

Peter D Keightley

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1499267/publications.pdf>

Version: 2024-02-01

123
papers

13,750
citations

38742

50
h-index

26613

107
g-index

141
all docs

141
docs citations

141
times ranked

11329
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
2	The distribution of fitness effects of new mutations. <i>Nature Reviews Genetics</i> , 2007, 8, 610-618.	16.3	1,234
3	Understanding quantitative genetic variation. <i>Nature Reviews Genetics</i> , 2002, 3, 11-21.	16.3	727
4	Estimating the Rate of Adaptive Molecular Evolution in the Presence of Slightly Deleterious Mutations and Population Size Change. <i>Molecular Biology and Evolution</i> , 2009, 26, 2097-2108.	8.9	413
5	High genomic deleterious mutation rates in hominids. <i>Nature</i> , 1999, 397, 344-347.	27.8	412
6	Spontaneous Mutation Accumulation Studies in Evolutionary Genetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2009, 40, 151-172.	8.3	396
7	Direct estimation of per nucleotide and genomic deleterious mutation rates in <i>Drosophila</i> . <i>Nature</i> , 2007, 445, 82-85.	27.8	381
8	Analysis of the genome sequences of three <i>Drosophila melanogaster</i> spontaneous mutation accumulation lines. <i>Genome Research</i> , 2009, 19, 1195-1201.	5.5	343
9	Joint Inference of the Distribution of Fitness Effects of Deleterious Mutations and Population Demography Based on Nucleotide Polymorphism Frequencies. <i>Genetics</i> , 2007, 177, 2251-2261.	2.9	336
10	Interference among deleterious mutations favours sex and recombination in finite populations. <i>Nature</i> , 2006, 443, 89-92.	27.8	328
11	Enhanced CpG Mutability and Tumorigenesis in MBD4-Deficient Mice. <i>Science</i> , 2002, 297, 403-405.	12.6	294
12	Estimation of the Spontaneous Mutation Rate per Nucleotide Site in a <i>Drosophila melanogaster</i> Full-Sib Family. <i>Genetics</i> , 2014, 196, 313-320.	2.9	248
13	Direct Estimation of the Mitochondrial DNA Mutation Rate in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2008, 6, e204.	5.6	239
14	Estimation of the Spontaneous Mutation Rate in <i>Heliconius melpomene</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 239-243.	8.9	220
15	Ubiquitous selective constraints in the <i>Drosophila</i> genome revealed by a genome-wide interspecies comparison. <i>Genome Research</i> , 2006, 16, 875-884.	5.5	217
16	Quantifying the Slightly Deleterious Mutation Model of Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2002, 19, 2142-2149.	8.9	191
17	Evidence for Widespread Degradation of Gene Control Regions in Hominid Genomes. <i>PLoS Biology</i> , 2005, 3, e42.	5.6	178
18	Rates and Fitness Consequences of New Mutations in Humans. <i>Genetics</i> , 2012, 190, 295-304.	2.9	174

#	ARTICLE	IF	CITATIONS
19	Nature of Deleterious Mutation Load in <i>Drosophila</i> . <i>Genetics</i> , 1996, 144, 1993-1999.	2.9	171
20	Current hypotheses for the evolution of sex and recombination. <i>Integrative Zoology</i> , 2012, 7, 192-209.	2.6	158
21	The Effect of Variation in the Effective Population Size on the Rate of Adaptive Molecular Evolution in Eukaryotes. <i>Genome Biology and Evolution</i> , 2012, 4, 658-667.	2.5	156
22	Terumi Mukai and the Riddle of Deleterious Mutation Rates. <i>Genetics</i> , 1999, 153, 515-523.	2.9	154
23	High Frequency of Cryptic Deleterious Mutations in <i>Caenorhabditis elegans</i> . <i>Science</i> , 1999, 285, 1748-1751.	12.6	153
24	TOWARD A REALISTIC MODEL OF MUTATIONS AFFECTING FITNESS. <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 683-685.	2.3	129
25	Evidence for Pervasive Adaptive Protein Evolution in Wild Mice. <i>PLoS Genetics</i> , 2010, 6, e1000825.	3.5	123
26	Estimate of the Spontaneous Mutation Rate in <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2012, 192, 1447-1454.	2.9	123
27	Functional constraints and frequency of deleterious mutations in noncoding DNA of rodents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13402-13406.	7.1	120
28	Global population divergence and admixture of the brown rat (<i>Rattus norvegicus</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161762.	2.6	119
29	A Comparison of Models to Infer the Distribution of Fitness Effects of New Mutations. <i>Genetics</i> , 2013, 193, 1197-1208.	2.9	114
30	A Method for Inferring the Rate of Occurrence and Fitness Effects of Advantageous Mutations. <i>Genetics</i> , 2011, 189, 1427-1437.	2.9	111
31	Quantitative genetic variability maintained by mutation-stabilizing selection balance in finite populations. <i>Genetical Research</i> , 1988, 52, 33-43.	0.9	108
32	Extensive de novo mutation rate variation between individuals and across the genome of <i>Chlamydomonas reinhardtii</i> . <i>Genome Research</i> , 2015, 25, 1739-1749.	5.5	107
33	Contributions of Protein-Coding and Regulatory Change to Adaptive Molecular Evolution in Murid Rodents. <i>PLoS Genetics</i> , 2013, 9, e1003995.	3.5	106
34	Intron Size and Exon Evolution in <i>Drosophila</i> . <i>Genetics</i> , 2005, 170, 481-485.	2.9	105
35	EMS-Induced Polygenic Mutation Rates for Nine Quantitative Characters in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1998, 148, 753-766.	2.9	100
36	Patterns of Evolutionary Constraints in Intronic and Intergenic DNA of <i>Drosophila</i> . <i>Genome Research</i> , 2004, 14, 273-279.	5.5	99

#	ARTICLE	IF	CITATIONS
37	A Genetic Map of Quantitative Trait Loci for Body Weight in the Mouse. <i>Genetics</i> , 1996, 142, 227-235.	2.9	99
38	Detecting positive selection in the genome. <i>BMC Biology</i> , 2017, 15, 98.	3.8	97
39	Dominance, Pleiotropy and Metabolic Structure. <i>Genetics</i> , 1987, 117, 319-329.	2.9	89
40	What can we learn about the distribution of fitness effects of new mutations from DNA sequence data?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1187-1193.	4.0	88
41	Distributions of Selectively Constrained Sites and Deleterious Mutation Rates in the Hominid and Murid Genomes. <i>Molecular Biology and Evolution</i> , 2010, 27, 177-192.	8.9	88
42	Inferring the Probability of the Derived <i>vs.</i> the Ancestral Allelic State at a Polymorphic Site. <i>Genetics</i> , 2018, 209, 897-906.	2.9	83
43	The scale of mutational variation in the murid genome. <i>Genome Research</i> , 2005, 15, 1086-1094.	5.5	75
44	Mapping of obesity QTLs in a cross between mouse lines divergently selected on fat content. <i>Mammalian Genome</i> , 2000, 11, 2-7.	2.2	74
45	Bottleneck Effect on Genetic Variance: A Theoretical Investigation of the Role of Dominance. <i>Genetics</i> , 1998, 150, 435-447.	2.9	70
46	Spontaneous Mutational Variation for Body Size in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2002, 162, 755-765.	2.9	67
47	Properties of Ethylmethane Sulfonate-Induced Mutations Affecting Life-History Traits in <i>Caenorhabditis elegans</i> and Inferences About Bivariate Distributions of Mutation Effects. <i>Genetics</i> , 2000, 156, 143-154.	2.9	64
48	Inference of Genome-Wide Mutation Rates and Distributions of Mutation Effects for Fitness Traits: A Simulation Study. <i>Genetics</i> , 1998, 150, 1283-1293.	2.9	63
49	Faster-X Adaptive Protein Evolution in House Mice. <i>Genetics</i> , 2014, 196, 1131-1143.	2.9	62
50	Genomic Selective Constraints in Murid Noncoding DNA. <i>PLoS Genetics</i> , 2006, 2, e204.	3.5	60
51	Directional Selection and Variation in Finite Populations. <i>Genetics</i> , 1987, 117, 573-582.	2.9	60
52	Recommendations for improving statistical inference in population genomics. <i>PLoS Biology</i> , 2022, 20, e3001669.	5.6	60
53	The Nature of Genetic Variation for Complex Traits Revealed by GWAS and Regional Heritability Mapping Analyses. <i>Genetics</i> , 2015, 201, 1601-1613.	2.9	58
54	A Metabolic Basis for Dominance and Recessivity. <i>Genetics</i> , 1996, 143, 621-625.	2.9	58

#	ARTICLE	IF	CITATIONS
55	Mitochondrial Mutation Rate, Spectrum and Heteroplasmy in <i>Caenorhabditis elegans</i> Spontaneous Mutation Accumulation Lines of Differing Population Size. <i>Molecular Biology and Evolution</i> , 2017, 34, msx051.	8.9	57
56	Multigeneration Maximum-Likelihood Analysis Applied to Mutation-Accumulation Experiments in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2000, 154, 1193-1201.	2.9	55
57	Inferring the Frequency Spectrum of Derived Variants to Quantify Adaptive Molecular Evolution in Protein-Coding Genes of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 203, 975-984.	2.9	53
58	A Test for Epistasis Among Induced Mutations in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2000, 156, 1635-1647.	2.9	53
59	MCALIGN: Stochastic Alignment of Noncoding DNA Sequences Based on an Evolutionary Model of Sequence Evolution. <i>Genome Research</i> , 2004, 14, 442-450.	5.5	52
60	Evolutionary constraints in conserved nongenic sequences of mammals. <i>Genome Research</i> , 2005, 15, 1373-1378.	5.5	50
61	A Resolution of the Mutation Load Paradox in Humans. <i>Genetics</i> , 2012, 191, 1321-1330.	2.9	50
62	Detection of quantitative trait loci from frequency changes of marker alleles under selection. <i>Genetical Research</i> , 1993, 62, 195-203.	0.9	49
63	Regulatory Variation at Glypican-3 Underlies a Major Growth QTL in Mice. <i>PLoS Biology</i> , 2005, 3, e135.	5.6	47
64	PAPPA2, an Enzyme That Cleaves an Insulin-Like Growth-Factor-Binding Protein, Is a Candidate Gene for a Quantitative Trait Locus Affecting Body Size in Mice. <i>Genetics</i> , 2006, 173, 1547-1553.	2.9	47
65	Inferring the distribution of fitness effects of spontaneous mutations in <i>Chlamydomonas reinhardtii</i> . <i>PLoS Biology</i> , 2019, 17, e3000192.	5.6	47
66	Test of candidate gene quantitative trait locus association applied to fatness in mice. <i>Heredity</i> , 1998, 81, 630-637.	2.6	46
67	Comparative genomics of <i>Chlamydomonas</i> . <i>Plant Cell</i> , 2021, 33, 1016-1041.	6.6	46
68	Metabolic Models of Selection Response. <i>Journal of Theoretical Biology</i> , 1996, 182, 311-316.	1.7	43
69	Analysis and implications of mutational variation. <i>Genetica</i> , 2009, 136, 359-369.	1.1	43
70	The Role of Advantageous Mutations in Enhancing the Evolution of a Recombination Modifier. <i>Genetics</i> , 2010, 184, 1153-1164.	2.9	42
71	Mapping quantitative trait loci for body weight on the X chromosome in mice. I. Analysis of a reciprocal F2 population. <i>Genetical Research</i> , 1997, 70, 117-124.	0.9	41
72	Microarray gene expression analysis of the Fob3b obesity QTL identifies positional candidate gene Sqle and perturbed cholesterol and glycolysis pathways. <i>Physiological Genomics</i> , 2005, 20, 224-232.	2.3	39

#	ARTICLE	IF	CITATIONS
73	Genetic Basis of Response to 50 Generations of Selection on Body Weight in Inbred Mice. <i>Genetics</i> , 1998, 148, 1931-1939.	2.9	39
74	DNA Sequence Error Rates in Genbank Records Estimated using the Mouse Genome as a Reference. <i>DNA Sequence</i> , 2004, 15, 362-364.	0.7	37
75	Genetic complexity of an obesity QTL (Fob3) revealed by detailed genetic mapping. <i>Mammalian Genome</i> , 2004, 15, 472-481.	2.2	37
76	Recent Evolution in <i>Rattus norvegicus</i> Is Shaped by Declining Effective Population Size. <i>Molecular Biology and Evolution</i> , 2015, 32, 2547-2558.	8.9	36
77	The Recombination Landscape in Wild House Mice Inferred Using Population Genomic Data. <i>Genetics</i> , 2017, 207, 297-309.	2.9	36
78	Inference of Site Frequency Spectra From High-Throughput Sequence Data: Quantification of Selection on Nonsynonymous and Synonymous Sites in Humans. <i>Genetics</i> , 2011, 188, 931-940.	2.9	35
79	Quantitative genetic variability maintained by mutation-stabilizing selection balance: sampling variation and response to subsequent directional selection. <i>Genetical Research</i> , 1989, 54, 45-58.	0.9	34
80	Estimating the Rate of Adaptive Molecular Evolution When the Evolutionary Divergence Between Species is Small. <i>Journal of Molecular Evolution</i> , 2012, 74, 61-68.	1.8	34
81	SPONTANEOUS MUTATION ACCUMULATION IN MULTIPLE STRAINS OF THE GREEN ALGA, <i>CHLAMYDOMONAS REINHARDTII</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2589-2602.	2.3	34
82	Understanding the factors that shape patterns of nucleotide diversity in the house mouse genome. <i>Molecular Biology and Evolution</i> , 2018, 35, 2971-2988.	8.9	34
83	TOWARD A REALISTIC MODEL OF MUTATIONS AFFECTING FITNESS. <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 683.	2.3	33
84	Direct Estimate of the Spontaneous Mutation Rate Uncovers the Effects of Drift and Recombination in the <i>Chlamydomonas reinhardtii</i> Plastid Genome. <i>Molecular Biology and Evolution</i> , 2016, 33, 800-808.	8.9	33
85	Mapping quantitative trait loci affecting sternopleural bristle number in <i>Drosophila melanogaster</i> using changes of marker allele frequencies in divergently selected lines. <i>Genetical Research</i> , 1998, 72, 79-91.	0.9	32
86	Positive and Negative Selection in Murine Ultraconserved Noncoding Elements. <i>Molecular Biology and Evolution</i> , 2011, 28, 2651-2660.	8.9	32
87	Population genetics: Surviving under mutation pressure. <i>Current Biology</i> , 1998, 8, R235-R237.	3.9	31
88	Positive and Negative Selection on Noncoding DNA Close to Protein-Coding Genes in Wild House Mice. <i>Molecular Biology and Evolution</i> , 2011, 28, 1183-1191.	8.9	31
89	Average Dominance for Polygenes: Drawbacks of Regression Estimates. <i>Genetics</i> , 1997, 147, 1487-1490.	2.9	29
90	Fine mapping of a murine growth locus to a 1.4-cM region and resolution of linked QTL. <i>Mammalian Genome</i> , 2004, 15, 482-491.	2.2	28

#	ARTICLE	IF	CITATIONS
91	Mapping quantitative trait loci for body weight on the X chromosome in mice. II. Analysis of congenic backcrosses. <i>Genetical Research</i> , 1997, 70, 125-133.	0.9	27
92	Accumulation of mutations affecting body weight in inbred mouse lines. <i>Genetical Research</i> , 1995, 65, 145-149.	0.9	24
93	Patterns of population structure and complex haplotype sharing among field isolates of the green alga <i>Chlamydomonas reinhardtii</i> . <i>Molecular Ecology</i> , 2019, 28, 3977-3993.	3.9	23
94	Testing the correspondence between map positions of quantitative trait loci. <i>Genetical Research</i> , 1999, 74, 323-328.	0.9	22
95	High-resolution quantitative trait locus mapping for body weight in mice by recombinant progeny testing. <i>Genetical Research</i> , 2001, 77, 191-197.	0.9	22
96	Characterization of a QTL affecting skeletal size in mice. <i>Mammalian Genome</i> , 2003, 14, 175-183.	2.2	22
97	Unexpected conserved non-coding DNA blocks in mammals. <i>Trends in Genetics</i> , 2004, 20, 332-337.	6.7	22
98	Effect of Divergence Time and Recombination Rate on Molecular Evolution of <i>Drosophila</i> INE-1 Transposable Elements and Other Candidates for Neutrally Evolving Sites. <i>Journal of Molecular Evolution</i> , 2007, 65, 627-639.	1.8	21
99	Nuclear Gene Variation in Wild Brown Rats. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1661-1664.	1.8	21
100	Fitness change in relation to mutation number in spontaneous mutation accumulation lines of <i>Chlamydomonas reinhardtii</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2918-2929.	2.3	21
101	Inference of Mutation Parameters and Selective Constraint in Mammalian Coding Sequences by Approximate Bayesian Computation. <i>Genetics</i> , 2011, 187, 1153-1161.	2.9	20
102	Fitness decline under osmotic stress in <i>Caenorhabditis elegans</i> populations subjected to spontaneous mutation accumulation at varying population sizes. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1000-1008.	2.3	20
103	Inbred lab mice are not isogenic: genetic variation within inbred strains used to infer the mutation rate per nucleotide site. <i>Heredity</i> , 2021, 126, 107-116.	2.6	20
104	Genetic instability of <i>C. elegans</i> comes naturally. <i>Trends in Genetics</i> , 2005, 21, 67-70.	6.7	19
105	De Novo Mutation Rate Variation and Its Determinants in <i>Chlamydomonas</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 3709-3723.	8.9	19
106	Effect of the assignment of ancestral CpG state on the estimation of nucleotide substitution rates in mammals. <i>BMC Evolutionary Biology</i> , 2008, 8, 265.	3.2	15
107	The use of retrotransposons as markers for mapping genes responsible for fitness differences between related <i>Drosophila melanogaster</i> strains. <i>Genetical Research</i> , 1993, 62, 125-131.	0.9	13
108	Estimating numbers of EMS-induced mutations affecting life history traits in <i>Caenorhabditis elegans</i> in crosses between inbred sublines. <i>Genetical Research</i> , 2003, 82, 191-205.	0.9	13

#	ARTICLE	IF	CITATIONS
109	How many lethal alleles?. Trends in Genetics, 2003, 19, 57-59.	6.7	12
110	Patterns of DNA-Sequence Divergence Between <i>Drosophila miranda</i> and <i>D. pseudoobscura</i> . Journal of Molecular Evolution, 2009, 69, 601-611.	1.8	12
111	Assessing Recent Selection and Functionality at Long Noncoding RNA Loci in the Mouse Genome. Genome Biology and Evolution, 2015, 7, 2432-2444.	2.5	12
112	Quantitative Genetics: Loci with large effects. Current Biology, 1995, 5, 485-487.	3.9	11
113	Response to Kondrashov. Trends in Genetics, 2001, 17, 77-78.	6.7	11
114	Comparing Analysis Methods for Mutation-Accumulation Data. Genetics, 2004, 167, 551-553.	2.9	10
115	Genetic variance and fixation probabilities at quantitative trait loci in mutation-selection balance. Genetical Research, 1991, 58, 139-144.	0.9	9
116	Analysis of mutation accumulation experiments: response to Deng, Li and Li. Genetical Research, 1999, 74, 87-91.	0.9	9
117	The distribution of fitness effects of spontaneous mutations in <i>Chlamydomonas reinhardtii</i> inferred using frequency changes under experimental evolution. PLoS Genetics, 2022, 18, e1009840.	3.5	9
118	Genetic Architecture: Dissecting the Genetic Basis of Phenotypic Variation. Current Biology, 2002, 12, R415-R416.	3.9	6
119	Chewing the fat. Nature Genetics, 1995, 10, 125-126.	21.4	4
120	Quantitative genetics: Resolving wing shape genes. Current Biology, 2000, 10, R113-R115.	3.9	3
121	Behavioural Genetics: Finding Genes that Cause Complex Trait Variation. Current Biology, 2005, 15, R19-R21.	3.9	1
122	Low rates of proviral integration in SWR/J \times RF/J hybrid mice. Genetical Research, 1995, 66, 45-52.	0.9	0
123	William G. Hill (1940–2021). Nature Ecology and Evolution, 2022, 6, 344-345.	7.8	0