Nathan D Pankratz

List of Publications by Year in Descending Order

147 papers	8,492 citations	48 h-index	91 g-index
164 ext. papers	11,003 ext. citations	8 avg, IF	5.15 L-index

#	Paper	IF	Citations
147	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. *Cell Genomics*, **2022**, 2, 100084-100084		1
146	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. *Nature Communications*, **2022**, 13, 1222	17.4	0
145	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
144	A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data.. *NAR Genomics and Bioinformatics*, **2022**, 4, lqac034	3.7	0
143	Association of mitochondrial DNA copy number with cardiometabolic diseases.. *Cell Genomics*, **2021**, 1,		1
142	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
141	FGL1 as a modulator of plasma D-dimer levels: Exome-wide marker analysis of plasma tPA, PAI-1, and D-dimer. *Journal of Thrombosis and Haemostasis*, **2021**, 19, 2019-2028	15.4	1
140	Potential Role for the RASD1 Glucocorticoid-Responsive Gene in Corticotroph Tumorigenesis. *Journal of the Endocrine Society*, **2021**, 5, A549-A549	0.4	78
139	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
138	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. *Human Genetics and Genomics Advances*, **2021**, 2,	0.8	1
137	Exome sequencing of child-parent trios with bladder exstrophy: Findings in 26 children. *American Journal of Medical Genetics, Part A*, **2021**, 185, 3028-3041	2.5	1
136	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 1836-1851	11	1
135	Prediction of False-Positive Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Molecular Results in a High-Throughput Open-Platform System. *Journal of Molecular Diagnostics*, **2021**, 23, 1085-1096	5.1	1
134	Whole genome sequence analysis of platelet traits in the NHLBI trans-omics for precision medicine initiative. *Human Molecular Genetics*, **2021**,	5.6	2
133	Germline CDKN1B Loss-of-Function Variants Cause Pediatric Cushing's Disease With or Without an MEN4 Phenotype. *Journal of Clinical Endocrinology and Metabolism*, **2020**, 105,	5.6	10
132	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. *JAMA Oncology*, **2020**, 6, 724-734	13.4	60
131	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. *American Journal of Human Genetics*, **2020**, 106, 112-120	11	2

130	Requirement of FAT and DCHS protocadherins during hypothalamic-pituitary development. *JCI Insight*, **2020**, 5,	9.9	2
129	Evaluation of mitochondrial DNA copy number estimation techniques. *PLoS ONE*, **2020**, 15, e0228166	3.7	38
128	OR06-01 The Role of Germline Defects in Cushing Disease. *Journal of the Endocrine Society*, **2020**, 4,	0.4	78
127	Association of polymorphisms in androgen production, uptake, and conversion chain (APUC) genes with mortality of prostate cancer patients.. *Journal of Clinical Oncology*, **2020**, 38, 5528-5528	2.2	
126	Replication of Newly Identified Genetic Associations Between Abdominal Aortic Aneurysm and SMYD2, LINC00540, PCIF1/MMP9/ZNF335, and ERG. *European Journal of Vascular and Endovascular Surgery*, **2020**, 59, 92-97	2.3	4
125	Burden of rare exome sequence variants in PROC gene is associated with venous thromboembolism: a population-based study. *Journal of Thrombosis and Haemostasis*, **2020**, 18, 445-453	15.4	6
124	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. *Genome Medicine*, **2020**, 12, 84	14.4	13
123	Nearly Half of Germline Variants Predicted To Be Pathogenic in Patients With Osteosarcoma Are De Novo: A Report From the Children's Oncology Group. *JCO Precision Oncology*, **2020**, 4,	3.6	3
122	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
121	Validation of a hybrid approach to standardize immunophenotyping analysis in large population studies: The Health and Retirement Study. *Scientific Reports*, **2020**, 10, 8759	4.9	1
120	A Mendelian randomization of and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. *Blood*, **2020**, 136, 3062-3069	2.2	6
119	Rare Germline Variants in Pediatric Patients With Cushing's Disease: What Is Their Role?. *Frontiers in Endocrinology*, **2020**, 11, 433	5.7	4
118	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
117	Mitochondrial DNA copy number and incident atrial fibrillation. *BMC Medicine*, **2020**, 18, 246	11.4	7
116	Evaluation of mitochondrial DNA copy number estimation techniques **2020**, 15, e0228166		
115	Evaluation of mitochondrial DNA copy number estimation techniques **2020**, 15, e0228166		
114	Evaluation of mitochondrial DNA copy number estimation techniques **2020**, 15, e0228166		
113	Evaluation of mitochondrial DNA copy number estimation techniques **2020**, 15, e0228166		

112	Genetic analysis of hsCRP in American Indians: The Strong Heart Family Study. *PLoS ONE*, **2019**, 14, e0223574	3.7	2
111	Discovering genetic interactions bridging pathways in genome-wide association studies. *Nature Communications*, **2019**, 10, 4274	17.4	26
110	A large-scale exome array analysis of venous thromboembolism. *Genetic Epidemiology*, **2019**, 43, 449-457	2.6	11
109	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. *PLoS ONE*, **2019**, 14, e0216222	3.7	11
108	Large Genomic Aberrations in Corticotropinomas Are Associated With Greater Aggressiveness. *Journal of Clinical Endocrinology and Metabolism*, **2019**, 104, 1792-1801	5.6	10
107	RE: "RACIAL AND ETHNIC DIFFERENCES IN SOCIOECONOMIC POSITION AND RISK OF CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIA". *American Journal of Epidemiology*, **2019**, 188, 1192-1193	3.8	3
106	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. *Blood*, **2019**, 134, 1645-1657	2.2	63
105	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. *Scientific Reports*, **2019**, 9, 15192	4.9	14
104	OR24-6 Non-syndromic Cushing's Disease Due To CDKN1B Mutations: Novel Mutations And Phenotypic Features In A Large Pediatric Cohort. *Journal of the Endocrine Society*, **2019**, 3,	0.4	1
103	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. *PLoS Genetics*, **2019**, 15, e1008500	6	90
102	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. *Circulation*, **2019**, 139, 620-635	16.7	51
101	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. *Blood*, **2019**, 133, 967-977	2.2	17
100	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. *Human Molecular Genetics*, **2019**, 28, 515-523	5.6	10
99	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. *Journal of Human Genetics*, **2018**, 63, 327-337	4.3	5
98	Functional variants in the gene confer shared effects on risk for Crohn's disease and Parkinson's disease. *Science Translational Medicine*, **2018**, 10,	17.5	165
97	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. *PLoS ONE*, **2018**, 13, e0200486	3.7	14
96	Evaluation of the relationship between plasma lipids and abdominal aortic aneurysm: A Mendelian randomization study. *PLoS ONE*, **2018**, 13, e0195719	3.7	26
95	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. *Human Molecular Genetics*, **2018**, 27, 2940-2953	5.6	8

94	Common β-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. *PLoS Genetics*, **2018**, 14, e1007293	6	25
93	Pleiotropic effects of n-6 and n-3 fatty acid-related genetic variants on circulating hemostatic variables. *Thrombosis Research*, **2018**, 168, 53-59	8.2	1
92	Rare copy number variants identified in prune belly syndrome. *European Journal of Medical Genetics* , **2018**, 61, 145-151	2.6	16
91	Klinefelter syndrome in males with germ cell tumors: A report from the Children's Oncology Group. *Cancer*, **2018**, 124, 3900-3908	6.4	29
90	Identification of Genetic Variants Linking Protein C and Lipoprotein Metabolism: The ARIC Study (Atherosclerosis Risk in Communities). *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2017**, 37, 589-597	8.4	8
89	Heritability of Vascular Structure and Function: A Parent-Child Study. *Journal of the American Heart Association*, **2017**, 6,	6	8
88	Somatic USP8 Gene Mutations Are a Common Cause of Pediatric Cushing Disease. *Journal of Clinical Endocrinology and Metabolism*, **2017**, 102, 2836-2843	5.6	61
87	Failure to replicate thrombomodulin genetic variant predictors of venous thromboembolism in African Americans. *Blood*, **2017**, 130, 688-690	2.2	2
86	Loss-of-function mutations in the gene are a novel cause of Cushing's disease. *Endocrine-Related Cancer*, **2017**, 24, 379-392	5.7	41
85	Variants in BAK1, SPRY4, and GAB2 are associated with pediatric germ cell tumors: A report from the children's oncology group. *Genes Chromosomes and Cancer*, **2017**, 56, 548-558	5	19
84	Association of Mitochondrial DNA Copy Number With Cardiovascular Disease. *JAMA Cardiology*, **2017**, 2, 1247-1255	16.2	109
83	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Mining*, **2017**, 10, 25	4.3	5
82	Corticotropinoma as a Component of Carney Complex. *Journal of the Endocrine Society*, **2017**, 1, 918-925	0.4	32
81	Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium. *Diabetologia*, **2017**, 60, 2384-2398	10.3	16
80	Association between mitochondrial DNA copy number and sudden cardiac death: findings from the Atherosclerosis Risk in Communities study (ARIC). *European Heart Journal*, **2017**, 38, 3443-3448	9.5	43
79	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. *PLoS Genetics*, **2017**, 13, e1006760	6	38
78	Replication of genome-wide association signals in Asian Indians with early-onset type 2 diabetes. *Acta Diabetologica*, **2016**, 53, 915-923	3.9	11
77	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. *American Journal of Human Genetics*, **2016**, 99, 40-55	11	61

76	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. *American Journal of Human Genetics*, **2016**, 99, 22-39	11	42
75	Association between Mitochondrial DNA Copy Number in Peripheral Blood and Incident CKD in the Atherosclerosis Risk in Communities Study. *Journal of the American Society of Nephrology: JASN*, **2016**, 27, 2467-73	12.7	79
74	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. *American Journal of Human Genetics*, **2016**, 99, 8-21	11	47
73	Rare copy number variants implicated in posterior urethral valves. *American Journal of Medical Genetics, Part A*, **2016**, 170, 622-33	2.5	16
72	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. *American Journal of Human Genetics*, **2016**, 99, 481-8	11	31
71	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. *Cancer Discovery*, **2015**, 5, 920-31	24.4	71
70	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. *Neurobiology of Aging*, **2015**, 36, 1605.e7-12	5.6	70
69	Genetic and nongenetic risk factors for childhood cancer. *Pediatric Clinics of North America*, **2015**, 62, 11-25	3.6	94
68	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. *Blood*, **2015**, 126, e19-29	2.2	45
67	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. *Human Molecular Genetics*, **2015**, 24, 559-71	5.6	31
66	Copy number variations and cognitive phenotypes in unselected populations. *JAMA - Journal of the American Medical Association*, **2015**, 313, 2044-54	27.4	96
65	The associations between 6-n-propylthiouracil (PROP) intensity and taste intensities differ by TAS2R38 haplotype. *Journal of Nutrigenetics and Nutrigenomics*, **2014**, 7, 143-52		24
64	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. *Nature Genetics*, **2014**, 46, 989-93	36.3	1261
63	Low-Frequency Copy-Number Variants and General Cognitive Ability: No Evidence of Association. *Intelligence*, **2014**, 42, 98-106	3	9
62	Rare nonsynonymous exonic variants in addiction and behavioral disinhibition. *Biological Psychiatry*, **2014**, 75, 783-9	7.9	39
61	Genetic associations of nonsynonymous exonic variants with psychophysiological endophenotypes. *Psychophysiology*, **2014**, 51, 1300-8	4.1	21
60	Multiancestral analysis of inflammation-related genetic variants and C-reactive protein in the population architecture using genomics and epidemiology study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 178-88		22
59	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131

58	Fine Mapping and Identification of BMI Loci in African Americans. *American Journal of Human Genetics*, **2013**, 93, 661-71	11	63
57	A genome-wide association study for venous thromboembolism: the extended cohorts for heart and aging research in genomic epidemiology (CHARGE) consortium. *Genetic Epidemiology*, **2013**, 37, 512-521	2.6	80
56	Odor identification and cognitive function in the Beaver Dam Offspring Study. *Journal of Clinical and Experimental Neuropsychology*, **2013**, 35, 669-76	2.1	22
55	Factors related to fungiform papillae density: the beaver dam offspring study. *Chemical Senses*, **2013**, 38, 669-77	4.8	76
54	An analysis of measures of effect size by age of onset in cancer genomewide association studies. *Genes Chromosomes and Cancer*, **2013**, 52, 855-9	5	5
53	A multicenter study of glucocerebrosidase mutations in dementia with Lewy bodies. *JAMA Neurology*, **2013**, 70, 727-35	17.2	285
52	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
51	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. *Annals of Neurology*, **2012** , 71, 370-84	9.4	214
50	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
49	Gene expression profiles in Parkinson disease prefrontal cortex implicate FOXO1 and genes under its transcriptional regulation. *PLoS Genetics*, **2012**, 8, e1002794	6	54
48	Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database. *PLoS Genetics*, **2012**, 8, e1002548	6	420
47	Voxelwise gene-wide association study (vGeneWAS): multivariate gene-based association testing in 731 elderly subjects. *NeuroImage*, **2011**, 56, 1875-91	7.9	96
46	Genomic Copy Number Analysis in Alzheimer's Disease and Mild Cognitive Impairment: An ADNI Study. *International Journal of Alzheimer's Disease*, **2011**, 2011, 729478	3.7	43
45	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
44	Translation initiator EIF4G1 mutations in familial Parkinson disease. *American Journal of Human Genetics*, **2011**, 89, 398-406	11	213
43	Identifying rare variants from exome scans: the GAW17 experience. *BMC Proceedings*, **2011**, 5 Suppl 9, S1	2.3	5
42	Genomewide linkage study of modifiers of LRRK2-related Parkinson's disease. *Movement Disorders*, **2011**, 26, 2039-44	7	7
41	Joint analyses of disease and correlated quantitative phenotypes using next-generation sequencing data. *Genetic Epidemiology*, **2011**, 35 Suppl 1, S67-73	2.6	3

40	Copy number variation in familial Parkinson disease. *PLoS ONE*, **2011**, 6, e20988	3.7	53
39	Genome-wide association of familial late-onset Alzheimer's disease replicates BIN1 and CLU and nominates CUGBP2 in interaction with APOE. *PLoS Genetics*, **2011**, 7, e1001308	6	179
38	A commonly carried allele of the obesity-related FTO gene is associated with reduced brain volume in the healthy elderly. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 8404-9	11.5	202
37	Voxelwise genome-wide association study (vGWAS). *NeuroImage*, **2010**, 53, 1160-74	7.9	197
36	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. *NeuroImage*, **2010**, 51, 542-54	7.9	119
35	Whole genome association study of brain-wide imaging phenotypes for identifying quantitative trait loci in MCI and AD: A study of the ADNI cohort. *NeuroImage*, **2010**, 53, 1051-63	7.9	266
34	Maternal inheritance and mitochondrial DNA variants in familial Parkinson's disease. *BMC Medical Genetics*, **2010**, 11, 53	2.1	26
33	Non-redundant summary scores applied to the North American Rheumatoid Arthritis Consortium dataset. *BMC Proceedings*, **2009**, 3 Suppl 7, S39	2.3	0
32	Alpha-synuclein and familial Parkinson's disease. *Movement Disorders*, **2009**, 24, 1125-31	7	32
31	Genomewide association study for susceptibility genes contributing to familial Parkinson disease. *Human Genetics*, **2009**, 124, 593-605	6.3	363
30	Genomewide association study for onset age in Parkinson disease. *BMC Medical Genetics*, **2009**, 10, 98	2.1	78
29	Clinical correlates of depressive symptoms in familial Parkinson's disease. *Movement Disorders*, **2008**, 23, 2216-23	7	25
28	Issues in association mapping with high-density SNP data and diverse family structures. *Genetic Epidemiology*, **2007**, 31 Suppl 1, S22-33	2.6	4
27	R1514Q substitution in Lrrk2 is not a pathogenic Parkinson's disease mutation. *Movement Disorders* , **2007**, 22, 254-7	7	8
26	Genetics of Parkinson disease. *Genetics in Medicine*, **2007**, 9, 801-11	8.1	77
25	A two-stage classification approach identifies seven susceptibility genes for a simulated complex disease. *BMC Proceedings*, **2007**, 1 Suppl 1, S30	2.3	3
24	Presence of an APOE4 allele results in significantly earlier onset of Parkinson's disease and a higher risk with dementia. *Movement Disorders*, **2006**, 21, 45-9	7	73
23	Mutations in LRRK2 other than G2019S are rare in a north American-based sample of familial Parkinson's disease. *Movement Disorders*, **2006**, 21, 2257-60	7	23

22	Mutations in DJ-1 are rare in familial Parkinson disease. *Neuroscience Letters*, **2006**, 408, 209-13	3.3	37
21	Hearing impairment susceptibility in elderly men and the DFNA18 locus. *JAMA Otolaryngology*, **2006**, 132, 506-10		38
20	Chromosome 5 and Parkinson disease. *European Journal of Human Genetics*, **2006**, 14, 1106-10	5.3	4
19	Genetic screening for a single common LRRK2 mutation in familial Parkinson's disease. *Lancet, The*, **2005**, 365, 410-2	40	145
18	Standard linkage and association methods identify the mechanism of four susceptibility genes for a simulated complex disease. *BMC Genetics*, **2005**, 6 Suppl 1, S142	2.6	1
17	The Familial Intracranial Aneurysm (FIA) study protocol. *BMC Medical Genetics*, **2005**, 6, 17	2.1	54
16	Evaluation of the role of Nurr1 in a large sample of familial Parkinson's disease. *Movement Disorders*, **2004**, 19, 649-55	7	33
15	Genetics of Parkinson disease. *NeuroRx*, **2004**, 1, 235-42		30
14	Genetics of Parkinson disease. *Neurotherapeutics*, **2004**, 1, 235-242	6.4	
13	Genome-wide linkage analysis and evidence of gene-by-gene interactions in a sample of 362 multiplex Parkinson disease families. *Human Molecular Genetics*, **2003**, 12, 2599-608	5.6	116
12	Identification of genes for complex disease using longitudinal phenotypes. *BMC Genetics*, **2003**, 4 Suppl 1, S58	2.6	3
11	Significant linkage of Parkinson disease to chromosome 2q36-37. *American Journal of Human Genetics*, **2003**, 72, 1053-7	11	138
10	Genome screen to identify susceptibility genes for Parkinson disease in a sample without parkin mutations. *American Journal of Human Genetics*, **2002**, 71, 124-35	11	150
9	Parametric linkage analysis and disequilibrium methods to identify loci for complex disease. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S528-33	2.6	1
8	Mitochondrial DNA Copy Number (mtDNA-CN) Can Influence Mortality and Cardiovascular Disease via Methylation of Nuclear DNA CpGs		2
7	Discovering genetic interactions bridging pathways in genome-wide association studies		2
6	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3
5	Elucidating mechanisms of genetic cross-disease associations: an integrative approach implicates protein C as a causal pathway in arterial and venous diseases		2

4	Association of mitochondrial DNA copy number with cardiometabolic diseases in a large cross-sectional study of multiple ancestries	2
3	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program	1
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program	68
1	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