

# 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	William G. Hill (1940–2021). <i>Nature Ecology and Evolution</i> , 2022, 6, 344-345.	7.8	0
2	Recommendations for improving statistical inference in population genomics. <i>PLoS Biology</i> , 2022, 20, e3001669.	5.6	60
3	The distribution of fitness effects of spontaneous mutations in <i>Chlamydomonas reinhardtii</i> inferred using frequency changes under experimental evolution. <i>PLoS Genetics</i> , 2022, 18, e1009840.	3.5	9
4	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
5	Comparative genomics of <i>Chlamydomonas</i> . <i>Plant Cell</i> , 2021, 33, 1016-1041.	6.6	46
6	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
7	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
8	Inferring the distribution of fitness effects of spontaneous mutations in <i>Chlamydomonas reinhardtii</i> . <i>PLoS Biology</i> , 2019, 17, e3000192.	5.6	47
9	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
10	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
11	Inferring the Probability of the Derived vs. the Ancestral Allelic State at a Polymorphic Site. <i>Genetics</i> , 2018, 209, 897-906.	2.9	83
12	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
13	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
14	The Recombination Landscape in Wild House Mice Inferred Using Population Genomic Data. <i>Genetics</i> , 2017, 207, 297-309.	2.9	36
15	Detecting positive selection in the genome. <i>BMC Biology</i> , 2017, 15, 98.	3.8	97
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Estimation of the Spontaneous Mutation Rate in <i>Heliconius melpomene</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 239-243.	8.9	220
20	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
21	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
22	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
23	Assessing Recent Selection and Functionality at Long Noncoding RNA Loci in the Mouse Genome. <i>Genome Biology and Evolution</i> , 2015, 7, 2432-2444.	2.5	12
24	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
25	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
26	Faster-X Adaptive Protein Evolution in House Mice. <i>Genetics</i> , 2014, 196, 1131-1143.	2.9	62
27	A Comparison of Models to Infer the Distribution of Fitness Effects of New Mutations. <i>Genetics</i> , 2013, 193, 1197-1208.	2.9	114
28	Contributions of Protein-Coding and Regulatory Change to Adaptive Molecular Evolution in Murid Rodents. <i>PLoS Genetics</i> , 2013, 9, e1003995.	3.5	106
29	A Resolution of the Mutation Load Paradox in Humans. <i>Genetics</i> , 2012, 191, 1321-1330.	2.9	50
30	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
31	Nuclear Gene Variation in Wild Brown Rats. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1661-1664.	1.8	21
32	Estimate of the Spontaneous Mutation Rate in <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2012, 192, 1447-1454.	2.9	123
33	Rates and Fitness Consequences of New Mutations in Humans. <i>Genetics</i> , 2012, 190, 295-304.	2.9	174
34	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
35	Current hypotheses for the evolution of sex and recombination. <i>Integrative Zoology</i> , 2012, 7, 192-209.	2.6	158
36	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

#	ARTICLE	IF	CITATIONS
37	A Method for Inferring the Rate of Occurrence and Fitness Effects of Advantageous Mutations. <i>Genetics</i> , 2011, 189, 1427-1437.	2.9	111
38	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
39	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
40	Positive and Negative Selection in Murine Ultraconserved Noncoding Elements. <i>Molecular Biology and Evolution</i> , 2011, 28, 2651-2660.	8.9	32
41	The Role of Advantageous Mutations in Enhancing the Evolution of a Recombination Modifier. <i>Genetics</i> , 2010, 184, 1153-1164.	2.9	42
42	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
43	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
44	Evidence for Pervasive Adaptive Protein Evolution in Wild Mice. <i>PLoS Genetics</i> , 2010, 6, e1000825.	3.5	123
45	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
46	Analysis and implications of mutational variation. <i>Genetica</i> , 2009, 136, 359-369.	1.1	43
47	Patterns of DNA-Sequence Divergence Between <i>Drosophila miranda</i> and <i>D. pseudoobscura</i> . <i>Journal of Molecular Evolution</i> , 2009, 69, 601-611.	1.8	12
48	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
49	Spontaneous Mutation Accumulation Studies in Evolutionary Genetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2009, 40, 151-172.	8.3	396
50	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
51	Direct Estimation of the Mitochondrial DNA Mutation Rate in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2008, 6, e204.	5.6	239
52	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
53	The distribution of fitness effects of new mutations. <i>Nature Reviews Genetics</i> , 2007, 8, 610-618.	16.3	1,234
54	Direct estimation of per nucleotide and genomic deleterious mutation rates in <i>Drosophila</i> . <i>Nature</i> , 2007, 445, 82-85.	27.8	381

#	ARTICLE	IF	CITATIONS
55	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
56	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
57	Interference among deleterious mutations favours sex and recombination in finite populations. <i>Nature</i> , 2006, 443, 89-92.	27.8	328
58	Genomic Selective Constraints in Murid Noncoding DNA. <i>PLoS Genetics</i> , 2006, 2, e204.	3.5	60
59	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
60	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
61	Microarray gene expression analysis of the <i>Fob3b</i> obesity QTL identifies positional candidate gene <i>Sqle</i> and perturbed cholesterol and glycolysis pathways. <i>Physiological Genomics</i> , 2005, 20, 224-232.	2.3	39
62	Behavioural Genetics: Finding Genes that Cause Complex Trait Variation. <i>Current Biology</i> , 2005, 15, R19-R21.	3.9	1
63	Genetic instability of <i>C. elegans</i> comes naturally. <i>Trends in Genetics</i> , 2005, 21, 67-70.	6.7	19
64	Regulatory Variation at Glypican-3 Underlies a Major Growth QTL in Mice. <i>PLoS Biology</i> , 2005, 3, e135.	5.6	47
65	Evidence for Widespread Degradation of Gene Control Regions in Hominid Genomes. <i>PLoS Biology</i> , 2005, 3, e42.	5.6	178
66	Intron Size and Exon Evolution in <i>Drosophila</i> . <i>Genetics</i> , 2005, 170, 481-485.	2.9	105
67	Evolutionary constraints in conserved nongenic sequences of mammals. <i>Genome Research</i> , 2005, 15, 1373-1378.	5.5	50
68	The scale of mutational variation in the murid genome. <i>Genome Research</i> , 2005, 15, 1086-1094.	5.5	75
69	Comparing Analysis Methods for Mutation-Accumulation Data. <i>Genetics</i> , 2004, 167, 551-553.	2.9	10
70	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
71	Patterns of Evolutionary Constraints in Intronic and Intergenic DNA of <i>Drosophila</i> . <i>Genome Research</i> , 2004, 14, 273-279.	5.5	99
72	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

#	ARTICLE	IF	CITATIONS
73	Unexpected conserved non-coding DNA blocks in mammals. Trends in Genetics, 2004, 20, 332-337.	6.7	22
74	Genetic complexity of an obesity QTL (Fob3) revealed by detailed genetic mapping. Mammalian Genome, 2004, 15, 472-481.	2.2	37
75	Fine mapping of a murine growth locus to a 1.4-cM region and resolution of linked QTL. Mammalian Genome, 2004, 15, 482-491.	2.2	28
76	Characterization of a QTL affecting skeletal size in mice. Mammalian Genome, 2003, 14, 175-183.	2.2	22
77	How many lethal alleles?. Trends in Genetics, 2003, 19, 57-59.	6.7	12
78	TOWARD A REALISTIC MODEL OF MUTATIONS AFFECTING FITNESS. Evolution; International Journal of Organic Evolution, 2003, 57, 683-685.	2.3	129
79	TOWARD A REALISTIC MODEL OF MUTATIONS AFFECTING FITNESS. Evolution; International Journal of Organic Evolution, 2003, 57, 683.	2.3	33
80	Functional constraints and frequency of deleterious mutations in noncoding DNA of rodents. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13402-13406.	7.1	120
81	Estimating numbers of EMS-induced mutations affecting life history traits in <i>Caenorhabditis elegans</i> in crosses between inbred sublines. Genetical Research, 2003, 82, 191-205.	0.9	13
82	Enhanced CpG Mutability and Tumorigenesis in MBD4-Deficient Mice. Science, 2002, 297, 403-405.	12.6	294
83	Quantifying the Slightly Deleterious Mutation Model of Molecular Evolution. Molecular Biology and Evolution, 2002, 19, 2142-2149.	8.9	191
84	Genetic Architecture: Dissecting the Genetic Basis of Phenotypic Variation. Current Biology, 2002, 12, R415-R416.	3.9	6
85	Understanding quantitative genetic variation. Nature Reviews Genetics, 2002, 3, 11-21.	16.3	727
86	Spontaneous Mutational Variation for Body Size in <i>Caenorhabditis elegans</i> . Genetics, 2002, 162, 755-765.	2.9	67
87	High-resolution quantitative trait locus mapping for body weight in mice by recombinant progeny testing. Genetical Research, 2001, 77, 191-197.	0.9	22
88	Response to Kondrashov. Trends in Genetics, 2001, 17, 77-78.	6.7	11
89	Quantitative genetics: Resolving wing shape genes. Current Biology, 2000, 10, R113-R115.	3.9	3
90	Mapping of obesity QTLs in a cross between mouse lines divergently selected on fat content. Mammalian Genome, 2000, 11, 2-7.	2.2	74

#	ARTICLE	IF	CITATIONS
91	Multigeneration Maximum-Likelihood Analysis Applied to Mutation-Accumulation Experiments in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2000, 154, 1193-1201.	2.9	55
92	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
93	A Test for Epistasis Among Induced Mutations in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2000, 156, 1635-1647.	2.9	53
94	High genomic deleterious mutation rates in hominids. <i>Nature</i> , 1999, 397, 344-347.	27.8	412
95	High Frequency of Cryptic Deleterious Mutations in <i>Caenorhabditis elegans</i> . <i>Science</i> , 1999, 285, 1748-1751.	12.6	153
96	Analysis of mutation accumulation experiments: response to Deng, Li and Li. <i>Genetical Research</i> , 1999, 74, 87-91.	0.9	9
97	Testing the correspondence between map positions of quantitative trait loci. <i>Genetical Research</i> , 1999, 74, 323-328.	0.9	22
98	Terumi Mukai and the Riddle of Deleterious Mutation Rates. <i>Genetics</i> , 1999, 153, 515-523.	2.9	154
99	Population genetics: Surviving under mutation pressure. <i>Current Biology</i> , 1998, 8, R235-R237.	3.9	31
100	Test of candidate gene quantitative trait locus association applied to fatness in mice. <i>Heredity</i> , 1998, 81, 630-637.	2.6	46
101	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
102	EMS-Induced Polygenic Mutation Rates for Nine Quantitative Characters in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1998, 148, 753-766.	2.9	100
103	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
104	Bottleneck Effect on Genetic Variance: A Theoretical Investigation of the Role of Dominance. <i>Genetics</i> , 1998, 150, 435-447.	2.9	70
105	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
106	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
107	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
108	Average Dominance for Polygenes: Drawbacks of Regression Estimates. <i>Genetics</i> , 1997, 147, 1487-1490.	2.9	29

#	ARTICLE	IF	CITATIONS
109	Metabolic Models of Selection Response. <i>Journal of Theoretical Biology</i> , 1996, 182, 311-316.	1.7	43
110	A Genetic Map of Quantitative Trait Loci for Body Weight in the Mouse. <i>Genetics</i> , 1996, 142, 227-235.	2.9	99
111	A Metabolic Basis for Dominance and Recessivity. <i>Genetics</i> , 1996, 143, 621-625.	2.9	58
112	Nature of Deleterious Mutation Load in <i>Drosophila</i> . <i>Genetics</i> , 1996, 144, 1993-1999.	2.9	171
113	Low rates of proviral integration in SWR/J $\times$ RF/J hybrid mice. <i>Genetical Research</i> , 1995, 66, 45-52.	0.9	0
114	Accumulation of mutations affecting body weight in inbred mouse lines. <i>Genetical Research</i> , 1995, 65, 145-149.	0.9	24
115	Quantitative Genetics: Loci with large effects. <i>Current Biology</i> , 1995, 5, 485-487.	3.9	11
116	Chewing the fat. <i>Nature Genetics</i> , 1995, 10, 125-126.	21.4	4
117	Detection of quantitative trait loci from frequency changes of marker alleles under selection. <i>Genetical Research</i> , 1993, 62, 195-203.	0.9	49
118	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
119	Genetic variance and fixation probabilities at quantitative trait loci in mutation-selection balance. <i>Genetical Research</i> , 1991, 58, 139-144.	0.9	9
120	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
121	Quantitative genetic variability maintained by mutation-stabilizing selection balance in finite populations. <i>Genetical Research</i> , 1988, 52, 33-43.	0.9	108
122	Dominance, Pleiotropy and Metabolic Structure. <i>Genetics</i> , 1987, 117, 319-329.	2.9	89
123	Directional Selection and Variation in Finite Populations. <i>Genetics</i> , 1987, 117, 573-582.	2.9	60