

# Christian Schlögl

## List of Publications by Year in descending order

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Version: 2024-02-01

232  
papers

20,463  
citations

16451

64  
h-index

14759

127  
g-index

262  
all docs

262  
docs citations

262  
times ranked

18361  
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.	3.9	4
2	Pool-GWAS on reproductive dormancy in <i>Drosophila simulans</i> suggests a polygenic architecture. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	1
3	Natural variation in <i>Drosophila</i> shows weak pleiotropic effects. <i>Genome Biology</i> , 2022, 23, 116.	8.8	4
4	The Transposition Rate Has Little Influence on the Plateauing Level of the P-element. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	11
5	Parallel gene expression evolution in natural and laboratory evolved populations. <i>Molecular Ecology</i> , 2021, 30, 884-894.	3.9	15
6	Detecting selected haplotype blocks in evolve and resequence experiments. <i>Molecular Ecology Resources</i> , 2021, 21, 93-109.	4.8	20
7	Fine Mapping without Phenotyping: Identification of Selection Targets in Secondary Evolve and Resequencing Experiments. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	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.	8.8	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, .	2.5	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.	2.6	4
11	Next-generation biological control: the need for integrating genetics and genomics. <i>Biological Reviews</i> , 2020, 95, 1838-1854.	10.4	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.	3.9	15
13	The Evolution of Phenotypic Plasticity in Response to Temperature Stress. <i>Genome Biology and Evolution</i> , 2020, 12, 2429-2440.	2.5	30
14	Fitness effects for Ace insecticide resistance mutations are determined by ambient temperature. <i>BMC Biology</i> , 2020, 18, 157.	3.8	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.	2.3	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.	8.9	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.	2.5	14
18	Polygenic adaptation: a unifying framework to understand positive selection. <i>Nature Reviews Genetics</i> , 2020, 21, 769-781.	16.3	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.	2.5	29
20	Rapid sex-specific adaptation to high temperature in <i>Drosophila</i> . <i>ELife</i> , 2020, 9, .	6.0	25
21	Benchmarking software tools for detecting and quantifying selection in evolve and resequencing studies. <i>Genome Biology</i> , 2019, 20, 169.	8.8	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.	2.4	11
23	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095.	3.3	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.	3.9	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.	2.5	24
26	Genetic redundancy fuels polygenic adaptation in <i>Drosophila</i> . <i>PLoS Biology</i> , 2019, 17, e3000128.	5.6	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.	2.0	46
28	High-throughput fecundity measurements in <i>Drosophila</i> . <i>Scientific Reports</i> , 2018, 8, 4469.	3.3	16
29	Asian horses deepen the MSY phylogeny. <i>Animal Genetics</i> , 2018, 49, 90-93.	1.7	32
30	Molecular dissection of a natural transposable element invasion. <i>Genome Research</i> , 2018, 28, 824-835.	5.5	64
31	Contesting the evidence for non-adaptive plasticity. <i>Nature</i> , 2018, 555, E21-E22.	27.8	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.	4.8	34
33	Evolution of longevity improves immunity in <i>Drosophila</i> . <i>Evolution Letters</i> , 2018, 2, 567-579.	3.3	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.	2.5	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.	3.9	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.	8.8	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.	4.8	3
38	<scp>Clear</scp>: Composition of Likelihoods for Evolve and Resequencing Experiments. <i>Genetics</i> , 2017, 206, 1011-1023.	2.9	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.	7.1	35
40	Quantifying Selection with Pool-Seq Time Series Data. <i>Molecular Biology and Evolution</i> , 2017, 34, 3023-3034.	8.9	69
41	Regulation of transposable elements: Interplay between TE-encoded regulatory sequences and host-specific <i>trans</i>-acting factors in <i>Drosophila melanogaster</i>. <i>Molecular Ecology</i> , 2017, 26, 5149-5159.	3.9	12
42	Unexpected high genetic diversity in small populations suggests maintenance by associative overdominance. <i>Molecular Ecology</i> , 2017, 26, 6510-6523.	3.9	40
43	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. <i>Current Biology</i> , 2017, 27, 2029-2035.e5.	3.9	75
44	Uncovering the genetic signature of quantitative trait evolution with replicated time series data. <i>Heredity</i> , 2017, 118, 42-51.	2.6	42
45	Reconstruction of Haplotype-Blocks Selected during Experimental Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 174-184.	8.9	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.	8.8	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.	1.8	25
48	<i>Drosophila</i> Adaptation to Viral Infection through Defensive Symbiont Evolution. <i>PLoS Genetics</i> , 2016, 12, e1006297.	3.5	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.	1.8	38
50	Ancestral population reconstitution from isofemale lines as a tool for experimental evolution. <i>Ecology and Evolution</i> , 2016, 6, 7169-7175.	1.9	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.	4.8	22
52	Estimating the Effective Population Size from Temporal Allele Frequency Changes in Experimental Evolution. <i>Genetics</i> , 2016, 204, 723-735.	2.9	58
53	PoPoolationTE2: Comparative Population Genomics of Transposable Elements Using Pool-Seq. <i>Molecular Biology and Evolution</i> , 2016, 33, 2759-2764.	8.9	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.	2.9	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.	21.4	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.	4.8	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.	2.9	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.	3.5	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.	1.7	51
60	Tempo and Mode of Transposable Element Activity in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2015, 11, e1005406.	3.5	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.	7.1	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.	2.3	36
63	Genome assembly and annotation of a <i>Drosophila simulans</i> strain from Madagascar. <i>Molecular Ecology Resources</i> , 2015, 15, 372-381.	4.8	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.	8.9	82
65	Multi-locus Analysis of Genomic Time Series Data from Experimental Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005069.	3.5	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.	2.9	35
67	Temperature Stress Mediates Decanalization and Dominance of Gene Expression in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2015, 11, e1004883.	3.5	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.	2.6	219
69	Genes from scratch – the evolutionary fate of de novo genes. <i>Trends in Genetics</i> , 2015, 31, 215-219.	6.7	206
70	Temperature-Related Reaction Norms of Gene Expression: Regulatory Architecture and Functional Implications. <i>Molecular Biology and Evolution</i> , 2015, 32, 2393-2402.	8.9	57
71	Genomic Resources Notes Accepted 1 August 2014-30 September 2014. <i>Molecular Ecology Resources</i> , 2015, 15, 228-229.	4.8	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.	8.9	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.	3.9	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.	7.1	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.	2.9	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.	3.9	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.	2.4	50
78	Sequencing pools of individuals "mining genome-wide polymorphism data without big funding. <i>Nature Reviews Genetics</i> , 2014, 15, 749-763.	16.3	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.	1.7	79
80	A Guide for the Design of Evolve and Resequencing Studies. <i>Molecular Biology and Evolution</i> , 2014, 31, 474-483.	8.9	138
81	The life cycle of <i>Drosophila</i> orphan genes. <i>ELife</i> , 2014, 3, e01311.	6.0	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.	2.3	72
83	Estimating Empirical Codon Hidden Markov Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 725-736.	8.9	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.	1.9	41
85	Evolution of mir-92a Underlies Natural Morphological Variation in <i>Drosophila melanogaster</i> . <i>Current Biology</i> , 2013, 23, 523-528.	3.9	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.	1.7	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.	8.9	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.	2.5	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.	5.5	73
90	A Perspective on Micro-Evo-Devo: Progress and Potential. <i>Genetics</i> , 2013, 195, 625-634.	2.9	48

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91	A Genome-Wide, Fine-Scale Map of Natural Pigmentation Variation in <i>Drosophila melanogaster</i> . PLoS Genetics, 2013, 9, e1003534.	3.5	146
92	Extensive paternal mtDNA leakage in natural populations of <i>Drosophila melanogaster</i> . Molecular Ecology, 2013, 22, 2106-2117.	3.9	57
93	PoolSeq: a Python program for estimating the allele frequency spectrum and detecting selective sweeps from next generation sequencing of pooled samples. Molecular Ecology Resources, 2013, 13, 337-340.	4.8	55
94	Allelic imbalance metre (AIlm), a new tool for measuring allele-specific gene expression with RNA-seq data. Molecular Ecology Resources, 2013, 13, 740-745.	4.8	36
95	Genetic and developmental analysis of differences in eye and face morphology between <i>Drosophila simulans</i> and <i>Drosophila mauritiana</i> . Evolution & Development, 2013, 15, 257-267.	2.0	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. PLoS ONE, 2013, 8, e67048.	2.5	41
97	DistMap: A Toolkit for Distributed Short Read Mapping on a Hadoop Cluster. PLoS ONE, 2013, 8, e72614.	2.5	50
98	Intra-Specific Regulatory Variation in <i>Drosophila pseudoobscura</i> . PLoS ONE, 2013, 8, e83547.	2.5	23
99	Sequencing of Pooled DNA Samples (Pool-Seq) Uncovers Complex Dynamics of Transposable Element Insertions in <i>Drosophila melanogaster</i> . PLoS Genetics, 2012, 8, e1002487.	3.5	223
100	Gowinda: unbiased analysis of gene set enrichment for genome-wide association studies. Bioinformatics, 2012, 28, 2084-2085.	4.1	116
101	The Genomic Signature of Splicing-Coupled Selection Differs between Long and Short Introns. Molecular Biology and Evolution, 2012, 29, 21-24.	8.9	28
102	The DAIBAM MITE element is involved in the origin of one fixed and two polymorphic <i>Drosophila virilis</i> phylad inversions. Fly, 2012, 6, 71-74.	1.7	13
103	Detecting Selective Sweeps from Pooled Next-Generation Sequencing Samples. Molecular Biology and Evolution, 2012, 29, 2177-2186.	8.9	75
104	Genome-wide patterns of latitudinal differentiation among populations of <i>Drosophila melanogaster</i> from North America. Molecular Ecology, 2012, 21, 4748-4769.	3.9	256
105	Combining evidence of selection with association analysis increases power to detect regions influencing complex traits in dairy cattle. BMC Genomics, 2012, 13, 48.	2.8	31
106	Evolution of Eye Morphology and Rhodopsin Expression in the <i>Drosophila melanogaster</i> Species Subgroup. PLoS ONE, 2012, 7, e37346.	2.5	53
107	Two fiber genes of nearly equal lengths are a common and distinctive feature of Fowl adenovirus C members. Veterinary Microbiology, 2012, 156, 411-417.	1.9	79
108	Adaptation of <i>Drosophila</i> to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. Molecular Ecology, 2012, 21, 4931-4941.	3.9	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.	2.5	20
110	PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals. PLoS ONE, 2011, 6, e15925.	2.5	556
111	Distinguishing Positive Selection From Neutral Evolution: Boosting the Performance of Summary Statistics. Genetics, 2011, 187, 229-244.	2.9	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.	1.7	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.	3.9	81
114	Genealogical lineage sorting leads to significant, but incorrect Bayesian multilocus inference of population structure. Molecular Ecology, 2011, 20, 1108-1121.	3.9	33
115	DNA double-strand break repair and the evolution of intron density. Trends in Genetics, 2011, 27, 1-6.	6.7	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.	1.4	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.	4.1	729
119	Developmental Stability: A Major Role for Cyclin G in <i>Drosophila melanogaster</i> . PLoS Genetics, 2011, 7, e1002314.	3.5	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.	3.5	19
121	A Comparative Study of the Short Term Cold Resistance Response in Distantly Related <i>Drosophila</i> Species: The Role of regucalcin and Frost. PLoS ONE, 2011, 6, e25520.	2.5	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.	1.4	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.	3.9	330
125	Contrasting seasonal niche separation between rare and abundant taxa conceals the extent of protist diversity. Molecular Ecology, 2010, 19, 2908-2915.	3.9	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.	3.9	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.	1.7	15
128	Host Range and Specificity of the <i>Drosophila C</i> Virus. <i>PLoS ONE</i> , 2010, 5, e12421.	2.5	36
129	The Next Generation of Molecular Markers From Massively Parallel Sequencing of Pooled DNA Samples. <i>Genetics</i> , 2010, 186, 207-218.	2.9	329
130	Nonsense-Mediated Decay Enables Intron Gain in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2010, 6, e1000819.	3.5	55
131	Detecting Selective Sweeps: A New Approach Based on Hidden Markov Models. <i>Genetics</i> , 2009, 181, 1567-1578.	2.9	48
132	Expression profiling of <i>Drosophila</i> mitochondrial genes via deep mRNA sequencing. <i>Nucleic Acids Research</i> , 2009, 37, 7509-7518.	14.5	53
133	PanGEA: Identification of allele specific gene expression using the 454 technology. <i>BMC Bioinformatics</i> , 2009, 10, 143.	2.6	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.	3.9	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.	2.5	19
136	Gene expression profiling by massively parallel sequencing. <i>Genome Research</i> , 2008, 18, 172-177.	5.5	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.	2.1	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.	2.3	36
139	The impact of shared ancestral variation on hybrid male lethality – a 16 codon indel in the <i>Drosophila simulans</i> Lhr gene. <i>Journal of Evolutionary Biology</i> , 2008, 21, 551-555.	1.7	7
140	Contrasting patterns of natural variation in global <i>Drosophila melanogaster</i> populations. <i>Molecular Ecology</i> , 2008, 17, 4470-4479.	3.9	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.	2.8	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.	2.9	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.	8.9	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.	2.9	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.	3.5	119
147	SciRoKo: a new tool for whole genome microsatellite search and investigation. <i>Bioinformatics</i> , 2007, 23, 1683-1685.	4.1	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.	1.7	13
149	<i>Silene tatarica</i> microsatellites are frequently located in repetitive DNA. <i>Journal of Evolutionary Biology</i> , 2006, 19, 1612-1619.	1.7	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 /Ov	3.9	17
152	Microsatellite variation and differentiation in African and non-African populations of <i>Drosophila simulans</i> . <i>Molecular Ecology</i> , 2006, 15, 3895-3905.	3.9	24
153	Phylogeographic patterns in <i>Drosophila montana</i> . <i>Molecular Ecology</i> , 2006, 16, 1085-1097.	3.9	31
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