

# 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	#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
2	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
3	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
4	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
5	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
6	Transposable elements generate regulatory novelty in a tissue-specific fashion. <i>BMC Genomics</i> , 2018, 19, 468.	2.8	86
7	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
8	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
9	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
10	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
11	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
12	Genomics of Ecological Adaptation in Cactophilic <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 349-366.	2.5	51
13	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
14	A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015, 6, 13.	3.6	83
15	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
16	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
17	Genomic Landscape of Human, Bat, and Ex Vivo DNA Transposon Integrations. <i>Molecular Biology and Evolution</i> , 2014, 31, 1816-1832.	8.9	30
18	Volatile evolution of long noncoding RNA repertoires: mechanisms and biological implications. <i>Trends in Genetics</i> , 2014, 30, 439-452.	6.7	235

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19	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20645-20650.	7.1	260
20	Transposable Elements Are Major Contributors to the Origin, Diversification, and Regulation of Vertebrate Long Noncoding RNAs. PLoS Genetics, 2013, 9, e1003470.	3.5	574
21	Functional characterization of <i>piggyBat</i> from the bat <i>Myotis lucifugus</i> unveils an active mammalian DNA transposon. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 234-239.	7.1	73
22	Functional specialization of Piwi proteins in <i>Paramecium tetraurelia</i> from post-transcriptional gene silencing to genome remodelling. Nucleic Acids Research, 2011, 39, 4249-4264.	14.5	82
23	Highly Precise and Developmentally Programmed Genome Assembly in <i>Paramecium</i> Requires Ligase IV-Dependent End Joining. PLoS Genetics, 2011, 7, e1002049.	3.5	56
24	Gene expression in a paleopolyploid: a transcriptome resource for the ciliate <i>Paramecium tetraurelia</i> . BMC Genomics, 2010, 11, 547.	2.8	64
25	The Relationship among Gene Expression, the Evolution of Gene Dosage, and the Rate of Protein Evolution. PLoS Genetics, 2010, 6, e1000944.	3.5	189
26	PiggyMac, a domesticated <i>piggyBac</i> transposase involved in programmed genome rearrangements in the ciliate <i>Paramecium tetraurelia</i> . Genes and Development, 2009, 23, 2478-2483.	5.9	177