Aurelie Hua-Van

List of Publications by Year
in descending order

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Version: 2024-02-01

40 papers	5,418 citations	279798 23 h-index	276875 41 g-index
42 all docs	42 docs citations	42 times ranked	7659 citing authors

#	Article	IF	Citations
1	<p>Integrative taxonomy and a new species description in the sturtevanti subgroup of the Drosophila saltans group (Diptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 737 Td (Dros	10.5	37
2	Allelic diversification after transposable element exaptation promotedgsdfas the master sex determining gene of sablefish. Genome Research, 2021, 31, 1366-1380.	5.5	23
3	Chromosomal scale assembly of parasitic wasp genome reveals symbiotic virus colonization. Communications Biology, 2021, 4, 104.	4.4	27
4	piRNA and Transposon Dynamics in Drosophila: A Female Story. Genome Biology and Evolution, 2020, 12, 931-947.	2.5	20
5	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	8.8	71
6	Symbiont-Driven Male Mating Success in the Neotropical Drosophila paulistorum Superspecies. Behavior Genetics, 2019, 49, 83-98.	2.1	31
7	The somatic mobilization of transposable element mariner-Mos1 during the Drosophila lifespan and its biological consequences. Gene, 2018, 679, 65-72.	2.2	10
8	Molecular evolution of piggyBac superfamily: from selfishness to domestication. Genome Biology and Evolution, 2017, 9, evw292.	2.5	21
9	Transcriptional polymorphism of pi<scp>RNA</scp> regulatory genes underlies the mariner activity in Drosophila simulans testes. Molecular Ecology, 2017, 26, 3715-3731.	3.9	10
10	Experimental evolution reveals hyperparasitic interactions among transposable elements. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14763-14768.	7.1	30
11	VHICA, a New Method to Discriminate between Vertical and Horizontal Transposon Transfer: Application to theMarinerFamily withinDrosophila. Molecular Biology and Evolution, 2016, 33, 1094-1109.	8.9	62
12	Mariner transposons are sailing in the genome of the blood-sucking bug Rhodnius prolixus. BMC Genomics, 2015, 16, 1061.	2.8	23
13	Recurrent Domestication by Lepidoptera of Genes from Their Parasites Mediated by Bracoviruses. PLoS Genetics, 2015, 11, e1005470.	3.5	60
14	A call for benchmarking transposable element annotation methods. Mobile DNA, 2015, 6, 13.	3.6	83
15	Genomic landscape and evolutionary dynamics of mariner transposable elements within the Drosophila genus. BMC Genomics, 2014, 15, 727.	2.8	31
16	Gene make-up: rapid and massive intron gains after horizontal transfer of a bacterial Î±-amylase gene to Basidiomycetes. BMC Evolutionary Biology, 2013, 13, 40.	3.2	49
17	Reconstructing the Evolutionary History of Transposable Elements. Genome Biology and Evolution, 2013, 5, 77-86.	2.5	27
18	Improving prokaryotic transposable elements identification using a combination of de novo and profile HMM methods. BMC Genomics, 2013, 14, 700.	2.8	19

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19	Fossil Rhabdoviral Sequences Integrated into Arthropod Genomes: Ontogeny, Evolution, and Potential Functionality. Molecular Biology and Evolution, 2012, 29, 381-390.	8.9	100
20	The evolutionary history of mariner-like elements in Neotropical drosophilids. Genetica, 2011, 139, 327-338.	1.1	8
21	Genome-Wide Comparative Analysis of pogo-Like Transposable Elements in Different Fusarium Species. Journal of Molecular Evolution, 2011, 73, 230-243.	1.8	20
22	The struggle for life of the genome's selfish architects. Biology Direct, 2011, 6, 19.	4.6	198
23	Comparative genomics reveals mobile pathogenicity chromosomes in Fusarium. Nature, 2010, 464, 367-373.	27.8	1,442
24	Reply: A unified classification system for eukaryotic transposable elements should reflect their phylogeny. Nature Reviews Genetics, 2009, 10, 276-276.	16.3	41
25	Automatic classification within families of transposable elements: Application to the mariner Family. Gene, 2009, 448, 227-232.	2.2	31
26	Analysis of the DDE Motif in the Mutator Superfamily. Journal of Molecular Evolution, 2008, 67, 670-681.	1.8	26
27	The mariner transposable element in natural populations of Drosophila simulans. Heredity, 2008, 101, 53-59.	2.6	19
28	A universal classification of eukaryotic transposable elements implemented in Repbase. Nature Reviews Genetics, 2008, 9, 414-414.	16.3	5
29	Transposition of a Fungal Miniature Inverted-Repeat Transposable Element Through the Action of a Tc1-Like Transposase. Genetics, 2007, 175, 441-452.	2.9	47
30	Amplification of the 1731 LTR retrotransposon in Drosophila melanogaster cultured cells: Origin of neocopies and impact on the genome. Gene, 2007, 393, 116-126.	2.2	16
31	A unified classification system for eukaryotic transposable elements. Nature Reviews Genetics, 2007, 8, 973-982.	16.3	2,396
32	Abundance, distribution and dynamics of retrotransposable elements and transposons: similarities and differences. Cytogenetic and Genome Research, 2005, 110, 426-440.	1.1	106
33	Aberrant transposition of a Tc1-mariner element, impala, in the fungus Fusarium oxysporum. Molecular Genetics and Genomics, 2002, 267, 79-87.	2.1	24
34	Germ line transformation of the yellow fever mosquito, Aedes aegypti, mediated by transpositional insertion of a piggyBac vector. Insect Molecular Biology, 2002, 11, 133-139.	2.0	58
35	Transposon impala, a Novel Tool for Gene Tagging in the Rice Blast Fungus Magnaporthe grisea. Molecular Plant-Microbe Interactions, 2001, 14, 308-315.	2.6	53
36	Evolutionary History of the impala Transposon in Fusarium oxysporum. Molecular Biology and Evolution, 2001, 18, 1959-1969.	8.9	37

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37	Mobility of the piggyBac transposon in embryos of the vectors of Dengue fever (Aedes albopictus) and La Crosse encephalitis (Ae. triseriatus). Molecular Genetics and Genomics, 2001, 265, 66-71.	2.1	20
38	Transposition of autonomous and engineered impala transposons in Fusarium oxysporum and a related species. Molecular Genetics and Genomics, 2001, 264, 724-731.	2.4	36
39	Genome organization in Fusarium oxysporum : clusters of class II transposons. Current Genetics, 2000, 37, 339-347.	1.7	78
40	Three highly divergent subfamilies of the impala transposable element coexist in the genome of the fungus Fusarium oxysporum. Molecular Genetics and Genomics, 1998, 259, 354-362.	2.4	51