

Nathan D Pankratz

List of Publications by Citations

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147
papers

8,492
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164
ext. papers

11,003
ext. citations

8
avg, IF

5.15
L-index

#	Paper	IF	Citations
147	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. <i>Nature Genetics</i> , 2014 , 46, 989-93	36.3	1261
146	Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database. <i>PLoS Genetics</i> , 2012 , 8, e1002548	6	420
145	Genomewide association study for susceptibility genes contributing to familial Parkinson disease. <i>Human Genetics</i> , 2009 , 124, 593-605	6.3	363
144	A multicenter study of glucocerebrosidase mutations in dementia with Lewy bodies. <i>JAMA Neurology</i> , 2013 , 70, 727-35	17.2	285
143	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021 , 590, 290-299	50.4	268
142	Whole genome association study of brain-wide imaging phenotypes for identifying quantitative trait loci in MCI and AD: A study of the ADNI cohort. <i>NeuroImage</i> , 2010 , 53, 1051-63	7.9	266
141	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. <i>Annals of Neurology</i> , 2012 , 71, 370-84	9.4	214
140	Translation initiator EIF4G1 mutations in familial Parkinson disease. <i>American Journal of Human Genetics</i> , 2011 , 89, 398-406	11	213
139	A commonly carried allele of the obesity-related FTO gene is associated with reduced brain volume in the healthy elderly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 8404-9	11.5	202
138	Voxelwise genome-wide association study (vGWAS). <i>NeuroImage</i> , 2010 , 53, 1160-74	7.9	197
137	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. <i>American Journal of Human Genetics</i> , 2012 , 91, 823-38	11	189
136	Genome-wide association of familial late-onset Alzheimer's disease replicates BIN1 and CLU and nominates CUGBP2 in interaction with APOE. <i>PLoS Genetics</i> , 2011 , 7, e1001308	6	179
135	Functional variants in the gene confer shared effects on risk for Crohn's disease and Parkinson's disease. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	165
134	Genome screen to identify susceptibility genes for Parkinson disease in a sample without parkin mutations. <i>American Journal of Human Genetics</i> , 2002 , 71, 124-35	11	150
133	Genetic screening for a single common LRRK2 mutation in familial Parkinson's disease. <i>Lancet, The</i> , 2005 , 365, 410-2	40	145
132	Significant linkage of Parkinson disease to chromosome 2q36-37. <i>American Journal of Human Genetics</i> , 2003 , 72, 1053-7	11	138
131	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. <i>American Journal of Human Genetics</i> , 2014 , 94, 349-60	11	131

130	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. <i>NeuroImage</i> , 2010 , 51, 542-54	7.9	119
129	Genome-wide linkage analysis and evidence of gene-by-gene interactions in a sample of 362 multiplex Parkinson disease families. <i>Human Molecular Genetics</i> , 2003 , 12, 2599-608	5.6	116
128	Association of Mitochondrial DNA Copy Number With Cardiovascular Disease. <i>JAMA Cardiology</i> , 2017 , 2, 1247-1255	16.2	109
127	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , 2011 , 88, 6-18	11	103
126	Copy number variations and cognitive phenotypes in unselected populations. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 313, 2044-54	27.4	96
125	Voxelwise gene-wide association study (vGeneWAS): multivariate gene-based association testing in 731 elderly subjects. <i>NeuroImage</i> , 2011 , 56, 1875-91	7.9	96
124	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020 , 182, 1214-1231.e11	56.2	96
123	Genetic and nongenetic risk factors for childhood cancer. <i>Pediatric Clinics of North America</i> , 2015 , 62, 11-25	3.6	94
122	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. <i>PLoS Genetics</i> , 2019 , 15, e1008500	6	90
121	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020 , 182, 1198-1213.e14	56.2	88
120	A genome-wide association study for venous thromboembolism: the extended cohorts for heart and aging research in genomic epidemiology (CHARGE) consortium. <i>Genetic Epidemiology</i> , 2013 , 37, 512-521	2.6	80
119	Association between Mitochondrial DNA Copy Number in Peripheral Blood and Incident CKD in the Atherosclerosis Risk in Communities Study. <i>Journal of the American Society of Nephrology: JASN</i> , 2016 , 27, 2467-73	12.7	79
118	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , 2012 , 90, 1116-1117	11	78
117	Genomewide association study for onset age in Parkinson disease. <i>BMC Medical Genetics</i> , 2009 , 10, 98	2.1	78
116	OR06-01 The Role of Germline Defects in Cushing's Disease. <i>Journal of the Endocrine Society</i> , 2020 , 4,	0.4	78
115	Potential Role for the RASD1 Glucocorticoid-Responsive Gene in Corticotroph Tumorigenesis. <i>Journal of the Endocrine Society</i> , 2021 , 5, A549-A549	0.4	78
114	Genetics of Parkinson disease. <i>Genetics in Medicine</i> , 2007 , 9, 801-11	8.1	77
113	Factors related to fungiform papillae density: the beaver dam offspring study. <i>Chemical Senses</i> , 2013 , 38, 669-77	4.8	76

112	Presence of an APOE4 allele results in significantly earlier onset of Parkinson's disease and a higher risk with dementia. <i>Movement Disorders</i> , 2006 , 21, 45-9	7	73
111	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. <i>Cancer Discovery</i> , 2015 , 5, 920-31	24.4	71
110	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. <i>Neurobiology of Aging</i> , 2015 , 36, 1605.e7-12	5.6	70
109	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program		68
108	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019 , 134, 1645-1657	2.2	63
107	Fine Mapping and Identification of BMI Loci in African Americans. <i>American Journal of Human Genetics</i> , 2013 , 93, 661-71	11	63
106	Somatic USP8 Gene Mutations Are a Common Cause of Pediatric Cushing Disease. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017 , 102, 2836-2843	5.6	61
105	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016 , 99, 40-55	11	61
104	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. <i>JAMA Oncology</i> , 2020 , 6, 724-734	13.4	60
103	Gene expression profiles in Parkinson disease prefrontal cortex implicate FOXO1 and genes under its transcriptional regulation. <i>PLoS Genetics</i> , 2012 , 8, e1002794	6	54
102	The Familial Intracranial Aneurysm (FIA) study protocol. <i>BMC Medical Genetics</i> , 2005 , 6, 17	2.1	54
101	Copy number variation in familial Parkinson disease. <i>PLoS ONE</i> , 2011 , 6, e20988	3.7	53
100	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 2019 , 139, 620-635	16.7	51
99	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016 , 99, 8-21	11	47
98	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015 , 126, e19-29	2.2	45
97	Association between mitochondrial DNA copy number and sudden cardiac death: findings from the Atherosclerosis Risk in Communities study (ARIC). <i>European Heart Journal</i> , 2017 , 38, 3443-3448	9.5	43
96	Genomic Copy Number Analysis in Alzheimer's Disease and Mild Cognitive Impairment: An ADNI Study. <i>International Journal of Alzheimer's Disease</i> , 2011 , 2011, 729478	3.7	43
95	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016 , 99, 22-39	11	42

94	Loss-of-function mutations in the gene are a novel cause of Cushing's disease. <i>Endocrine-Related Cancer</i> , 2017 , 24, 379-392	5.7	41
93	Rare nonsynonymous exonic variants in addiction and behavioral disinhibition. <i>Biological Psychiatry</i> , 2014 , 75, 783-9	7.9	39
92	Hearing impairment susceptibility in elderly men and the DFNA18 locus. <i>JAMA Otolaryngology</i> , 2006 , 132, 506-10		38
91	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. <i>PLoS Genetics</i> , 2017 , 13, e1006760	6	38
90	Evaluation of mitochondrial DNA copy number estimation techniques. <i>PLoS ONE</i> , 2020 , 15, e0228166	3.7	38
89	Mutations in DJ-1 are rare in familial Parkinson disease. <i>Neuroscience Letters</i> , 2006 , 408, 209-13	3.3	37
88	Evaluation of the role of Nurr1 in a large sample of familial Parkinson's disease. <i>Movement Disorders</i> , 2004 , 19, 649-55	7	33
87	Corticotropinoma as a Component of Carney Complex. <i>Journal of the Endocrine Society</i> , 2017 , 1, 918-925	5.4	32
86	Alpha-synuclein and familial Parkinson's disease. <i>Movement Disorders</i> , 2009 , 24, 1125-31	7	32
85	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. <i>Human Molecular Genetics</i> , 2015 , 24, 559-71	5.6	31
84	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. <i>American Journal of Human Genetics</i> , 2016 , 99, 481-8	11	31
83	Genetics of Parkinson disease. <i>NeuroRx</i> , 2004 , 1, 235-42		30
82	Klinefelter syndrome in males with germ cell tumors: A report from the Children's Oncology Group. <i>Cancer</i> , 2018 , 124, 3900-3908	6.4	29
81	Discovering genetic interactions bridging pathways in genome-wide association studies. <i>Nature Communications</i> , 2019 , 10, 4274	17.4	26
80	Evaluation of the relationship between plasma lipids and abdominal aortic aneurysm: A Mendelian randomization study. <i>PLoS ONE</i> , 2018 , 13, e0195719	3.7	26
79	Maternal inheritance and mitochondrial DNA variants in familial Parkinson's disease. <i>BMC Medical Genetics</i> , 2010 , 11, 53	2.1	26
78	Common globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. <i>PLoS Genetics</i> , 2018 , 14, e1007293	6	25
77	Clinical correlates of depressive symptoms in familial Parkinson's disease. <i>Movement Disorders</i> , 2008 , 23, 2216-23	7	25

76	The associations between 6-n-propylthiouracil (PROP) intensity and taste intensities differ by TAS2R38 haplotype. <i>Journal of Nutrigenetics and Nutrigenomics</i> , 2014 , 7, 143-52		24
75	Mutations in LRRK2 other than G2019S are rare in a north American-based sample of familial Parkinson's disease. <i>Movement Disorders</i> , 2006 , 21, 2257-60	7	23
74	Odor identification and cognitive function in the Beaver Dam Offspring Study. <i>Journal of Clinical and Experimental Neuropsychology</i> , 2013 , 35, 669-76	2.1	22
73	Multiancestral analysis of inflammation-related genetic variants and C-reactive protein in the population architecture using genomics and epidemiology study. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 178-88		22
72	Genetic associations of nonsynonymous exonic variants with psychophysiological endophenotypes. <i>Psychophysiology</i> , 2014 , 51, 1300-8	4.1	21
71	Variants in BAK1, SPRY4, and GAB2 are associated with pediatric germ cell tumors: A report from the children's oncology group. <i>Genes Chromosomes and Cancer</i> , 2017 , 56, 548-558	5	19
70	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. <i>Blood</i> , 2019 , 133, 967-977	2.2	17
69	Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium. <i>Diabetologia</i> , 2017 , 60, 2384-2398	10.3	16
68	Rare copy number variants implicated in posterior urethral valves. <i>American Journal of Medical Genetics, Part A</i> , 2016 , 170, 622-33	2.5	16
67	Rare copy number variants identified in prune belly syndrome. <i>European Journal of Medical Genetics</i> , 2018 , 61, 145-151	2.6	16
66	The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. <i>PLoS ONE</i> , 2018 , 13, e0200486	3.7	14
65	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. <i>Scientific Reports</i> , 2019 , 9, 15192	4.9	14
64	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. <i>Genome Medicine</i> , 2020 , 12, 84	14.4	13
63	A large-scale exome array analysis of venous thromboembolism. <i>Genetic Epidemiology</i> , 2019 , 43, 449-457	2.6	11
62	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , 2019 , 14, e0216222	3.7	11
61	Replication of genome-wide association signals in Asian Indians with early-onset type 2 diabetes. <i>Acta Diabetologica</i> , 2016 , 53, 915-923	3.9	11
60	Large Genomic Aberrations in Corticotropinomas Are Associated With Greater Aggressiveness. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019 , 104, 1792-1801	5.6	10
59	Germline CDKN1B Loss-of-Function Variants Cause Pediatric Cushing's Disease With or Without an MEN4 Phenotype. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020 , 105,	5.6	10

58	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. <i>Human Molecular Genetics</i> , 2019 , 28, 515-523	5.6	10
57	Low-Frequency Copy-Number Variants and General Cognitive Ability: No Evidence of Association. <i>Intelligence</i> , 2014 , 42, 98-106	3	9
56	Identification of Genetic Variants Linking Protein C and Lipoprotein Metabolism: The ARIC Study (Atherosclerosis Risk in Communities). <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017 , 37, 589-597	8.4	8
55	Heritability of Vascular Structure and Function: A Parent-Child Study. <i>Journal of the American Heart Association</i> , 2017 , 6,	6	8
54	Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the Metabochip in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>Human Molecular Genetics</i> , 2018 , 27, 2940-2953	5.6	8
53	R1514Q substitution in Lrrk2 is not a pathogenic Parkinson's disease mutation. <i>Movement Disorders</i> , 2007 , 22, 254-7	7	8
52	Genomewide linkage study of modifiers of LRRK2-related Parkinson's disease. <i>Movement Disorders</i> , 2011 , 26, 2039-44	7	7
51	Mitochondrial DNA copy number and incident atrial fibrillation. <i>BMC Medicine</i> , 2020 , 18, 246	11.4	7
50	Burden of rare exome sequence variants in PROC gene is associated with venous thromboembolism: a population-based study. <i>Journal of Thrombosis and Haemostasis</i> , 2020 , 18, 445-453	15.4	6
49	A Mendelian randomization of Γ and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. <i>Blood</i> , 2020 , 136, 3062-3069	2.2	6
48	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. <i>BioData Mining</i> , 2017 , 10, 25	4.3	5
47	Genome-wide association study of homocysteine in African Americans from the Jackson Heart Study, the Multi-Ethnic Study of Atherosclerosis, and the Coronary Artery Risk in Young Adults study. <i>Journal of Human Genetics</i> , 2018 , 63, 327-337	4.3	5
46	An analysis of measures of effect size by age of onset in cancer genomewide association studies. <i>Genes Chromosomes and Cancer</i> , 2013 , 52, 855-9	5	5
45	Identifying rare variants from exome scans: the GAW17 experience. <i>BMC Proceedings</i> , 2011 , 5 Suppl 9, S1	2.3	5
44	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021 , 108, 874-893	11	5
43	Issues in association mapping with high-density SNP data and diverse family structures. <i>Genetic Epidemiology</i> , 2007 , 31 Suppl 1, S22-33	2.6	4
42	Chromosome 5 and Parkinson disease. <i>European Journal of Human Genetics</i> , 2006 , 14, 1106-10	5.3	4
41	Replication of Newly Identified Genetic Associations Between Abdominal Aortic Aneurysm and SMYD2, LINC00540, PCIF1/MMP9/ZNF335, and ERG. <i>European Journal of Vascular and Endovascular Surgery</i> , 2020 , 59, 92-97	2.3	4

40	Rare Germline Variants in Pediatric Patients With Cushing's Disease: What Is Their Role?. <i>Frontiers in Endocrinology</i> , 2020 , 11, 433	5.7	4
39	RE: "RACIAL AND ETHNIC DIFFERENCES IN SOCIOECONOMIC POSITION AND RISK OF CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIA". <i>American Journal of Epidemiology</i> , 2019 , 188, 1192-1193	3.8	3
38	Joint analyses of disease and correlated quantitative phenotypes using next-generation sequencing data. <i>Genetic Epidemiology</i> , 2011 , 35 Suppl 1, S67-73	2.6	3
37	A two-stage classification approach identifies seven susceptibility genes for a simulated complex disease. <i>BMC Proceedings</i> , 2007 , 1 Suppl 1, S30	2.3	3
36	Identification of genes for complex disease using longitudinal phenotypes. <i>BMC Genetics</i> , 2003 , 4 Suppl 1, S58	2.6	3
35	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3
34	Nearly Half of Germline Variants Predicted To Be Pathogenic in Patients With Osteosarcoma Are De Novo: A Report From the Children's Oncology Group. <i>JCO Precision Oncology</i> , 2020 , 4,	3.6	3
33	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. <i>Science Advances</i> , 2022 , 8, eabl6579	14.3	3
32	Failure to replicate thrombomodulin genetic variant predictors of venous thromboembolism in African Americans. <i>Blood</i> , 2017 , 130, 688-690	2.2	2
31	Genetic analysis of hsCRP in American Indians: The Strong Heart Family Study. <i>PLoS ONE</i> , 2019 , 14, e0223574	3.7	2
30	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. <i>American Journal of Human Genetics</i> , 2020 , 106, 112-120	11	2
29	Requirement of FAT and DCHS protocadherins during hypothalamic-pituitary development. <i>JCI Insight</i> , 2020 , 5,	9.9	2
28	Mitochondrial DNA Copy Number (mtDNA-CN) Can Influence Mortality and Cardiovascular Disease via Methylation of Nuclear DNA CpGs		2
27	Discovering genetic interactions bridging pathways in genome-wide association studies		2
26	Elucidating mechanisms of genetic cross-disease associations: an integrative approach implicates protein C as a causal pathway in arterial and venous diseases		2
25	Association of mitochondrial DNA copy number with cardiometabolic diseases in a large cross-sectional study of multiple ancestries		2
24	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations		2
23	Whole genome sequence analysis of platelet traits in the NHLBI trans-omics for precision medicine initiative. <i>Human Molecular Genetics</i> , 2021 ,	5.6	2

22	Pleiotropic effects of n-6 and n-3 fatty acid-related genetic variants on circulating hemostatic variables. <i>Thrombosis Research</i> , 2018 , 168, 53-59	8.2	1
21	Standard linkage and association methods identify the mechanism of four susceptibility genes for a simulated complex disease. <i>BMC Genetics</i> , 2005 , 6 Suppl 1, S142	2.6	1
20	Parametric linkage analysis and disequilibrium methods to identify loci for complex disease. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S528-33	2.6	1
19	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. <i>Cell Genomics</i> , 2022 , 2, 100084-100084		1
18	OR24-6 Non-syndromic Cushing's Disease Due To CDKN1B Mutations: Novel Mutations And Phenotypic Features In A Large Pediatric Cohort. <i>Journal of the Endocrine Society</i> , 2019 , 3,	0.4	1
17	Association of mitochondrial DNA copy number with cardiometabolic diseases.. <i>Cell Genomics</i> , 2021 , 1,		1
16	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
15	Validation of a hybrid approach to standardize immunophenotyping analysis in large population studies: The Health and Retirement Study. <i>Scientific Reports</i> , 2020 , 10, 8759	4.9	1
14	FGL1 as a modulator of plasma D-dimer levels: Exome-wide marker analysis of plasma tPA, PAI-1, and D-dimer. <i>Journal of Thrombosis and Haemostasis</i> , 2021 , 19, 2019-2028	15.4	1
13	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. <i>Human Genetics and Genomics Advances</i> , 2021 , 2,	0.8	1
12	Exome sequencing of child-parent trios with bladder exstrophy: Findings in 26 children. <i>American Journal of Medical Genetics, Part A</i> , 2021 , 185, 3028-3041	2.5	1
11	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021 , 108, 1836-1851	11	1
10	Prediction of False-Positive Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Molecular Results in a High-Throughput Open-Platform System. <i>Journal of Molecular Diagnostics</i> , 2021 , 23, 1085-1096	5.1	1
9	Non-redundant summary scores applied to the North American Rheumatoid Arthritis Consortium dataset. <i>BMC Proceedings</i> , 2009 , 3 Suppl 7, S39	2.3	0
8	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. <i>Nature Communications</i> , 2022 , 13, 1222	17.4	0
7	A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data.. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqac034	3.7	0
6	Genetics of Parkinson disease. <i>Neurotherapeutics</i> , 2004 , 1, 235-242	6.4	
5	Association of polymorphisms in androgen production, uptake, and conversion chain (APUC) genes with mortality of prostate cancer patients.. <i>Journal of Clinical Oncology</i> , 2020 , 38, 5528-5528	2.2	

4 Evaluation of mitochondrial DNA copy number estimation techniques **2020**, 15, e0228166

3 Evaluation of mitochondrial DNA copy number estimation techniques **2020**, 15, e0228166

2 Evaluation of mitochondrial DNA copy number estimation techniques **2020**, 15, e0228166

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