2016 , 44, 1-4	2.8	9
55	Interaction effect of alcohol consumption and Alzheimer disease polygenic risk score on the brain cortical thickness of cognitively normal subjects. <i>Alcohol</i> , 2020 , 85, 1-12	2.7	9

(2019-2019)

54	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 208-216	4	9
53	A latent unknown clustering integrating multi-omics data (LUCID) with phenotypic traits. <i>Bioinformatics</i> , 2020 , 36, 842-850	7.2	9
52	Evaluation of 71 Coronary Artery Disease Risk Variants in a Multiethnic Cohort. <i>Frontiers in Cardiovascular Medicine</i> , 2018 , 5, 19	5.4	8
51	Prenatal exposure to persistent organic pollutants and childhood obesity: A systematic review and meta-analysis of human studies. <i>Obesity Reviews</i> , 2021 , e13383	10.6	8
50	Exposure to per- and Polyfluoroalkyl Substances and Markers of Liver Injury: A Systematic Review and Meta-Analysis <i>Environmental Health Perspectives</i> , 2022 , 130, 46001	8.4	8
49	DNA methylation patterns of adult survivors of adolescent/young adult Hodgkin lymphoma compared to their unaffected monozygotic twin. <i>Leukemia and Lymphoma</i> , 2019 , 60, 1429-1437	1.9	7
48	Telomerase Variants in Patients with Cirrhosis Awaiting Liver Transplantation. <i>Hepatology</i> , 2019 , 69, 2652-2663	11.2	7
47	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	11	7
46	Genetic architectures of proximal and distal colorectal cancer are partly distinct. <i>Gut</i> , 2021 , 70, 1325-13	34 9.2	7
45	Combined Effect of a Polygenic Risk Score and Rare Genetic Variants on Prostate Cancer Risk. <i>European Urology</i> , 2021 , 80, 134-138	10.2	7
44	Joint analysis for integrating two related studies of different data types and different study designs using hierarchical modeling approaches. <i>Human Heredity</i> , 2012 , 74, 83-96	1.1	5
43	A meta-analysis of genome-wide association studies of multiple myeloma among men and women of African ancestry. <i>Blood Advances</i> , 2020 , 4, 181-190	7.8	5
42	Fine-Mapping of Common Genetic Variants Associated with Colorectal Tumor Risk Identified Potential Functional Variants. <i>PLoS ONE</i> , 2016 , 11, e0157521	3.7	5
41	Functional informed genome-wide interaction analysis of body mass index, diabetes and colorectal cancer risk. <i>Cancer Medicine</i> , 2020 , 9, 3563-3573	4.8	4
40	Multistage Genetic Association Studies 2007 , 1		4
39	HiLDA: a statistical approach to investigate differences in mutational signatures. <i>PeerJ</i> , 2019 , 7, e7557	3.1	4
38	Prostate cancer meta-analysis from more than 145,000 men to identify 65 novel prostate cancer susceptibility loci <i>Journal of Clinical Oncology</i> , 2017 , 2017, 1-1	2.2	4
37	Using Bayes model averaging to leverage both gene main effects and G IE interactions to identify genomic regions in genome-wide association studies. <i>Genetic Epidemiology</i> , 2019 , 43, 150-165	2.6	4

36	Prenatal and postnatal exposure to PFAS and cardiometabolic factors and inflammation status in children from six European cohorts. <i>Environment International</i> , 2021 , 157, 106853	12.9	4
35	Replication and Genetic Risk Score Analysis for Pancreatic Cancer in a Diverse Multiethnic Population. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 2686-2692	4	3
34	Evaluation of a Multiethnic Polygenic Risk Score Model for Prostate Cancer. <i>Journal of the National Cancer Institute</i> , 2021 ,	9.7	3
33	In Utero Exposure to Mercury Is Associated With Increased Susceptibility to Liver Injury and Inflammation in Childhood. <i>Hepatology</i> , 2021 , 74, 1546-1559	11.2	3
32	Exposure to Perfluoroalkyl Substances and Glucose Homeostasis in Youth. <i>Environmental Health Perspectives</i> , 2021 , 129, 97002	8.4	3
31	Variability in Cytogenetic Testing for Multiple Myeloma: A Comprehensive Analysis From Across the United States. <i>JCO Oncology Practice</i> , 2020 , 16, e1169-e1180	2.3	2
30	Infectious mononucleosis, immune genotypes, and non-Hodgkin lymphoma (NHL): an InterLymph Consortium study. <i>Cancer Causes and Control</i> , 2020 , 31, 451-462	2.8	2
29	Improvements to the Escalation with Overdose Control design and a comparison with the restricted Continual Reassessment Method. <i>Pharmaceutical Statistics</i> , 2019 , 18, 659-670	1	2
28	Advancing tools for human early lifecourse exposome research and translation (ATHLETE): Project overview <i>Environmental Epidemiology</i> , 2021 , 5, e166	0.2	2
27	A Unified Model for the Analysis of Gene-Environment Interaction. <i>American Journal of Epidemiology</i> , 2019 , 188, 760-767	3.8	2
26	Association of a Pathway-Specific Genetic Risk Score With Risk of Radiation-Associated Contralateral Breast Cancer. <i>JAMA Network Open</i> , 2019 , 2, e1912259	10.4	1
25	Epstein-Barr virus load is higher in long-term Hodgkin lymphoma survivors compared to their unaffected twins and unrelated controls. <i>British Journal of Haematology</i> , 2019 , 185, 377-380	4.5	1
24	Genome-wide association study of circulating folate one-carbon metabolites. <i>Genetic Epidemiology</i> , 2019 , 43, 1030-1045	2.6	1
23	HLA Haplotypes Are Associated with Multiple Myeloma Risk in the African American Multiple Myeloma Study (AAMMS). <i>Blood</i> , 2016 , 128, 3250-3250	2.2	1
22	Bayesian variable selection with a pleiotropic loss function in Mendelian randomization. <i>Statistics in Medicine</i> , 2021 , 40, 5025-5045	2.3	1
21	An integrated risk and epidemiological model to estimate risk-stratified COVID-19 outcomes for Los Angeles County: March 1, 2020-March 1, 2021. <i>PLoS ONE</i> , 2021 , 16, e0253549	3.7	1
20	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021 , 12, 4198	17.4	1
19	Sign-based Shrinkage Based on an Asymmetric LASSO Penalty <i>Journal of Data Science</i> , 2021 , 19, 429-4	4 9 .1	1

A Hierarchical Approach Using Marginal Summary Statistics for Multiple Intermediates in a 18 Mendelian Randomization or Transcriptome Analysis. *American Journal of Epidemiology*, **2021**, 190, 1148³1858 ¹ Rare Variants in the DNA Repair Pathway and the Risk of Colorectal Cancer. Cancer Epidemiology 17 Biomarkers and Prevention, 2021, 30, 895-903 Novel strategy for disease risk prediction incorporating predicted gene expression and DNA 16 9.4 1 methylation data: a multi-phased study of prostate cancer. Cancer Communications, 2021, Plasma concentrations of lipophilic persistent organic pollutants and glucose homeostasis in youth 15 7.9 populations.. Environmental Research, 2022, 212, 113296 Characteristics associated with COVID-19 vaccination status among staff and faculty of a large, diverse University in Los Angeles: The Trojan Pandemic Response Initiative.. Preventive Medicine 2.6 1 14 Reports, 2022, 27, 101802 Whole-Exome Sequencing in Multiplex Families to Identify Novel AYA Classical Hodgkin Lymphoma 13 2.2 Predisposition Genes. *Blood*, **2021**, 138, 3499-3499 Prenatal and childhood exposure to air pollution and traffic and the risk of liver injury in European 12 0.2 O children. Environmental Epidemiology, **2021**, 5, e153 Association of Genetic Risk Score With NAFLD in An Ethnically Diverse Cohort. Hepatology 6 11 Communications, 2021, 5, 1689-1703 Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium.. Human Genetics and Genomics Advances, 0.8 О 10 2022, 3, 100099 Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region.. Cancer Epidemiology Biomarkers and Prevention, 9 4 2022, OF1-OF13 Reply to Xiaoling Lin, Brian T. Helfand, and Jianfeng Xuß Letter to the Editor re: Daniel A. Leongamornlert, Edward J. Saunders, Sarah Wakerell, et al. Germline DNA Repair Gene Mutations 8 10.2 in Young-onset Prostate Cancer Cases in the UK: Evidence for a More Extensive Genetic Panel. Eur Differential Gene Expression in Circulating T-Cells in Long-Term Adolescent/Young Adult Hodgkin 2.2 Lymphoma (AYAHL) Survivors and Their Unaffected Twins. Blood, 2021, 138, 1332-1332 DNA repair gene panel mutations in young onset prostate cancer cases in the.. Journal of Clinical 2.2 Oncology, 2018, 36, 18-18 Comprehensive Investigation of White Blood Cell and Gene Expression Profiles As Risk Factors for 2.2 Multiple Myeloma in African Americans. Blood, 2019, 134, 4379-4379 Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common 2.2 variants in GATA3. Blood, 2014, 124, 135-135 Genetic Susceptibility Markers of Multiple Myeloma in African-Americans. Blood, 2014, 124, 2030-2030 2.2 DNA Methylation Differences in Twins Discordant for Adolescent/Young Adult Hodgkin Lymphoma. 2.2 Blood, 2015, 126, 179-179 IC-P-056: INTERACTION EFFECT OF APOE-4 AND SUBJECTIVE SLEEP QUALITY ON CORTICAL THICKNESS IN COGNITIVELY HEALTHY ADULTS 2019, 15, P57-P57