Masatoshi Nei

List of Publications by Year
in descending order

173 papers	139,362 citations	5896 81 h-index	5120 166 g-index
178 all docs	178 docs citations	178 times ranked	95005 citing authors

#	Article	IF	Citations
1	The Reproducibility of an Inferred Tree and the Diploidization of Gene Segregation after Genome Duplication. Genome Biology and Evolution, 2020, 12, 3792-3796.	2.5	0
2	The Reliability and Stability of an Inferred Phylogenetic Tree from Empirical Data. Molecular Biology and Evolution, 2017, 34, msw272.	8.9	4
3	Efficiencies of the NJp, Maximum Likelihood, and Bayesian Methods of Phylogenetic Construction for Compositional and Noncompositional Genes. Molecular Biology and Evolution, 2016, 33, 1618-1624.	8.9	30
4	My Memory of Walter Fitch (1929-2011) and Starting Molecular Biology and Evolution. Molecular Biology and Evolution, 2014, 31, 1329-1332.	8.9	0
5	POPTREEW: Web Version of POPTREE for Constructing Population Trees from Allele Frequency Data and Computing Some Other Quantities. Molecular Biology and Evolution, 2014, 31, 1622-1624.	8.9	156
6	Evolution of the Sex-lethal Gene in Insects and Origin of the Sex-Determination System in Drosophila. Journal of Molecular Evolution, 2014, 78, 50-65.	1.8	16
7	Random fluctuation of selection coefficients and the extent of nucleotide variation in human populations. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10676-10681.	7.1	9
8	Origins and Evolution of MicroRNA Genes in Plant Species. Genome Biology and Evolution, 2012, 4, 230-239.	2.5	231
9	MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution, 2011, 28, 2731-2739.	8.9	36,550
10	Evolutionary Changes of the Target Sites of Two MicroRNAs Encoded in the Hox Gene Cluster of Drosophila and Other Insect Species. Genome Biology and Evolution, 2011, 3, 129-139.	2.5	18
11	Roles of Mutation and Selection in Speciation: From Hugo de Vries to the Modern Genomic Era. Genome Biology and Evolution, 2011, 3, 812-829.	2.5	66
12	Origins and Evolution of MicroRNA Genes in Drosophila Species. Genome Biology and Evolution, 2010, 2, 180-189.	2.5	101
13	Analysis of the Immunoglobulin Light Chain Genes in Zebra Finch: Evolutionary Implications. Molecular Biology and Evolution, 2010, 27, 113-120.	8.9	30
14	POPTREE2: Software for Constructing Population Trees from Allele Frequency Data and Computing Other Population Statistics with Windows Interface. Molecular Biology and Evolution, 2010, 27, 747-752.	8.9	587
15	The Neutral Theory of Molecular Evolution in the Genomic Era. Annual Review of Genomics and Human Genetics, 2010, 11, 265-289.	6.2	197
16	Is positive selection responsible for the evolution of a duplicate UV-sensitive opsin gene in <i>Heliconius</i> butterflies?. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, E96; author reply E97.	7.1	6
17	Reliabilities of identifying positive selection by the branch-site and the site-prediction methods. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6700-6705.	7.1	136
18	Evolution of F-box genes in plants: Different modes of sequence divergence and their relationships with functional diversification. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 835-840.	7.1	268

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19	Genomic Drift and Evolution of Microsatellite DNAs in Human Populations. Molecular Biology and Evolution, 2009, 26, 1835-1840.	8.9	12
20	Genomic organization and evolution of immunoglobulin kappa gene enhancers and kappa deleting element in mammals. Molecular Immunology, 2009, 46, 3171-3177.	2.2	20
21	Evolutionary dynamics of the immunoglobulin heavy chain variable region genes in vertebrates. Immunogenetics, 2008, 60, 47-55.	2.4	53
22	MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences. Briefings in Bioinformatics, 2008, 9, 299-306.	6.5	3,073
23	The evolution of animal chemosensory receptor gene repertoires: roles of chance and necessity. Nature Reviews Genetics, 2008, 9, 951-963.	16.3	533
24	Ultraconserved coding regions outside the homeobox of mammalian Hox genes. BMC Evolutionary Biology, 2008, 8, 260.	3.2	17
25	Empirical Tests of the Reliability of Phylogenetic Trees Constructed With Microsatellite DNA. Genetics, 2008, 178, 385-392.	2.9	84
26	Origins and Evolution of the Formin Multigene Family That Is Involved in the Formation of Actin Filaments. Molecular Biology and Evolution, 2008, 25, 2717-2733.	8.9	65
27	Evolutionary redefinition of immunoglobulin light chain isotypes in tetrapods using molecular markers. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16647-16652.	7.1	54
28	Evolutionary dynamics of olfactory receptor genes in Drosophila species. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7122-7127.	7.1	109
29	The new mutation theory of phenotypic evolution. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12235-12242.	7.1	196
30	The origins and early evolution of DNA mismatch repair genes—multiple horizontal gene transfers and co-evolution. Nucleic Acids Research, 2007, 35, 7591-7603.	14.5	94
31	Genomic drift and copy number variation of sensory receptor genes in humans. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20421-20426.	7.1	139
32	MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) Software Version 4.0. Molecular Biology and Evolution, 2007, 24, 1596-1599.	8.9	25,988
33	Extensive Gains and Losses of Olfactory Receptor Genes in Mammalian Evolution. PLoS ONE, 2007, 2, e708.	2.5	270
34	Heterogeneous but conserved natural killer receptor gene complexes in four major orders of mammals. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3192-3197.	7.1	86
35	Evolutionary dynamics of olfactory and other chemosensory receptor genes in vertebrates. Journal of Human Genetics, 2006, 51, 505-517.	2.3	199
36	Origins and evolution of the recA/RAD51 gene family: Evidence for ancient gene duplication and endosymbiotic gene transfer. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10328-10333.	7.1	268

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37	Concerted and Birth-and-Death Evolution of Multigene Families. Annual Review of Genetics, 2005, 39, 121-152.	7.6	1,150
38	Origin and evolution of the Ig-like domains present in mammalian leukocyte receptors: insights from chicken, frog, and fish homologues. Immunogenetics, 2005, 57, 151-157.	2.4	36
39	Evolutionary Change of the Numbers of Homeobox Genes in Bilateral Animals. Molecular Biology and Evolution, 2005, 22, 2386-2394.	8.9	79
40	Evolutionary dynamics of olfactory receptor genes in fishes and tetrapods. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6039-6044.	7.1	278
41	Origin and evolution of the chicken leukocyte receptor complex. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4057-4062.	7.1	36
42	A simple method for predicting the functional differentiation of duplicate genes and its application to MIKC-type MADS-box genes. Nucleic Acids Research, 2005, 33, e12-e12.	14.5	23
43	Selectionism and Neutralism in Molecular Evolution. Molecular Biology and Evolution, 2005, 22, 2318-2342.	8.9	293
44	Comparative evolutionary analysis of olfactory receptor gene clusters between humans and mice. Gene, 2005, 346, 13-21.	2.2	105
45	Evolutionary changes of the number of olfactory receptor genes in the human and mouse lineages. Gene, 2005, 346, 23-28.	2.2	54
46	Eighty percent of proteins are different between humans and chimpanzees. Gene, 2005, 346, 215-219.	2.2	32
47	Rapid expansion of killer cell immunoglobulin-like receptor genes in primates and their coevolution with MHC Class I genes. Gene, 2005, 347, 149-159.	2.2	36
48	Bottlenecks, Genetic Polymorphism and SpeciationThis article is dedicated to the memory of Takeo Maruyama.. Genetics, 2005, 170, 1-4.	2.9	31
49	Concerted and Nonconcerted Evolution of the Hsp70 Gene Superfamily in Two Sibling Species of Nematodes. Molecular Biology and Evolution, 2004, 21, 498-505.	8.9	67
50	False-Positive Selection Identified by ML-Based Methods: Examples from the Sig1 Gene of the Diatom Thalassiosira weissflogii and the tax Gene of a Human T-cell Lymphotropic Virus. Molecular Biology and Evolution, 2004, 21, 914-921.	8.9	107
51	Prospects for inferring very large phylogenies by using the neighbor-joining method. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11030-11035.	7.1	4,158
52	Type I MADS-box genes have experienced faster birth-and-death evolution than type II MADS-box genes in angiosperms. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1910-1915.	7.1	209
53	Genomic organization and evolutionary analysis of Ly49 genes encoding the rodent natural killer cell receptors: rapid evolution by repeated gene duplication. Immunogenetics, 2004, 56, 343-54.	2.4	32
54	MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. Briefings in Bioinformatics, 2004, 5, 150-163.	6.5	10,598

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55	Reanalysis of Murphy et al.?s Data Gives Various Mammalian Phylogenies and Suggests Overcredibility of Bayesian Trees. Journal of Molecular Evolution, 2003, 57, S290-S296.	1.8	36
56	Antiquity and Evolution of the MADS-Box Gene Family Controlling Flower Development in Plants. Molecular Biology and Evolution, 2003, 20, 1435-1447.	8.9	122
57	Estimation of Divergence Times for Major Lineages of Primate Species. Molecular Biology and Evolution, 2003, 20, 424-434.	8.9	345
58	Evolution of olfactory receptor genes in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12235-12240.	7.1	232
59	Birth-and-Death Evolution in Primate MHC Class I Genes: Divergence Time Estimates. Molecular Biology and Evolution, 2003, 20, 601-609.	8.9	70
60	Acceleration of genomic evolution caused by enhanced mutation rate in endocellular symbionts. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12944-12948.	7.1	151
61	Overcredibility of molecular phylogenies obtained by Bayesian phylogenetics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16138-16143.	7.1	598
62	Simulation Study of the Reliability and Robustness of the Statistical Methods for Detecting Positive Selection at Single Amino Acid Sites. Molecular Biology and Evolution, 2002, 19, 1865-1869.	8.9	91
63	Purifying Selection and Birth-and-death Evolution in the Histone H4 Gene Family. Molecular Biology and Evolution, 2002, 19, 689-697.	8.9	98
64	The Wilhelmine E. Key 2001 Invitational Lecture. Estimation of Divergence Times for a Few Mammalian and Several Primate Species. , 2002, 93, 157-164.		59
65	Molecular Evolution of the Nontandemly Repeated Genes of the Histone 3 Multigene Family. Molecular Biology and Evolution, 2002, 19, 68-75.	8.9	86
66	Adaptive Evolution of Variable Region Genes Encoding an Unusual Type of Immunoglobulin in Camelids. Molecular Biology and Evolution, 2002, 19, 205-215.	8.9	48
67	Reliabilities of Parsimony-based and Likelihood-based Methods for Detecting Positive Selection at Single Amino Acid Sites. Molecular Biology and Evolution, 2001, 18, 2179-2185.	8.9	79
68	Evolutionary Dynamics of the T-Cell Receptor VB Gene Family as Inferred from the Human and Mouse Genomic Sequences. Molecular Biology and Evolution, 2001, 18, 503-513.	8.9	34
69	Positive Selection in the Evolution of Mammalian Interleukin-2 Genes. Molecular Biology and Evolution, 2000, 17, 1413-1416.	8.9	36
70	An Unusual Form of Purifying Selection in a Sperm Protein. Molecular Biology and Evolution, 2000, 17, 278-283.	8.9	69
71	Efficiencies of Fast Algorithms of Phylogenetic Inference Under the Criteria of Maximum Parsimony, Minimum Evolution, and Maximum Likelihood When a Large Number of Sequences Are Used. Molecular Biology and Evolution, 2000, 17, 1251-1258.	8.9	269
72	Accuracies of ancestral amino acid sequences inferred by the parsimony, likelihood, and distance methods. Journal of Molecular Evolution, 1997, 44, S139-S146.	1.8	256

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73	Natural selection at the class II major histocompatibility complex loci of mammals. , 1997, , 89-97.		70
74	PHYLOGENETIC ANALYSIS IN MOLECULAR EVOLUTIONARY GENETICS. Annual Review of Genetics, 1996, 30, 371-403.	7.6	297
75	Evolution of Antennapedia-Class Homeobox Genes. Genetics, 1996, 142, 295-303.	2.9	130
76	Genetic Distances and Reconstruction of Phylogenetic Trees From Microsatellite DNA. Genetics, 1996, 144, 389-399.	2.9	1,038
77	Unbiased estimates of the number of nucleotide substitutions when substitution rate varies among different sites. Journal of Molecular Evolution, 1994, 38, 295-9.	1.8	81
78	MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. Bioinformatics, 1994, 10, 189-191.	4.1	711
79	Inconsistency of the maximum parsimony method when the rate of nucleotide substitution is constant. Journal of Molecular Evolution, 1994, 39, 210-218.	1.8	41
80	Effective population size, genetic diversity, and coalescence time in subdivided populations. Journal of Molecular Evolution, 1993, 37, 240-4.	1.8	147
81	Evolutionary relationships of the classes of major histocompatibility complex genes. Immunogenetics, 1993, 37, 337-346.	2.4	57
82	Statistical properties of the ordinary least-squares, generalized least-squares, and minimum-evolution methods of phylogenetic inference. Journal of Molecular Evolution, 1992, 35, 367-375.	1.8	318
83	Neutral mutation hypothesis test. Nature, 1991, 354, 115-116.	27.8	24
84	Evolutionary Relationships of Human Populations at the Molecular Level. , 1991, , 415-428.		13
85	Relationships between intrapopulational and interpopulational genetic diversity in man. Annals of Human Biology, 1990, 17, 501-513.	1.0	45
86	Genetic Relationships of Europeans, Asians and Africans and the Origin of Modern <i>Homo sapiens</i>. Human Heredity, 1989, 39, 276-281.	0.8	64
87	Pattern of nucleotide substitution at major histocompatibility complex class I loci reveals overdominant selection. Nature, 1988, 335, 167-170.	27.8	1,912
88	Accumulation of mutations in sexual and asexual populations. Genetical Research, 1987, 49, 135-146.	0.9	153
89	Definition and Estimation of Fixation Indices. Evolution; International Journal of Organic Evolution, 1986, 40, 643.	2.3	71
90	DEFINITION AND ESTIMATION OF FIXATION INDICES. Evolution; International Journal of Organic Evolution, 1986, 40, 643-645.	2.3	164

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91	Genetic variation in subdivided populations and conservation genetics. Heredity, 1986, 57, 189-198.	2.6	167
92	The number of nucleotides required to determine the branching order of three species, with special reference to the human-chimpanzee-gorilla divergence. Journal of Molecular Evolution, 1986, 24, 189-204.	1.8	232
93	Phylogenetic analysis of polymorphic DNA sequences at the Adh locus inDrosophila melanogaster and its sibling species. Journal of Molecular Evolution, 1985, 22, 289-300.	1.8	63
94	GENE GENEALOGY AND VARIANCE OF INTERPOPULATIONAL NUCLEOTIDE DIFFERENCES. Genetics, 1985, 110, 325-344.	2.9	292
95	On the Positive Identification of Paternity. Human Heredity, 1984, 34, 258-260.	0.8	2
96	Extent of Protein Polymorphism and the Neutral Mutation Theory. , 1984, , 73-118.		179
97	Genetic Polymorphism and Neomutationism. Lecture Notes in Biomathematics, 1984, , 214-241.	0.3	8
98	Accuracy of estimated phylogenetic trees from molecular data. Journal of Molecular Evolution, 1983, 19, 153-170.	1.8	2,194
99	A Note on Positive Identification of Paternity by Using Genetic Markers. Human Heredity, 1983, 33, 29-35.	0.8	12
100	MODELS OF EVOLUTION OF REPRODUCTIVE ISOLATION. Genetics, 1983, 103, 557-579.	2.9	180
101	MAXIMUM LIKELIHOOD ESTIMATION OF THE NUMBER OF NUCLEOTIDE SUBSTITUTIONS FROM RESTRICTION SITES DATA. Genetics, 1983, 105, 207-217.	2.9	487
102	Genetic differentiation of quantitative characters between populations or species: I. Mutation and random genetic drift. Genetical Research, 1982, 39, 303-314.	0.9	111
103	Biases of the estimates of DNA divergence obtained by the restriction enzyme technique. Journal of Molecular Evolution, 1982, 18, 115-120.	1.8	88
104	Accuracy of estimated phylogenetic trees from molecular data. Journal of Molecular Evolution, 1982, 18, 387-404.	1.8	220
105	Estimation of average number of nucleotide substitutions when the rate of substitution varies with nucleotide. Journal of Molecular Evolution, 1982, 18, 414-422.	1.8	282
106	Positive selection causes purifying selection (reply). Nature, 1982, 295, 630-630.	27.8	3
107	Statistical properties of the Jukes-Holmquist method of estimating the number of nucleotide substitutions: Reply to Holmquist and Conroy's criticism. Journal of Molecular Evolution, 1981, 17, 182-187.	1.8	0
108	Polymorphism and evolution of the Rh blood groups. Japanese Journal of Human Genetics, 1981, 26, 263-278.	0.8	8

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109	Pseudogenes as a paradigm of neutral evolution. Nature, 1981, 292, 237-239.	27.8	487
110	DNA POLYMORPHISM DETECTABLE BY RESTRICTION ENDONUCLEASES. Genetics, 1981, 97, 145-163.	2.9	1,167
111	GENETIC VARIABILITY MAINTAINED BY MUTATION AND OVERDOMINANT SELECTION IN FINITE POPULATIONS. Genetics, 1981, 98, 441-459.	2.9	124
112	GENETIC DRIFT AND ESTIMATION OF EFFECTIVE POPULATION SIZE. Genetics, 1981, 98, 625-640.	2.9	459
113	STATISTICAL STUDIES OF PROTEIN POLYMORPHISM. Genetics, 1981, 97, 494A-494A.	2.9	3
114	Non-random association between electromorphs and inversion chromosomes in finite populations. Genetical Research, 1980, 35, 65-83.	0.9	85
115	Stochastic Theory of Population Genetics and Evolution. Lecture Notes in Biomathematics, 1980, , 17-47.	0.3	8
116	STATISTICAL STUDIES ON PROTEIN POLYMORPHISM IN NATURAL POPULATIONS. III. DISTRIBUTION OF ALLELE FREQUENCIES AND THE NUMBER OF ALLELES PER LOCUS. Genetics, 1980, 94, 1039-1063.	2.9	125
117	PROTEIN POLYMORPHISM AND THE SAS-CFF MODEL. Genetics, 1980, 94, 1085-1087.	2.9	8
118	Augmentation algorithm: A reply to holmquist. Journal of Molecular Evolution, 1979, 13, 167-171.	1.8	5
119	Proportion of informative families for genetic counseling with linked marker genes. Japanese Journal of Human Genetics, 1979, 24, 131-142.	0.8	14
120	POPULATION DYNAMICS OF SEX-DETERMINING ALLELES IN HONEY BEES AND SELF-INCOMPATIBILITY ALLELES IN PLANTS. Genetics, 1979, 91, 609-626.	2.9	147
121	Goodman et al.'s method for augmenting the number of nucleotide substitutions. Journal of Molecular Evolution, 1978, 11, 67-73.	1.8	22
122	The theory of genetic distance and evolution of human races. Japanese Journal of Human Genetics, 1978, 23, 341-369.	0.8	154
123	Nonrandom amino acid substitution and estimation of the number of nucleotide substitutions in evolution. Journal of Molecular Evolution, 1978, 11, 333-347.	1.8	16
124	STATISTICAL STUDIES ON PROTEIN POLYMORPHISM IN NATURAL POPULATIONS II. GENE DIFFERENTIATION BETWEEN POPULATIONS. Genetics, 1978, 88, 367-390.	2.9	69
125	ESTIMATION OF AVERAGE HETEROZYGOSITY AND GENETIC DISTANCE FROM A SMALL NUMBER OF INDIVIDUALS. Genetics, 1978, 89, 583-590.	2.9	9,389
126	BOTTLENECK EFFECTS ON AVERAGE HETEROZYGOSITY AND GENETIC DISTANCE WITH THE STEPWISE MUTATION MODEL. Evolution; International Journal of Organic Evolution, 1977, 31, 347-356.	2.3	246

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127	Bottleneck Effects on Average Heterozygosity and Genetic Distance with the Stepwise Mutation Model. Evolution; International Journal of Organic Evolution, 1977, 31, 347.	2.3	128
128	Mean and variance of FST in a finite number of incompletely isolated populations. Theoretical Population Biology, 1977, 11, 291-306.	1.1	88
129	Drift variances of FST and GST statistics obtained from a finite number of isolated populations. Theoretical Population Biology, 1977, 11, 307-325.	1.1	93
130	<i>F</i>â€statistics and analysis of gene diversity in subdivided populations. Annals of Human Genetics, 1977, 41, 225-233.	0.8	1,103
131	Standard error of immunological dating of evolutionary time. Journal of Molecular Evolution, 1977, 9, 203-211.	1.8	43
132	STATISTICAL STUDIES ON PROTEIN POLYMORPHISM IN NATURAL POPULATIONS I. DISTRIBUTION OF SINGLE LOCUS HETEROZYGOSITY. Genetics, 1977, 86, 455-483.	2.9	147
133	PERSISTENCE OF COMMON ALLELES IN TWO RELATED POPULATIONS OR SPECIES. Genetics, 1977, 86, 901-914.	2.9	47
134	EFFECTS OF RANDOM FLUCTUATION OF SELECTION INTENSITY ON GENETIC VARIABILITY IN A FINITE POPULATION. Japanese Journal of Genetics, 1976, 51, 355-369.	1.0	21
135	Testing the neutral mutation hypothesis by distribution of single locus heterozygosity. Nature, 1976, 262, 491-493.	27.8	71
136	Electrophoretically silent alleles in a finite population. Journal of Molecular Evolution, 1976, 8, 381-385.	1.8	15
137	Empirical relationship between the number of nucleotide substitutions and interspecific identity of amino acid sequences in some proteins. Journal of Molecular Evolution, 1976, 7, 313-323.	1.8	22
138	The transient distribution of allele frequencies under mutation pressure. Genetical Research, 1976, 28, 205-214.	0.9	57
139	HIDDEN GENETIC VARIABILITY WITHIN ELECTROMORPHS IN FINITE POPULATIONS. Genetics, 1976, 84, 385-393.	2.9	25
140	Probability of identical monomorphism in related species. Genetical Research, 1975, 26, 31-43.	0.9	47
141	THE BOTTLENECK EFFECT AND GENETIC VARIABILITY IN POPULATIONS. Evolution; International Journal of Organic Evolution, 1975, 29, 1-10.	2.3	2,013
142	Drift variances of heterozygosity and genetic distance in transient states. Genetical Research, 1975, 25, 229-247.	0.9	106
143	Lewontin-Krakauer <i>test for neutral genes</i>. Genetics, 1975, 80, 395-395.	2.9	150
144	Stable linkage disequilibrium without epistasis in subdivided populations. Theoretical Population Biology, 1974, 6, 173-183.	1.1	111

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145	Dynamics of gene differentiation between incompletely isolated populations of unequal sizes. Theoretical Population Biology, 1974, 5, 460-469.	1.1	65
146	A New Measure of Genetic Distance. , 1974, , 63-76.		25
147	SAMPLING VARIANCES OF HETEROZYGOSITY AND GENETIC DISTANCE. Genetics, 1974, 76, 379-390.	2.9	1,404
148	Genetic distance and electrophoretic identity of proteins between taxa. Journal of Molecular Evolution, 1973, 2, 323-328.	1.8	102
149	Probability of Fixation of Nonfunctional Genes at Duplicate Loci. American Naturalist, 1973, 107, 362-372.	2.1	106
150	PROBABILITY OF FIXATION AND MEAN FIXATION TIME OF AN OVERDOMINANT MUTATION. Genetics, 1973, 74, 371-380.	2.9	52
151	LINKAGE DISEQUILIBRIUM IN SUBDIVIDED POPULATIONS. Genetics, 1973, 75, 213-219.	2.9	288
152	Genetic Distance between Populations. American Naturalist, 1972, 106, 283-292.	2.1	8,261
153	Identity of genes by descent within and between populations under mutation and migration pressures. Theoretical Population Biology, 1972, 3, 460-465.	1.1	112
154	Extinction time of deleterious mutant genes in large populations. Theoretical Population Biology, 1971, 2, 419-425.	1.1	26
155	Total number of individuals affected by a single deleterious mutation in large populations. Theoretical Population Biology, 1971, 2, 426-430.	1.1	17
156	Interspecific Gene Differences and Evolutionary Time Estimated from Electrophoretic Data on Protein Identity. American Naturalist, 1971, 105, 385-398.	2.1	216
157	FERTILITY EXCESS NECESSARY FOR GENE SUBSTITUTION IN REGULATED POPULATIONS. Genetics, 1971, 68, 169-184.	2.9	23
158	Variability and heritability of human fertility. Annals of Human Genetics, 1970, 33, 251-259.	0.8	58
159	Gene Duplication and Nucleotide Substitution in Evolution. Nature, 1969, 221, 40-42.	27.8	153
160	Evolutionary Change of Linkage Intensity. Nature, 1968, 218, 1160-1161.	27.8	21
161	MODIFICATION OF LINKAGE INTENSITY BY NATURAL SELECTION. Genetics, 1967, 57, 625-641.	2.9	245
162	FREQUENCY CHANGES OF NEW INVERSIONS IN POPULATIONS UNDER MUTATION-SELECTION EQUILIBRIA. Genetics, 1967, 57, 741-750.	2.9	68

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163	Effective population size when fertility is inherited. Genetical Research, 1966, 8, 257-260.	0.9	66
164	Genetic structure of human populations II. Differentiation of blood group gene frequencies among isolated populations. Heredity, 1966, 21, 183-190.	2.6	90
165	Genetic structure of human populations I. Local differentiation of blood group gene frequencies in Japan. Heredity, 1966, 21, 9-35.	2.6	81
166	Genetic structure of human populations III. Differentiation of Abo blood group gene frequencies in small areas of Japan. Heredity, 1966, 21, 461-472.	2.6	13
167	EFFECTS OF RESTRICTED POPULATION SIZE AND INCREASE IN MUTATION RATE ON THE GENETIC VARIATION OF QUANTITATIVE CHARACTERS. Genetics, 1966, 54, 763-782.	2.9	11
168	VARIATION AND COVARIATION OF GENE FREQUENCIES IN SUBDIVIDED POPULATIONS. Evolution; International Journal of Organic Evolution, 1965, 19, 256-258.	2.3	42
169	EFFECT OF LINKAGE ON THE GENETIC LOAD MANIFESTED UNDER INBREEDING. Genetics, 1965, 51, 679-688.	2.9	6
170	GENETIC EFFECTS OF X RAYS ON QUANTITATIVE CHARACTERS IN A HETEROGENEOUS POPULATION OF <i>DROSOPHILA MELANOGASTER</i>. Genetics, 1965, 52, 1007-1015.	2.9	8
171	EFFECTS OF LINKAGE AND EPISTASIS ON THE EQUILIBRIUM FREQUENCIES OF LETHAL GENES. II. NUMERICAL SOLUTIONS. Japanese Journal of Genetics, 1964, 39, 7-25.	1.0	5
172	EFFECTS OF LINKAGE AND EPISTASIS ON THE EQUILIBRIUM FREQUENCIES OF LETHAL GENES. I. LINKAGE EQUILIBRIUM. Japanese Journal of Genetics, 1964, 39, 1-6.	1.0	5
173	The efficiency of haploid method of plant breeding. Heredity, 1963, 18, 95-100.	2.6	38