Andrew Singleton

List of Publications by Year
in descending order

164 papers	28,952 citations	12330 69 h-index	5539 163 g-index
185 all docs	185 docs citations	185 times ranked	37026 citing authors

#	Article	IF	Citations
1	Clinical Variability of SYNJ1-Associated Early-Onset Parkinsonism. Frontiers in Neurology, 2021, 12, 648457.	2.4	11
2	Exploring dementia and neuronal ceroid lipofuscinosis genes in 100 FTD-like patients from 6 towns and rural villages on the Adriatic Sea cost of Apulia. Scientific Reports, 2021, 11, 6353.	3.3	7
3	Anticholinergic Drug Induced Cognitive and Physical Impairment: Results from the InCHIANTI Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 995-1002.	3.6	34
4	Clinical and dopamine transporter imaging characteristics of non-manifest LRRK2 and GBA mutation carriers in the Parkinson's Progression Markers Initiative (PPMI): a cross-sectional study. Lancet Neurology, The, 2020, 19, 71-80.	10.2	94
5	Shared mechanisms for cognitive impairment and physical frailty: A model for complex systems. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2020, 6, e12027.	3.7	28
6	Genetic and Phenotypic Basis of Autosomal Dominant Parkinson's Disease in a Large Multi-Center Cohort. Frontiers in Neurology, 2020, 11, 682.	2.4	28
7	Longitudinal Measurements of Glucocerebrosidase activity in Parkinsonâ€™s patients. Annals of Clinical and Translational Neurology, 2020, 7, 1816-1830.	3.7	23
8	Characterization of Recessive Parkinson Disease in a Large Multicenter Study. Annals of Neurology, 2020, 88, 843-850.	5.3	40
9	Clinical and Dopamine Transporter Imaging Characteristics of Leucine Rich Repeat Kinase 2 (LRRK2) and Glucosylceramidase Beta (GBA) Parkinson's Disease Participants in the Parkinson's Progression Markers Initiative: A Crossâ€Sectional Study. Movement Disorders, 2020, 35, 833-844.	3.9	48
10	Analysis of neurodegenerative disease-causing genes in dementia with Lewy bodies. Acta Neuropathologica Communications, 2020, 8, 5.	5.2	27
11	The Genetic Architecture of Parkinson Disease in Spain: Characterizing Populationâ€Specific Risk, Differential Haplotype Structures, and Providing Etiologic Insight. Movement Disorders, 2019, 34, 1851-1863.	3.9	47
12	Feasibility and safety of lumbar puncture in the Parkinson's disease research participants: Parkinson's Progression Marker Initiative (PPMI). Parkinsonism and Related Disorders, 2019, 62, 201-209.	2.2	15
13	Mitochondria function associated genes contribute to Parkinsonâ€™s Disease risk and later age at onset. Npj Parkinson's Disease, 2019, 5, 8.	5.3	95
14	Blepharospasm: A genetic screening study in 132 patients. Parkinsonism and Related Disorders, 2019, 64, 315-318.	2.2	13
15	Heritability and genetic variance of dementia with Lewy bodies. Neurobiology of Disease, 2019, 127, 492-501.	4.4	29
16	Peripheral GRN mRNA and Serum Progranulin Levels as a Potential Indicator for Both the Presence of Splice Site Mutations and Individuals at Risk for Frontotemporal Dementia. Journal of Alzheimer's Disease, 2019, 67, 159-167.	2.6	11
17	A comprehensive screening of copy number variability in dementia with Lewy bodies. Neurobiology of Aging, 2019, 75, 223.e1-223.e10.	3.1	13
18	Longitudinal Change of Clinical and Biological Measures in Early Parkinson's Disease: Parkinson's Progression Markers Initiative Cohort. Movement Disorders, 2018, 33, 771-782.	3.9	136

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19	Polygenic risk score in postmortem diagnosed sporadic early-onset Alzheimer's disease. Neurobiology of Aging, 2018, 62, 244.e1-244.e8.	3.1	30
20	Investigating the genetic architecture of dementia with Lewy bodies: a two-stage genome-wide association study. Lancet Neurology, The, 2018, 17, 64-74.	10.2	195
21	The Parkinson's progression markers initiative (PPMI) â€“ establishing a PD biomarker cohort. Annals of Clinical and Translational Neurology, 2018, 5, 1460-1477.	3.7	330
22	A C6orf10/LOC101929163 locus is associated with age of onset in C9orf72 carriers. Brain, 2018, 141, 2895-2907.	7.6	39
23	Shared biological pathways for frailty and cognitive impairment: A systematic review. Ageing Research Reviews, 2018, 47, 149-158.	10.9	48
24	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
25	Effects of Multiple Genetic Loci on Age atÂOnset in Frontotemporal Dementia. Journal of Alzheimer's Disease, 2017, 56, 1271-1278.	2.6	4
26	Genetics of early-onset Parkinson's disease in Finland: exome sequencing and genome-wide association study. Neurobiology of Aging, 2017, 53, 195.e7-195.e10.	3.1	46
27	Mutations in TYROBP are not a common cause of dementia in a Turkish cohort. Neurobiology of Aging, 2017, 58, 240.e1-240.e3.	3.1	6
28	Analysis of C9orf72 repeat expansions in a large international cohort of dementia with Lewy bodies. Neurobiology of Aging, 2017, 49, 214.e13-214.e15.	3.1	12
29	Mutation analysis of sporadic early-onset Alzheimer's disease using the NeuroX array. Neurobiology of Aging, 2017, 49, 215.e1-215.e8.	3.1	21
30	Linkage, whole genome sequence, and biological data implicate variants in RAB10 in Alzheimerâ€™s disease resilience. Genome Medicine, 2017, 9, 100.	8.2	67
31	Estimating the causal influence of body mass index on risk of Parkinson disease: A Mendelian randomisation study. PLoS Medicine, 2017, 14, e1002314.	8.4	152
32	Multiple modality biomarker prediction of cognitive impairment in prospectively followed de novo Parkinson disease. PLoS ONE, 2017, 12, e0175674.	2.5	110
33	A Bayesian mathematical model of motor and cognitive outcomes in Parkinsonâ€™s disease. PLoS ONE, 2017, 12, e0178982.	2.5	11
34	Anatomy of Subsidence in Tianjin from Time Series InSAR. Remote Sensing, 2016, 8, 266.	4.0	33
35	Mutation Frequency of the Major Frontotemporal Dementia Genes, MAPT, GRN and C9ORF72 in a Turkish Cohort of Dementia Patients. PLoS ONE, 2016, 11, e0162592.	2.5	19
36	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213

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37	Genome-wide assessment of Parkinson's disease in a Southern Spanish population. Neurobiology of Aging, 2016, 45, 213.e3-213.e9.	3.1	35
38	The Evolution of Genetics: Alzheimerâ€™s and Parkinsonâ€™s Diseases. Neuron, 2016, 90, 1154-1163.	8.1	81
39	Genome-wide analysis of genetic correlation in dementia with Lewy bodies, Parkinson's and Alzheimer's diseases. Neurobiology of Aging, 2016, 38, 214.e7-214.e10.	3.1	78
40	CSF biomarkers associated with disease heterogeneity in early Parkinsonâ€™s disease: the Parkinsonâ€™s Progression Markers Initiative study. Acta Neuropathologica, 2016, 131, 935-949.	7.7	190
41	Loss of VPS13C Function in Autosomal-Recessive Parkinsonism Causes Mitochondrial Dysfunction and Increases PINK1/Parkin-Dependent Mitophagy. American Journal of Human Genetics, 2016, 98, 500-513.	6.2	333
42	Extracting Vertical Displacement Rates in Shanghai (China) with Multi-Platform SAR Images. Remote Sensing, 2015, 7, 9542-9562.	4.0	62
43	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	27.8	772
44	Multiple system atrophy: the application of genetics in understanding etiology. Clinical Autonomic Research, 2015, 25, 19-36.	2.5	20
45	A genome-wide screening and SNPs-to-genes approach to identify novel genetic risk factors associated with frontotemporal dementia. Neurobiology of Aging, 2015, 36, 2904.e13-2904.e26.	3.1	48
46	Gene expression markers of age-related inflammation in two human cohorts. Experimental Gerontology, 2015, 70, 37-45.	2.8	23
47	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
48	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 110-118.	3.6	250
49	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	2.9	8
50	A systematic screening to identifyde novomutations causing sporadic early-onset Parkinson's disease. Human Molecular Genetics, 2015, 24, 6711-6720.	2.9	59
51	Mutation analysis of patients with neurodegenerative disorders using NeuroX array. Neurobiology of Aging, 2015, 36, 545.e9-545.e14.	3.1	36
52	Genetic analysis implicates APOE, SNCA and suggests lysosomal dysfunction in the etiology of dementia with Lewy bodies. Human Molecular Genetics, 2014, 23, 6139-6146.	2.9	178
53	Investigating the role of rare coding variability in Mendelian dementia genes (APP , PSEN1 , PSEN2 , GRN) Tj ETQq1 1 0.784314 rgBT	3.1	53
54	Whole blood gene expression and interleukin-6 levels. Genomics, 2014, 104, 490-495.	2.9	24

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55	Next generation sequencing techniques in neurological diseases: redefining clinical and molecular associations. Human Molecular Genetics, 2014, 23, R47-R53.	2.9	57
56	Exome sequencing identifies 2 novel presenilin 1 mutations (p.L166V and p.S230R) in British early-onset Alzheimer's disease. Neurobiology of Aging, 2014, 35, 2422.e13-2422.e16.	3.1	28
57	Identical twins with the C9orf72 repeat expansion are discordant for ALS. Neurology, 2014, 83, 1476-1478.	1.1	40
58	Splicing factor 3B1 hypomethylation is associated with altered SF3B1 transcript expression in older humans. Mechanisms of Ageing and Development, 2014, 135, 50-56.	4.6	7
59	Association of Cerebrospinal Fluid Î²-Amyloid 1-42, T-tau, P-tau₁₈₁, and Î±-Synuclein Levels With Clinical Features of Drug-Naive Patients With Early Parkinson Disease. JAMA Neurology, 2013, 70, 1277-87.	9.0	318
60	TREM2 Variants in Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 117-127.	27.0	2,385
61	Using Exome Sequencing to Reveal Mutations in TREM2 Presenting as a Frontotemporal Dementiaâ€“like Syndrome Without Bone Involvement. JAMA Neurology, 2013, 70, 78.	9.0	311
62	Initial Assessment of the Pathogenic Mechanisms of the Recently Identified Alzheimer Risk Loci. Annals of Human Genetics, 2013, 77, 85-105.	0.8	41
63	NOTCH3 Variants and Risk of Ischemic Stroke. PLoS ONE, 2013, 8, e75035.	2.5	30
64	Exome sequencing reveals an unexpected genetic cause of disease: NOTCH3 mutation in a Turkish family with Alzheimer's disease. Neurobiology of Aging, 2012, 33, 1008.e17-1008.e23.	3.1	86
65	Identification of PSEN1 and PSEN2 gene mutations and variants in Turkish dementia patients. Neurobiology of Aging, 2012, 33, 1850.e17-1850.e27.	3.1	44
66	Advancing age is associated with gene expression changes resembling mTOR inhibition: Evidence from two human populations. Mechanisms of Ageing and Development, 2012, 133, 556-562.	4.6	54
67	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
68	The Parkinson Progression Marker Initiative (PPMI). Progress in Neurobiology, 2011, 95, 629-635.	5.7	1,278
69	A Hexanucleotide Repeat Expansion in C9ORF72 Is the Cause of Chromosome 9p21-Linked ALS-FTD. Neuron, 2011, 72, 257-268.	8.1	3,833
70	APOE and AÎ²PP Gene Variation in Cortical and Cerebrovascular Amyloid-Î² Pathology and Alzheimer's Disease: A Population-Based Analysis. Journal of Alzheimer's Disease, 2011, 26, 377-385.	2.6	15
71	Genomic Risk Profiling of Ischemic Stroke: Results of an International Genome-Wide Association Meta-Analysis. PLoS ONE, 2011, 6, e23161.	2.5	14
72	SCA15 Due to Large ITPR1 Deletions in a Cohort of 333 White Families With Dominant Ataxia. Archives of Neurology, 2011, 68, 637-43.	4.5	65

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73	Human aging is characterized by focused changes in gene expression and deregulation of alternative splicing. Aging Cell, 2011, 10, 868-878.	6.7	230
74	Clinical features, with video documentation, of the original familial lewy body parkinsonism caused by Î±â€šynuclein triplication (Iowa kindred). Movement Disorders, 2011, 26, 2134-2136.	3.9	32
75	Parkinson's disease and Î±â€šynuclein expression. Movement Disorders, 2011, 26, 2160-2168.	3.9	186
76	A generalizable hypothesis for the genetic architecture of disease: pleomorphic risk loci. Human Molecular Genetics, 2011, 20, R158-R162.	2.9	79
77	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
78	A genome-wide association analysis of serum iron concentrations. Blood, 2010, 115, 94-96.	1.4	142
79	A thorough assessment of benign genetic variability inGRNandMAPT. Human Mutation, 2010, 31, E1126-E1140.	2.5	23
80	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
81	Genetic screening of Alzheimer's disease genes in Iberian and African samples yields novel mutations in presenilins and APP. Neurobiology of Aging, 2010, 31, 725-731.	3.1	196
82	Human ataxias: a genetic dissection of inositol triphosphate receptor (ITPR1)-dependent signaling. Trends in Neurosciences, 2010, 33, 211-219.	8.6	81
83	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
84	Genetic Variability in CLU and Its Association with Alzheimer's Disease. PLoS ONE, 2010, 5, e9510.	2.5	52
85	Characterization of PLA2G6 as a locus for dystoniaâ€parkinsonism. Annals of Neurology, 2009, 65, 19-23.	5.3	399
86	A two-stage genome-wide association study of sporadic amyotrophic lateral sclerosis. Human Molecular Genetics, 2009, 18, 1524-1532.	2.9	106
87	A simple and efficient algorithm for genomeâ€wide homozygosity analysis in disease. Molecular Systems Biology, 2009, 5, 304.	7.2	1
88	Candidate Gene Polymorphisms for Ischemic Stroke. Stroke, 2009, 40, 3436-3442.	2.0	46
89	Glucocerebrosidase mutations in clinical and pathologically proven Parkinson's disease. Brain, 2009, 132, 1783-1794.	7.6	612
90	Sequential Use of Transcriptional Profiling, Expression Quantitative Trait Mapping, and Gene Association Implicates MMP20 in Human Kidney Aging. PLoS Genetics, 2009, 5, e1000685.	3.5	50

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91	Genome-Wide Association Study of Plasma Polyunsaturated Fatty Acids in the InCHIANTI Study. PLoS Genetics, 2009, 5, e1000338.	3.5	351
92	Familial Parkinsonism and early onset Parkinson's disease in a Brazilian movement disorders clinic: Phenotypic characterization and frequency of SNCA, PRKN, PINK1, and LRRK2 mutations. Movement Disorders, 2009, 24, 662-666.	3.9	63
93	The TOR1A polymorphism rs1182 and the risk of spread in primary blepharospasm. Movement Disorders, 2009, 24, 613-616.	3.9	35
94	Genome-wide Association Study of Vitamin B6, Vitamin B12, Folate, and Homocysteine Blood Concentrations. American Journal of Human Genetics, 2009, 84, 477-482.	6.2	225
95	Common Variation in the Î²-Carotene 15,15â€²-Monooxygenase 1 Gene Affects Circulating Levels of Carotenoids: A Genome-wide Association Study. American Journal of Human Genetics, 2009, 84, 123-133.	6.2	203
96	A Nonsense Mutation in COQ9 Causes Autosomal-Recessive Neonatal-Onset Primary Coenzyme Q10 Deficiency: A Potentially Treatable Form of Mitochondrial Disease. American Journal of Human Genetics, 2009, 84, 558-566.	6.2	206
97	Genetic susceptibility in Parkinson's disease. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2009, 1792, 597-603.	3.8	37
98	Complete screening for glucocerebrosidase mutations in Parkinson disease patients from Portugal. Neurobiology of Aging, 2009, 30, 1515-1517.	3.1	97
99	Genomewide Association Studies and Human Disease. New England Journal of Medicine, 2009, 360, 1759-1768.	27.0	683
100	Susceptibility genes in movement disorders. Movement Disorders, 2008, 23, 927-934.	3.9	2
101	Novel progranulin mutation: Screening for PGRN mutations in a Portuguese series of FTD/CBS cases. Movement Disorders, 2008, 23, 1269-1273.	3.9	30
102	Genomewide SNP assay reveals mutations underlying Parkinson disease. Human Mutation, 2008, 29, 315-322.	2.5	46
103	Whole genome association studies: Deciding when persistence becomes perseveration. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 131-133.	1.7	6
104	Neurofibrillary tau pathology modulated by genetic variation of Î±â€synuclein. Annals of Neurology, 2008, 64, 348-352.	5.3	22
105	A Genome-Wide Association Study Identifies Protein Quantitative Trait Loci (pQTLs). PLoS Genetics, 2008, 4, e1000072.	3.5	415
106	Population-Based Genome-wide Association Studies Reveal Six Loci Influencing Plasma Levels of Liver Enzymes. American Journal of Human Genetics, 2008, 83, 520-528.	6.2	402
107	Emerging pathways in genetic Parkinson's disease: Potential role of ceramide metabolism in Lewy body disease. FEBS Journal, 2008, 275, 5767-5773.	4.7	121
108	Analysis of Parkinson disease patients from Portugal for mutations in SNCA, PRKN, PINK1 and LRRK2. BMC Neurology, 2008, 8, 1.	1.8	52

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109	Genome-wide association studies in neurological disorders. Lancet Neurology, The, 2008, 7, 1067-1072.	10.2	49
110	Whole Genome Analyses Suggest Ischemic Stroke and Heart Disease Share an Association With Polymorphisms on Chromosome 9p21. Stroke, 2008, 39, 1586-1589.	2.0	153
111	The HapMap. Archives of Neurology, 2008, 65, 319-21.	4.5	7
112	Analysis of Nigerians with Apparently Sporadic Parkinson Disease for Mutations in LRRK2, PRKN and ATXN3. PLoS ONE, 2008, 3, e3421.	2.5	61
113	TDP-43 Is Not a Common Cause of Sporadic Amyotrophic Lateral Sclerosis. PLoS ONE, 2008, 3, e2450.	2.5	60
114	REPORTING AND INTERPRETATION OF GENETIC VARIANTS IN CASES AND CONTROLS. Neurology, 2007, 69, 111-112.	1.1	5
115	Kinase signaling pathways as potential targets in the treatment of Parkinsonâ€™s disease. Expert Review of Proteomics, 2007, 4, 783-792.	3.0	21
116	Genome-wide SNP assay reveals structural genomic variation, extended homozygosity and cell-line induced alterations in normal individuals. Human Molecular Genetics, 2007, 16, 1-14.	2.9	211
117	Linkage Disequilibrium and Association Analysis of ?-Synuclein and Alcohol and Drug Dependence in Two American Indian Populations. Alcoholism: Clinical and Experimental Research, 2007, 31, 070212174136004-???.	2.4	23
118	Genome-wide genotyping in amyotrophic lateral sclerosis and neurologically normal controls: first stage analysis and public release of data. Lancet Neurology, The, 2007, 6, 322-328.	10.2	206
119	A genome-wide genotyping study in patients with ischaemic stroke: initial analysis and data release. Lancet Neurology, The, 2007, 6, 414-420.	10.2	175
120	Genome-wide association studies and ALS: are we there yet?. Lancet Neurology, The, 2007, 6, 841-843.	10.2	4
121	Amyotrophic Lateral Sclerosis: An Emerging Era of Collaborative Gene Discovery. PLoS ONE, 2007, 2, e1254.	2.5	13
122	Conflicting Results Regarding the Semaphorin Gene (SEMA5A) and the Risk for Parkinson Disease. American Journal of Human Genetics, 2006, 78, 1082-1083.	6.2	50
123	Genome-wide genotyping in Parkinson's disease and neurologically normal controls: first stage analysis and public release of data. Lancet Neurology, The, 2006, 5, 911-916.	10.2	360
124	Kinase activity is required for the toxic effects of mutant LRRK2/dardarin. Neurobiology of Disease, 2006, 23, 329-341.	4.4	683
125	Analysis of IFT74as a candidate gene for chromosome 9p-linked ALS-FTD. BMC Neurology, 2006, 6, 44.	1.8	70
126	Association of Î±-synuclein Rep1 polymorphism and Parkinson's disease: Influence of Rep1 on age at onset. Movement Disorders, 2006, 21, 534-539.	3.9	49

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127	Glucocerebrosidase mutations are also found in subjects with early-onset parkinsonism from Venezuela. Movement Disorders, 2006, 21, 282-283.	3.9	64
128	Prion genotypes in Central America suggest selection for the V129 allele. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 33-35.	1.7	3
129	Genetics of Parkinson's disease and parkinsonism. Annals of Neurology, 2006, 60, 389-398.	5.3	281
130	Application of Genome-Wide Single Nucleotide Polymorphism Typing: Simple Association and Beyond. PLoS Genetics, 2006, 2, e150.	3.5	85
131	How genetics research in Parkinson's disease is enhancing understanding of the common idiopathic forms of the disease. Current Opinion in Neurology, 2005, 18, 706-711.	3.6	62
132	Tyrosinase exacerbates dopamine toxicity but is not genetically associated with Parkinson's disease. Journal of Neurochemistry, 2005, 93, 246-256.	3.9	103
133	Defining the ends of Parkin exon 4 deletions in two different families with Parkinson's disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 133B, 120-123.	1.7	18
134	Torsin A haplotype predisposes to idiopathic dystonia. Annals of Neurology, 2005, 57, 765-767.	5.3	73
135	Parkin disease in a Brazilian kindred: Manifesting heterozygotes and clinical follow-up over 10 years. Movement Disorders, 2005, 20, 479-484.	3.9	32
136	Mutation of the Parkin gene in a Persian family: Clinical progression over a 40-year period. Movement Disorders, 2005, 20, 887-890.	3.9	4
137	G2019S dardarin substitution is a common cause of Parkinson's disease in a Portuguese cohort. Movement Disorders, 2005, 20, 1653-1655.	3.9	106
138	A Rare Truncating Mutation in ADH1C (G78Stop) Shows Significant Association With Parkinson Disease in a Large International Sample. Archives of Neurology, 2005, 62, 74.	4.5	57
139	Genetic screening for a single common LRRK2 mutation in familial Parkinson's disease. Lancet, The, 2005, 365, 410-412.	13.7	243
140	A common LRRK2 mutation in idiopathic Parkinson's disease. Lancet, The, 2005, 365, 415-416.	13.7	391
141	The dardarin G2019S mutation is a common cause of Parkinson's disease but not other neurodegenerative diseases. Neuroscience Letters, 2005, 389, 137-139.	2.1	105
142	The law of mass action applied to neurodegenerative disease: a hypothesis concerning the etiology and pathogenesis of complex diseases. Human Molecular Genetics, 2004, 13, 123R-126.	2.9	86
143	A consanguineous Turkish family with early-onset Parkinson's disease and an exon 4 parkin deletion. Movement Disorders, 2004, 19, 812-816.	3.9	20
144	Analysis of an earlyâ€onset Parkinson's disease cohort for DJâ€1 mutations. Movement Disorders, 2004, 19, 796-800.	3.9	71

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145	Smell testing is abnormal in â€˜lubagâ€™ or X-linked dystonia-parkinsonism: a pilot study. Parkinsonism and Related Disorders, 2004, 10, 407-410.	2.2	18
146	No evidence for tau duplications in frontal temporal dementia families showing genetic linkage to the tau locus in which tau mutations have not been found. Neuroscience Letters, 2004, 363, 99-101.	2.1	7
147	Paraoxonase 1 (PON1) gene polymorphisms and Parkinsonâ€™s disease in a Finnish population. Neuroscience Letters, 2004, 367, 168-170.	2.1	26
148	The tau H2 haplotype is almost exclusively Caucasian in origin. Neuroscience Letters, 2004, 369, 183-185.	2.1	102
149	Parkinson's disease and dementia with Lewy bodies: a difference in dose?. Lancet, The, 2004, 364, 1105-1107.	13.7	80
150	Primary hyperhidrosis. Clinical Autonomic Research, 2003, 13, 96-98.	2.5	74
151	Familiality in simple and complex disease. Clinical Autonomic Research, 2003, 13, 88-90.	2.5	1
152	Genes and parkinsonism. Lancet Neurology, The, 2003, 2, 221-228.	10.2	98
153	Earlyâ€onset Parkinson's disease caused by a compound heterozygous DJâ€1 mutation. Annals of Neurology, 2003, 54, 271-274.	5.3	233
154	Mutation at the SCA17 locus is not a common cause of parkinsonism. Parkinsonism and Related Disorders, 2003, 9, 317-320.	2.2	15
155	Ethnic Differences and Disease Phenotypes. Science, 2003, 300, 739-740.	12.6	20
156	Ethnic differences in the expression of neurodegenerative disease: Machado-Joseph disease in Africans and Caucasians. Movement Disorders, 2002, 17, 1068-1071.	3.9	77
157	Phenomenology of ?Lubag? or X-linked dystonia-parkinsonism. Movement Disorders, 2002, 17, 1271-1277.	3.9	92
158	Xâ€linked dystonia (â€œLubagâ€) presenting predominantly with parkinsonism: A more benign phenotype?. Movement Disorders, 2002, 17, 200-202.	3.9	37
159	Lewy bodies and parkinsonism in families withparkin mutations. Annals of Neurology, 2001, 50, 293-300.	5.3	479
160	Refinement of the PARK3 locus on chromosome 2p13 and the analysis of 14 candidate genes. European Journal of Human Genetics, 2001, 9, 659-666.	2.8	46
161	Spinocerebellar Ataxia Type 3 Phenotypically Resembling Parkinson Disease in a Black Family. Archives of Neurology, 2001, 58, 296.	4.5	135
162	The Future of Genetic Analysis of Neurological Disorders. Neurobiology of Disease, 2000, 7, 65-69.	4.4	11

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163	An evaluation of the Team Objective Structured Clinical Examination (TOSCE). Medical Education, 1999, 33, 34-41.	2.1	37
164	Using Exome Sequencing to Reveal Mutations in TREM2 Presenting as a Frontotemporal Dementiaâ€“like Syndrome Without Bone Involvement. JAMA Neurology, 0, , 1.	9.0	6