

AurÃ©lie Kapusta

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

3,232
citations

304743

22
h-index

580821

25
g-index

32
all docs

32
docs citations

32
times ranked

5310
citing authors

#	ARTICLE	IF	CITATIONS
1	Transposable Elements Are Major Contributors to the Origin, Diversification, and Regulation of Vertebrate Long Noncoding RNAs. <i>PLoS Genetics</i> , 2013, 9, e1003470.	3.5	574
2	Dynamics of genome size evolution in birds and mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1460-E1469.	7.1	324
3	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20645-20650.	7.1	260
4	Ancient Transposable Elements Transformed the Uterine Regulatory Landscape and Transcriptome during the Evolution of Mammalian Pregnancy. <i>Cell Reports</i> , 2015, 10, 551-561.	6.4	249
5	Volatile evolution of long noncoding RNA repertoires: mechanisms and biological implications. <i>Trends in Genetics</i> , 2014, 30, 439-452.	6.7	235
6	The Relationship among Gene Expression, the Evolution of Gene Dosage, and the Rate of Protein Evolution. <i>PLoS Genetics</i> , 2010, 6, e1000944.	3.5	189
7	PiggyMac, a domesticated <i>piggyBac</i> transposase involved in programmed genome rearrangements in the ciliate <i>Paramecium tetraurelia</i> . <i>Genes and Development</i> , 2009, 23, 2478-2483.	5.9	177
8	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. <i>Genome Biology</i> , 2016, 17, 111.	8.8	152
9	Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. <i>ELife</i> , 2016, 5, .	6.0	130
10	Evolution of bird genomes—a transposon's-eye view. <i>Annals of the New York Academy of Sciences</i> , 2017, 1389, 164-185.	3.8	114
11	A comprehensive analysis of piRNAs from adult human testis and their relationship with genes and mobile elements. <i>BMC Genomics</i> , 2014, 15, 545.	2.8	105
12	Transposable elements generate regulatory novelty in a tissue-specific fashion. <i>BMC Genomics</i> , 2018, 19, 468.	2.8	86
13	A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015, 6, 13.	3.6	83
14	Functional specialization of Piwi proteins in <i>Paramecium tetraurelia</i> from post-transcriptional gene silencing to genome remodelling. <i>Nucleic Acids Research</i> , 2011, 39, 4249-4264.	14.5	82
15	Functional characterization of <i>piggyBat</i> from the bat <i>Myotis lucifugus</i> unveils an active mammalian DNA transposon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 234-239.	7.1	73
16	Gene expression in a paleopolyploid: a transcriptome resource for the ciliate <i>Paramecium tetraurelia</i> . <i>BMC Genomics</i> , 2010, 11, 547.	2.8	64
17	Improved Genome Assembly and Annotation for the Rock Pigeon (<i>Columba livia</i>). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1391-1398.	1.8	62
18	Highly Precise and Developmentally Programmed Genome Assembly in <i>Paramecium</i> Requires Ligase IV-Dependent End Joining. <i>PLoS Genetics</i> , 2011, 7, e1002049.	3.5	56

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19	Genomics of Ecological Adaptation in Cactophilic <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 349-366.	2.5	51
20	RNAi-dependent <i>Polycomb</i> repression controls transposable elements in <i>Tetrahymena</i> . <i>Genes and Development</i> , 2019, 33, 348-364.	5.9	42
21	Ku-Mediated Coupling of DNA Cleavage and Repair during Programmed Genome Rearrangements in the Ciliate <i>Paramecium tetraurelia</i> . <i>PLoS Genetics</i> , 2014, 10, e1004552.	3.5	38
22	Genomic Landscape of Human, Bat, and Ex Vivo DNA Transposon Integrations. <i>Molecular Biology and Evolution</i> , 2014, 31, 1816-1832.	8.9	30
23	Exploration of the <i>Drosophila buzzatii</i> transposable element content suggests underestimation of repeats in <i>Drosophila</i> genomes. <i>BMC Genomics</i> , 2016, 17, 344.	2.8	22
24	Clinical and molecular epidemiology of invasive <i>Staphylococcus aureus</i> infection in Utah children; continued dominance of MSSA over MRSA. <i>PLoS ONE</i> , 2020, 15, e0238991.	2.5	20
25	Identification of a miniature <i>Sae2/Ctp1/CtIP</i> ortholog from <i>Paramecium tetraurelia</i> required for sexual reproduction and DNA double-strand break repair. <i>DNA Repair</i> , 2019, 77, 96-108.	2.8	8
26	#64: An odyssey Beyond the Capsule: Genetic Determinants of Pediatric Invasive <i>Streptococcus pneumoniae</i> Empyema. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021, 10, S7-S7.	1.3	0