

Christian Schläpfer

List of Publications by Year in descending order

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Version: 2024-02-01

232
papers

20,463
citations

18887

64
h-index

16791

127
g-index

262
all docs

262
docs citations

262
times ranked

20444
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of phenotypic variance in response to a novel hot environment. <i>Molecular Ecology</i> , 2022, 31, 934-945.	2.0	4
2	Pool-GWAS on reproductive dormancy in <i>Drosophila simulans</i> suggests a polygenic architecture. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	1
3	Natural variation in <i>Drosophila</i> shows weak pleiotropic effects. <i>Genome Biology</i> , 2022, 23, 116.	3.8	4
4	The Transposition Rate Has Little Influence on the Plateauing Level of the P-element. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	11
5	Parallel gene expression evolution in natural and laboratory evolved populations. <i>Molecular Ecology</i> , 2021, 30, 884-894.	2.0	15
6	Detecting selected haplotype blocks in evolve and resequence experiments. <i>Molecular Ecology Resources</i> , 2021, 21, 93-109.	2.2	20
7	Fine Mapping without Phenotyping: Identification of Selection Targets in Secondary Evolve and Resequencing Experiments. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
8	The genetic architecture of temperature adaptation is shaped by population ancestry and not by selection regime. <i>Genome Biology</i> , 2021, 22, 211.	3.8	11
9	Highly Parallel Genomic Selection Response in Replicated <i>Drosophila melanogaster</i> Populations with Reduced Genetic Variation. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
10	Long-term gut microbiome dynamics in <i>Drosophila melanogaster</i> reveal environment-specific associations between bacterial taxa at the family level. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20212193.	1.2	4
11	Next-generation biological control: the need for integrating genetics and genomics. <i>Biological Reviews</i> , 2020, 95, 1838-1854.	4.7	67
12	Low concordance of short-term and long-term selection responses in experimental <i>Drosophila</i> populations. <i>Molecular Ecology</i> , 2020, 29, 3466-3475.	2.0	15
13	The Evolution of Phenotypic Plasticity in Response to Temperature Stress. <i>Genome Biology and Evolution</i> , 2020, 12, 2429-2440.	1.1	30
14	Fitness effects for Ace insecticide resistance mutations are determined by ambient temperature. <i>BMC Biology</i> , 2020, 18, 157.	1.7	8
15	Long-Term Dynamics Among Wolbachia Strains During Thermal Adaptation of Their <i>Drosophila melanogaster</i> Hosts. <i>Frontiers in Genetics</i> , 2020, 11, 482.	1.1	7
16	Neuronal Function and Dopamine Signaling Evolve at High Temperature in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2630-2640.	3.5	22
17	Secondary Evolve and Resequencing: An Experimental Confirmation of Putative Selection Targets without Phenotyping. <i>Genome Biology and Evolution</i> , 2020, 12, 151-159.	1.1	14
18	Polygenic adaptation: a unifying framework to understand positive selection. <i>Nature Reviews Genetics</i> , 2020, 21, 769-781.	7.7	238

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19	Distinct Patterns of Selective Sweep and Polygenic Adaptation in Evolve and Resequencing Studies. <i>Genome Biology and Evolution</i> , 2020, 12, 890-904.	1.1	29
20	Rapid sex-specific adaptation to high temperature in <i>Drosophila</i> . <i>ELife</i> , 2020, 9, .	2.8	25
21	Benchmarking software tools for detecting and quantifying selection in evolve and resequencing studies. <i>Genome Biology</i> , 2019, 20, 169.	3.8	33
22	A 24 h Age Difference Causes Twice as Much Gene Expression Divergence as 100 Generations of Adaptation to a Novel Environment. <i>Genes</i> , 2019, 10, 89.	1.0	11
23	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095.	1.6	39
24	Shifting the paradigm in Evolve and Resequencing studies: From analysis of single nucleotide polymorphisms to selected haplotype blocks. <i>Molecular Ecology</i> , 2019, 28, 521-524.	2.0	18
25	DNA Motifs Are Not General Predictors of Recombination in Two <i>Drosophila</i> Sister Species. <i>Genome Biology and Evolution</i> , 2019, 11, 1345-1357.	1.1	24
26	Genetic redundancy fuels polygenic adaptation in <i>Drosophila</i> . <i>PLoS Biology</i> , 2019, 17, e3000128.	2.6	212
27	Redefining reproductive dormancy in <i>Drosophila</i> as a general stress response to cold temperatures. <i>Journal of Insect Physiology</i> , 2018, 107, 175-185.	0.9	46
28	High-throughput fecundity measurements in <i>Drosophila</i> . <i>Scientific Reports</i> , 2018, 8, 4469.	1.6	16
29	Asian horses deepen the MSY phylogeny. <i>Animal Genetics</i> , 2018, 49, 90-93.	0.6	32
30	Molecular dissection of a natural transposable element invasion. <i>Genome Research</i> , 2018, 28, 824-835.	2.4	64
31	Contesting the evidence for non-adaptive plasticity. <i>Nature</i> , 2018, 555, E21-E22.	13.7	29
32	<i>ReadTools</i> : A universal toolkit for handling sequence data from different sequencing platforms. <i>Molecular Ecology Resources</i> , 2018, 18, 676-680.	2.2	34
33	Evolution of longevity improves immunity in <i>Drosophila</i> . <i>Evolution Letters</i> , 2018, 2, 567-579.	1.6	62
34	Readapting to DCV Infection without Wolbachia: Frequency Changes of <i>Drosophila</i> Antiviral Alleles Can Replace Endosymbiont Protection. <i>Genome Biology and Evolution</i> , 2018, 10, 1783-1791.	1.1	13
35	Pleiotropic effects of regulatory variation in <i>tan</i> result in correlation of two pigmentation traits in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2018, 27, 3207-3218.	2.0	22
36	A simple genetic basis of adaptation to a novel thermal environment results in complex metabolic rewiring in <i>Drosophila</i> . <i>Genome Biology</i> , 2018, 19, 119.	3.8	71

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37	Polymorphism-aware protein databases – a prerequisite for an unbiased proteomic analysis of natural populations. <i>Molecular Ecology Resources</i> , 2017, 17, 1148-1155.	2.2	3
38	<scp>Clear</scp>: Composition of Likelihoods for Evolve and Resequencing Experiments. <i>Genetics</i> , 2017, 206, 1011-1023.	1.2	32
39	High rate of translocation-based gene birth on the <i>Drosophila</i> Y chromosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11721-11726.	3.3	35
40	Quantifying Selection with Pool-Seq Time Series Data. <i>Molecular Biology and Evolution</i> , 2017, 34, 3023-3034.	3.5	69
41	Regulation of transposable elements: Interplay between TE-encoded regulatory sequences and host-specific trans-acting factors in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2017, 26, 5149-5159.	2.0	12
42	Unexpected high genetic diversity in small populations suggests maintenance by associative overdominance. <i>Molecular Ecology</i> , 2017, 26, 6510-6523.	2.0	40
43	Y Chromosome Unravels the Recent Oriental Origin of Modern Stallions. <i>Current Biology</i> , 2017, 27, 2029-2035.e5.	1.8	75
44	Uncovering the genetic signature of quantitative trait evolution with replicated time series data. <i>Heredity</i> , 2017, 118, 42-51.	1.2	42
45	Reconstruction of Haplotype-Blocks Selected during Experimental Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 174-184.	3.5	32
46	Strong epistatic and additive effects of linked candidate SNPs for <i>Drosophila</i> pigmentation have implications for analysis of genome-wide association studies results. <i>Genome Biology</i> , 2017, 18, 126.	3.8	11
47	<i>Drosophila simulans</i> : A Species with Improved Resolution in Evolve and Resequencing Studies. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2337-2343.	0.8	25
48	<i>Drosophila</i> Adaptation to Viral Infection through Defensive Symbiont Evolution. <i>PLoS Genetics</i> , 2016, 12, e1006297.	1.5	29
49	Suitability of Different Mapping Algorithms for Genome-Wide Polymorphism Scans with Pool-Seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3507-3515.	0.8	38
50	Ancestral population reconstitution from isofemale lines as a tool for experimental evolution. <i>Ecology and Evolution</i> , 2016, 6, 7169-7175.	0.8	25
51	The impact of library preparation protocols on the consistency of allele frequency estimates in Pool-Seq data. <i>Molecular Ecology Resources</i> , 2016, 16, 118-122.	2.2	22
52	Estimating the Effective Population Size from Temporal Allele Frequency Changes in Experimental Evolution. <i>Genetics</i> , 2016, 204, 723-735.	1.2	58
53	PoPoolationTE2: Comparative Population Genomics of Transposable Elements Using Pool-Seq. <i>Molecular Biology and Evolution</i> , 2016, 33, 2759-2764.	3.5	86
54	The Interplay of Temperature and Genotype on Patterns of Alternative Splicing in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 204, 315-325.	1.2	50

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55	Sequencing of the genus <i>Arabidopsis</i> identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. <i>Nature Genetics</i> , 2016, 48, 1077-1082.	9.4	198
56	High rates of phasing errors in highly polymorphic species with low levels of linkage disequilibrium. <i>Molecular Ecology Resources</i> , 2016, 16, 874-882.	2.2	13
57	Reconciling Differences in Pool-GWAS Between Populations: A Case Study of Female Abdominal Pigmentation in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 202, 843-855.	1.2	39
58	Hybrid Dysgenesis in <i>Drosophila simulans</i> Associated with a Rapid Invasion of the P-Element. <i>PLoS Genetics</i> , 2016, 12, e1005920.	1.5	60
59	Spatially varying selection shapes life history clines among populations of <i>Drosophila melanogaster</i> from sub-Saharan Africa. <i>Journal of Evolutionary Biology</i> , 2015, 28, 826-840.	0.8	51
60	Tempo and Mode of Transposable Element Activity in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2015, 11, e1005406.	1.5	97
61	The recent invasion of natural <i>Drosophila simulans</i> populations by the P-element. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6659-6663.	3.3	101
62	Parallel trait adaptation across opposing thermal environments in experimental <i>Drosophila melanogaster</i> populations. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1745-1759.	1.1	36
63	Genome assembly and annotation of a <i>Drosophila simulans</i> strain from Madagascar. <i>Molecular Ecology Resources</i> , 2015, 15, 372-381.	2.2	46
64	Patterns of Linkage Disequilibrium and Long Range Hitchhiking in Evolving Experimental <i>Drosophila melanogaster</i> Populations. <i>Molecular Biology and Evolution</i> , 2015, 32, 495-509.	3.5	82
65	Multi-locus Analysis of Genomic Time Series Data from Experimental Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005069.	1.5	63
66	Genetic Architecture and Functional Characterization of Genes Underlying the Rapid Diversification of Male External Genitalia Between <i>Drosophila simulans</i> and <i>Drosophila mauritiana</i> . <i>Genetics</i> , 2015, 200, 357-369.	1.2	35
67	Temperature Stress Mediates Decanalization and Dominance of Gene Expression in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2015, 11, e1004883.	1.5	81
68	Combining experimental evolution with next-generation sequencing: a powerful tool to study adaptation from standing genetic variation. <i>Heredity</i> , 2015, 114, 431-440.	1.2	219
69	Genes from scratch – the evolutionary fate of de novo genes. <i>Trends in Genetics</i> , 2015, 31, 215-219.	2.9	206
70	Temperature-Related Reaction Norms of Gene Expression: Regulatory Architecture and Functional Implications. <i>Molecular Biology and Evolution</i> , 2015, 32, 2393-2402.	3.5	57
71	Genomic Resources Notes Accepted 1 August 2014-30 September 2014. <i>Molecular Ecology Resources</i> , 2015, 15, 228-229.	2.2	31
72	Massive Habitat-Specific Genomic Response in <i>D. melanogaster</i> Populations during Experimental Evolution in Hot and Cold Environments. <i>Molecular Biology and Evolution</i> , 2014, 31, 364-375.	3.5	138

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73	Inference of chromosomal inversion dynamics from PoolSeq data in natural and laboratory populations of <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2014, 23, 1813-1827.	2.0	101
74	Host adaptation to viruses relies on few genes with different cross-resistance properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5938-5943.	3.3	122
75	Whole-genome sequences of two turkey adenovirus types reveal the existence of two unknown lineages that merit the establishment of novel species within the genus <i>Aviadenovirus</i> . <i>Journal of General Virology</i> , 2014, 95, 156-170.	1.3	31
76	Experimental evolution reveals habitat-specific fitness dynamics among <i>Wolbachia</i> clades in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2014, 23, 802-814.	2.0	43
77	Complete genome sequences of pigeon adenovirus 1 and duck adenovirus 2 extend the number of species within the genus <i>Aviadenovirus</i> . <i>Virology</i> , 2014, 462-463, 107-114.	1.1	50
78	Sequencing pools of individuals " mining genome-wide polymorphism data without big funding. <i>Nature Reviews Genetics</i> , 2014, 15, 749-763.	7.7	654
79	A <i>Drosophila</i> laboratory evolution experiment points to low evolutionary potential under increased temperatures likely to be experienced in the future. <i>Journal of Evolutionary Biology</i> , 2014, 27, 1859-1868.	0.8	79
80	A Guide for the Design of Evolve and Resequencing Studies. <i>Molecular Biology and Evolution</i> , 2014, 31, 474-483.	3.5	138
81	The life cycle of <i>Drosophila</i> orphan genes. <i>ELife</i> , 2014, 3, e01311.	2.8	163
82	VARIATION IN THERMAL PERFORMANCE AND REACTION NORMS AMONG POPULATIONS OF <i>DROSOPHILA MELANOGASTER</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3573-3587.	1.1	72
83	Estimating Empirical Codon Hidden Markov Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 725-736.	3.5	51
84	The first whole genome sequence of a Fowl adenovirus B strain enables interspecies comparisons within the genus <i>Aviadenovirus</i> . <i>Veterinary Microbiology</i> , 2013, 166, 250-256.	0.8	41
85	Evolution of mir-92a Underlies Natural Morphological Variation in <i>Drosophila melanogaster</i> . <i>Current Biology</i> , 2013, 23, 523-528.	1.8	47
86	Reproductive and post-reproductive life history of wild-caught <i>Drosophila melanogaster</i> under laboratory conditions. <i>Journal of Evolutionary Biology</i> , 2013, 26, 1508-1520.	0.8	59
87	Linking Great Apes Genome Evolution across Time Scales Using Polymorphism-Aware Phylogenetic Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 2249-2262.	3.5	73
88	<i>Drosophila americana</i> as a Model Species for Comparative Studies on the Molecular Basis of Phenotypic Variation. <i>Genome Biology and Evolution</i> , 2013, 5, 661-679.	1.1	24
89	Genome-wide patterns of natural variation reveal strong selective sweeps and ongoing genomic conflict in <i>Drosophila mauritiana</i> . <i>Genome Research</i> , 2013, 23, 99-110.	2.4	73
90	A Perspective on Micro-Evo-Devo: Progress and Potential. <i>Genetics</i> , 2013, 195, 625-634.	1.2	48

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91	A Genome-Wide, Fine-Scale Map of Natural Pigmentation Variation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2013, 9, e1003534.	1.5	146
92	Extensive paternal mtDNA leakage in natural populations of <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2013, 22, 2106-2117.	2.0	57
93	PoolSeq: a Python program for estimating the allele frequency spectrum and detecting selective sweeps from next generation sequencing of pooled samples. <i>Molecular Ecology Resources</i> , 2013, 13, 337-340.	2.2	55
94	Allelic imbalance metre (A llim), a new tool for measuring allele-specific gene expression with RNA-seq data. <i>Molecular Ecology Resources</i> , 2013, 13, 740-745.	2.2	36
95	Genetic and developmental analysis of differences in eye and face morphology between <i>Drosophila simulans</i> and <i>Drosophila mauritiana</i> . <i>Evolution & Development</i> , 2013, 15, 257-267.	1.1	33
96	Complete Mitochondrial DNA Sequences of the Threadfin Cichlid (<i>Petrochromis trewavasae</i>) and the Blunthead Cichlid (<i>Tropheus moorii</i>) and Patterns of Mitochondrial Genome Evolution in Cichlid Fishes. <i>PLoS ONE</i> , 2013, 8, e67048.	1.1	41
97	DistMap: A Toolkit for Distributed Short Read Mapping on a Hadoop Cluster. <i>PLoS ONE</i> , 2013, 8, e72614.	1.1	50
98	Intra-Specific Regulatory Variation in <i>Drosophila pseudoobscura</i> . <i>PLoS ONE</i> , 2013, 8, e83547.	1.1	23
99	Sequencing of Pooled DNA Samples (Pool-Seq) Uncovers Complex Dynamics of Transposable Element Insertions in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1002487.	1.5	223
100	Gowinda: unbiased analysis of gene set enrichment for genome-wide association studies. <i>Bioinformatics</i> , 2012, 28, 2084-2085.	1.8	116
101	The Genomic Signature of Splicing-Coupled Selection Differs between Long and Short Introns. <i>Molecular Biology and Evolution</i> , 2012, 29, 21-24.	3.5	28
102	The DAIBAM MITE element is involved in the origin of one fixed and two polymorphic <i>Drosophila virilis</i> phylad inversions. <i>Fly</i> , 2012, 6, 71-74.	0.9	13
103	Detecting Selective Sweeps from Pooled Next-Generation Sequencing Samples. <i>Molecular Biology and Evolution</i> , 2012, 29, 2177-2186.	3.5	75
104	Genome-wide patterns of latitudinal differentiation among populations of <i>Drosophila melanogaster</i> from North America. <i>Molecular Ecology</i> , 2012, 21, 4748-4769.	2.0	256
105	Combining evidence of selection with association analysis increases power to detect regions influencing complex traits in dairy cattle. <i>BMC Genomics</i> , 2012, 13, 48.	1.2	31
106	Evolution of Eye Morphology and Rhodopsin Expression in the <i>Drosophila melanogaster</i> Species Subgroup. <i>PLoS ONE</i> , 2012, 7, e37346.	1.1	53
107	Two fiber genes of nearly equal lengths are a common and distinctive feature of Fowl adenovirus C members. <i>Veterinary Microbiology</i> , 2012, 156, 411-417.	0.8	79
108	Adaptation of <i>Drosophila</i> to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. <i>Molecular Ecology</i> , 2012, 21, 4931-4941.	2.0	194

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109	Evaluation of Different Reference Based Annotation Strategies Using RNA-Seq – A Case Study in <i>Drosophila pseudoobscura</i> . PLoS ONE, 2012, 7, e46415.	1.1	20
110	PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals. PLoS ONE, 2011, 6, e15925.	1.1	556
111	Distinguishing Positive Selection From Neutral Evolution: Boosting the Performance of Summary Statistics. Genetics, 2011, 187, 229-244.	1.2	102
112	Multiple quantitative trait loci influence intra-specific variation in genital morphology between phylogenetically distinct lines of <i>Drosophila montana</i> . Journal of Evolutionary Biology, 2011, 24, 1879-1886.	0.8	10
113	Phylogeography, genetic structure and population divergence time of cheetahs in Africa and Asia: evidence for long-term geographic isolates. Molecular Ecology, 2011, 20, 706-724.	2.0	81
114	Genealogical lineage sorting leads to significant, but incorrect Bayesian multilocus inference of population structure. Molecular Ecology, 2011, 20, 1108-1121.	2.0	33
115	DNA double-strand break repair and the evolution of intron density. Trends in Genetics, 2011, 27, 1-6.	2.9	54
116	CANGS DB: a stand-alone web-based database tool for processing, managing and analyzing 454 data in biodiversity studies. BMC Research Notes, 2011, 4, 227.	0.6	4
117	PoPoolation DB: a user-friendly web-based database for the retrieval of natural polymorphisms in <i>Drosophila</i> . BMC Genetics, 2011, 12, 27.	2.7	11
118	PoPoolation2: identifying differentiation between populations using sequencing of pooled DNA samples (Pool-Seq). Bioinformatics, 2011, 27, 3435-3436.	1.8	729
119	Developmental Stability: A Major Role for Cyclin G in <i>Drosophila melanogaster</i> . PLoS Genetics, 2011, 7, e1002314.	1.5	50
120	Segregating Variation in the Polycomb Group Gene <i>cramped</i> Alters the Effect of Temperature on Multiple Traits. PLoS Genetics, 2011, 7, e1001280.	1.5	19
121	A Comparative Study of the Short Term Cold Resistance Response in Distantly Related <i>Drosophila</i> Species: The Role of <i>regucalcin</i> and <i>Frost</i> . PLoS ONE, 2011, 6, e25520.	1.1	23
122	Non-random genomic integration - an intrinsic property of retrogenes in <i>Drosophila</i> ?. BMC Evolutionary Biology, 2010, 10, 114.	3.2	13
123	CANGS: a user-friendly utility for processing and analyzing 454 GS-FLX data in biodiversity studies. BMC Research Notes, 2010, 3, 3.	0.6	50
124	Diversity in a hidden world: potential and limitation of next-generation sequencing for surveys of molecular diversity of eukaryotic microorganisms. Molecular Ecology, 2010, 19, 32-40.	2.0	330
125	Contrasting seasonal niche separation between rare and abundant taxa conceals the extent of protist diversity. Molecular Ecology, 2010, 19, 2908-2915.	2.0	209
126	Multiple hybridization events between <i>Drosophila simulans</i> and <i>Drosophila mauritiana</i> are supported by mtDNA introgression. Molecular Ecology, 2010, 19, 4695-4707.	2.0	37

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127	A microsatellite linkage map for <i>Drosophila montana</i> shows large variation in recombination rates, and a courtship song trait maps to an area of low recombination. <i>Journal of Evolutionary Biology</i> , 2010, 23, 518-527.	0.8	15
128	Host Range and Specificity of the <i>Drosophila C</i> Virus. <i>PLoS ONE</i> , 2010, 5, e12421.	1.1	36
129	The Next Generation of Molecular Markers From Massively Parallel Sequencing of Pooled DNA Samples. <i>Genetics</i> , 2010, 186, 207-218.	1.2	329
130	Nonsense-Mediated Decay Enables Intron Gain in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2010, 6, e1000819.	1.5	55
131	Detecting Selective Sweeps: A New Approach Based on Hidden Markov Models. <i>Genetics</i> , 2009, 181, 1567-1578.	1.2	48
132	Expression profiling of <i>Drosophila</i> mitochondrial genes via deep mRNA sequencing. <i>Nucleic Acids Research</i> , 2009, 37, 7509-7518.	6.5	53
133	PanGEA: Identification of allele specific gene expression using the 454 technology. <i>BMC Bioinformatics</i> , 2009, 10, 143.	1.2	24
134	A Single Amino Acid Replacement in ETC2 Shapes Trichome Patterning in Natural <i>Arabidopsis</i> Populations. <i>Current Biology</i> , 2009, 19, 1747-1751.	1.8	38
135	Mapping Accuracy of Short Reads from Massively Parallel Sequencing and the Implications for Quantitative Expression Profiling. <i>PLoS ONE</i> , 2009, 4, e6323.	1.1	19
136	Gene expression profiling by massively parallel sequencing. <i>Genome Research</i> , 2008, 18, 172-177.	2.4	210
137	Variation in Male Courtship Song Traits in <i>Drosophila virilis</i> : The Effects of Selection and Drift on Song Divergence at the Intraspecific Level. <i>Behavior Genetics</i> , 2008, 38, 82-92.	1.4	13
138	CLINAL DISTRIBUTION OF A CHROMOSOMAL REARRANGEMENT: A PRECURSOR TO CHROMOSOMAL SPECIATION?. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 1852-1865.	1.1	36
139	The impact of shared ancestral variation on hybrid male lethality – a 16 codon indel in the <i>Drosophila simulans Lhr</i> gene. <i>Journal of Evolutionary Biology</i> , 2008, 21, 551-555.	0.8	7
140	Contrasting patterns of natural variation in global <i>Drosophila melanogaster</i> populations. <i>Molecular Ecology</i> , 2008, 17, 4470-4479.	2.0	29
141	Male-biased genes are overrepresented among novel <i>Drosophila pseudoobscura</i> sex-biased genes. <i>BMC Evolutionary Biology</i> , 2008, 8, 182.	3.2	8
142	Survey of microsatellite clustering in eight fully sequenced species sheds light on the origin of compound microsatellites. <i>BMC Genomics</i> , 2008, 9, 612.	1.2	59
143	African <i>Drosophila melanogaster</i> and <i>D. simulans</i> Populations Have Similar Levels of Sequence Variability, Suggesting Comparable Effective Population Sizes. <i>Genetics</i> , 2008, 178, 405-412.	1.2	33
144	Nonrandom <i>Wolbachia</i> Infection Status of <i>Drosophila melanogaster</i> Strains with Different mtDNA Haplotypes. <i>Molecular Biology and Evolution</i> , 2008, 25, 2493-2498.	3.5	44

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145	Identification of Selective Sweeps Using a Dynamically Adjusted Number of Linked Microsatellites. <i>Genetics</i> , 2007, 175, 207-218.	1.2	32
146	Phenotypic Plasticity in <i>Drosophila</i> Pigmentation Caused by Temperature Sensitivity of a Chromatin Regulator Network. <i>PLoS Genetics</i> , 2007, 3, e30.	1.5	119
147	SciRoKo: a new tool for whole genome microsatellite search and investigation. <i>Bioinformatics</i> , 2007, 23, 1683-1685.	1.8	304
148	Low abundance of <i>Escherichia coli</i> microsatellites is associated with an extremely low mutation rate. <i>Journal of Evolutionary Biology</i> , 2006, 19, 1671-1676.	0.8	13
149	<i>Silene tatarica</i> microsatellites are frequently located in repetitive DNA. <i>Journal of Evolutionary Biology</i> , 2006, 19, 1612-1619.	0.8	24
150	ms2ms.pl: a PERL script for generating microsatellite data. <i>Molecular Ecology Notes</i> , 2006, 6, 580-581.	1.7	6
151	COMMENT: Moving beyond single-locus studies to characterize hybridization between oaks (<i>Quercus</i>) Tj ETQq1 1.0.784314 rgBT / 2.0 17	2.0	17
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