Aya Takahashi

List of Publications by Year
in descending order

36 papers	1,305 citations	516710 16 h-index	377865 34 g-index
44 all docs	44 docs citations	44 times ranked	1653 citing authors

#	Article	IF	Citations
1	A SNP in the ABCC11 gene is the determinant of human earwax type. Nature Genetics, 2006, 38, 324-330.	21.4	267
2	The nucleotide changes governing cuticular hydrocarbon variation and their evolution in Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 3920-3925.	7.1	180
3	Incipient speciation by sexual isolation in Drosophila: Concurrent evolution at multiple loci. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 6709-6713.	7.1	124
4	Highly contiguous assemblies of 101 drosophilid genomes. ELife, 2021, 10, .	6.0	108
5	<i>Cis</i>- and <i>Trans</i>-regulatory Effects on Gene Expression in a Natural Population of <i>Drosophila melanogaster</i>. Genetics, 2017, 206, 2139-2148.	2.9	57
6	Characteristics of genes up-regulated and down-regulated after 24Âh starvation in the head of Drosophila. Gene, 2009, 446, 11-17.	2.2	48
7	Pigmentation and behavior: potential association through pleiotropic genes in <i>Drosophila</i>. Genes and Genetic Systems, 2013, 88, 165-174.	0.7	46
8	Natural Variation of <i>ebony</i> Gene Controlling Thoracic Pigmentation in <i>Drosophila melanogaster</i>. Genetics, 2007, 177, 1233-1237.	2.9	42
9	Pleiotropic Effects of ebony and tan on Pigmentation and Cuticular Hydrocarbon Composition in Drosophila melanogaster. Frontiers in Physiology, 2019, 10, 518.	2.8	38
10	Effects of Density on Growth of Head Size in Larvae of the Salamander Hynobius retardatus. Copeia, 1996, 1996, 478.	1.3	34
11	Divergent enhancer haplotype of ebony on inversion In(3R)Payne associated with pigmentation variation in a tropical population of Drosophila melanogaster. Molecular Ecology, 2011, 20, 4277-4287.	3.9	34
12	Complex patterns of <i>cis</i>â€regulatory polymorphisms in <i>ebony</i> underlie standing pigmentation variation in <i>Drosophila melanogaster</i>. Molecular Ecology, 2015, 24, 5829-5841.	3.9	32
13	An innovative ovipositor for niche exploitation impacts genital coevolution between sexes in a fruit-damaging <i>Drosophila</i>. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20181635.	2.6	30
14	Introgression of <i>Drosophila simulans Nuclear Pore Protein 160</i> in <i>Drosophila melanogaster</i> Alone Does Not Cause Inviability but Does Cause Female Sterility. Genetics, 2010, 186, 669-676.	2.9	21
15	Mechanical incompatibility caused by modifications of multiple male genital structures using genomic introgression in<i>Drosophila</i>*. Evolution; International Journal of Organic Evolution, 2018, 72, 2406-2418.	2.3	21
16	Genetic Basis of Sexual Isolation in Drosophila melanogaster. Genetica, 2004, 120, 273-284.	1.1	20
17	Mosaic genealogy of the Mus musculus genome revealed by 21 nuclear genes from its three subspecies. Genes and Genetic Systems, 2008, 83, 77-88.	0.7	20
18	Molecular Spectrum of Spontaneous <i>de Novo</i> Mutations in Male and Female Germline Cells of <i>Drosophila melanogaster</i>. Genetics, 2009, 181, 1035-1043.	2.9	19

#	Article	IF	Citations
19	<i>Drosophila suzukii</i>avoidance of microbes in oviposition choice. Royal Society Open Science, 2021, 8, 201601.	2.4	19
20	Genetic Variation Versus Recombination Rate in a Structured Population of Mice. Molecular Biology and Evolution, 2003, 21, 404-409.	8.9	17
21	Starvation-Induced Elevation of Taste Responsiveness and Expression of a Sugar Taste Receptor Gene in<i>Drosophila melanogaster</i>. Journal of Neurogenetics, 2012, 26, 206-215.	1.4	17
22	Wholeâ€genome sequencing reveals small genomic regions of introgression in an introduced crater lake population of threespine stickleback. Ecology and Evolution, 2016, 6, 2190-2204.	1.9	17
23	A High-Frequency Null Mutant of an Odorant-Binding Protein Gene, Obp57e, in Drosophila melanogaster. Genetics, 2005, 170, 709-718.	2.9	13
24	Cold tolerance and metabolic rate increased by cold acclimation in <i>Drosophila albomicans</i> from natural populations. Genes and Genetic Systems, 2013, 88, 289-300.	0.7	11
25	A Generalized Linear Model for Decomposing <i>Cis</i>-regulatory, Parent-of-Origin, and Maternal Effects on Allele-Specific Gene Expression. G3: Genes, Genomes, Genetics, 2017, 7, 2227-2234.	1.8	11
26	A standardized nomenclature and atlas of the female terminalia of <i>Drosophila melanogaster</i>. Fly, 2022, 16, 128-151.	1.7	11
27	Effect of exonic splicing regulation on synonymous codon usage in alternatively spliced exons of Dscam. BMC Evolutionary Biology, 2009, 9, 214.	3.2	7
28	Inferring the demographic history of Japanese cedar, Cryptomeria japonica, using amplicon sequencing. Heredity, 2019, 123, 371-383.	2.6	7
29	A Novel Cell Death Gene Acts to Repair Patterning Defects in Drosophila melanogaster. Genetics, 2014, 197, 739-742.	2.9	4
30	Starvation tolerance associated with prolonged sleep bouts upon starvation in a single natural population of <i>Drosophila melanogaster</i>. Journal of Evolutionary Biology, 2019, 32, 1117-1123.	1.7	4
31	The role of the epidermis enhancer element in positive and negative transcriptional regulation of <i>ebony</i> in <i>Drosophila melanogaster</i>. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	4
32	Cuticular Hydrocarbon Content that Affects Male Mate Preference of<i>Drosophila melanogaster</i>from West Africa. International Journal of Evolutionary Biology, 2012, 2012, 1-10.	1.0	3
33	Factors underlying natural variation in body pigmentation of <i>Drosophila melanogaster</i>. Genes and Genetic Systems, 2016, 91, 127-137.	0.7	3
34	Population genetic analysis of two species of Distylium: D. racemosum growing in East Asian evergreen broad-leaved forests and D. lepidotum endemic to the Ogasawara (Bonin) Islands. Tree Genetics and Genomes, 2019, 15, 1.	1.6	3
35	Genetic basis of sexual isolation in Drosophila melanogaster. Contemporary Issues in Genetics and Evolution, 2004, , 273-284.	0.9	1
36	Ecology, genetics, and evolution of body color variations. Genes and Genetic Systems, 2013, 88, 143-143.	0.7	0