

# Dmitri A Petrov

## List of Publications by Year in descending order

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Version: 2024-02-01

152  
papers

17,269  
citations

16411

64  
h-index

20900

115  
g-index

204  
all docs

204  
docs citations

204  
times ranked

17382  
citing authors

#	ARTICLE	IF	CITATIONS
1	Widespread introgression across a phylogeny of 155 <i>Drosophila</i> genomes. <i>Current Biology</i> , 2022, 32, 111-123.e5.	1.8	132
2	Revisiting the malaria hypothesis: accounting for polygenicity and pleiotropy. <i>Trends in Parasitology</i> , 2022, 38, 290-301.	1.5	5
3	Tumor suppressor pathways shape EGFR-driven lung tumor progression and response to treatment. <i>Molecular and Cellular Oncology</i> , 2022, 9, 1994328.	0.3	0
4	Direct observation of adaptive tracking on ecological time scales in <i>Drosophila</i> . <i>Science</i> , 2022, 375, eabj7484.	6.0	71
5	Combinatorial Inactivation of Tumor Suppressors Efficiently Initiates Lung Adenocarcinoma with Therapeutic Vulnerabilities. <i>Cancer Research</i> , 2022, 82, 1589-1602.	0.4	7
6	Genetic Adaptation in New York City Rats. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	13
7	The clarifying role of time series data in the population genetics of HIV. <i>PLoS Genetics</i> , 2021, 17, e1009050.	1.5	26
8	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021, 38, 2366-2379.	3.5	35
9	A Functional Taxonomy of Tumor Suppression in Oncogenic KRAS-Driven Lung Cancer. <i>Cancer Discovery</i> , 2021, 11, 1754-1773.	7.7	35
10	Detection of hard and soft selective sweeps from <i>Drosophila melanogaster</i> population genomic data. <i>PLoS Genetics</i> , 2021, 17, e1009373.	1.5	35
11	Human-chimpanzee fused cells reveal cis-regulatory divergence underlying skeletal evolution. <i>Nature Genetics</i> , 2021, 53, 467-476.	9.4	46
12	Genetic Determinants of EGFR-Driven Lung Cancer Growth and Therapeutic Response <i>In Vivo</i> . <i>Cancer Discovery</i> , 2021, 11, 1736-1753.	7.7	59
13	Historical trends and new surveillance of <i>Plasmodium falciparum</i> drug resistance markers in Angola. <i>Malaria Journal</i> , 2021, 20, 175.	0.8	7
14	The AMBRA1 E3 ligase adaptor regulates the stability of cyclin D. <i>Nature</i> , 2021, 592, 794-798.	13.7	76
15	The cis-regulatory effects of modern human-specific variants. <i>ELife</i> , 2021, 10, .	2.8	36
16	Functional biology in its natural context: A search for emergent simplicity. <i>ELife</i> , 2021, 10, .	2.8	34
17	Broad geographic sampling reveals the shared basis and environmental correlates of seasonal adaptation in <i>Drosophila</i> . <i>ELife</i> , 2021, 10, .	2.8	66
18	Highly contiguous assemblies of 101 drosophilid genomes. <i>ELife</i> , 2021, 10, .	2.8	108

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19	Quantitative <i>In Vivo</i> Analyses Reveal a Complex Pharmacogenomic Landscape in Lung Adenocarcinoma. <i>Cancer Research</i> , 2021, 81, 4570-4580.	0.4	13
20	Richard C. Lewontin (1929–2021). <i>Science</i> , 2021, 373, 745-745.	6.0	2
21	<i>Drosophila</i> Evolution over Space and Time (DEST): A New Population Genomics Resource. <i>Molecular Biology and Evolution</i> , 2021, 38, 5782-5805.	3.5	37
22	Common host variation drives malaria parasite fitness in healthy human red cells. <i>ELife</i> , 2021, 10, .	2.8	17
23	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. <i>Nature Neuroscience</i> , 2021, 24, 186-196.	7.1	22
24	The <i>Tetragnatha kauaiensis</i> Genome Sheds Light on the Origins of Genomic Novelty in Spiders. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	16
25	Long live the king: chromosome-level assembly of the lion ( <i>Panthera leo</i> ) using linked-read, Hi-C, and long-read data. <i>BMC Biology</i> , 2020, 18, 3.	1.7	34
26	Pervasive Strong Selection at the Level of Codon Usage Bias in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2020, 214, 511-528.	1.2	42
27	Ancient RNA virus epidemics through the lens of recent adaptation in human genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190575.	1.8	37
28	Fitness variation across subtle environmental perturbations reveals local modularity and global pleiotropy of adaptation. <i>ELife</i> , 2020, 9, .	2.8	69
29	Single nucleotide mapping of trait space reveals Pareto fronts that constrain adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 1539-1551.	3.4	60
30	Microbiome composition shapes rapid genomic adaptation of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20025-20032.	3.3	103
31	Exploiting selection at linked sites to infer the rate and strength of adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 977-984.	3.4	43
32	Empowering conservation practice with efficient and economical genotyping from poor quality samples. <i>Methods in Ecology and Evolution</i> , 2019, 10, 853-859.	2.2	40
33	Stress response, behavior, and development are shaped by transposable element-induced mutations in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2019, 15, e1007900.	1.5	64
34	Evolutionary Dynamics in Structured Populations Under Strong Population Genetic Forces. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3395-3407.	0.8	23
35	Accurate Allele Frequencies from Ultra-low Coverage Pool-Seq Samples in Evolve-and-Resequencing Experiments. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 4159-4168.	0.8	29
36	Cost-effective assembly of the African wild dog ( <i>Lycaon pictus</i> ) genome using linked reads. <i>GigaScience</i> , 2019, 8, .	3.3	22

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37	Hidden Complexity of Yeast Adaptation under Simple Evolutionary Conditions. <i>Current Biology</i> , 2018, 28, 515-525.e6.	1.8	63
38	Rapid seasonal evolution in innate immunity of wild <i>Drosophila melanogaster</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20172599.	1.2	82
39	Tripolar chromosome segregation drives the association between maternal genotype at variants spanning PLK4 and aneuploidy in human preimplantation embryos. <i>Human Molecular Genetics</i> , 2018, 27, 2573-2585.	1.4	55
40	Mapping the in vivo fitness landscape of lung adenocarcinoma tumor suppression in mice. <i>Nature Genetics</i> , 2018, 50, 483-486.	9.4	101
41	Common variants associated with mitotic-origin of aneuploidy in human embryos. <i>Reproductive BioMedicine Online</i> , 2018, 36, e1.	1.1	0
42	Tissue-Specific cis-Regulatory Divergence Implicates eIoF in Inhibiting Interspecies Mating in <i>Drosophila</i> . <i>Current Biology</i> , 2018, 28, 3969-3975.e3.	1.8	37
43	Evidence that RNA Viruses Drove Adaptive Introgression between Neanderthals and Modern Humans. <i>Cell</i> , 2018, 175, 360-371.e13.	13.5	164
44	Spatiotemporal dynamics and genome-wide association analysis of desiccation tolerance in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2018, 27, 3525-3540.	2.0	33
45	Soft Selective Sweeps in Evolutionary Rescue. <i>Genetics</i> , 2017, 205, 1573-1586.	1.2	41
46	A quantitative and multiplexed approach to uncover the fitness landscape of tumor suppression in vivo. <i>Nature Methods</i> , 2017, 14, 737-742.	9.0	105
47	Deep sequencing of natural and experimental populations of <i>Drosophila melanogaster</i> reveals biases in the spectrum of new mutations. <i>Genome Research</i> , 2017, 27, 1988-2000.	2.4	45
48	Seasonally fluctuating selection can maintain polymorphism at many loci via segregation lift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9932-E9941.	3.3	100
49	Multiplexed in vivo homology-directed repair and tumor barcoding enables parallel quantification of Kras variant oncogenicity. <i>Nature Communications</i> , 2017, 8, 2053.	5.8	78
50	Extremely Rare Polymorphisms in <i>Saccharomyces cerevisiae</i> Allow Inference of the Mutational Spectrum. <i>PLoS Genetics</i> , 2017, 13, e1006455.	1.5	13
51	High rate of adaptation of mammalian proteins that interact with Plasmodium and related parasites. <i>PLoS Genetics</i> , 2017, 13, e1007023.	1.5	37
52	Seeking Goldilocks During Evolution of Drug Resistance. <i>PLoS Biology</i> , 2017, 15, e2001872.	2.6	2
53	A spatio-temporal assessment of simian/human immunodeficiency virus (SHIV) evolution reveals a highly dynamic process within the host. <i>PLoS Pathogens</i> , 2017, 13, e1006358.	2.1	25
54	SNP genotyping to monitor wild tigers for conservation. <i>Canadian Journal of Biotechnology</i> , 2017, 1, 19-19.	0.3	0

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55	Secondary contact and local adaptation contribute to genome-wide patterns of clinal variation in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2016, 25, 1157-1174.	2.0	149
56	Comparative population genomics of latitudinal variation in <i>Drosophila simulans</i> and <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2016, 25, 723-740.	2.0	128
57	Elevated Linkage Disequilibrium and Signatures of Soft Sweeps Are Common in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 203, 863-880.	1.2	44
58	Heterozygote Advantage Is a Common Outcome of Adaptation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 203, 1401-1413.	1.2	38
59	Whole Genome Analysis of 132 Clinical <i>Saccharomyces cerevisiae</i> Strains Reveals Extensive Ploidy Variation. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2421-2434.	0.8	129
60	An Intrinsically Disordered Region of the DNA Repair Protein Nbs1 Is a Species-Specific Barrier to Herpes Simplex Virus 1 in Primates. <i>Cell Host and Microbe</i> , 2016, 20, 178-188.	5.1	33
61	Development of a Comprehensive Genotype-to-Fitness Map of Adaptation-Driving Mutations in Yeast. <i>Cell</i> , 2016, 166, 1585-1596.e22.	13.5	205
62	Global Transcriptional Profiling of Diapause and Climatic Adaptation in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 707-720.	3.5	59
63	Effects of maternal age on euploidy rates in a large cohort of embryos analyzed with 24-chromosome single-nucleotide polymorphism-based preimplantation genetic screening. <i>Fertility and Sterility</i> , 2016, 105, 1307-1313.	0.5	131
64	More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. <i>ELife</i> , 2016, 5, .	2.8	70
65	Viruses are a dominant driver of protein adaptation in mammals. <i>ELife</i> , 2016, 5, .	2.8	267
66	Evidence of Selection against Complex Mitotic-Origin Aneuploidy during Preimplantation Development. <i>PLoS Genetics</i> , 2015, 11, e1005601.	1.5	170
67	Quantification of GC-biased gene conversion in the human genome. <i>Genome Research</i> , 2015, 25, 1215-1228.	2.4	127
68	Quantitative evolutionary dynamics using high-resolution lineage tracking. <i>Nature</i> , 2015, 519, 181-186.	13.7	372
69	Imperfect drug penetration leads to spatial monotherapy and rapid evolution of multidrug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2874-83.	3.3	142
70	Recent Selective Sweeps in North American <i>Drosophila melanogaster</i> Show Signatures of Soft Sweeps. <i>PLoS Genetics</i> , 2015, 11, e1005004.	1.5	392
71	Obstruction of adaptation in diploids by recessive, strongly deleterious alleles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2658-66.	3.3	34
72	T-lex2: genotyping, frequency estimation and re-annotation of transposable elements using single or pooled next-generation sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, e22-e22.	6.5	61

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73	Common variants spanning <i>PLK4</i> are associated with mitotic-origin aneuploidy in human embryos. <i>Science</i> , 2015, 348, 235-238.	6.0	106
74	Illumina TruSeq Synthetic Long-Reads Empower De Novo Assembly and Resolve Complex, Highly-Repetitive Transposable Elements. <i>PLoS ONE</i> , 2014, 9, e106689.	1.1	180
75	Precise estimates of mutation rate and spectrum in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2310-8.	3.3	362
76	Genomic Evidence of Rapid and Stable Adaptive Oscillations over Seasonal Time Scales in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2014, 10, e1004775.	1.5	473
77	Soft Selective Sweeps in Complex Demographic Scenarios. <i>Genetics</i> , 2014, 198, 669-684.	1.2	69
78	Genome-wide signals of positive selection in human evolution. <i>Genome Research</i> , 2014, 24, 885-895.	2.4	200
79	Comparative population genomics: power and principles for the inference of functionality. <i>Trends in Genetics</i> , 2014, 30, 133-139.	2.9	48
80	Genomic inference accurately predicts the timing and severity of a recent bottleneck in a nonmodel insect population. <i>Molecular Ecology</i> , 2014, 23, 136-150.	2.0	40
81	Population Genomics of Transposable Elements in <i>Drosophila</i> . <i>Annual Review of Genetics</i> , 2014, 48, 561-581.	3.2	144
82	Reply to Chen and Zhang: On interpreting genome-wide trends from yeast mutation accumulation data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4063-E4063.	3.3	0
83	Population genomics of rapid adaptation by soft selective sweeps. <i>Trends in Ecology and Evolution</i> , 2013, 28, 659-669.	4.2	471
84	Strong Purifying Selection at Synonymous Sites in <i>D. melanogaster</i> . <i>PLoS Genetics</i> , 2013, 9, e1003527.	1.5	187
85	Evolutionary Biology for the 21st Century. <i>PLoS Biology</i> , 2013, 11, e1001466.	2.6	115
86	Frequent adaptation and the McDonald-Kreitman test. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8615-8620.	3.3	231
87	Host Species and Environmental Effects on Bacterial Communities Associated with <i>Drosophila</i> in the Laboratory and in the Natural Environment. <i>PLoS ONE</i> , 2013, 8, e70749.	1.1	216
88	LDx: Estimation of Linkage Disequilibrium from High-Throughput Pooled Resequencing Data. <i>PLoS ONE</i> , 2012, 7, e48588.	1.1	88
89	Evolution of Genome Content: Population Dynamics of Transposable Elements in Flies and Humans. <i>Methods in Molecular Biology</i> , 2012, 855, 361-383.	0.4	41
90	Origins and rates of aneuploidy in human blastomeres. <i>Fertility and Sterility</i> , 2012, 97, 395-401.	0.5	110

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91	Empirical Validation of Pooled Whole Genome Population Re-Sequencing in <i>Drosophila melanogaster</i> . PLoS ONE, 2012, 7, e41901.	1.1	84
92	On the Limitations of Using Ribosomal Genes as References for the Study of Codon Usage: A Rebuttal. PLoS ONE, 2012, 7, e49060.	1.1	17
93	Population Genomics of Transposable Elements in <i>Drosophila melanogaster</i> . Molecular Biology and Evolution, 2011, 28, 1633-1644.	3.5	160
94	Faster than Neutral Evolution of Constrained Sequences: The Complex Interplay of Mutational Biases and Weak Selection. Genome Biology and Evolution, 2011, 3, 383-395.	1.1	30
95	Heterozygote advantage as a natural consequence of adaptation in diploids. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20666-20671.	3.3	174
96	High sensitivity to aligner and high rate of false positives in the estimates of positive selection in the 12 <i>Drosophila</i> genomes. Genome Research, 2011, 21, 863-874.	2.4	137
97	T-lex: a program for fast and accurate assessment of transposable element presence using next-generation sequencing data. Nucleic Acids Research, 2011, 39, e36-e36.	6.5	53
98	Relaxed Purifying Selection and Possibly High Rate of Adaptation in Primate Lineage-Specific Genes. Genome Biology and Evolution, 2010, 2, 393-409.	1.1	100
99	Broker Genes in Human Disease. Genome Biology and Evolution, 2010, 2, 815-825.	1.1	68
100	Adaptive Evolution of Pelvic Reduction in Sticklebacks by Recurrent Deletion of a <i>Pitx1</i> Enhancer. Science, 2010, 327, 302-305.	6.0	901
101	Evidence that Adaptation in <i>Drosophila</i> Is Not Limited by Mutation at Single Sites. PLoS Genetics, 2010, 6, e1000924.	1.5	255
102	Genome-Wide Patterns of Adaptation to Temperate Environments Associated with Transposable Elements in <i>Drosophila</i> . PLoS Genetics, 2010, 6, e1000905.	1.5	137
103	<i>Drosophila melanogaster</i> recombination rate calculator. Gene, 2010, 463, 18-20.	1.0	142
104	Evidence That Mutation Is Universally Biased towards AT in Bacteria. PLoS Genetics, 2010, 6, e1001115.	1.5	386
105	General Rules for Optimal Codon Choice. PLoS Genetics, 2009, 5, e1000556.	1.5	203
106	MITEs – The Ultimate Parasites. Science, 2009, 325, 1352-1353.	6.0	17
107	Similarly Strong Purifying Selection Acts on Human Disease Genes of All Evolutionary Ages. Genome Biology and Evolution, 2009, 1, 131-144.	1.1	45
108	Pervasive Natural Selection in the <i>Drosophila</i> Genome?. PLoS Genetics, 2009, 5, e1000495.	1.5	329

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109	Pervasive Hitchhiking at Coding and Regulatory Sites in Humans. <i>PLoS Genetics</i> , 2009, 5, e1000336.	1.5	134
110	Molecular Evolution of the Testis TAFs of <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 1103-1116.	3.5	15
111	A Recent Adaptive Transposable Element Insertion Near Highly Conserved Developmental Loci in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 1949-1961.	3.5	58
112	The adaptive role of transposable elements in the <i>Drosophila</i> genome. <i>Gene</i> , 2009, 448, 124-133.	1.0	82
113	Selection on Codon Bias. <i>Annual Review of Genetics</i> , 2008, 42, 287-299.	3.2	827
114	Pervasive and Persistent Redundancy among Duplicated Genes in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000113.	1.5	181
115	Nonadaptive Explanations for Signatures of Partial Selective Sweeps in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1025-1042.	3.5	21
116	High Rate of Recent Transposable Element-Induced Adaptation in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2008, 6, e251.	2.6	176
117	High Functional Diversity in <i>Mycobacterium tuberculosis</i> Driven by Genetic Drift and Human Demography. <i>PLoS Biology</i> , 2008, 6, e311.	2.6	507
118	Inferring the Strength of Selection in <i>Drosophila</i> under Complex Demographic Models. <i>Molecular Biology and Evolution</i> , 2008, 26, 513-526.	3.5	28
119	Genomewide Spatial Correspondence Between Nonsynonymous Divergence and Neutral Polymorphism Reveals Extensive Adaptation in <i>Drosophila</i> . <i>Genetics</i> , 2007, 177, 2083-2099.	1.2	115
120	The mode and tempo of genome size evolution in eukaryotes. <i>Genome Research</i> , 2007, 17, 594-601.	2.4	140
121	Reduced selection leads to accelerated gene loss in <i>Shigella</i> . <i>Genome Biology</i> , 2007, 8, R164.	13.9	64
122	Similar Levels of X-linked and Autosomal Nucleotide Variation in African and non-African populations of <i>Drosophila melanogaster</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 202.	3.2	46
123	Minor shift in background substitutional patterns in the <i>Drosophila saltans</i> and <i>willistoni</i> lineages is insufficient to explain GC content of coding sequences. <i>BMC Biology</i> , 2006, 4, 37.	1.7	17
124	A Novel Method Distinguishes Between Mutation Rates and Fixation Biases in Patterns of Single-Nucleotide Substitution. <i>Journal of Molecular Evolution</i> , 2006, 62, 168-175.	0.8	10
125	Do disparate mechanisms of duplication add similar genes to the genome?. <i>Trends in Genetics</i> , 2005, 21, 548-551.	2.9	91
126	Substantial Regional Variation in Substitution Rates in the Human Genome: Importance of GC Content, Gene Density, and Telomere-Specific Effects. <i>Journal of Molecular Evolution</i> , 2005, 60, 748-763.	0.8	85



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127	Protein Evolution in the Context of <i>Drosophila</i> Development. <i>Journal of Molecular Evolution</i> , 2005, 60, 774-785.	0.8	54
128	Codon Bias and Noncoding GC Content Correlate Negatively with Recombination Rate on the <i>Drosophila</i> X Chromosome. <i>Journal of Molecular Evolution</i> , 2005, 61, 315-324.	0.8	50
129	Paucity of chimeric gene-transposable element transcripts in the <i>Drosophila melanogaster</i> genome. <i>BMC Biology</i> , 2005, 3, 24.	1.7	54
130	X-Linked Genes Evolve Higher Codon Bias in <i>Drosophila</i> and <i>Caenorhabditis</i> . <i>Genetics</i> , 2005, 171, 145-155.	1.2	60
131	Elevated evolutionary rates in the laboratory strain of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1092-1097.	3.3	90
132	Pesticide Resistance via Transposition-Mediated Adaptive Gene Truncation in <i>Drosophila</i> . <i>Science</i> , 2005, 309, 764-767.	6.0	226
133	The Large Genome Constraint Hypothesis: Evolution, Ecology and Phenotype. <i>Annals of Botany</i> , 2005, 95, 177-190.	1.4	429
134	Genomic Heterogeneity of Background Substitutional Patterns in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2005, 169, 709-722.	1.2	90
135	Rapid Sequence Turnover at an Intergenic Locus in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 670-680.	3.5	48
136	Enhancer Choice in Cis and in Trans in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004, 167, 1739-1747.	1.2	36
137	Rates of DNA Duplication and Mitochondrial DNA Insertion in the Human Genome. <i>Journal of Molecular Evolution</i> , 2003, 57, 343-354.	0.8	112
138	Transposable elements in clonal lineages: lethal hangover from sex. <i>Biological Journal of the Linnean Society</i> , 2003, 79, 33-41.	0.7	46
139	Distinct Changes of Genomic Biases in Nucleotide Substitution at the Time of Mammalian Radiation. <i>Molecular Biology and Evolution</i> , 2003, 20, 1887-1896.	3.5	95
140	Size Matters: Non-LTR Retrotransposable Elements and Ectopic Recombination in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 880-892.	3.5	208
141	Mutational Equilibrium Model of Genome Size Evolution. <i>Theoretical Population Biology</i> , 2002, 61, 531-544.	0.5	231
142	DNA loss and evolution of genome size in <i>Drosophila</i> . <i>Genetica</i> , 2002, 115, 81-91.	0.5	133
143	How Intron Splicing Affects the Deletion and Insertion Profile in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2002, 162, 1233-1244.	1.2	22
144	Evolution of genome size: new approaches to an old problem. <i>Trends in Genetics</i> , 2001, 17, 23-28.	2.9	378

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145	Genomic Gigantism: DNA Loss Is Slow in Mountain Grasshoppers. <i>Molecular Biology and Evolution</i> , 2001, 18, 246-253.	3.5	111
146	Genome size as a mutation-selection-drift process.. <i>Genes and Genetic Systems</i> , 1999, 74, 201-207.	0.2	19
147	Slow but Steady: Reduction of Genome Size through Biased Mutation [with Reply]. <i>Plant Cell</i> , 1997, 9, 1900.	3.1	10
148	Trash DNA is what gets thrown away: high rate of DNA loss in <i>Drosophila</i> . <i>Gene</i> , 1997, 205, 279-289.	1.0	67
149	High intrinsic rate of DNA loss in <i>Drosophila</i> . <i>Nature</i> , 1996, 384, 346-349.	13.7	374
150	A combined molecular and cytogenetic approach to genome evolution in <i>Drosophila</i> using large-fragment DNA cloning. <i>Chromosoma</i> , 1993, 102, 253-266.	1.0	54
151	A repetitive DNA element, associated with telomeric sequences in <i>Drosophila melanogaster</i> , contains open reading frames. <i>Chromosoma</i> , 1992, 102, 32-40.	1.0	53
152	Characterization of bacteriophage P1 library containing inserts of <i>Drosophila</i> DNA of 75?100 kilobase pairs. <i>Chromosoma</i> , 1991, 100, 487-494.	1.0	117