Peter Andolfatto

List of Publications by Year
in descending order

90 papers	9,960 citations	34076 52 h-index	46771 89 g-index
105 all docs	105 docs citations	105 times ranked	8907 citing authors

#	Article	IF	Citations
1	The Genetic Architecture of Variation in the Sexually Selected Sword Ornament and Its Evolution in Hybrid Populations. Current Biology, 2021, 31, 923-935.e11.	1.8	21
2	A novel family of secreted insect proteins linked to plant gall development. Current Biology, 2021, 31, 1836-1849.e12.	1.8	37
3	Concerted evolution reveals co-adapted amino acid substitutions in Na+K+-ATPase of frogs that prey on toxic toads. Current Biology, 2021, 31, 2530-2538.e10.	1.8	20
4	Genomic signatures of spatially divergent selection at clownfish range margins. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210407.	1.2	6
5	WHotLAMP: A simple, inexpensive, and sensitive molecular test for the detection of SARS-CoV-2 in saliva. PLoS ONE, 2021, 16, e0257464.	1.1	2
6	Population genetics of the coral Acropora millepora : Toward genomic prediction of bleaching. Science, 2020, 369, .	6.0	167
7	Natural hybridization reveals incompatible alleles that cause melanoma in swordtail fish. Science, 2020, 368, 731-736.	6.0	86
8	Changes throughout a Genetic Network Mask the Contribution of Hox Gene Evolution. Current Biology, 2019, 29, 2157-2166.e6.	1.8	33
9	Predictability in the evolution of Orthopteran cardenolide insensitivity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180246.	1.8	33
10	Dichotomy of Dosage Compensation along the Neo Z Chromosome of the Monarch Butterfly. Current Biology, 2019, 29, 4071-4077.e3.	1.8	66
11	Adaptive substitutions underlying cardiac glycoside insensitivity in insects exhibit epistasis in vivo. ELife, 2019, 8, .	2.8	28
12	Natural selection interacts with recombination to shape the evolution of hybrid genomes. Science, 2018, 360, 656-660.	6.0	314
13	How the manakin got its crown: A novel trait that is unlikely to cause speciation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4144-E4145.	3.3	8
14	What do we mean when we talk about hybrid speciation?. Heredity, 2018, 120, 379-382.	1.2	43
15	The withinâ€host dynamics of infection in transâ€generationally primed flour beetles. Molecular Ecology, 2017, 26, 3794-3807.	2.0	70
16	Sexual Dimorphism and Retinal Mosaic Diversification following the Evolution of a Violet Receptor in Butterflies. Molecular Biology and Evolution, 2017, 34, 2271-2284.	3.5	46
17	Different Evolutionary Strategies To Conserve Chromatin Boundary Function in the Bithorax Complex. Genetics, 2017, 205, 589-603.	1.2	14
18	Assortative mating and persistent reproductive isolation in hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10936-10941.	3.3	77

#	Article	IF	Citations
19	A Genomic Map of the Effects of Linked Selection in Drosophila. PLoS Genetics, 2016, 12, e1006130.	1.5	145
20	Ancient hybridization and genomic stabilization in a swordtail fish. Molecular Ecology, 2016, 25, 2661-2679.	2.0	91
21	simMSG: an experimental design tool for highâ€throughput genotyping of hybrids. Molecular Ecology Resources, 2016, 16, 183-192.	2.2	8
22	Population differences in olfaction accompany host shift in Drosophila mojavensis. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161562.	1.2	40
23	Phylogenetic incongruence and the evolutionary origins of cardenolide-resistant forms of Na⁺,K⁺-ATPase inDanausbutterflies. Evolution; International Journal of Organic Evolution, 2016, 70, 1913-1921.	1.1	16
24	Genetics of Intraspecies Variation in Avoidance Behavior Induced by a Thermal Stimulus in Caenorhabditis elegans. Genetics, 2015, 200, 1327-1339.	1.2	9
25	Tandem Duplications and the Limits of Natural Selection in Drosophila yakuba and Drosophila simulans. PLoS ONE, 2015, 10, e0132184.	1.1	25
26	Reproductive Isolation of Hybrid Populations Driven by Genetic Incompatibilities. PLoS Genetics, 2015, 11, e1005041.	1.5	93
27	Genome-wide QTL mapping of saltwater tolerance in sibling species of Anopheles (malaria vector) mosquitoes. Heredity, 2015, 115, 471-479.	1.2	17
28	HOW COMMON IS HOMOPLOID HYBRID SPECIATION?. Evolution; International Journal of Organic Evolution, 2014, 68, 1553-1560.	1.1	273
29	Revised Annotations, Sex-Biased Expression, and Lineage-Specific Genes in the Drosophila melanogaster Group. G3: Genes, Genomes, Genetics, 2014, 4, 2345-2351.	0.8	17
30	Landscape of Standing Variation for Tandem Duplications in Drosophila yakuba and Drosophila simulans. Molecular Biology and Evolution, 2014, 31, 1750-1766.	3.5	89
31	High-resolution mapping reveals hundreds of genetic incompatibilities in hybridizing fish species. ELife, 2014, 3, .	2.8	115
32	AN EVALUATION OF THE HYBRID SPECIATION HYPOTHESIS FORXIPHOPHORUS CLEMENCIAEBASED ON WHOLE GENOME SEQUENCES. Evolution; International Journal of Organic Evolution, 2013, 67, 1155-1168.	1.1	25
33	PHYLOGENOMICS REVEALS EXTENSIVE RETICULATE EVOLUTION INXIPHOPHORUSFISHES. Evolution; International Journal of Organic Evolution, 2013, 67, 2166-2179.	1.1	176
34	The Capsella rubella genome and the genomic consequences of rapid mating system evolution. Nature Genetics, 2013, 45, 831-835.	9.4	374
35	A second-generation assembly of the Drosophila simulans genome provides new insights into patterns of lineage-specific divergence. Genome Research, 2013, 23, 89-98.	2.4	157
36	Revisiting an Old Riddle: What Determines Genetic Diversity Levels within Species?. PLoS Biology, 2012, 10, e1001388.	2.6	485

#	Article	IF	Citations
37	Parallel Molecular Evolution in an Herbivore Community. Science, 2012, 337, 1634-1637.	6.0	252
38	Methods to Detect Selection on Noncoding DNA. Methods in Molecular Biology, 2012, 856, 141-159.	0.4	29
39	Evolution of Multiple Additive Loci Caused Divergence between Drosophila yakuba and D. santomea in Wing Rowing during Male Courtship. PLoS ONE, 2012, 7, e43888.	1.1	33
40	Genome sequencing reveals complex speciation in the Drosophila simulans clade. Genome Research, 2012, 22, 1499-1511.	2.4	220
41	The evolution of cardenolideâ€resistant forms of Na⁺,K⁺â€ATPase in Danainae butterflies. Molecular Ecology, 2012, 21, 340-349.	2.0	38
42	GENETIC ARCHITECTURE AND ADAPTIVE SIGNIFICANCE OF THE SELFING SYNDROME INCAPSELLA. Evolution; International Journal of Organic Evolution, 2012, 66, 1360-1374.	1.1	79
43	Multiplexed shotgun genotyping for rapid and efficient genetic mapping. Genome Research, 2011, 21, 610-617.	2.4	390
44	Effective Population Size and the Efficacy of Selection on the X Chromosomes of Two Closely Related Drosophila Species. Genome Biology and Evolution, 2011, 3, 114-128.	1.1	59
45	Structurama: Bayesian Inference of Population Structure. Evolutionary Bioinformatics, 2011, 7, EBO.S6761.	0.6	95
46	A Population Genetics-Phylogenetics Approach to Inferring Natural Selection in Coding Sequences. PLoS Genetics, 2011, 7, e1002395.	1.5	78
47	Correlated Evolution of Nearby Residues in Drosophilid Proteins. PLoS Genetics, 2011, 7, e1001315.	1.5	48
48	On the Utility of Short Intron Sequences as a Reference for the Detection of Positive and Negative Selection in Drosophila. Molecular Biology and Evolution, 2010, 27, 1226-1234.	3.5	105
49	Pervasive Natural Selection in the Drosophila Genome?. PLoS Genetics, 2009, 5, e1000495.	1.5	329
50	Evolution of the tan Locus Contributed to Pigment Loss in Drosophila santomea: A Response to Matute etÂal.. Cell, 2009, 139, 1189-1196.	13.5	32
51	The Impact of Natural Selection on the Genome: Emerging Patterns in Drosophila and Arabidopsis. Annual Review of Ecology, Evolution, and Systematics, 2008, 39, 193-213.	3.8	97
52	The Evolution of Gene Regulation Underlies a Morphological Difference between Two Drosophila Sister Species. Cell, 2008, 132, 783-793.	13.5	269
53	Controlling Type-I Error of the McDonaldâ€“Kreitman Test in Genomewide Scans for Selection on Noncoding DNA. Genetics, 2008, 180, 1767-1771.	1.2	41
54	Positive and Negative Selection on Noncoding DNA in Drosophila simulans. Molecular Biology and Evolution, 2008, 25, 1825-1834.	3.5	91

#	Article	IF	Citations
55	An Approximate Bayesian Estimator Suggests Strong, Recurrent Selective Sweeps in Drosophila. PLoS Genetics, 2008, 4, e1000198.	1.5	94
56	Inference of Population Structure Under a Dirichlet Process Model. Genetics, 2007, 175, 1787-1802.	1.2	246
57	Hitchhiking effects of recurrent beneficial amino acid substitutions in the Drosophila melanogaster genome. Genome Research, 2007, 17, 1755-1762.	2.4	188
58	Progress and prospects in mapping recent selection in the genome. Heredity, 2007, 98, 340-348.	1.2	121
59	DISCORDANT DIVERGENCE TIMES AMONG Z-CHROMOSOME REGIONS BETWEEN TWO ECOLOGICALLY DISTINCT SWALLOWTAIL BUTTERFLY SPECIES. Evolution; International Journal of Organic Evolution, 2007, 61, 912-927.	1.1	65
60	EXTENSIVE INTROGRESSION OF MITOCHONDRIAL DNA RELATIVE TO NUCLEAR GENES IN THE DROSOPHILA YAKUBA SPECIES GROUP. Evolution; International Journal of Organic Evolution, 2006, 60, 292.	1.1	4
61	EXTENSIVE INTROGRESSION OF MITOCHONDRIAL DNA RELATIVE TO NUCLEAR GENES IN THE DROSOPHILA YAKUBA SPECIES GROUP. Evolution; International Journal of Organic Evolution, 2006, 60, 292-302.	1.1	187
62	Approximate Bayesian Inference Reveals Evidence for a Recent, Severe Bottleneck in a Netherlands Population of Drosophila melanogaster. Genetics, 2006, 172, 1607-1619.	1.2	239
63	Selection, Recombination and Demographic History in Drosophila miranda. Genetics, 2006, 174, 2045-2059.	1.2	73
64	X chromosomes and autosomes evolve at similar rates in Drosophila: No evidence for faster-X protein evolution. Genome Research, 2006, 16, 498-504.	2.4	67
65	Extensive introgression of mitochondrial DNA relative to nuclear genes in the Drosophila yakuba species group. Evolution; International Journal of Organic Evolution, 2006, 60, 292-302.	1.1	69
66	Adaptive evolution of non-coding DNA in Drosophila. Nature, 2005, 437, 1149-1152.	13.7	576
67	Multilocus patterns of nucleotide variability and the demographic and selection history of Drosophila melanogaster populations. Genome Research, 2005, 15, 790-799.	2.4	247
68	Patterns of intron sequence evolution in Drosophila are dependent upon length and GC content. Genome Biology, 2005, 6, R67.	13.9	158
69	Patterns of Evolutionary Constraints in Intronic and Intergenic DNA of Drosophila. Genome Research, 2004, 14, 273-279.	2.4	99
70	NO ASSOCIATION BETWEEN MITOCHONDRIAL DNA HAPLOTYPES AND A FEMALE-LIMITED MIMICRY PHENOTYPE IN PAPILIO GLAUCUS. Evolution; International Journal of Organic Evolution, 2003, 57, 305-316.	1.1	28
71	NO ASSOCIATION BETWEEN MITOCHONDRIAL DNA HAPLOTYPES AND A FEMALE-LIMITED MIMICRY PHENOTYPE IN PAPILIO GLAUCUS. Evolution; International Journal of Organic Evolution, 2003, 57, 305.	1.1	13
72	Linkage Disequilibrium Patterns Across a Recombination Gradient in African Drosophila melanogaster. Genetics, 2003, 165, 1289-1305.	1.2	55

#	Article	IF	Citations
73	Testing Models of Selection and Demography in Drosophila simulans. Genetics, 2002, 162, 203-216.	1.2	181
74	Adaptive hitchhiking effects on genome variability. Current Opinion in Genetics and Development, 2001, 11, 635-641.	1.5	168
75	Cloning and sequence of the gene encoding the muscle fatty acid binding protein from the desert locust, Schistocerca gregaria. Insect Biochemistry and Molecular Biology, 2001, 31, 553-562.	1.2	32
76	Inversion polymorphisms and nucleotide variability in Drosophila. Genetical Research, 2001, 77, 1-8.	0.3	136
77	Contrasting Patterns of X-Linked and Autosomal Nucleotide Variation in Drosophila melanogaster and Drosophila simulans. Molecular Biology and Evolution, 2001, 18, 279-290.	3.5	242
78	Recombination and the Frequency Spectrum in Drosophila melanogaster and Drosophila simulans. Molecular Biology and Evolution, 2001, 18, 291-298.	3.5	55
79	Regions of Lower Crossing Over Harbor More Rare Variants in African Populations of Drosophila melanogaster. Genetics, 2001, 158, 657-665.	1.2	111
80	Molecular Variation at the In(2L)t Proximal Breakpoint Site in Natural Populations of Drosophila melanogaster and D. simulans. Genetics, 2000, 154, 1681-1691.	1.2	44
81	A Genome-Wide Departure From the Standard Neutral Model in Natural Populations of Drosophila. Genetics, 2000, 156, 257-268.	1.2	163
82	The Population Genetics of the Origin and Divergence of the Drosophila simulans Complex Species. Genetics, 2000, 156, 1913-1931.	1.2	356
83	Unusual Haplotype Structure at the Proximal Breakpoint of In(2L)t in a Natural Population of Drosophila melanogaster. Genetics, 1999, 153, 1297-1311.	1.2	151
84	The Effect of Gene Conversion on Intralocus Associations. Genetics, 1998, 148, 1397-1399.	1.2	115
85	Transformed hairy roots of Mesembryantemum crystallinum: gene expression patterns upon salt stress. Physiologia Plantarum, 1994, 90, 708-714.	2.6	25
86	Transformed hairy roots of Mesembryanthemum crystauinum: gene expression patterns upon salt stress. Physiologia Plantarum, 1994, 90, 708-714.	2.6	7
87	Developmental changes of FABP concentration, expression, and intracellular distribution in locust flight muscle. Molecular and Cellular Biochemistry, 1993, 123, 153-158.	1.4	20
88	Developmental changes of FABP concentration, expression, and intracellular distribution in locust flight muscle. , 1993, , 153-158.		0
89	Fatty-acid-binding protein in locust flight muscle. Developmental changes of expression, concentration and intracellular distribution. FEBS Journal, 1992, 210, 1045-1051.	0.2	54
90	Alleleâ€specific knockouts reveal a role for aponticâ€like in the evolutionary loss of larval melanin pigmentation in the domesticated silkworm, Bombyx mori. Insect Molecular Biology, 0, , .	1.0	4