Penelope R Haddrill

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Research trends in forensic science: A scientometric approach to analyze the content of the <scp>INTERPOL</scp> reviews. Wiley Interdisciplinary Reviews Forensic Science, 2022, 4, e1447.	2.1	5
2	Developments in forensic DNA analysis. Emerging Topics in Life Sciences, 2021, 5, 381-393.	2.6	36
3	Population genetics and forensic utility of 23 autosomal PowerPlex Fusion 6C STR loci in the Kuwaiti population. Scientific Reports, 2021, 11, 1865.	3.3	6
4	Population genetics of 30 insertion/deletion polymorphisms in the Kuwaiti population. International Journal of Legal Medicine, 2020, 134, 985-986.	2.2	5
5	Evaluating the effect of body fluid mixture on the relative expression ratio of blood-specific RNA markers. Forensic Science International, 2020, 307, 110116.	2.2	9
6	Determination of the most effective enhancement process for latent fingermarks on Clydesdale Bank and Royal Bank of Scotland £5 and £10 polymer banknotes. Forensic Science International, 2020, 312, 110334.	2.2	7
7	Identifying blood-specific age-related DNA methylation markers on the Illumina MethylationEPIC® BeadChip. Forensic Science International, 2019, 303, 109944.	2.2	22
8	Estimating time since deposition using quantification of RNA degradation in body fluid-specific markers. Forensic Science International, 2019, 298, 58-63.	2.2	40
9	Evaluation of 30 insertion/deletion polymorphisms as forensic markers in the Kuwaiti population. Forensic Science International: Genetics Supplement Series, 2019, 7, 737-738.	0.3	1
10	A multi-tissue age prediction model based on DNA methylation analysis. Forensic Science International: Genetics Supplement Series, 2017, 6, e62-e64.	0.3	10
11	Quantification of RNA degradation of blood-specific markers to indicate the age of bloodstains. Forensic Science International: Genetics Supplement Series, 2017, 6, e453-e455.	0.3	14
12	Variation in the intensity of selection on codon bias over time causes contrasting patterns of base composition evolution in <i>Drosophila</i> . Genome Biology and Evolution, 2017, 9, evw291.	2.5	38
13	Strain-specific and pooled genome sequences for populations of Drosophila melanogaster from three continents F1000Research, 2015, 4, 31.	1.6	15
14	The Discovery, Distribution, and Evolution of Viruses Associated with Drosophila melanogaster. PLoS Biology, 2015, 13, e1002210.	5.6	272
15	The Relation between Recombination Rate and Patterns of Molecular Evolution and Variation in Drosophila melanogaster. Molecular Biology and Evolution, 2014, 31, 1010-1028.	8.9	144
16	Estimation of the Spontaneous Mutation Rate per Nucleotide Site in a <i>Drosophila melanogaster</i> Full-Sib Family. Genetics, 2014, 196, 313-320.	2.9	248
17	Codon Usage Bias and Effective Population Sizes on the X Chromosome versus the Autosomes in Drosophila melanogaster. Molecular Biology and Evolution, 2013, 30, 811-823.	8.9	41
18	Variation in male and female mating behaviour among different populations of the two-spot ladybird, Adalia bipunctata (Coleoptera: Coccinellidae). European Journal of Entomology, 2013, 110, 87-93.	1.2	10

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19	Molecular Evolution in Nonrecombining Regions of the Drosophila melanogaster Genome. Genome Biology and Evolution, 2012, 4, 278-288.	2.5	51
20	Ancestral polymorphisms in <i>Drosophila pseudoobscura</i> and <i>Drosophila miranda</i> . Genetical Research, 2011, 93, 255-263.	0.9	10
21	Determinants of Synonymous and Nonsynonymous Variability in Three Species of Drosophila. Molecular Biology and Evolution, 2011, 28, 1731-1743.	8.9	36
22	Genetic Diversity, Population Structure and Wolbachia Infection Status in a Worldwide Sample of Drosophila melanogaster and D. simulans Populations. PLoS ONE, 2011, 6, e26318.	2.5	44
23	Estimating the Parameters of Selection on Nonsynonymous Mutations in <i>Drosophila pseudoobscura</i> and <i>D. miranda</i> . Genetics, 2010, 185, 1381-1396.	2.9	61
24	Female multiple mating in wild and laboratory populations of the twoâ€spot ladybird, <i>Adalia bipunctata</i> . Molecular Ecology, 2008, 17, 3189-3197.	3.9	39
25	Non-neutral processes drive the nucleotide composition of non-coding sequences in <i>Drosophila</i> . Biology Letters, 2008, 4, 438-441.	2.3	40
26	Elevated levels of expression associated with regions of the Drosophila genome that lack crossing over. Biology Letters, 2008, 4, 758-761.	2.3	15
27	Positive and Negative Selection on Noncoding DNA in Drosophila simulans. Molecular Biology and Evolution, 2008, 25, 1825-1834.	8.9	91
28	A multispecies approach for comparing sequence evolution of X-linked and autosomal sites in <i>Drosophila</i> . Genetical Research, 2008, 90, 421-431.	0.9	29
29	The age and evolution of an antiviral resistance mutation in Drosophila melanogaster. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 2027-2034.	2.6	48
30	Reduced efficacy of selection in regions of the Drosophila genome that lack crossing over. Genome Biology, 2007, 8, R18.	9.6	140
31	Temporal effects of multiple mating on components of fitness in the two-spot ladybird, Adalia bipunctata (Coleoptera: Coccinellidae). European Journal of Entomology, 2007, 104, 393-398.	1.2	23
32	Multilocus patterns of nucleotide variability and the demographic and selection history of Drosophila melanogaster populations. Genome Research, 2005, 15, 790-799.	5.5	247
33	Patterns of intron sequence evolution in Drosophila are dependent upon length and GC content. Genome Biology, 2005, 6, R67.	9.6	158