

# Christian Schläpfer

## List of Publications by Year in descending order

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232  
papers

20,463  
citations

16450

64  
h-index

14758

127  
g-index

262  
all docs

262  
docs citations

262  
times ranked

18361  
citing authors

#	ARTICLE	IF	CITATIONS
1	microsatellite analyser(MSA): a platform independent analysis tool for large microsatellite data sets. <i>Molecular Ecology Notes</i> , 2003, 3, 167-169.	1.7	1,413
2	Slippage synthesis of simple sequence DNA. <i>Nucleic Acids Research</i> , 1992, 20, 211-215.	14.5	1,000
3	PoPoolation2: identifying differentiation between populations using sequencing of pooled DNA samples (Pool-Seq). <i>Bioinformatics</i> , 2011, 27, 3435-3436.	4.1	729
4	Sequencing pools of individuals " mining genome-wide polymorphism data without big funding. <i>Nature Reviews Genetics</i> , 2014, 15, 749-763.	16.3	654
5	The evolution of molecular markers " just a matter of fashion?. <i>Nature Reviews Genetics</i> , 2004, 5, 63-69.	16.3	635
6	Evolutionary dynamics of microsatellite DNA. <i>Chromosoma</i> , 2000, 109, 365-371.	2.2	604
7	PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals. <i>PLoS ONE</i> , 2011, 6, e15925.	2.5	556
8	Conservation of polymorphic simple sequence loci in cetacean species. <i>Nature</i> , 1991, 354, 63-65.	27.8	336
9	Social structure of pilot whales revealed by analytical DNA profiling. <i>Science</i> , 1993, 260, 670-672.	12.6	334
10	Diversity in a hidden world: potential and limitation of next-generation sequencing for surveys of molecular diversity of eukaryotic microorganisms. <i>Molecular Ecology</i> , 2010, 19, 32-40.	3.9	330
11	The Next Generation of Molecular Markers From Massively Parallel Sequencing of Pooled DNA Samples. <i>Genetics</i> , 2010, 186, 207-218.	2.9	329
12	Isolation of simple-sequence loci for use in polymerase chain reaction-based DNA fingerprinting. <i>Electrophoresis</i> , 1991, 12, 113-118.	2.4	327
13	SciRoKo: a new tool for whole genome microsatellite search and investigation. <i>Bioinformatics</i> , 2007, 23, 1683-1685.	4.1	304
14	Simple sequences. <i>Current Opinion in Genetics and Development</i> , 1994, 4, 832-837.	3.3	282
15	Genome-wide patterns of latitudinal differentiation among populations of <i>Drosophila melanogaster</i> from North America. <i>Molecular Ecology</i> , 2012, 21, 4748-4769.	3.9	256
16	Chromosomal homogeneity of <i>Drosophila</i> ribosomal DNA arrays suggests intrachromosomal exchanges drive concerted evolution. <i>Current Biology</i> , 1994, 4, 777-783.	3.9	252
17	Polygenic adaptation: a unifying framework to understand positive selection. <i>Nature Reviews Genetics</i> , 2020, 21, 769-781.	16.3	238
18	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.	3.5	223

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19	Fitness effects of advantageous mutations in evolving <i>Escherichia coli</i> populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 1113-1117.	7.1	222
20	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
21	Amplification of hypervariable simple sequence repeats (microsatellites) from excremental DNA of wild living bonobos ( <i>Pan paniscus</i> ). <i>Molecular Ecology</i> , 1995, 4, 515-518.	3.9	218
22	Genetic redundancy fuels polygenic adaptation in <i>Drosophila</i> . <i>PLoS Biology</i> , 2019, 17, e3000128.	5.6	212
23	Gene expression profiling by massively parallel sequencing. <i>Genome Research</i> , 2008, 18, 172-177.	5.5	210
24	Contrasting seasonal niche separation between rare and abundant taxa conceals the extent of protist diversity. <i>Molecular Ecology</i> , 2010, 19, 2908-2915.	3.9	209
25	Hitchhiking mapping – functional genomics from the population genetics perspective. <i>Trends in Genetics</i> , 2003, 19, 32-38.	6.7	208
26	Genes from scratch – the evolutionary fate of de novo genes. <i>Trends in Genetics</i> , 2015, 31, 215-219.	6.7	206
27	A Microsatellite-Based Multilocus Screen for the Identification of Local Selective Sweeps. <i>Genetics</i> , 2002, 160, 753-763.	2.9	203
28	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
29	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.	3.9	194
30	Evidence for shared ancestral polymorphism rather than recurrent gene flow at microsatellite loci differentiating two hybridizing oaks ( <i>Quercus</i> spp.). <i>Molecular Ecology</i> , 2004, 14, 549-561.	3.9	176
31	High mutation rate of a long microsatellite allele in <i>Drosophila melanogaster</i> provides evidence for allele-specific mutation rates. <i>Molecular Biology and Evolution</i> , 1998, 15, 1269-1274.	8.9	174
32	Hitchhiking mapping: A population-based fine-mapping strategy for adaptive mutations in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12949-12954.	7.1	174
33	The life cycle of <i>Drosophila</i> orphan genes. <i>ELife</i> , 2014, 3, e01311.	6.0	163
34	Two Distinct Modes of Microsatellite Mutation Processes: Evidence From the Complete Genomic Sequences of Nine Species. <i>Genome Research</i> , 2003, 13, 2242-2251.	5.5	162
35	Three Divergent rDNA Clusters Predate the Species Divergence in <i>Quercus petraea</i> (Matt.) Liebl. and <i>Quercus robur</i> L. <i>Molecular Biology and Evolution</i> , 2001, 18, 112-119.	8.9	156
36	A Genome-Wide, Fine-Scale Map of Natural Pigmentation Variation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2013, 9, e1003534.	3.5	146

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37	Molecular Phylogeny of European Muroid Rodents Based on Complete Cytochrome b Sequences. <i>Molecular Phylogenetics and Evolution</i> , 2000, 16, 37-47.	2.7	138
38	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
39	A Guide for the Design of Evolve and Resequencing Studies. <i>Molecular Biology and Evolution</i> , 2014, 31, 474-483.	8.9	138
40	Multiple mating in wild <i>Drosophila melanogaster</i> revisited by microsatellite analysis. <i>Molecular Ecology</i> , 1998, 7, 915-917.	3.9	136
41	World-wide survey of an Accord insertion and its association with DDT resistance in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2004, 13, 2491-2504.	3.9	131
42	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
43	Distribution of dinucleotide microsatellites in the <i>Drosophila melanogaster</i> genome. <i>Molecular Biology and Evolution</i> , 1999, 16, 602-610.	8.9	119
44	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
45	Gowinda: unbiased analysis of gene set enrichment for genome-wide association studies. <i>Bioinformatics</i> , 2012, 28, 2084-2085.	4.1	116
46	Long Microsatellite Alleles in <i>Drosophila melanogaster</i> Have a Downward Mutation Bias and Short Persistence Times, Which Cause Their Genome-Wide Underrepresentation. <i>Genetics</i> , 2000, 155, 1213-1220.	2.9	115
47	Polymorphism and Locus-Specific Effects on Polymorphism at Microsatellite Loci in Natural <i>Drosophila melanogaster</i> Populations. <i>Genetics</i> , 1997, 146, 309-320.	2.9	112
48	Trichome Distribution in <i>Arabidopsis thaliana</i> and its Close Relative <i>Arabidopsis lyrata</i> : Molecular Analysis of the Candidate Gene <i>GLABROUS1</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 1754-1763.	8.9	111
49	Genetic Differentiation Between American and European <i>Drosophila melanogaster</i> Populations Could Be Attributed to Admixture of African Alleles. <i>Molecular Biology and Evolution</i> , 2003, 20, 792-799.	8.9	110
50	Distinguishing Positive Selection From Neutral Evolution: Boosting the Performance of Summary Statistics. <i>Genetics</i> , 2011, 187, 229-244.	2.9	102
51	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
52	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
53	Complex patterns of colonization and refugia revealed for European grayling <i>Thymallus thymallus</i> , based on complete sequencing of the mitochondrial DNA control region. <i>Molecular Ecology</i> , 2002, 11, 1393-1407.	3.9	100
54	Tempo and Mode of Transposable Element Activity in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2015, 11, e1005406.	3.5	97

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55	PoPoolationTE2: Comparative Population Genomics of Transposable Elements Using Pool-Seq. <i>Molecular Biology and Evolution</i> , 2016, 33, 2759-2764.	8.9	86
56	Microsatellite Variability Differs Between Dinucleotide Repeat Motifsâ€”Evidence from <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 1277-1285.	8.9	83
57	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
58	Genome evolution: Are microsatellites really simple sequences?. <i>Current Biology</i> , 1998, 8, R132-R134.	3.9	81
59	Comparison of algorithms for the analysis of Affymetrix microarray data as evaluated by co-expression of genes in known operons. <i>Nucleic Acids Research</i> , 2006, 34, e8-e8.	14.5	81
60	Phylogeography, genetic structure and population divergence time of cheetahs in Africa and Asia: evidence for long-term geographic isolates. <i>Molecular Ecology</i> , 2011, 20, 706-724.	3.9	81
61	Temperature Stress Mediates Decanalization and Dominance of Gene Expression in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2015, 11, e1004883.	3.5	81
62	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.	1.9	79
63	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
64	Detecting Selective Sweeps from Pooled Next-Generation Sequencing Samples. <i>Molecular Biology and Evolution</i> , 2012, 29, 2177-2186.	8.9	75
65	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. <i>Current Biology</i> , 2017, 27, 2029-2035.e5.	3.9	75
66	Mitochondrial and nuclear DNA phylogeography of <i>Thymallus</i> spp. (grayling) provides evidence of ice-age mediated environmental perturbations in the world's oldest body of fresh water, Lake Baikal. <i>Molecular Ecology</i> , 2002, 11, 2599-2611.	3.9	74
67	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
68	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
69	Haplotype (mtDNA) diversity of brown trout <i>Salmo trutta</i> in tributaries of the Austrian Danube: massive introgression of Atlantic basin fish - by man or nature?. <i>Molecular Ecology</i> , 2001, 10, 1241-1246.	3.9	72
70	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
71	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
72	Quantifying Selection with Pool-Seq Time Series Data. <i>Molecular Biology and Evolution</i> , 2017, 34, 3023-3034.	8.9	69

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73	Next-generation biological control: the need for integrating genetics and genomics. <i>Biological Reviews</i> , 2020, 95, 1838-1854.	10.4	67
74	A microsatellite-based multilocus phylogeny of the <i>Drosophila melanogaster</i> species complex. <i>Current Biology</i> , 1998, 8, 1183-1187.	3.9	65
75	Molecular dissection of a natural transposable element invasion. <i>Genome Research</i> , 2018, 28, 824-835.	5.5	64
76	Towards a molecular characterization of adaptation in local populations. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 683-687.	3.3	63
77	Multi-locus Analysis of Genomic Time Series Data from Experimental Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005069.	3.5	63
78	Conservation of locus-specific microsatellite variability across species: a comparison of two <i>Drosophila</i> sibling species, <i>D. melanogaster</i> and <i>D. simulans</i> . <i>Molecular Biology and Evolution</i> , 1998, 15, 176-184.	8.9	62
79	Mitochondrial haplotype diversity among Portuguese brown trout <i>Salmo trutta</i> L. populations: relevance to the post-Pleistocene recolonization of northern Europe. <i>Molecular Ecology</i> , 2000, 9, 691-698.	3.9	62
80	Evolution of longevity improves immunity in <i>Drosophila</i> . <i>Evolution Letters</i> , 2018, 2, 567-579.	3.3	62
81	Isolation and characterization of microsatellite loci from <i>Apodemus flavicollis</i> (rodentia, muridae) and <i>Clethrionomys glareolus</i> (rodentia, cricetidae). <i>Molecular Ecology</i> , 1997, 6, 597-599.	3.9	61
82	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
83	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
84	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
85	Estimating the Effective Population Size from Temporal Allele Frequency Changes in Experimental Evolution. <i>Genetics</i> , 2016, 204, 723-735.	2.9	58
86	Extensive paternal mtDNA leakage in natural populations of <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2013, 22, 2106-2117.	3.9	57
87	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
88	Nonsense-Mediated Decay Enables Intron Gain in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2010, 6, e1000819.	3.5	55
89	PoolHMM: 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.	4.8	55
90	DNA double-strand break repair and the evolution of intron density. <i>Trends in Genetics</i> , 2011, 27, 1-6.	6.7	54

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91	Expression profiling of <i>Drosophila</i> mitochondrial genes via deep mRNA sequencing. <i>Nucleic Acids Research</i> , 2009, 37, 7509-7518.	14.5	53
92	Evolution of Eye Morphology and Rhodopsin Expression in the <i>Drosophila melanogaster</i> Species Subgroup. <i>PLoS ONE</i> , 2012, 7, e37346.	2.5	53
93	Estimating Empirical Codon Hidden Markov Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 725-736.	8.9	51
94	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
95	CANGS: a user-friendly utility for processing and analyzing 454 GS-FLX data in biodiversity studies. <i>BMC Research Notes</i> , 2010, 3, 3.	1.4	50
96	Developmental Stability: A Major Role for Cyclin G in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2011, 7, e1002314.	3.5	50
97	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
98	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
99	DistMap: A Toolkit for Distributed Short Read Mapping on a Hadoop Cluster. <i>PLoS ONE</i> , 2013, 8, e72614.	2.5	50
100	The use of microsatellites for genetic analysis of natural populations – a critical review. , 1998, , 71-86.		48
101	Removal of Microsatellite Interruptions by DNA Replication Slippage: Phylogenetic Evidence from <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 1001-1009.	8.9	48
102	Detecting Selective Sweeps: A New Approach Based on Hidden Markov Models. <i>Genetics</i> , 2009, 181, 1567-1578.	2.9	48
103	A Perspective on Micro-Evo-Devo: Progress and Potential. <i>Genetics</i> , 2013, 195, 625-634.	2.9	48
104	A Novel Test Statistic for the Identification of Local Selective Sweeps Based on Microsatellite Gene Diversity. , 2005, , 55-64.		47
105	Evolution of mir-92a Underlies Natural Morphological Variation in <i>Drosophila melanogaster</i> . <i>Current Biology</i> , 2013, 23, 523-528.	3.9	47
106	Mismatch Repair-Driven Mutational Bias in <i>D. melanogaster</i> . <i>Molecular Cell</i> , 2002, 10, 199-205.	9.7	46
107	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
108	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

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109	<i>Drosophila virilis</i> Has Long and Highly Polymorphic Microsatellites. <i>Molecular Biology and Evolution</i> , 2000, 17, 1641-1646.	8.9	44
110	Microsatellite analysis reveals substantial genetic differentiation between contemporary New World and Old World Holstein Friesian populations. <i>Animal Genetics</i> , 2000, 31, 31-38.	1.7	44
111	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
112	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
113	Patterns of Microsatellite Variability Among X Chromosomes and Autosomes Indicate a High Frequency of Beneficial Mutations in Non-African <i>D. simulans</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 1384-1390.	8.9	42
114	Uncovering the genetic signature of quantitative trait evolution with replicated time series data. <i>Heredity</i> , 2017, 118, 42-51.	2.6	42
115	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
116	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.	2.5	41
117	Unexpected high genetic diversity in small populations suggests maintenance by associative overdominance. <i>Molecular Ecology</i> , 2017, 26, 6510-6523.	3.9	40
118	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
119	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095.	3.3	39
120	Genealogical inference of closely related species based on microsatellites. <i>Genetical Research</i> , 2001, 78, 209-212.	0.9	38
121	Nonneutral Admixture of Immigrant Genotypes in African <i>Drosophila melanogaster</i> Populations from Zimbabwe. <i>Molecular Biology and Evolution</i> , 2003, 20, 1329-1337.	8.9	38
122	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
123	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
124	Multiple hybridization events between <i>Drosophila simulans</i> and <i>Drosophila mauritiana</i> are supported by mtDNA introgression. <i>Molecular Ecology</i> , 2010, 19, 4695-4707.	3.9	37
125	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
126	Host Range and Specificity of the <i>Drosophila C</i> Virus. <i>PLoS ONE</i> , 2010, 5, e12421.	2.5	36



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127	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.	4.8	36
128	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
129	No Accelerated Rate of Protein Evolution in Male-Biased <i>Drosophila pseudoobscura</i> Genes. <i>Genetics</i> , 2006, 174, 411-420.	2.9	35
130	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
131	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
132	<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
133	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
134	Genealogical lineage sorting leads to significant, but incorrect Bayesian multilocus inference of population structure. <i>Molecular Ecology</i> , 2011, 20, 1108-1121.	3.9	33
135	Genetic and developmental analysis of differences in eye and face morphology between <i>Drosophila simulans</i> and <i>Drosophila mauritiana</i> . <i>Evolution &amp; Development</i> , 2013, 15, 257-267.	2.0	33
136	Benchmarking software tools for detecting and quantifying selection in evolve and resequencing studies. <i>Genome Biology</i> , 2019, 20, 169.	8.8	33
137	Population structure in African <i>Drosophila melanogaster</i> revealed by microsatellite analysis. <i>Molecular Ecology</i> , 2004, 14, 563-573.	3.9	32
138	Identification of Selective Sweeps Using a Dynamically Adjusted Number of Linked Microsatellites. <i>Genetics</i> , 2007, 175, 207-218.	2.9	32
139	<i>Clear</i> : Composition of Likelihoods for Evolve and Resequencing Experiments. <i>Genetics</i> , 2017, 206, 1011-1023.	2.9	32
140	Reconstruction of Haplotype-Blocks Selected during Experimental Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 174-184.	8.9	32
141	Asian horses deepen the MSY phylogeny. <i>Animal Genetics</i> , 2018, 49, 90-93.	1.7	32
142	The Use of Imperfect Microsatellites for DNA Fingerprinting and Population Genetics. , 1999, , 153-165.		32
143	Phylogeographic patterns in <i>Drosophila montana</i> . <i>Molecular Ecology</i> , 2006, 16, 1085-1097.	3.9	31
144	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.	2.8	31

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145	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 Aviadenovirus. <i>Journal of General Virology</i> , 2014, 95, 156-170.	2.9	31
146	Genomic Resources Notes Accepted 1 August 2014-30 September 2014. <i>Molecular Ecology Resources</i> , 2015, 15, 228-229.	4.8	31
147	Single nucleotide polymorphisms derived from ancestral populations show no evidence for biased diversity estimates in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2002, 11, 947-950.	3.9	30
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