Nathan D Pankratz

List of Publications by Year
in descending order

144	12,565	41344 49	30087 103
papers	citations	h-index	g-index

164	164	164	20936
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	2.9	9
2	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
3	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	12.8	5
4	Exome sequencing identifies variants in infants with sacral agenesis. Birth Defects Research, 2022, 114, 215-227.	1.5	2
5	Predicted leukocyte telomere length and risk of germ cell tumours. British Journal of Cancer, 2022, 127, 301-312.	6.4	3
6	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
7	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.	2.9	3
8	A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data. NAR Genomics and Bioinformatics, 2022, 4, lqac034.	3.2	12
9	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
10	Prostate Cancer Mortality Associated with Aggregate Polymorphisms in Androgen-Regulating Genes: The Atherosclerosis Risk in the Communities (ARIC) Study. Cancers, 2021, 13, 1958.	3.7	6
11	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
12	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.	3.8	1
13	Potential Role for the RASD1 Glucocorticoid-Responsive Gene in Corticotroph Tumorigenesis. Journal of the Endocrine Society, 2021, 5, A549-A549.	0.2	0
14	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.	1.7	2
15	Exome sequencing of childâ€“parent trios with bladder exstrophy: Findings in 26 children. American Journal of Medical Genetics, Part A, 2021, 185, 3028-3041.	1.2	4
16	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.	6.2	14
17	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.	2.8	2
18	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	6.5	26

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19	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.	1.5	11
20	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.	3.8	11
21	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. Genome Medicine, 2020, 12, 84.	8.2	63
22	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.	3.0	10
23	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
24	Validation of a hybrid approach to standardize immunophenotyping analysis in large population studies: The Health and Retirement Study. Scientific Reports, 2020, 10, 8759.	3.3	9
25	A Mendelian randomization of Î³â€² and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. Blood, 2020, 136, 3062-3069.	1.4	25
26	Rare Germline DICER1 Variants in Pediatric Patients With Cushing's Disease: What Is Their Role?. Frontiers in Endocrinology, 2020, 11, 433.	3.5	7
27	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
28	Mitochondrial DNA copy number and incident atrial fibrillation. BMC Medicine, 2020, 18, 246.	5.5	21
29	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.	3.6	31
30	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	7.1	139
31	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	6.2	9
32	Requirement of FAT and DCHS protocadherins during hypothalamic-pituitary development. JCI Insight, 2020, 5, .	5.0	10
33	Evaluation of mitochondrial DNA copy number estimation techniques. PLoS ONE, 2020, 15, e0228166.	2.5	97
34	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.	1.6	0
35	OR06-01 The Role of Germline Defects in Cushingâ€™s Disease. Journal of the Endocrine Society, 2020, 4, .	0.2	0
36	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0

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37	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
38	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
39	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
40	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
41	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. Scientific Reports, 2019, 9, 15192.	3.3	32
42	Genetic analysis of hsCRP in American Indians: The Strong Heart Family Study. PLoS ONE, 2019, 14, e0223574.	2.5	5
43	Discovering genetic interactions bridging pathways in genome-wide association studies. Nature Communications, 2019, 10, 4274.	12.8	52
44	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	1.3	22
45	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
46	Large Genomic Aberrations in Corticotropinomas Are Associated With Greater Aggressiveness. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 1792-1801.	3.6	20
47	RE: â€œRACIAL AND ETHNIC DIFFERENCES IN SOCIOECONOMIC POSITION AND RISK OF CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIAâ€. American Journal of Epidemiology, 2019, 188, 1192-1193.	3.4	5
48	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.	3.5	203
49	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
50	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	1.4	34
51	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. Human Molecular Genetics, 2019, 28, 515-523.	2.9	15
52	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, .	0.2	3
53	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.	2.3	7
54	Functional variants in the LRRK2 gene confer shared effects on risk for Crohnâ€™s disease and Parkinsonâ€™s disease. Science Translational Medicine, 2018, 10, .	12.4	273

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55	Rare copy number variants identified in prune belly syndrome. European Journal of Medical Genetics, 2018, 61, 145-151.	1.3	21
56	Klinefelter syndrome in males with germ cell tumors: A report from the Children's Oncology Group. Cancer, 2018, 124, 3900-3908.	4.1	46
57	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.	2.5	25
58	Evaluation of the relationship between plasma lipids and abdominal aortic aneurysm: A Mendelian randomization study. PLoS ONE, 2018, 13, e0195719.	2.5	39
59	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.	2.9	16
60	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	3.5	45
61	Pleiotropic effects of n-6 and n-3 fatty acid-related genetic variants on circulating hemostatic variables. Thrombosis Research, 2018, 168, 53-59.	1.7	1
62	Identification of Genetic Variants Linking Protein C and Lipoprotein Metabolism. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 589-597.	2.4	17
63	Heritability of Vascular Structure and Function: A Parentâ€“Child Study. Journal of the American Heart Association, 2017, 6, .	3.7	12
64	Somatic USP8 Gene Mutations Are a Common Cause of Pediatric Cushing Disease. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2836-2843.	3.6	81
65	Failure to replicate thrombomodulin genetic variant predictors of venous thromboembolism in African Americans. Blood, 2017, 130, 688-690.	1.4	2
66	Loss-of-function mutations in the CABLES1 gene are a novel cause of Cushingâ€™s disease. Endocrine-Related Cancer, 2017, 24, 379-392.	3.1	66
67	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.	2.8	27
68	Association of Mitochondrial DNA Copy Number With Cardiovascular Disease. JAMA Cardiology, 2017, 2, 1247.	6.1	194
69	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.	6.3	20
70	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.	2.2	68
71	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	4.0	7
72	Corticotropinoma as a Component of Carney Complex. Journal of the Endocrine Society, 2017, 1, 918-925.	0.2	45

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73	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.	3.5	53
74	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
75	Rare copy number variants implicated in posterior urethral valves. American Journal of Medical Genetics, Part A, 2016, 170, 622-633.	1.2	25
76	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.	6.2	45
77	Replication of genome-wide association signals in Asian Indians with early-onset type 2 diabetes. Acta Diabetologica, 2016, 53, 915-923.	2.5	15
78	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
79	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.	6.2	50
80	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.	6.1	112
81	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
82	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. Obstetrical and Gynecological Survey, 2015, 70, 559-560.	0.4	2
83	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
84	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	7.4	143
85	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	9.4	88
86	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. Neurobiology of Aging, 2015, 36, 1605.e7-1605.e12.	3.1	96
87	The Associations between 6-n-Propylthiouracil (PROP) Intensity and Taste Intensities Differ by TAS2R38 Haplotype. Journal of Nutrigenetics and Nutrigenomics, 2015, 7, 143-152.	1.3	29
88	Genetic and Nongenetic Risk Factors for Childhood Cancer. Pediatric Clinics of North America, 2015, 62, 11-25.	1.8	149
89	Genetic associations of nonsynonymous exonic variants with psychophysiological endophenotypes. Psychophysiology, 2014, 51, 1300-1308.	2.4	21
90	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

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91	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.	6.2	158
92	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Nature Genetics, 2014, 46, 989-993.	21.4	1,685
93	Low-frequency copy-number variants and general cognitive ability: No evidence of association. Intelligence, 2014, 42, 98-106.	3.0	10
94	Rare Nonsynonymous Exonic Variants in Addiction and Behavioral Disinhibition. Biological Psychiatry, 2014, 75, 783-789.	1.3	41
95	Fine Mapping and Identification of BMI Loci in African Americans. American Journal of Human Genetics, 2013, 93, 661-671.	6.2	77
96	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.	1.3	99
97	Odor identification and cognitive function in the Beaver Dam Offspring Study. Journal of Clinical and Experimental Neuropsychology, 2013, 35, 669-676.	1.3	29
98	Factors Related to Fungiform Papillae Density: The Beaver Dam Offspring Study. Chemical Senses, 2013, 38, 669-677.	2.0	96
99	An analysis of measures of effect size by age of onset in cancer genomewide association studies. Genes Chromosomes and Cancer, 2013, 52, 855-859.	2.8	8
100	A Multicenter Study of Glucocerebrosidase Mutations in Dementia With Lewy Bodies. JAMA Neurology, 2013, 70, 727.	9.0	374
101	Gene Expression Profiles in Parkinson Disease Prefrontal Cortex Implicate FOXO1 and Genes under Its Transcriptional Regulation. PLoS Genetics, 2012, 8, e1002794.	3.5	76
102	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. PLoS Genetics, 2012, 8, e1002548.	3.5	495
103	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
104	Metaâ€analysis of Parkinson's Disease: Identification of a novel locus, RIT2. Annals of Neurology, 2012, 71, 370-384.	5.3	264
105	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	6.2	0
106	Voxelwise gene-wide association study (vGeneWAS): Multivariate gene-based association testing in 731 elderly subjects. NeuroImage, 2011, 56, 1875-1891.	4.2	116
107	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.	2.0	51
108	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122

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109	Translation Initiator EIF4G1 Mutations in Familial Parkinson Disease. American Journal of Human Genetics, 2011, 89, 398-406.	6.2	250
110	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.6	6
111	Genomewide linkage study of modifiers of LRRK2â€related Parkinson's disease. Movement Disorders, 2011, 26, 2039-2044.	3.9	8
112	Joint analyses of disease and correlated quantitative phenotypes using nextâ€generation sequencing data. Genetic Epidemiology, 2011, 35, S67-73.	1.3	4
113	Copy Number Variation in Familial Parkinson Disease. PLoS ONE, 2011, 6, e20988.	2.5	67
114	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.	3.5	223
115	Maternal inheritance and mitochondrial DNA variants in familial Parkinson's disease. BMC Medical Genetics, 2010, 11, 53.	2.1	26
116	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.	7.1	227
117	Voxelwise genome-wide association study (vGWAS). NeuroImage, 2010, 53, 1160-1174.	4.2	239
118	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. NeuroImage, 2010, 51, 542-554.	4.2	141
119	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.	4.2	340
120	Non-redundant summary scores applied to the North American Rheumatoid Arthritis Consortium dataset. BMC Proceedings, 2009, 3, S39.	1.6	1
121	Alphaâ€synuclein and familial Parkinson's disease. Movement Disorders, 2009, 24, 1125-1131.	3.9	45
122	Genomewide association study for susceptibility genes contributing to familial Parkinson disease. Human Genetics, 2009, 124, 593-605.	3.8	410
123	Genomewide association study for onset age in Parkinson disease. BMC Medical Genetics, 2009, 10, 98.	2.1	104
124	Clinical correlates of depressive symptoms in familial Parkinson's disease. Movement Disorders, 2008, 23, 2216-2223.	3.9	37
125	Genetics of Parkinson disease. Genetics in Medicine, 2007, 9, 801-811.	2.4	101
126	A two-stage classification approach identifies seven susceptibility genes for a simulated complex disease. BMC Proceedings, 2007, 1, S30.	1.6	3

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127	Issues in association mapping with high-density SNP data and diverse family structures. Genetic Epidemiology, 2007, 31, S22-S33.	1.3	4
128	R1514Q substitution in Lrrk2 is not a pathogenic Parkinson's disease mutation. Movement Disorders, 2007, 22, 254-256.	3.9	8
129	Mutations in DJ-1 are rare in familial Parkinson disease. Neuroscience Letters, 2006, 408, 209-213.	2.1	45
130	Hearing Impairment Susceptibility in Elderly Men and the DFNA18 Locus. JAMA Otolaryngology, 2006, 132, 506.	1.2	41
131	Chromosome 5 and Parkinson disease. European Journal of Human Genetics, 2006, 14, 1106-1110.	2.8	4
132	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.	3.9	91
133	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.	3.9	26
134	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
135	The Familial Intracranial Aneurysm (FIA) study protocol. BMC Medical Genetics, 2005, 6, 17.	2.1	60
136	Genetic screening for a single common LRRK2 mutation in familial Parkinson's disease. Lancet, The, 2005, 365, 410-412.	13.7	243
137	Evaluation of the role of Nurr1 in a large sample of familial Parkinson's disease. Movement Disorders, 2004, 19, 649-655.	3.9	33
138	Genetics of Parkinson disease. NeuroRx, 2004, 1, 235-242.	6.0	35
139	Genetics of Parkinson disease. Neurotherapeutics, 2004, 1, 235-242.	4.4	0
140	Identification of genes for complex disease using longitudinal phenotypes. BMC Genetics, 2003, 4, S58.	2.7	3
141	Significant Linkage of Parkinson Disease to Chromosome 2q36-37. American Journal of Human Genetics, 2003, 72, 1053-1057.	6.2	158
142	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.	2.9	131
143	Genome Screen to Identify Susceptibility Genes for Parkinson Disease in a Sample without parkin Mutations. American Journal of Human Genetics, 2002, 71, 124-135.	6.2	162
144	Parametric Linkage Analysis and Disequilibrium Methods to Identify Loci for Complex Disease. Genetic Epidemiology, 2001, 21, S528-33.	1.3	1