

Masatoshi Nei

List of Publications by Year in descending order

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papers

139,362
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#	ARTICLE	IF	CITATIONS
1	MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. <i>Molecular Biology and Evolution</i> , 2011, 28, 2731-2739.	8.9	36,550
2	MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) Software Version 4.0. <i>Molecular Biology and Evolution</i> , 2007, 24, 1596-1599.	8.9	25,988
3	MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. <i>Briefings in Bioinformatics</i> , 2004, 5, 150-163.	6.5	10,598
4	ESTIMATION OF AVERAGE HETEROZYGOSITY AND GENETIC DISTANCE FROM A SMALL NUMBER OF INDIVIDUALS. <i>Genetics</i> , 1978, 89, 583-590.	2.9	9,389
5	Genetic Distance between Populations. <i>American Naturalist</i> , 1972, 106, 283-292.	2.1	8,261
6	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.	7.1	4,158
7	MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences. <i>Briefings in Bioinformatics</i> , 2008, 9, 299-306.	6.5	3,073
8	Accuracy of estimated phylogenetic trees from molecular data. <i>Journal of Molecular Evolution</i> , 1983, 19, 153-170.	1.8	2,194
9	THE BOTTLENECK EFFECT AND GENETIC VARIABILITY IN POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 1975, 29, 1-10.	2.3	2,013
10	Pattern of nucleotide substitution at major histocompatibility complex class I loci reveals overdominant selection. <i>Nature</i> , 1988, 335, 167-170.	27.8	1,912
11	SAMPLING VARIANCES OF HETEROZYGOSITY AND GENETIC DISTANCE. <i>Genetics</i> , 1974, 76, 379-390.	2.9	1,404
12	DNA POLYMORPHISM DETECTABLE BY RESTRICTION ENDONUCLEASES. <i>Genetics</i> , 1981, 97, 145-163.	2.9	1,167
13	Concerted and Birth-and-Death Evolution of Multigene Families. <i>Annual Review of Genetics</i> , 2005, 39, 121-152.	7.6	1,150
14	<i>F</i> -statistics and analysis of gene diversity in subdivided populations. <i>Annals of Human Genetics</i> , 1977, 41, 225-233.	0.8	1,103
15	Genetic Distances and Reconstruction of Phylogenetic Trees From Microsatellite DNA. <i>Genetics</i> , 1996, 144, 389-399.	2.9	1,038
16	MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. <i>Bioinformatics</i> , 1994, 10, 189-191.	4.1	711
17	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.	7.1	598
18	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.	8.9	587

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19	The evolution of animal chemosensory receptor gene repertoires: roles of chance and necessity. <i>Nature Reviews Genetics</i> , 2008, 9, 951-963.	16.3	533
20	Pseudogenes as a paradigm of neutral evolution. <i>Nature</i> , 1981, 292, 237-239.	27.8	487
21	MAXIMUM LIKELIHOOD ESTIMATION OF THE NUMBER OF NUCLEOTIDE SUBSTITUTIONS FROM RESTRICTION SITES DATA. <i>Genetics</i> , 1983, 105, 207-217.	2.9	487
22	GENETIC DRIFT AND ESTIMATION OF EFFECTIVE POPULATION SIZE. <i>Genetics</i> , 1981, 98, 625-640.	2.9	459
23	Estimation of Divergence Times for Major Lineages of Primate Species. <i>Molecular Biology and Evolution</i> , 2003, 20, 424-434.	8.9	345
24	Statistical properties of the ordinary least-squares, generalized least-squares, and minimum-evolution methods of phylogenetic inference. <i>Journal of Molecular Evolution</i> , 1992, 35, 367-375.	1.8	318
25	PHYLOGENETIC ANALYSIS IN MOLECULAR EVOLUTIONARY GENETICS. <i>Annual Review of Genetics</i> , 1996, 30, 371-403.	7.6	297
26	Selectionism and Neutralism in Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2005, 22, 2318-2342.	8.9	293
27	GENE GENEALOGY AND VARIANCE OF INTERPOPULATIONAL NUCLEOTIDE DIFFERENCES. <i>Genetics</i> , 1985, 110, 325-344.	2.9	292
28	LINKAGE DISEQUILIBRIUM IN SUBDIVIDED POPULATIONS. <i>Genetics</i> , 1973, 75, 213-219.	2.9	288
29	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.	1.8	282
30	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.	7.1	278
31	Extensive Gains and Losses of Olfactory Receptor Genes in Mammalian Evolution. <i>PLoS ONE</i> , 2007, 2, e708.	2.5	270
32	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.	8.9	269
33	Origins and evolution of the recA/RAD51 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.	7.1	268
34	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.	7.1	268
35	Accuracies of ancestral amino acid sequences inferred by the parsimony, likelihood, and distance methods. <i>Journal of Molecular Evolution</i> , 1997, 44, S139-S146.	1.8	256
36	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.	2.3	246

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37	MODIFICATION OF LINKAGE INTENSITY BY NATURAL SELECTION. <i>Genetics</i> , 1967, 57, 625-641.	2.9	245
38	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.	1.8	232
39	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.	7.1	232
40	Origins and Evolution of MicroRNA Genes in Plant Species. <i>Genome Biology and Evolution</i> , 2012, 4, 230-239.	2.5	231
41	Accuracy of estimated phylogenetic trees from molecular data. <i>Journal of Molecular Evolution</i> , 1982, 18, 387-404.	1.8	220
42	Interspecific Gene Differences and Evolutionary Time Estimated from Electrophoretic Data on Protein Identity. <i>American Naturalist</i> , 1971, 105, 385-398.	2.1	216
43	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.	7.1	209
44	Evolutionary dynamics of olfactory and other chemosensory receptor genes in vertebrates. <i>Journal of Human Genetics</i> , 2006, 51, 505-517.	2.3	199
45	The Neutral Theory of Molecular Evolution in the Genomic Era. <i>Annual Review of Genomics and Human Genetics</i> , 2010, 11, 265-289.	6.2	197
46	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.	7.1	196
47	MODELS OF EVOLUTION OF REPRODUCTIVE ISOLATION. <i>Genetics</i> , 1983, 103, 557-579.	2.9	180
48	Extent of Protein Polymorphism and the Neutral Mutation Theory. , 1984, , 73-118.		179
49	Genetic variation in subdivided populations and conservation genetics. <i>Heredity</i> , 1986, 57, 189-198.	2.6	167
50	DEFINITION AND ESTIMATION OF FIXATION INDICES. <i>Evolution; International Journal of Organic Evolution</i> , 1986, 40, 643-645.	2.3	164
51	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.	8.9	156
52	The theory of genetic distance and evolution of human races. <i>Japanese Journal of Human Genetics</i> , 1978, 23, 341-369.	0.8	154
53	Gene Duplication and Nucleotide Substitution in Evolution. <i>Nature</i> , 1969, 221, 40-42.	27.8	153
54	Accumulation of mutations in sexual and asexual populations. <i>Genetical Research</i> , 1987, 49, 135-146.	0.9	153

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55	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
56	Lewontin-Krakauer <i><i>test for neutral genes</i></i> . Genetics, 1975, 80, 395-395.	2.9	150
57	Effective population size, genetic diversity, and coalescence time in subdivided populations. Journal of Molecular Evolution, 1993, 37, 240-4.	1.8	147
58	STATISTICAL STUDIES ON PROTEIN POLYMORPHISM IN NATURAL POPULATIONS I. DISTRIBUTION OF SINGLE LOCUS HETEROZYGOSITY. Genetics, 1977, 86, 455-483.	2.9	147
59	POPULATION DYNAMICS OF SEX-DETERMINING ALLELES IN HONEY BEES AND SELF-INCOMPATIBILITY ALLELES IN PLANTS. Genetics, 1979, 91, 609-626.	2.9	147
60	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
61	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
62	Evolution of Antennapedia-Class Homeobox Genes. Genetics, 1996, 142, 295-303.	2.9	130
63	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
64	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
65	GENETIC VARIABILITY MAINTAINED BY MUTATION AND OVERDOMINANT SELECTION IN FINITE POPULATIONS. Genetics, 1981, 98, 441-459.	2.9	124
66	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
67	Identity of genes by descent within and between populations under mutation and migration pressures. Theoretical Population Biology, 1972, 3, 460-465.	1.1	112
68	Stable linkage disequilibrium without epistasis in subdivided populations. Theoretical Population Biology, 1974, 6, 173-183.	1.1	111
69	Genetic differentiation of quantitative characters between populations or species: I. Mutation and random genetic drift. Genetical Research, 1982, 39, 303-314.	0.9	111
70	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
71	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
72	Probability of Fixation of Nonfunctional Genes at Duplicate Loci. American Naturalist, 1973, 107, 362-372.	2.1	106

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73	Drift variances of heterozygosity and genetic distance in transient states. <i>Genetical Research</i> , 1975, 25, 229-247.	0.9	106
74	Comparative evolutionary analysis of olfactory receptor gene clusters between humans and mice. <i>Gene</i> , 2005, 346, 13-21.	2.2	105
75	Genetic distance and electrophoretic identity of proteins between taxa. <i>Journal of Molecular Evolution</i> , 1973, 2, 323-328.	1.8	102
76	Origins and Evolution of MicroRNA Genes in <i>Drosophila</i> Species. <i>Genome Biology and Evolution</i> , 2010, 2, 180-189.	2.5	101
77	Purifying Selection and Birth-and-death Evolution in the Histone H4 Gene Family. <i>Molecular Biology and Evolution</i> , 2002, 19, 689-697.	8.9	98
78	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.	14.5	94
79	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.	1.1	93
80	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.	8.9	91
81	Genetic structure of human populations II. Differentiation of blood group gene frequencies among isolated populations. <i>Heredity</i> , 1966, 21, 183-190.	2.6	90
82	Mean and variance of F_{ST} in a finite number of incompletely isolated populations. <i>Theoretical Population Biology</i> , 1977, 11, 291-306.	1.1	88
83	Biases of the estimates of DNA divergence obtained by the restriction enzyme technique. <i>Journal of Molecular Evolution</i> , 1982, 18, 115-120.	1.8	88
84	Molecular Evolution of the Nontandemly Repeated Genes of the Histone 3 Multigene Family. <i>Molecular Biology and Evolution</i> , 2002, 19, 68-75.	8.9	86
85	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.	7.1	86
86	Non-random association between electromorphs and inversion chromosomes in finite populations. <i>Genetical Research</i> , 1980, 35, 65-83.	0.9	85
87	Empirical Tests of the Reliability of Phylogenetic Trees Constructed With Microsatellite DNA. <i>Genetics</i> , 2008, 178, 385-392.	2.9	84
88	Genetic structure of human populations I. Local differentiation of blood group gene frequencies in Japan. <i>Heredity</i> , 1966, 21, 9-35.	2.6	81
89	Unbiased estimates of the number of nucleotide substitutions when substitution rate varies among different sites. <i>Journal of Molecular Evolution</i> , 1994, 38, 295-9.	1.8	81
90	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.	8.9	79

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91	Evolutionary Change of the Numbers of Homeobox Genes in Bilateral Animals. <i>Molecular Biology and Evolution</i> , 2005, 22, 2386-2394.	8.9	79
92	Testing the neutral mutation hypothesis by distribution of single locus heterozygosity. <i>Nature</i> , 1976, 262, 491-493.	27.8	71
93	Definition and Estimation of Fixation Indices. <i>Evolution; International Journal of Organic Evolution</i> , 1986, 40, 643.	2.3	71
94	Birth-and-Death Evolution in Primate MHC Class I Genes: Divergence Time Estimates. <i>Molecular Biology and Evolution</i> , 2003, 20, 601-609.	8.9	70
95	Natural selection at the class II major histocompatibility complex loci of mammals. , 1997, , 89-97.		70
96	An Unusual Form of Purifying Selection in a Sperm Protein. <i>Molecular Biology and Evolution</i> , 2000, 17, 278-283.	8.9	69
97	STATISTICAL STUDIES ON PROTEIN POLYMORPHISM IN NATURAL POPULATIONS II. GENE DIFFERENTIATION BETWEEN POPULATIONS. <i>Genetics</i> , 1978, 88, 367-390.	2.9	69
98	FREQUENCY CHANGES OF NEW INVERSIONS IN POPULATIONS UNDER MUTATION-SELECTION EQUILIBRIA. <i>Genetics</i> , 1967, 57, 741-750.	2.9	68
99	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.	8.9	67
100	Effective population size when fertility is inherited. <i>Genetical Research</i> , 1966, 8, 257-260.	0.9	66
101	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.	2.5	66
102	Dynamics of gene differentiation between incompletely isolated populations of unequal sizes. <i>Theoretical Population Biology</i> , 1974, 5, 460-469.	1.1	65
103	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.	8.9	65
104	Genetic Relationships of Europeans, Asians and Africans and the Origin of Modern &i>Homo sapiens&i>. <i>Human Heredity</i> , 1989, 39, 276-281.	0.8	64
105	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.	1.8	63
106	The Wilhelmine E. Key 2001 Invitational Lecture. Estimation of Divergence Times for a Few Mammalian and Several Primate Species. , 2002, 93, 157-164.		59
107	Variability and heritability of human fertility. <i>Annals of Human Genetics</i> , 1970, 33, 251-259.	0.8	58
108	The transient distribution of allele frequencies under mutation pressure. <i>Genetical Research</i> , 1976, 28, 205-214.	0.9	57

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109	Evolutionary relationships of the classes of major histocompatibility complex genes. Immunogenetics, 1993, 37, 337-346.	2.4	57
110	Evolutionary changes of the number of olfactory receptor genes in the human and mouse lineages. Gene, 2005, 346, 23-28.	2.2	54
111	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
112	Evolutionary dynamics of the immunoglobulin heavy chain variable region genes in vertebrates. Immunogenetics, 2008, 60, 47-55.	2.4	53
113	PROBABILITY OF FIXATION AND MEAN FIXATION TIME OF AN OVERDOMINANT MUTATION. Genetics, 1973, 74, 371-380.	2.9	52
114	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
115	Probability of identical monomorphism in related species. Genetical Research, 1975, 26, 31-43.	0.9	47
116	PERSISTENCE OF COMMON ALLELES IN TWO RELATED POPULATIONS OR SPECIES. Genetics, 1977, 86, 901-914.	2.9	47
117	Relationships between intrapopulational and interpopulational genetic diversity in man. Annals of Human Biology, 1990, 17, 501-513.	1.0	45
118	Standard error of immunological dating of evolutionary time. Journal of Molecular Evolution, 1977, 9, 203-211.	1.8	43
119	VARIATION AND COVARIATION OF GENE FREQUENCIES IN SUBDIVIDED POPULATIONS. Evolution; International Journal of Organic Evolution, 1965, 19, 256-258.	2.3	42
120	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
121	The efficiency of haploid method of plant breeding. Heredity, 1963, 18, 95-100.	2.6	38
122	Positive Selection in the Evolution of Mammalian Interleukin-2 Genes. Molecular Biology and Evolution, 2000, 17, 1413-1416.	8.9	36
123	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
124	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
125	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
126	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

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127	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.	8.9	34
128	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.	2.4	32
129	Eighty percent of proteins are different between humans and chimpanzees. <i>Gene</i> , 2005, 346, 215-219.	2.2	32
130	Bottlenecks, Genetic Polymorphism and Speciation This article is dedicated to the memory of Takeo Maruyama.. <i>Genetics</i> , 2005, 170, 1-4.	2.9	31
131	Analysis of the Immunoglobulin Light Chain Genes in Zebra Finch: Evolutionary Implications. <i>Molecular Biology and Evolution</i> , 2010, 27, 113-120.	8.9	30
132	Efficiencies of the Njp, Maximum Likelihood, and Bayesian Methods of Phylogenetic Construction for Compositional and Noncompositional Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1618-1624.	8.9	30
133	Extinction time of deleterious mutant genes in large populations. <i>Theoretical Population Biology</i> , 1971, 2, 419-425.	1.1	26
134	A New Measure of Genetic Distance. , 1974, , 63-76.		25
135	HIDDEN GENETIC VARIABILITY WITHIN ELECTROMORPHS IN FINITE POPULATIONS. <i>Genetics</i> , 1976, 84, 385-393.	2.9	25
136	Neutral mutation hypothesis test. <i>Nature</i> , 1991, 354, 115-116.	27.8	24
137	A simple method for predicting the functional differentiation of duplicate genes and its application to MIKC-type MADS-box genes. <i>Nucleic Acids Research</i> , 2005, 33, e12-e12.	14.5	23
138	FERTILITY EXCESS NECESSARY FOR GENE SUBSTITUTION IN REGULATED POPULATIONS. <i>Genetics</i> , 1971, 68, 169-184.	2.9	23
139	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.	1.8	22
140	Goodman et al.'s method for augmenting the number of nucleotide substitutions. <i>Journal of Molecular Evolution</i> , 1978, 11, 67-73.	1.8	22
141	Evolutionary Change of Linkage Intensity. <i>Nature</i> , 1968, 218, 1160-1161.	27.8	21
142	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
143	Genomic organization and evolution of immunoglobulin kappa gene enhancers and kappa deleting element in mammals. <i>Molecular Immunology</i> , 2009, 46, 3171-3177.	2.2	20
144	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.	2.5	18

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145	Total number of individuals affected by a single deleterious mutation in large populations. Theoretical Population Biology, 1971, 2, 426-430.	1.1	17
146	Ultraconserved coding regions outside the homeobox of mammalian Hox genes. BMC Evolutionary Biology, 2008, 8, 260.	3.2	17
147	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
148	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
149	Electrophoretically silent alleles in a finite population. Journal of Molecular Evolution, 1976, 8, 381-385.	1.8	15
150	Proportion of informative families for genetic counseling with linked marker genes. Japanese Journal of Human Genetics, 1979, 24, 131-142.	0.8	14
151	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
152	Evolutionary Relationships of Human Populations at the Molecular Level. , 1991, , 415-428.		13
153	A Note on Positive Identification of Paternity by Using Genetic Markers. Human Heredity, 1983, 33, 29-35.	0.8	12
154	Genomic Drift and Evolution of Microsatellite DNAs in Human Populations. Molecular Biology and Evolution, 2009, 26, 1835-1840.	8.9	12
155	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
156	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
157	Polymorphism and evolution of the Rh blood groups. Japanese Journal of Human Genetics, 1981, 26, 263-278.	0.8	8
158	Genetic Polymorphism and Neomutationism. Lecture Notes in Biomathematics, 1984, , 214-241.	0.3	8
159	Stochastic Theory of Population Genetics and Evolution. Lecture Notes in Biomathematics, 1980, , 17-47.	0.3	8
160	PROTEIN POLYMORPHISM AND THE SAS-CFF MODEL. Genetics, 1980, 94, 1085-1087.	2.9	8
161	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
162	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

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163	EFFECT OF LINKAGE ON THE GENETIC LOAD MANIFESTED UNDER INBREEDING. <i>Genetics</i> , 1965, 51, 679-688.	2.9	6
164	EFFECTS OF LINKAGE AND EPISTASIS ON THE EQUILIBRIUM FREQUENCIES OF LETHAL GENES. II. NUMERICAL SOLUTIONS. <i>Japanese Journal of Genetics</i> , 1964, 39, 7-25.	1.0	5
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