Nathan D Pankratz

List of Publications by Year
in descending order

144 papers	12,565 citations	41258 49 h-index	30010 103 g-index
164 all docs	164 docs citations	164 times ranked	20936 citing authors

#	Article	IF	Citations
1	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Nature Genetics, 2014, 46, 989-993.	9.4	1,685
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
3	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. PLoS Genetics, 2012, 8, e1002548.	1.5	495
4	Genomewide association study for susceptibility genes contributing to familial Parkinson disease. Human Genetics, 2009, 124, 593-605.	1.8	410
5	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
6	A Multicenter Study of Glucocerebrosidase Mutations in Dementia With Lewy Bodies. JAMA Neurology, 2013, 70, 727.	4.5	374
7	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
8	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, 1051-1063.	2.1	340
9	Functional variants in the LRRK2 gene confer shared effects on risk for Crohnâ€™s disease and Parkinsonâ€™s disease. Science Translational Medicine, 2018, 10, .	5.8	273
10	Metaâ€analysis of Parkinson's Disease: Identification of a novel locus, RIT2. Annals of Neurology, 2012, 71, 370-384.	2.8	264
11	Translation Initiator EIF4G1 Mutations in Familial Parkinson Disease. American Journal of Human Genetics, 2011, 89, 398-406.	2.6	250
12	Genetic screening for a single common LRRK2 mutation in familial Parkinson's disease. Lancet, The, 2005, 365, 410-412.	6.3	243
13	Voxelwise genome-wide association study (vGWAS). NeuroImage, 2010, 53, 1160-1174.	2.1	239
14	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, 8404-8409.	3.3	227
15	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
16	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.	1.5	223
17	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.	1.5	203
18	Association of Mitochondrial DNA Copy Number With Cardiovascular Disease. JAMA Cardiology, 2017, 2, 1247.	3.0	194

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19	Genome Screen to Identify Susceptibility Genes for Parkinson Disease in a Sample without parkin Mutations. American Journal of Human Genetics, 2002, 71, 124-135.	2.6	162
20	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
21	Significant Linkage of Parkinson Disease to Chromosome 2q36-37. American Journal of Human Genetics, 2003, 72, 1053-1057.	2.6	158
22	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
23	Genetic and Nongenetic Risk Factors for Childhood Cancer. Pediatric Clinics of North America, 2015, 62, 11-25.	0.9	149
24	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	3.8	143
25	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. NeuroImage, 2010, 51, 542-554.	2.1	141
26	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	3.4	139
27	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, 2599-2608.	1.4	131
28	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
29	Voxelwise gene-wide association study (vGeneWAS): Multivariate gene-based association testing in 731 elderly subjects. NeuroImage, 2011, 56, 1875-1891.	2.1	116
30	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, 2467-2473.	3.0	112
31	Genomewide association study for onset age in Parkinson disease. BMC Medical Genetics, 2009, 10, 98.	2.1	104
32	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
33	Genetics of Parkinson disease. Genetics in Medicine, 2007, 9, 801-811.	1.1	101
34	A Genomeâ€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.	0.6	99
35	Evaluation of mitochondrial DNA copy number estimation techniques. PLoS ONE, 2020, 15, e0228166.	1.1	97
36	Factors Related to Fungiform Papillae Density: The Beaver Dam Offspring Study. Chemical Senses, 2013, 38, 669-677.	1.1	96

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37	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. Neurobiology of Aging, 2015, 36, 1605.e7-1605.e12.	1.5	96
38	Presence of an APOE4 allele results in significantly earlier onset of Parkinson's disease and a higher risk with dementia. Movement Disorders, 2006, 21, 45-49.	2.2	91
39	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	7.7	88
40	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
41	Somatic USP8 Gene Mutations Are a Common Cause of Pediatric Cushing Disease. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2836-2843.	1.8	81
42	Fine Mapping and Identification of BMI Loci in African Americans. American Journal of Human Genetics, 2013, 93, 661-671.	2.6	77
43	Gene Expression Profiles in Parkinson Disease Prefrontal Cortex Implicate FOXO1 and Genes under Its Transcriptional Regulation. PLoS Genetics, 2012, 8, e1002794.	1.5	76
44	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.	1.0	68
45	Copy Number Variation in Familial Parkinson Disease. PLoS ONE, 2011, 6, e20988.	1.1	67
46	Loss-of-function mutations in the CABLES1 gene are a novel cause of Cushingâ€™s disease. Endocrine-Related Cancer, 2017, 24, 379-392.	1.6	66
47	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. Genome Medicine, 2020, 12, 84.	3.6	63
48	The Familial Intracranial Aneurysm (FIA) study protocol. BMC Medical Genetics, 2005, 6, 17.	2.1	60
49	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
50	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	0.6	55
51	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.	1.5	53
52	Discovering genetic interactions bridging pathways in genome-wide association studies. Nature Communications, 2019, 10, 4274.	5.8	52
53	Genomic Copy Number Analysis in Alzheimer's Disease and Mild Cognitive Impairment: An ADNI Study. International Journal of Alzheimer's Disease, 2011, 2011, 1-10.	1.1	51
54	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.	2.6	50

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55	Klinefelter syndrome in males with germ cell tumors: A report from the Children's Oncology Group. Cancer, 2018, 124, 3900-3908.	2.0	46
56	Mutations in DJ-1 are rare in familial Parkinson disease. Neuroscience Letters, 2006, 408, 209-213.	1.0	45
57	Alphaâ€synuclein and familial Parkinson's disease. Movement Disorders, 2009, 24, 1125-1131.	2.2	45
58	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, 481-488.	2.6	45
59	Corticotropinoma as a Component of Carney Complex. Journal of the Endocrine Society, 2017, 1, 918-925.	0.1	45
60	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
61	Hearing Impairment Susceptibility in Elderly Men and the DFNA18 Locus. JAMA Otolaryngology, 2006, 132, 506.	1.5	41
62	Rare Nonsynonymous Exonic Variants in Addiction and Behavioral Disinhibition. Biological Psychiatry, 2014, 75, 783-789.	0.7	41
63	Evaluation of the relationship between plasma lipids and abdominal aortic aneurysm: A Mendelian randomization study. PLoS ONE, 2018, 13, e0195719.	1.1	39
64	Clinical correlates of depressive symptoms in familial Parkinson's disease. Movement Disorders, 2008, 23, 2216-2223.	2.2	37
65	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	1.4	36
66	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
67	Genetics of Parkinson disease. NeuroRx, 2004, 1, 235-242.	6.0	35
68	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	0.6	34
69	Evaluation of the role of Nurr1 in a large sample of familial Parkinson's disease. Movement Disorders, 2004, 19, 649-655.	2.2	33
70	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. Scientific Reports, 2019, 9, 15192.	1.6	32
71	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, 178-188.	5.1	31
72	Germline CDKN1B Loss-of-Function Variants Cause Pediatric Cushingâ€™s Disease With or Without an MEN4 Phenotype. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1983-2005.	1.8	31

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73	Odor identification and cognitive function in the Beaver Dam Offspring Study. Journal of Clinical and Experimental Neuropsychology, 2013, 35, 669-676.	0.8	29
74	The Associations between 6-n-Propylthiouracil (PROP) Intensity and Taste Intensities Differ by TAS2R38 Haplotype. Journal of Nutrigenetics and Nutrigenomics, 2015, 7, 143-152.	1.8	29
75	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
76	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
77	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.	1.5	27
78	Mutations in LRRK2 other than G2019S are rare in a north americanâ€“based sample of familial Parkinson's disease. Movement Disorders, 2006, 21, 2257-2260.	2.2	26
79	Maternal inheritance and mitochondrial DNA variants in familial Parkinson's disease. BMC Medical Genetics, 2010, 11, 53.	2.1	26
80	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	3.0	26
81	Rare copy number variants implicated in posterior urethral valves. American Journal of Medical Genetics, Part A, 2016, 170, 622-633.	0.7	25
82	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.	1.1	25
83	A Mendelian randomization of Î³â€² and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. Blood, 2020, 136, 3062-3069.	0.6	25
84	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
85	Genetic associations of nonsynonymous exonic variants with psychophysiological endophenotypes. Psychophysiology, 2014, 51, 1300-1308.	1.2	21
86	Rare copy number variants identified in prune belly syndrome. European Journal of Medical Genetics, 2018, 61, 145-151.	0.7	21
87	Mitochondrial DNA copy number and incident atrial fibrillation. BMC Medicine, 2020, 18, 246.	2.3	21
88	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.	2.9	20
89	Large Genomic Aberrations in Corticotropinomas Are Associated With Greater Aggressiveness. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 1792-1801.	1.8	20
90	Identification of Genetic Variants Linking Protein C and Lipoprotein Metabolism. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 589-597.	1.1	17

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91	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	1.1	17
92	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.	1.4	16
93	Replication of genome-wide association signals in Asian Indians with early-onset type 2 diabetes. Acta Diabetologica, 2016, 53, 915-923.	1.2	15
94	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. Human Molecular Genetics, 2019, 28, 515-523.	1.4	15
95	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.	2.6	14
96	Heritability of Vascular Structure and Function: A Parentâ€“Child Study. Journal of the American Heart Association, 2017, 6, .	1.6	12
97	A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data. NAR Genomics and Bioinformatics, 2022, 4, lqac034.	1.5	12
98	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.	0.8	11
99	Burden of rare exome sequence variants in PROC gene is associated with venous thromboembolism: a populationâ€based study. Journal of Thrombosis and Haemostasis, 2020, 18, 445-453.	1.9	11
100	Low-frequency copy-number variants and general cognitive ability: No evidence of association. Intelligence, 2014, 42, 98-106.	1.6	10
101	Nearly Half of TP53 Germline Variants Predicted To Be Pathogenic in Patients With Osteosarcoma Are De Novo: A Report From the Childrenâ€™s Oncology Group. JCO Precision Oncology, 2020, 4, 1187-1195.	1.5	10
102	Requirement of FAT and DCHS protocadherins during hypothalamic-pituitary development. JCI Insight, 2020, 5, .	2.3	10
103	Validation of a hybrid approach to standardize immunophenotyping analysis in large population studies: The Health and Retirement Study. Scientific Reports, 2020, 10, 8759.	1.6	9
104	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	2.6	9
105	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	1.4	9
106	R1514Q substitution in Lrrk2 is not a pathogenic Parkinson's disease mutation. Movement Disorders, 2007, 22, 254-256.	2.2	8
107	Genomewide linkage study of modifiers of LRRK2â€related Parkinson's disease. Movement Disorders, 2011, 26, 2039-2044.	2.2	8
108	An analysis of measures of effect size by age of onset in cancer genomewide association studies. Genes Chromosomes and Cancer, 2013, 52, 855-859.	1.5	8

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109	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
110	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.	1.1	7
111	Rare Germline DICER1 Variants in Pediatric Patients With Cushing's Disease: What Is Their Role?. Frontiers in Endocrinology, 2020, 11, 433.	1.5	7
112	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.8	6
113	Prostate Cancer Mortality Associated with Aggregate Polymorphisms in Androgen-Regulating Genes: The Atherosclerosis Risk in the Communities (ARIC) Study. Cancers, 2021, 13, 1958.	1.7	6
114	Genetic analysis of hsCRP in American Indians: The Strong Heart Family Study. PLoS ONE, 2019, 14, e0223574.	1.1	5
115	RE: â€œRACIAL AND ETHNIC DIFFERENCES IN SOCIOECONOMIC POSITION AND RISK OF CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIAâ€• American Journal of Epidemiology, 2019, 188, 1192-1193.	1.6	5
116	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	5.8	5
117	Chromosome 5 and Parkinson disease. European Journal of Human Genetics, 2006, 14, 1106-1110.	1.4	4
118	Issues in association mapping with high-density SNP data and diverse family structures. Genetic Epidemiology, 2007, 31, S22-S33.	0.6	4
119	Joint analyses of disease and correlated quantitative phenotypes using nextâ€generation sequencing data. Genetic Epidemiology, 2011, 35, S67-73.	0.6	4
120	Exome sequencing of childâ€“parent trios with bladder exstrophy: Findings in 26 children. American Journal of Medical Genetics, Part A, 2021, 185, 3028-3041.	0.7	4
121	Identification of genes for complex disease using longitudinal phenotypes. BMC Genetics, 2003, 4, S58.	2.7	3
122	A two-stage classification approach identifies seven susceptibility genes for a simulated complex disease. BMC Proceedings, 2007, 1, S30.	1.8	3
123	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, .	0.1	3
124	Predicted leukocyte telomere length and risk of germ cell tumours. British Journal of Cancer, 2022, 127, 301-312.	2.9	3
125	Whole-exome sequencing of 14â€‰389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. Human Molecular Genetics, 2022, 31, 3120-3132.	1.4	3
126	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. Obstetrical and Gynecological Survey, 2015, 70, 559-560.	0.2	2

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127	Failure to replicate thrombomodulin genetic variant predictors of venous thromboembolism in African Americans. Blood, 2017, 130, 688-690.	0.6	2
128	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, 100040.	1.0	2
129	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.	1.2	2
130	Exome sequencing identifies variants in infants with sacral agenesis. Birth Defects Research, 2022, 114, 215-227.	0.8	2
131	Parametric Linkage Analysis and Disequilibrium Methods to Identify Loci for Complex Disease. Genetic Epidemiology, 2001, 21, S528-33.	0.6	1
132	Standard linkage and association methods identify the mechanism of four susceptibility genes for a simulated complex disease. BMC Genetics, 2005, 6, S142.	2.7	1
133	Non-redundant summary scores applied to the North American Rheumatoid Arthritis Consortium dataset. BMC Proceedings, 2009, 3, S39.	1.8	1
134	Pleiotropic effects of n-6 and n-3 fatty acid-related genetic variants on circulating hemostatic variables. Thrombosis Research, 2018, 168, 53-59.	0.8	1
135	FGL1 as a modulator of plasma Dâ€dimer levels: Exomeâ€wide marker analysis of plasma tPA, PAIâ€1, and Dâ€dimer. Journal of Thrombosis and Haemostasis, 2021, 19, 2019-2028.	1.9	1
136	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	2.6	0
137	Potential Role for the RASD1 Glucocorticoid-Responsive Gene in Corticotroph Tumorigenesis. Journal of the Endocrine Society, 2021, 5, A549-A549.	0.1	0
138	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.	0.8	0
139	OR06-01 The Role of Germline Defects in Cushingâ€™s Disease. Journal of the Endocrine Society, 2020, 4, .	0.1	0
140	Genetics of Parkinson disease. Neurotherapeutics, 2004, 1, 235-242.	2.1	0
141	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
142	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
143	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
144	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0