Kenneth K Kidd

List of Publications by Year
in descending order

166	15,229	41344	19190
papers	citations	49 h-index	118 g-index

168	168	168	14173
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	New Insight into the human genetic diversity in North African populations by genotyping of <scp>SNPs</scp> in <scp>DRD3</scp>, <scp>CSMD1</scp> and <scp>NRG1</scp> genes. Molecular Genetics & Genomic Medicine, 2022, 10, e1871.	1.2	2
2	North Asian population relationships in a global context. Scientific Reports, 2022, 12, 7214.	3.3	3
3	A multipurpose panel of microhaplotypes for use with STR markers in casework. Forensic Science International: Genetics, 2022, 60, 102729.	3.1	6
4	Ancient DNA reveals five streams of migration into Micronesia and matrilocality in early Pacific seafarers. Science, 2022, 377, 72-79.	12.6	13
5	Genetic diversity of the North African population revealed by the typing of SNPs in the DRD2/ANKK1 genomic region. Gene, 2021, 777, 145466.	2.2	2
6	Editorial: Current and Emerging Trends in Human Identification and Molecular Anthropology. Frontiers in Genetics, 2021, 12, 708222.	2.3	2
7	Genetic relationships of Southwest Asian and Mediterranean populations. Forensic Science International: Genetics, 2021, 53, 102528.	3.1	7
8	STAT3 polymorphisms in North Africa and its implication in breast cancer. Molecular Genetics & Genomic Medicine, 2021, 9, e1744.	1.2	1
9	The population genetics characteristics of a 90 locus panel of microhaplotypes. Human Genetics, 2021, 140, 1753-1773.	3.8	15
10	Population genetic data of 74 microhaplotypes in four major U.S. population groups. Forensic Science International: Genetics, 2020, 49, 102398.	3.1	13
11	A sequence-based 74plex microhaplotype assay for analysis of forensic DNA mixtures. Forensic Science International: Genetics, 2020, 49, 102367.	3.1	39
12	The distinctive geographic patterns of common pigmentation variants at the OCA2 gene. Scientific Reports, 2020, 10, 15433.	3.3	8
13	FrogAncestryCalc: A standalone batch likelihood computation tool for ancestry inference panels catalogued in FROG-kb. Forensic Science International: Genetics, 2020, 46, 102237.	3.1	8
14	Validation of novel forensic DNA markers using multiplex microhaplotype sequencing. Forensic Science International: Genetics, 2020, 47, 102275.	3.1	42
15	Genetic relationships of European, Mediterranean, and SW Asian populations using a panel of 55 AISNPs. European Journal of Human Genetics, 2019, 27, 1885-1893.	2.8	22
16	Genetic history of the population of Crete. Annals of Human Genetics, 2019, 83, 373-388.	0.8	2
17	Usefulness of COMT gene polymorphisms in North African populations. Gene, 2019, 696, 186-196.	2.2	7
18	Mixture deconvolution by massively parallel sequencing of microhaplotypes. International Journal of Legal Medicine, 2019, 133, 719-729.	2.2	47

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19	Population relationships based on 170 ancestry SNPs from the combined Kidd and Seldin panels. Scientific Reports, 2019, 9, 18874.	3.3	15
20	A massively parallel sequencing assay of microhaplotypes for mixture deconvolution. Forensic Science International: Genetics Supplement Series, 2019, 7, 522-524.	0.3	4
21	Microhaplotypes in forensic genetics. Forensic Science International: Genetics, 2019, 38, 54-69.	3.1	131
22	Ancestry inference of 96 population samples using microhaplotypes. International Journal of Legal Medicine, 2018, 132, 703-711.	2.2	48
23	Improving ancestry distinctions among Southwest Asian populations. Forensic Science International: Genetics, 2018, 35, 14-20.	3.1	40
24	The redesigned Forensic Research/Reference on Genetics-knowledge base, FROG-kb. Forensic Science International: Genetics, 2018, 33, 33-37.	3.1	21
25	Recent Selection on a Class I ADH Locus Distinguishes Southwest Asian Populations Including Ashkenazi Jews. Genes, 2018, 9, 452.	2.4	9
26	Selecting microhaplotypes optimized for different purposes. Electrophoresis, 2018, 39, 2815-2823.	2.4	39
27	Increasing the reference populations for the 55 AISNP panel: the need and benefits. International Journal of Legal Medicine, 2017, 131, 913-917.	2.2	38
28	Confounding effects of microbiome on the susceptibility of TNFSF15 to Crohnâ€™s disease in the Ryukyu Islands. Human Genetics, 2017, 136, 387-397.	3.8	14
29	Genetics of the peloponnesean populations and the theory of extinction of the medieval peloponnesean Greeks. European Journal of Human Genetics, 2017, 25, 637-645.	2.8	22
30	Evaluating 130 microhaplotypes across a global set of 83 populations. Forensic Science International: Genetics, 2017, 29, 29-37.	3.1	117
31	Microhaplotypes for ancestry prediction. Forensic Science International: Genetics Supplement Series, 2017, 6, e513-e515.	0.3	34
32	A panel of 74 AISNPs: Improved ancestry inference within Eastern Asia. Forensic Science International: Genetics, 2016, 23, 101-110.	3.1	63
33	Evaluating a subset of ancestry informative SNPs for discriminating among Southwest Asian and circum-Mediterranean populations. Forensic Science International: Genetics, 2016, 23, 153-158.	3.1	25
34	Genetic variation in Tunisia in the context of human diversity worldwide. American Journal of Physical Anthropology, 2016, 161, 62-71.	2.1	29
35	Thoughts on Estimating Ancestry. Security Science and Technology, 2016, , 131-144.	0.5	0
36	Proposed nomenclature for microhaplotypes. Human Genomics, 2016, 10, 16.	2.9	48

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37	Minimal SNP overlap among multiple panels of ancestry informative markers argues for more international collaboration. Forensic Science International: Genetics, 2016, 23, 25-32.	3.1	40
38	Genetic markers for massively parallel sequencing in forensics. Forensic Science International: Genetics Supplement Series, 2015, 5, e677-e679.	0.3	12
39	Mongolians in the Genetic Landscape of Central Asia: Exploring the Genetic Relations among Mongolians and Other World Populations. Human Biology, 2015, 87, 73.	0.2	14
40	Criteria for selecting microhaplotypes: mixture detection and deconvolution. Investigative Genetics, 2015, 6, 1.	3.3	117
41	52 additional reference population samples for the 55 AISNP panel. Forensic Science International: Genetics, 2015, 19, 269-271.	3.1	41
42	Extensive sequence variation in the 3â€² untranslated region of theKRASgene in lung and ovarian cancer cases. Cell Cycle, 2014, 13, 1030-1040.	2.6	39
43	Current sequencing technology makes microhaplotypes a powerful new type of genetic marker for forensics. Forensic Science International: Genetics, 2014, 12, 215-224.	3.1	182
44	Haplotype structure and positive selection at TLR1. European Journal of Human Genetics, 2014, 22, 551-557.	2.8	20
45	Application of six IrisPlex SNPs and comparison of two eye color prediction systems in diverse Eurasia populations. International Journal of Legal Medicine, 2014, 128, 447-453.	2.2	35
46	A Form of the Metabolic Syndrome Associated with Mutations inDYRK1B. New England Journal of Medicine, 2014, 370, 1909-1919.	27.0	116
47	An historical perspective on â€œThe world-wide distribution of allele frequencies at the human dopamine D4 receptor locusâ€• Human Genetics, 2014, 133, 431-433.	3.8	12
48	Progress toward an efficient panel of SNPs for ancestry inference. Forensic Science International: Genetics, 2014, 10, 23-32.	3.1	211
49	Maritime route of colonization of Europe. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9211-9216.	7.1	71
50	Inference of human continental origin and admixture proportions using a highly discriminative ancestry informative 41-SNP panel. Investigative Genetics, 2013, 4, 13.	3.3	93
51	First all-in-one diagnostic tool for DNA intelligence: genome-wide inference of biogeographic ancestry, appearance, relatedness, and sex with the Identitas v1 Forensic Chip. International Journal of Legal Medicine, 2013, 127, 559-572.	2.2	51
52	Worldwide Population Variation and Haplotype Analysis at the Serotonin Transporter Gene SLC6A4 and Implications for Association Studies. Biological Psychiatry, 2013, 74, 879-889.	1.3	52
53	ALFRED: an allele frequency resource for research and teaching. Nucleic Acids Research, 2012, 40, D1010-D1015.	14.5	87
54	Expanding data and resources for forensic use of SNPs in individual identification. Forensic Science International: Genetics, 2012, 6, 646-652.	3.1	43

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55	Mini-haplotypes as lineage informative SNPs and ancestry inference SNPs. European Journal of Human Genetics, 2012, 20, 1148-1154.	2.8	45
56	Introducing the Forensic Research/Reference on Genetics knowledge base, FROG-kb. Investigative Genetics, 2012, 3, 18.	3.3	42
57	High diversity and no significant selection signal of human ADH1B gene in Tibet. Investigative Genetics, 2012, 3, 23.	3.3	3
58	Duplicated Gene Evolution of the Primate Alcohol Dehydrogenase Family. Primatology Monographs, 2012, , 149-161.	0.8	2
59	Reconstructing Native American population history. Nature, 2012, 488, 370-374.	27.8	699
60	A global view of the OCA2-HERC2 region and pigmentation. Human Genetics, 2012, 131, 683-696.	3.8	113
61	Diversification of the ADH1B Gene during Expansion of Modern Humans. Annals of Human Genetics, 2011, 75, 497-507.	0.8	27
62	Analyses of a set of 128 ancestry informative single-nucleotide polymorphisms in a global set of 119 population samples. Investigative Genetics, 2011, 2, 1.	3.3	147
63	Single nucleotide polymorphisms and haplotypes in Native American populations. American Journal of Physical Anthropology, 2011, 146, 495-502.	2.1	21
64	RareBRCA1haplotypes including 3â€™UTR SNPs associated with breast cancer risk. Cell Cycle, 2011, 10, 90-99.	2.6	36
65	Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5154-5162.	7.1	394
66	The Distribution and Most Recent Common Ancestor of the 17q21 Inversion in Humans. American Journal of Human Genetics, 2010, 86, 161-171.	6.2	59
67	SNPs for a universal individual identification panel. Human Genetics, 2010, 127, 315-324.	3.8	194
68	Population-specific variation in haplotype composition and heterozygosity at the POLB locus. DNA Repair, 2009, 8, 579-584.	2.8	20
69	Global variation in CYP2C8â€“CYP2C9 functional haplotypes. Pharmacogenomics Journal, 2009, 9, 283-290.	2.0	47
70	Refined Geographic Distribution of the Oriental ALDH2*504Lys (nee 487Lys) Variant. Annals of Human Genetics, 2009, 73, 335-345.	0.8	232
71	Low Allele Frequency of ADH1Bâˆ—47His in West China and Different ADH1B Haplotypes in Western and Eastern Asia. American Journal of Human Genetics, 2009, 84, 92-94.	6.2	7
72	Genetic Landscape of Eurasia and â€œAdmixtureâ€•in Uyghurs. American Journal of Human Genetics, 2009, 85, 934-937.	6.2	49

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73	Multiplexed SNP detection panels for human identification. Forensic Science International: Genetics Supplement Series, 2009, 2, 538-539.	0.3	13
74	Haplotype evolution of SLITRK1, a candidate gene for Gilles de la Tourette Syndrome. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 463-466.	1.7	16
75	A SNP in a let-7 microRNA Complementary Site in the KRAS 3â€² Untranslated Region Increases Nonâ€“Small Cell Lung Cancer Risk. Cancer Research, 2008, 68, 8535-8540.	0.9	609
76	Ethnic Related Selection for an ADH Class I Variant within East Asia. PLoS ONE, 2008, 3, e1881.	2.5	40
77	Conservative evolution in duplicated genes of the primate Class I ADH cluster. Gene, 2007, 392, 64-76.	2.2	40
78	Evidence of Positive Selection on a Class I ADH Locus. American Journal of Human Genetics, 2007, 80, 441-456.	6.2	110
79	Geographically Separate Increases in the Frequency of the Derived ADH1B*47His Allele in Eastern and Western Asia. American Journal of Human Genetics, 2007, 81, 842-846.	6.2	90
80	Significant variation in haplotype block structure but conservation in tagSNP patterns among global populations. European Journal of Human Genetics, 2007, 15, 302-312.	2.8	72
81	Candidate SNPs for a universal individual identification panel. Human Genetics, 2007, 121, 305-317.	3.8	96
82	ALFRED: an allele frequency database for microevolutionary studies. Evolutionary Bioinformatics, 2007, 1, 1-10.	1.2	9
83	Developing a SNP panel for forensic identification of individuals. Forensic Science International, 2006, 164, 20-32.	2.2	227
84	ALFRED: An Allele Frequency Database for Microevolutionary Studies. Evolutionary Bioinformatics, 2005, 1, 117693430500100.	1.2	12
85	Human genome diversity project. Evolutionary Anthropology, 2005, 1, 80-82.	3.4	13
86	Linkage disequilibrium patterns vary substantially among populations. European Journal of Human Genetics, 2005, 13, 677-686.	2.8	138
87	Considerable Haplotype Diversity within the 23kb Encompassing the ADH7 Gene. Alcoholism: Clinical and Experimental Research, 2005, 29, 2091-2100.	2.4	18
88	Use of autosomal loci for clustering individuals and populations of East Asian origin. Human Genetics, 2005, 117, 511-519.	3.8	42
89	HAPLOT: a graphical comparison of haplotype blocks, tagSNP sets and SNP variation for multiple populations. Bioinformatics, 2005, 21, 3938-3939.	4.1	32
90	Implications of biogeography of human populations for 'race' and medicine. Nature Genetics, 2004, 36, S21-S27.	21.4	403

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91	The evolution and population genetics of the ALDH2 locus: random genetic drift, selection, and low levels of recombination. Annals of Human Genetics, 2004, 68, 93-109.	0.8	166
92	Response to Comment on "Genetic Structure of Human Populations". Science, 2003, 300, 1877c-1877.	12.6	20
93	A Human Genome Diversity Cell Line Panel. Science, 2002, 296, 261-262.	12.6	907
94	Genetic Structure of Human Populations. Science, 2002, 298, 2381-2385.	12.6	2,434
95	Genomewide Scan of Hoarding in Sib Pairs in Which Both Sibs Have Gilles de la Tourette Syndrome. American Journal of Human Genetics, 2002, 70, 896-904.	6.2	174
96	A Global Perspective on Genetic Variation at the ADH Genes Reveals Unusual Patterns of Linkage Disequilibrium and Diversity. American Journal of Human Genetics, 2002, 71, 84-99.	6.2	261
97	ALFRED: An allele frequency database for anthropology. American Journal of Physical Anthropology, 2002, 119, 77-83.	2.1	58
98	Population variation in linkage disequilibrium across the COMT gene considering promoter region and coding region variation. Human Genetics, 2002, 111, 521-537.	3.8	70
99	A Proline-Threonine Substitution in Codon 351 of ADH1C Is Common in Native Americans. Alcoholism: Clinical and Experimental Research, 2002, 26, 1759-1763.	2.4	33
100	A Proline-Threonine Substitution in Codon 351 of ADH1C Is Common in Native Americans. Alcoholism: Clinical and Experimental Research, 2002, 26, 1759-1763.	2.4	0
101	A proline-threonine substitution in codon 351 of ADH1C is common in Native Americans. Alcoholism: Clinical and Experimental Research, 2002, 26, 1759-63.	2.4	12
102	Identifying conservation units within captive chimpanzee populations. American Journal of Physical Anthropology, 2000, 111, 25-44.	2.1	40
103	Evolution of exon 1 of the dopamine D4 receptor (DRD4) gene in primates. The Journal of Experimental Zoology, 2000, 288, 32-38.	1.4	17
104	Haplotypes and Linkage Disequilibrium at the Phenylalanine Hydroxylase Locus, PAH, in a Global Representation of Populations. American Journal of Human Genetics, 2000, 66, 1882-1899.	6.2	160
105	Identifying conservation units within captive chimpanzee populationsA previous version of this paper was awarded the 1995 Sherwood Washburn Prize for a studen-presented paper to A.S.D.. American Journal of Physical Anthropology, 2000, 111, 25.	2.1	5
106	A Primate Genome Project Deserves High Priority. Science, 2000, 289, 1295b-1296.	12.6	31
107	Experience and Preliminary Results in Human Genome Diversity Research. Politics and the Life Sciences, 1999, 18, 314-316.	0.7	2
108	No Association Between DRD2 Locus and Alcoholism After Controlling the ADH and ALDH Genotypes in Chinese Han Population. Alcoholism: Clinical and Experimental Research, 1999, 23, 592-599.	2.4	42

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109	Genome scan for linkage to Gilles de la Tourette syndrome. , 1999, 88, 437-445.		82
110	Genealogy reconstruction from short tandem repeat genotypes in an Amazonian population. , 1999, 108, 137-146.		13
111	Evolution of the HOXB6 intergenic region: Motif conservation at the lateral plate mesoderm (LPM) enhancer element. , 1999, 285, 170-176.		3
112	Linkage Disequilibrium at the ADH2 and ADH3 Loci and Risk of Alcoholism. American Journal of Human Genetics, 1999, 64, 1147-1157.	6.2	239
113	A more powerful method to evaluate p-values in GENEHUNTER. Genetic Epidemiology, 1999, 17, S415-S420.	1.3	2
114	No Association Between DRD2 Locus and Alcoholism After Controlling the ADH and ALDH Genotypes in Chinese Han Population. Alcoholism: Clinical and Experimental Research, 1999, 23, 592.	2.4	5
115	ALFRED: A WEB-ACCESSIBLE ALLELE FREQUENCY DATABASE. , 1999, , 639-50.		12
116	A global survey of haplotype frequencies and linkage disequilibrium at the DRD2 locus. Human Genetics, 1998, 103, 211-227.	3.8	197
117	Long CAG/CTG repeats in mice. Mammalian Genome, 1998, 9, 392-393.	2.2	2
118	Genetic Structure of the Ancestral Population of Modern Humans. Journal of Molecular Evolution, 1998, 47, 146-155.	1.8	100
119	Analyses of Cross Species Polymerase Chain Reaction Products to Infer the Ancestral State of Human Polymorphisms. DNA Sequence, 1998, 8, 317-327.	0.7	34
120	Evolution of a D2 Dopamine Receptor Intron Within the Great Apes and Humans. DNA Sequence, 1998, 8, 289-301.	0.7	11
121	Survey of Maximum CTG/CAG Repeat Lengths in Humans and Non-Human Primates: Total Genome Scan in Populations Using the Repeat Expansion Detection Method. Human Molecular Genetics, 1997, 6, 403-408.	2.9	28
122	The dopamine D4 receptor gene (DRD4) is not associated with alcoholism in three Taiwanese populations: Six polymorphisms tested separately and as haplotypes. Biological Psychiatry, 1997, 41, 394-405.	1.3	48
123	Editorial: Can we find genes for schizophrenia?. , 1997, 74, 104-111.		31
124	Rapid molecular haplotyping of the first exon of the human dopamine D4 receptor gene by heteroduplex analysis. , 1997, 74, 91-94.		20
125	Population genetics of a functional variant of the dopamine Î²-hydroxylase gene (DBH). American Journal of Medical Genetics Part A, 1997, 74, 374-379.	2.4	104
126	Detection of a large CTG/CAG trinucleotide repeat expansion in a Danish schizophrenia kindred. , 1997, 74, 546-548.		15

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127	Detection of major genes underlying several quantitative traits associated with a common disease using different ascertainment schemes. Genetic Epidemiology, 1997, 14, 809-814.	1.3	8
128	DRD2 Haplotypes Containing the TaqI A1 Allele: Implications for Alcoholism Research. Alcoholism: Clinical and Experimental Research, 1996, 20, 697-705.	2.4	63
129	Nucleotide polymorphism, effective population size, and dispersal distances in the yellow baboons (Papio hamadryas cynocephalus) of Mikumi National Park, Tanzania. , 1996, 38, 157-168.		16
130	Chromosomal localization of long trinucleotide repeats in the human genome by fluorescence in situ hybridization. Nature Genetics, 1996, 12, 183-185.	21.4	36
131	Minisatellite diversity supports a recent African origin for modern humans. Nature Genetics, 1996, 13, 154-160.	21.4	173
132	Molecular haplotyping of genetic markers 10 kb apart by allele-specific long-range PCR. Nucleic Acids Research, 1996, 24, 4841-4843.	14.5	137
133	Associations of disease with genetic markers: DÃ©jÃ vu all over again. American Journal of Medical Genetics Part A, 1993, 48, 71-73.	2.4	160
134	Alleles at the dopamine D4 receptor locus do not contribute to the genetic susceptibility to schizophrenia in a large Swedish kindred. American Journal of Medical Genetics Part A, 1993, 48, 218-222.	2.4	56
135	A new polymorphic marker (D10S97) tightly linked to the multiple endocrine neoplasia type 2A (MEN2A) locus. Human Genetics, 1993, 90, 516-20.	3.8	1
136	A hypervariable segment in the human dopamine receptor D₄ (DRD4) gene. Human Molecular Genetics, 1993, 2, 767-773.	2.9	524
137	Population frequencies of the A1 allele at the dopamine D2 receptor locus. Biological Psychiatry, 1993, 34, 204-209.	1.3	119
138	Response : Forensic DNA Typing. Science, 1992, 255, 1052-1053.	12.6	1
139	Trials and tribulations in the search for genes causing neuropsychiatric disorders. Biodemography and Social Biology, 1991, 38, 163-178.	1.0	1
140	Segregation and Linkage Analyses of Tourette's Syndrome and Related Disorders. Journal of the American Academy of Child and Adolescent Psychiatry, 1990, 29, 195-203.	0.5	133
141	The human genome map 1990. Science, 1990, 250, suppl-4.	12.6	15
142	Re-evaluation of the linkage relationship between chromosome 11p loci and the gene for bipolar affective disorder in the Old Order Amish. Nature, 1989, 342, 238-243.	27.8	448
143	Linkage Analysis in Psychiatry. International Review of Psychiatry, 1989, 1, 231-242.	2.8	4
144	Some effects of selection strategies on linkage analysis. Genetic Epidemiology, 1988, 5, 289-297.	1.3	9

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145	Predicting genotypes at loci for autosomal recessive disorders using linked genetic markers: application to Wilson's disease. Human Genetics, 1988, 79, 109-117.	3.8	20
146	Evidence against linkage of schizophrenia to markers on chromosome 5 in a northern Swedish pedigree. Nature, 1988, 336, 167-170.	27.8	405
147	Family-Genetic Studies and Identification of Valid Diagnostic Categories in Adult and Child Psychiatry. British Journal of Psychiatry, 1987, 151, 39-44.	2.8	19
148	Bipolar affective disorders linked to DNA markers on chromosome 11. Nature, 1987, 325, 783-787.	27.8	827
149	Population genetics of a disease. Nature, 1987, 327, 282-283.	27.8	23
150	Searching for Major Genes for Psychiatric Disorders. Novartis Foundation Symposium, 1987, 130, 184-196.	1.1	3
151	Development of a map of chromosome 11p. Genetic Epidemiology, 1986, 3, 153-158.	1.3	17
152	Genetics of a wild population of rhesus monkeys (Macaca mulatta): II. The Dunga Gali population in species-wide perspective. American Journal of Physical Anthropology, 1986, 71, 129-140.	2.1	14
153	Genetic analysis workshop III: Sampling considerations and assumptions in gene mapping. Genetic Epidemiology, 1985, 2, 219-220.	1.3	0
154	The detection of major loci by segregation and linkage analysis: A simulation study. Genetic Epidemiology, 1984, 1, 285-296.	1.3	39
155	Utilizing automated methods to improve estimates of recurrence risk with linked genetic markers. American Journal of Medical Genetics Part A, 1984, 17, 621-625.	2.4	3
156	The genetics of a wild population of rhesus monkeys (Macaca mulatta). I. Genetic variability within and between social groups. American Journal of Physical Anthropology, 1984, 63, 341-360.	2.1	61
157	Some Environmental Factors and Hypotheses for Stuttering in Families with Several Stutterers. Journal of Speech, Language, and Hearing Research, 1984, 27, 543-548.	1.6	36
158	Recovery and Persistence of Stuttering among Relatives of Stutterers. The Journal of Speech and Hearing Disorders, 1983, 48, 402-409.	1.3	35
159	Language Onset and Concomitant Speech and Language Problems in Subgroups of Stutterers and Their Siblings. Journal of Speech, Language, and Hearing Research, 1982, 25, 482-486.	1.6	12
160	Analysis of the Sibship Patterns of Stutterers. Journal of Speech, Language, and Hearing Research, 1981, 24, 460-462.	1.6	11
161	Dermo-distortive urticaria: An autosomal dominant dermatologic disorder. American Journal of Medical Genetics Part A, 1981, 9, 307-315.	2.4	24
162	Genetic linkage analysis of dermo-distortive urticaria. American Journal of Medical Genetics Part A, 1981, 9, 317-321.	2.4	1

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163	The effects of variable ageâ€ofâ€onset and diagnostic criteria on the estimates of linkage: An example using manicâ€depressive illness and color blindness. Social Biology, 1980, 27, 1-10.	0.5	37
164	Familial Stuttering Patterns Are Not Related to One Measure of Severity. Journal of Speech, Language, and Hearing Research, 1980, 23, 539-545.	1.6	24
165	The value of dual mating data in estimating genetic parameters. Annals of Human Genetics, 1978, 41, 477-480.	0.8	5
166	Increased frequency of heterozygotes for Î±1 antitrypsin variants in individuals with either sex chromosome mosaicism or trisomy 21. Nature, 1976, 260, 320-321.	27.8	24