

Masatoshi Nei

List of Publications by Year in descending order

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papers

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104842
citing authors

#	ARTICLE	IF	CITATIONS
1	The Reproducibility of an Inferred Tree and the Diploidization of Gene Segregation after Genome Duplication. <i>Genome Biology and Evolution</i> , 2020, 12, 3792-3796.	1.1	0
2	The Reliability and Stability of an Inferred Phylogenetic Tree from Empirical Data. <i>Molecular Biology and Evolution</i> , 2017, 34, msw272.	3.5	4
3	Efficiencies of the Nj, Maximum Likelihood, and Bayesian Methods of Phylogenetic Construction for Compositional and Noncompositional Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1618-1624.	3.5	30
4	My Memory of Walter Fitch (1929-2011) and Starting <i>Molecular Biology and Evolution</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 1329-1332.	3.5	0
5	POPTREEW: Web Version of POPTREE for Constructing Population Trees from Allele Frequency Data and Computing Some Other Quantities. <i>Molecular Biology and Evolution</i> , 2014, 31, 1622-1624.	3.5	156
6	Evolution of the Sex-lethal Gene in Insects and Origin of the Sex-Determination System in <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2014, 78, 50-65.	0.8	16
7	Random fluctuation of selection coefficients and the extent of nucleotide variation in human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10676-10681.	3.3	9
8	Origins and Evolution of MicroRNA Genes in Plant Species. <i>Genome Biology and Evolution</i> , 2012, 4, 230-239.	1.1	231
9	MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. <i>Molecular Biology and Evolution</i> , 2011, 28, 2731-2739.	3.5	36,550
10	Evolutionary Changes of the Target Sites of Two MicroRNAs Encoded in the Hox Gene Cluster of <i>Drosophila</i> and Other Insect Species. <i>Genome Biology and Evolution</i> , 2011, 3, 129-139.	1.1	18
11	Roles of Mutation and Selection in Speciation: From Hugo de Vries to the Modern Genomic Era. <i>Genome Biology and Evolution</i> , 2011, 3, 812-829.	1.1	66
12	Origins and Evolution of MicroRNA Genes in <i>Drosophila</i> Species. <i>Genome Biology and Evolution</i> , 2010, 2, 180-189.	1.1	101
13	Analysis of the Immunoglobulin Light Chain Genes in Zebra Finch: Evolutionary Implications. <i>Molecular Biology and Evolution</i> , 2010, 27, 113-120.	3.5	30
14	POPTREE2: Software for Constructing Population Trees from Allele Frequency Data and Computing Other Population Statistics with Windows Interface. <i>Molecular Biology and Evolution</i> , 2010, 27, 747-752.	3.5	587
15	The Neutral Theory of Molecular Evolution in the Genomic Era. <i>Annual Review of Genomics and Human Genetics</i> , 2010, 11, 265-289.	2.5	197
16	Is positive selection responsible for the evolution of a duplicate UV-sensitive opsin gene in <i>Heliconius</i> butterflies?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, E96; author reply E97.	3.3	6
17	Reliabilities of identifying positive selection by the branch-site and the site-prediction methods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6700-6705.	3.3	136
18	Evolution of F-box genes in plants: Different modes of sequence divergence and their relationships with functional diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 835-840.	3.3	268

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19	Genomic Drift and Evolution of Microsatellite DNAs in Human Populations. <i>Molecular Biology and Evolution</i> , 2009, 26, 1835-1840.	3.5	12
20	Genomic organization and evolution of immunoglobulin kappa gene enhancers and kappa deleting element in mammals. <i>Molecular Immunology</i> , 2009, 46, 3171-3177.	1.0	20
21	Evolutionary dynamics of the immunoglobulin heavy chain variable region genes in vertebrates. <i>Immunogenetics</i> , 2008, 60, 47-55.	1.2	53
22	MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences. <i>Briefings in Bioinformatics</i> , 2008, 9, 299-306.	3.2	3,073
23	The evolution of animal chemosensory receptor gene repertoires: roles of chance and necessity. <i>Nature Reviews Genetics</i> , 2008, 9, 951-963.	7.7	533
24	Ultraconserved coding regions outside the homeobox of mammalian Hox genes. <i>BMC Evolutionary Biology</i> , 2008, 8, 260.	3.2	17
25	Empirical Tests of the Reliability of Phylogenetic Trees Constructed With Microsatellite DNA. <i>Genetics</i> , 2008, 178, 385-392.	1.2	84
26	Origins and Evolution of the Formin Multigene Family That Is Involved in the Formation of Actin Filaments. <i>Molecular Biology and Evolution</i> , 2008, 25, 2717-2733.	3.5	65
27	Evolutionary redefinition of immunoglobulin light chain isotypes in tetrapods using molecular markers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16647-16652.	3.3	54
28	Evolutionary dynamics of olfactory receptor genes in <i>Drosophila</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7122-7127.	3.3	109
29	The new mutation theory of phenotypic evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12235-12242.	3.3	196
30	The origins and early evolution of DNA mismatch repair genes—multiple horizontal gene transfers and co-evolution. <i>Nucleic Acids Research</i> , 2007, 35, 7591-7603.	6.5	94
31	Genomic drift and copy number variation of sensory receptor genes in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20421-20426.	3.3	139
32	MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) Software Version 4.0. <i>Molecular Biology and Evolution</i> , 2007, 24, 1596-1599.	3.5	25,988
33	Extensive Gains and Losses of Olfactory Receptor Genes in Mammalian Evolution. <i>PLoS ONE</i> , 2007, 2, e708.	1.1	270
34	Heterogeneous but conserved natural killer receptor gene complexes in four major orders of mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3192-3197.	3.3	86
35	Evolutionary dynamics of olfactory and other chemosensory receptor genes in vertebrates. <i>Journal of Human Genetics</i> , 2006, 51, 505-517.	1.1	199
36	Origins and evolution of the <i>recA/RAD51</i> gene family: Evidence for ancient gene duplication and endosymbiotic gene transfer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10328-10333.	3.3	268

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37	Concerted and Birth-and-Death Evolution of Multigene Families. <i>Annual Review of Genetics</i> , 2005, 39, 121-152.	3.2	1,150
38	Origin and evolution of the Ig-like domains present in mammalian leukocyte receptors: insights from chicken, frog, and fish homologues. <i>Immunogenetics</i> , 2005, 57, 151-157.	1.2	36
39	Evolutionary Change of the Numbers of Homeobox Genes in Bilateral Animals. <i>Molecular Biology and Evolution</i> , 2005, 22, 2386-2394.	3.5	79
40	Evolutionary dynamics of olfactory receptor genes in fishes and tetrapods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6039-6044.	3.3	278
41	Origin and evolution of the chicken leukocyte receptor complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4057-4062.	3.3	36
42	A simple method for predicting the functional differentiation of duplicate genes and its application to MIRC-type MADS-box genes. <i>Nucleic Acids Research</i> , 2005, 33, e12-e12.	6.5	23
43	Selectionism and Neutralism in Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2005, 22, 2318-2342.	3.5	293
44	Comparative evolutionary analysis of olfactory receptor gene clusters between humans and mice. <i>Gene</i> , 2005, 346, 13-21.	1.0	105
45	Evolutionary changes of the number of olfactory receptor genes in the human and mouse lineages. <i>Gene</i> , 2005, 346, 23-28.	1.0	54
46	Eighty percent of proteins are different between humans and chimpanzees. <i>Gene</i> , 2005, 346, 215-219.	1.0	32
47	Rapid expansion of killer cell immunoglobulin-like receptor genes in primates and their coevolution with MHC Class I genes. <i>Gene</i> , 2005, 347, 149-159.	1.0	36
48	Bottlenecks, Genetic Polymorphism and Speciation This article is dedicated to the memory of Takeo Maruyama.. <i>Genetics</i> , 2005, 170, 1-4.	1.2	31
49	Concerted and Nonconcerted Evolution of the Hsp70 Gene Superfamily in Two Sibling Species of Nematodes. <i>Molecular Biology and Evolution</i> , 2004, 21, 498-505.	3.5	67
50	False-Positive Selection Identified by ML-Based Methods: Examples from the Sig1 Gene of the Diatom <i>Thalassiosira weissflogii</i> and the tax Gene of a Human T-cell Lymphotropic Virus. <i>Molecular Biology and Evolution</i> , 2004, 21, 914-921.	3.5	107
51	Prospects for inferring very large phylogenies by using the neighbor-joining method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11030-11035.	3.3	4,158
52	Type I MADS-box genes have experienced faster birth-and-death evolution than type II MADS-box genes in angiosperms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1910-1915.	3.3	209
53	Genomic organization and evolutionary analysis of Ly49 genes encoding the rodent natural killer cell receptors: rapid evolution by repeated gene duplication. <i>Immunogenetics</i> , 2004, 56, 343-54.	1.2	32
54	MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. <i>Briefings in Bioinformatics</i> , 2004, 5, 150-163.	3.2	10,598

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55	Reanalysis of Murphy et al.'s Data Gives Various Mammalian Phylogenies and Suggests Overcredibility of Bayesian Trees. <i>Journal of Molecular Evolution</i> , 2003, 57, S290-S296.	0.8	36
56	Antiquity and Evolution of the MADS-Box Gene Family Controlling Flower Development in Plants. <i>Molecular Biology and Evolution</i> , 2003, 20, 1435-1447.	3.5	122
57	Estimation of Divergence Times for Major Lineages of Primate Species. <i>Molecular Biology and Evolution</i> , 2003, 20, 424-434.	3.5	345
58	Evolution of olfactory receptor genes in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12235-12240.	3.3	232
59	Birth-and-Death Evolution in Primate MHC Class I Genes: Divergence Time Estimates. <i>Molecular Biology and Evolution</i> , 2003, 20, 601-609.	3.5	70
60	Acceleration of genomic evolution caused by enhanced mutation rate in endocellular symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12944-12948.	3.3	151
61	Overcredibility of molecular phylogenies obtained by Bayesian phylogenetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16138-16143.	3.3	598
62	Simulation Study of the Reliability and Robustness of the Statistical Methods for Detecting Positive Selection at Single Amino Acid Sites. <i>Molecular Biology and Evolution</i> , 2002, 19, 1865-1869.	3.5	91
63	Purifying Selection and Birth-and-death Evolution in the Histone H4 Gene Family. <i>Molecular Biology and Evolution</i> , 2002, 19, 689-697.	3.5	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. <i>Molecular Biology and Evolution</i> , 2002, 19, 68-75.	3.5	86
66	Adaptive Evolution of Variable Region Genes Encoding an Unusual Type of Immunoglobulin in Camelids. <i>Molecular Biology and Evolution</i> , 2002, 19, 205-215.	3.5	48
67	Reliabilities of Parsimony-based and Likelihood-based Methods for Detecting Positive Selection at Single Amino Acid Sites. <i>Molecular Biology and Evolution</i> , 2001, 18, 2179-2185.	3.5	79
68	Evolutionary Dynamics of the T-Cell Receptor VB Gene Family as Inferred from the Human and Mouse Genomic Sequences. <i>Molecular Biology and Evolution</i> , 2001, 18, 503-513.	3.5	34
69	Positive Selection in the Evolution of Mammalian Interleukin-2 Genes. <i>Molecular Biology and Evolution</i> , 2000, 17, 1413-1416.	3.5	36
70	An Unusual Form of Purifying Selection in a Sperm Protein. <i>Molecular Biology and Evolution</i> , 2000, 17, 278-283.	3.5	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. <i>Molecular Biology and Evolution</i> , 2000, 17, 1251-1258.	3.5	269
72	Accuracies of ancestral amino acid sequences inferred by the parsimony, likelihood, and distance methods. <i>Journal of Molecular Evolution</i> , 1997, 44, S139-S146.	0.8	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.	3.2	297
75	Evolution of Antennapedia-Class Homeobox Genes. Genetics, 1996, 142, 295-303.	1.2	130
76	Genetic Distances and Reconstruction of Phylogenetic Trees From Microsatellite DNA. Genetics, 1996, 144, 389-399.	1.2	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.	0.8	81
78	MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. Bioinformatics, 1994, 10, 189-191.	1.8	711
79	Inconsistency of the maximum parsimony method when the rate of nucleotide substitution is constant. Journal of Molecular Evolution, 1994, 39, 210-218.	0.8	41
80	Effective population size, genetic diversity, and coalescence time in subdivided populations. Journal of Molecular Evolution, 1993, 37, 240-4.	0.8	147
81	Evolutionary relationships of the classes of major histocompatibility complex genes. Immunogenetics, 1993, 37, 337-346.	1.2	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.	0.8	318
83	Neutral mutation hypothesis test. Nature, 1991, 354, 115-116.	13.7	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.	0.4	45
86	Genetic Relationships of Europeans, Asians and Africans and the Origin of Modern &i>Homo sapiens&i>. Human Heredity, 1989, 39, 276-281.	0.4	64
87	Pattern of nucleotide substitution at major histocompatibility complex class I loci reveals overdominant selection. Nature, 1988, 335, 167-170.	13.7	1,912
88	Accumulation of mutations in sexual and asexual populations. Genetical Research, 1987, 49, 135-146.	0.3	153
89	Definition and Estimation of Fixation Indices. Evolution; International Journal of Organic Evolution, 1986, 40, 643.	1.1	71
90	DEFINITION AND ESTIMATION OF FIXATION INDICES. Evolution; International Journal of Organic Evolution, 1986, 40, 643-645.	1.1	164

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91	Genetic variation in subdivided populations and conservation genetics. <i>Heredity</i> , 1986, 57, 189-198.	1.2	167
92	The number of nucleotides required to determine the branching order of three species, with special reference to the human-chimpanzee-gorilla divergence. <i>Journal of Molecular Evolution</i> , 1986, 24, 189-204.	0.8	232
93	Phylogenetic analysis of polymorphic DNA sequences at the Adh locus in <i>Drosophila melanogaster</i> and its sibling species. <i>Journal of Molecular Evolution</i> , 1985, 22, 289-300.	0.8	63
94	GENE GENEALOGY AND VARIANCE OF INTERPOPULATIONAL NUCLEOTIDE DIFFERENCES. <i>Genetics</i> , 1985, 110, 325-344.	1.2	292
95	On the Positive Identification of Paternity. <i>Human Heredity</i> , 1984, 34, 258-260.	0.4	2
96	Extent of Protein Polymorphism and the Neutral Mutation Theory. , 1984, , 73-118.		179
97	Genetic Polymorphism and Neomutationism. <i>Lecture Notes in Biomathematics</i> , 1984, , 214-241.	0.3	8
98	Accuracy of estimated phylogenetic trees from molecular data. <i>Journal of Molecular Evolution</i> , 1983, 19, 153-170.	0.8	2,194
99	A Note on Positive Identification of Paternity by Using Genetic Markers. <i>Human Heredity</i> , 1983, 33, 29-35.	0.4	12
100	MODELS OF EVOLUTION OF REPRODUCTIVE ISOLATION. <i>Genetics</i> , 1983, 103, 557-579.	1.2	180
101	MAXIMUM LIKELIHOOD ESTIMATION OF THE NUMBER OF NUCLEOTIDE SUBSTITUTIONS FROM RESTRICTION SITES DATA. <i>Genetics</i> , 1983, 105, 207-217.	1.2	487
102	Genetic differentiation of quantitative characters between populations or species: I. Mutation and random genetic drift. <i>Genetical Research</i> , 1982, 39, 303-314.	0.3	111
103	Biases of the estimates of DNA divergence obtained by the restriction enzyme technique. <i>Journal of Molecular Evolution</i> , 1982, 18, 115-120.	0.8	88
104	Accuracy of estimated phylogenetic trees from molecular data. <i>Journal of Molecular Evolution</i> , 1982, 18, 387-404.	0.8	220
105	Estimation of average number of nucleotide substitutions when the rate of substitution varies with nucleotide. <i>Journal of Molecular Evolution</i> , 1982, 18, 414-422.	0.8	282
106	Positive selection causes purifying selection (reply). <i>Nature</i> , 1982, 295, 630-630.	13.7	3
107	Statistical properties of the Jukes-Holmquist method of estimating the number of nucleotide substitutions: Reply to Holmquist and Conroy's criticism. <i>Journal of Molecular Evolution</i> , 1981, 17, 182-187.	0.8	0
108	Polymorphism and evolution of the Rh blood groups. <i>Japanese Journal of Human Genetics</i> , 1981, 26, 263-278.	0.8	8

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109	Pseudogenes as a paradigm of neutral evolution. <i>Nature</i> , 1981, 292, 237-239.	13.7	487
110	DNA POLYMORPHISM DETECTABLE BY RESTRICTION ENDONUCLEASES. <i>Genetics</i> , 1981, 97, 145-163.	1.2	1,167
111	GENETIC VARIABILITY MAINTAINED BY MUTATION AND OVERDOMINANT SELECTION IN FINITE POPULATIONS. <i>Genetics</i> , 1981, 98, 441-459.	1.2	124
112	GENETIC DRIFT AND ESTIMATION OF EFFECTIVE POPULATION SIZE. <i>Genetics</i> , 1981, 98, 625-640.	1.2	459
113	STATISTICAL STUDIES OF PROTEIN POLYMORPHISM. <i>Genetics</i> , 1981, 97, 494A-494A.	1.2	3
114	Non-random association between electromorphs and inversion chromosomes in finite populations. <i>Genetical Research</i> , 1980, 35, 65-83.	0.3	85
115	Stochastic Theory of Population Genetics and Evolution. <i>Lecture Notes in Biomathematics</i> , 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. <i>Genetics</i> , 1980, 94, 1039-1063.	1.2	125
117	PROTEIN POLYMORPHISM AND THE SAS-CFF MODEL. <i>Genetics</i> , 1980, 94, 1085-1087.	1.2	8
118	Augmentation algorithm: A reply to holmquist. <i>Journal of Molecular Evolution</i> , 1979, 13, 167-171.	0.8	5
119	Proportion of informative families for genetic counseling with linked marker genes. <i>Japanese Journal of Human Genetics</i> , 1979, 24, 131-142.	0.8	14
120	POPULATION DYNAMICS OF SEX-DETERMINING ALLELES IN HONEY BEES AND SELF-INCOMPATIBILITY ALLELES IN PLANTS. <i>Genetics</i> , 1979, 91, 609-626.	1.2	147
121	Goodman et al.'s method for augmenting the number of nucleotide substitutions. <i>Journal of Molecular Evolution</i> , 1978, 11, 67-73.	0.8	22
122	The theory of genetic distance and evolution of human races. <i>Japanese Journal of Human Genetics</i> , 1978, 23, 341-369.	0.8	154
123	Nonrandom amino acid substitution and estimation of the number of nucleotide substitutions in evolution. <i>Journal of Molecular Evolution</i> , 1978, 11, 333-347.	0.8	16
124	STATISTICAL STUDIES ON PROTEIN POLYMORPHISM IN NATURAL POPULATIONS II. GENE DIFFERENTIATION BETWEEN POPULATIONS. <i>Genetics</i> , 1978, 88, 367-390.	1.2	69
125	ESTIMATION OF AVERAGE HETEROZYGOSITY AND GENETIC DISTANCE FROM A SMALL NUMBER OF INDIVIDUALS. <i>Genetics</i> , 1978, 89, 583-590.	1.2	9,389
126	BOTTLENECK EFFECTS ON AVERAGE HETEROZYGOSITY AND GENETIC DISTANCE WITH THE STEPWISE MUTATION MODEL. <i>Evolution; International Journal of Organic Evolution</i> , 1977, 31, 347-356.	1.1	246

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127	Bottleneck Effects on Average Heterozygosity and Genetic Distance with the Stepwise Mutation Model. <i>Evolution; International Journal of Organic Evolution</i> , 1977, 31, 347.	1.1	128
128	Mean and variance of F_{ST} in a finite number of incompletely isolated populations. <i>Theoretical Population Biology</i> , 1977, 11, 291-306.	0.5	88
129	Drift variances of F_{ST} and G_{ST} statistics obtained from a finite number of isolated populations. <i>Theoretical Population Biology</i> , 1977, 11, 307-325.	0.5	93
130	F_{ST} statistics and analysis of gene diversity in subdivided populations. <i>Annals of Human Genetics</i> , 1977, 41, 225-233.	0.3	1,103
131	Standard error of immunological dating of evolutionary time. <i>Journal of Molecular Evolution</i> , 1977, 9, 203-211.	0.8	43
132	STATISTICAL STUDIES ON PROTEIN POLYMORPHISM IN NATURAL POPULATIONS I. DISTRIBUTION OF SINGLE LOCUS HETEROZYGOSITY. <i>Genetics</i> , 1977, 86, 455-483.	1.2	147
133	PERSISTENCE OF COMMON ALLELES IN TWO RELATED POPULATIONS OR SPECIES. <i>Genetics</i> , 1977, 86, 901-914.	1.2	47
134	EFFECTS OF RANDOM FLUCTUATION OF SELECTION INTENSITY ON GENETIC VARIABILITY IN A FINITE POPULATION. <i>Japanese Journal of Genetics</i> , 1976, 51, 355-369.	1.0	21
135	Testing the neutral mutation hypothesis by distribution of single locus heterozygosity. <i>Nature</i> , 1976, 262, 491-493.	13.7	71
136	Electrophoretically silent alleles in a finite population. <i>Journal of Molecular Evolution</i> , 1976, 8, 381-385.	0.8	15
137	Empirical relationship between the number of nucleotide substitutions and interspecific identity of amino acid sequences in some proteins. <i>Journal of Molecular Evolution</i> , 1976, 7, 313-323.	0.8	22
138	The transient distribution of allele frequencies under mutation pressure. <i>Genetical Research</i> , 1976, 28, 205-214.	0.3	57
139	HIDDEN GENETIC VARIABILITY WITHIN ELECTROMORPHS IN FINITE POPULATIONS. <i>Genetics</i> , 1976, 84, 385-393.	1.2	25
140	Probability of identical monomorphism in related species. <i>Genetical Research</i> , 1975, 26, 31-43.	0.3	47
141	THE BOTTLENECK EFFECT AND GENETIC VARIABILITY IN POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 1975, 29, 1-10.	1.1	2,013
142	Drift variances of heterozygosity and genetic distance in transient states. <i>Genetical Research</i> , 1975, 25, 229-247.	0.3	106
143	Lewontin-Krakauer test for neutral genes. <i>Genetics</i> , 1975, 80, 395-395.	1.2	150
144	Stable linkage disequilibrium without epistasis in subdivided populations. <i>Theoretical Population Biology</i> , 1974, 6, 173-183.	0.5	111

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145	Dynamics of gene differentiation between incompletely isolated populations of unequal sizes. <i>Theoretical Population Biology</i> , 1974, 5, 460-469.	0.5	65
146	A New Measure of Genetic Distance. , 1974, , 63-76.		25
147	SAMPLING VARIANCES OF HETEROZYGOSITY AND GENETIC DISTANCE. <i>Genetics</i> , 1974, 76, 379-390.	1.2	1,404
148	Genetic distance and electrophoretic identity of proteins between taxa. <i>Journal of Molecular Evolution</i> , 1973, 2, 323-328.	0.8	102
149	Probability of Fixation of Nonfunctional Genes at Duplicate Loci. <i>American Naturalist</i> , 1973, 107, 362-372.	1.0	106
150	PROBABILITY OF FIXATION AND MEAN FIXATION TIME OF AN OVERDOMINANT MUTATION. <i>Genetics</i> , 1973, 74, 371-380.	1.2	52
151	LINKAGE DISEQUILIBRIUM IN SUBDIVIDED POPULATIONS. <i>Genetics</i> , 1973, 75, 213-219.	1.2	288
152	Genetic Distance between Populations. <i>American Naturalist</i> , 1972, 106, 283-292.	1.0	8,261
153	Identity of genes by descent within and between populations under mutation and migration pressures. <i>Theoretical Population Biology</i> , 1972, 3, 460-465.	0.5	112
154	Extinction time of deleterious mutant genes in large populations. <i>Theoretical Population Biology</i> , 1971, 2, 419-425.	0.5	26
155	Total number of individuals affected by a single deleterious mutation in large populations. <i>Theoretical Population Biology</i> , 1971, 2, 426-430.	0.5	17
156	Interspecific Gene Differences and Evolutionary Time Estimated from Electrophoretic Data on Protein Identity. <i>American Naturalist</i> , 1971, 105, 385-398.	1.0	216
157	FERTILITY EXCESS NECESSARY FOR GENE SUBSTITUTION IN REGULATED POPULATIONS. <i>Genetics</i> , 1971, 68, 169-184.	1.2	23
158	Variability and heritability of human fertility. <i>Annals of Human Genetics</i> , 1970, 33, 251-259.	0.3	58
159	Gene Duplication and Nucleotide Substitution in Evolution. <i>Nature</i> , 1969, 221, 40-42.	13.7	153
160	Evolutionary Change of Linkage Intensity. <i>Nature</i> , 1968, 218, 1160-1161.	13.7	21
161	MODIFICATION OF LINKAGE INTENSITY BY NATURAL SELECTION. <i>Genetics</i> , 1967, 57, 625-641.	1.2	245
162	FREQUENCY CHANGES OF NEW INVERSIONS IN POPULATIONS UNDER MUTATION-SELECTION EQUILIBRIA. <i>Genetics</i> , 1967, 57, 741-750.	1.2	68

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