## Esther Lizano

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8762788/publications.pdf

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687363 552781 2,816 27 13 26 h-index citations g-index papers 30 30 30 8140 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	27.8	1,857
2	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
3	Evidence for the biogenesis of more than 1,000 novel human microRNAs. Genome Biology, 2014, 15, R57.	9.6	222
4	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. Nature Communications, 2019, 10, 4.	12.8	90
5	Differential DNA methylation of vocal and facial anatomy genes in modern humans. Nature Communications, 2020, 11, 1189.	12.8	69
6	A comparative analysis of CCA-adding enzymes from human and E. coli: Differences in CCA addition and tRNA 3′-end repair. Biochimie, 2008, 90, 762-772.	2.6	42
7	The genomics of ecological flexibility, large brains, and long lives in capuchin monkeys revealed with fecalFACS. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	34
8	Transcription Factors Are Targeted by Differentially Expressed miRNAs in Primates. Genome Biology and Evolution, 2012, 4, 552-564.	2.5	30
9	Specific small-RNA signatures in the amygdala at premotor and motor stages of Parkinson's disease revealed by deep sequencing analysis. Bioinformatics, 2016, 32, 673-681.	4.1	29
10	<scp>MicroRNA</scp> expression profiling in blood from fragile Xâ€associated tremor/ataxia syndrome patients. Genes, Brain and Behavior, 2013, 12, 595-603.	2.2	25
11	A roadmap for highâ€throughput sequencing studies of wild animal populations using noninvasive samples and hybridization capture. Molecular Ecology Resources, 2019, 19, 609-622.	4.8	24
12	Maximizing the acquisition of unique reads in noninvasive capture sequencing experiments. Molecular Ecology Resources, 2021, 21, 745-761.	4.8	18
13	Population dynamics and genetic connectivity in recent chimpanzee history. Cell Genomics, 2022, 2, 100133.	6.5	18
14	Annotation of primate miRNAs by high throughput sequencing of small RNA libraries. BMC Genomics, 2012, 13, 116.	2.8	16
15	Evolution of Neuronal and Endothelial Transcriptomes in Primates. Genome Biology and Evolution, 2010, 2, 284-292.	2.5	14
16	Production of RNAs with Homogeneous 5′ and 3′ Ends. , 0, , 22-35.		13
17	A Splice Variant of the Human CCA-adding Enzyme with Modified Activity. Journal of Molecular Biology, 2007, 366, 1258-1265.	4.2	13
18	Targeted conservation genetics of the endangered chimpanzee. Heredity, 2020, 125, 15-27.	2.6	11

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#	Article	IF	CITATION
19	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	1.7	7
20	Transcriptome innovations in primates revealed by single-molecule long-read sequencing. Genome Research, 2022, 32, 1448-1462.	5 <b>.</b> 5	6
21	Flow Sorting Enrichment and Nanopore Sequencing of Chromosome 1 From a Chinese Individual. Frontiers in Genetics, 2019, 10, 1315.	2.3	5
22	Genetic data from the extinct giant rat from Tenerife (Canary Islands) points to a recent divergence from mainland relatives. Biology Letters, 2021, 17, 20210533.	2.3	5
23	Recovering the genomes hidden in museum wet collections. Molecular Ecology Resources, 2022, , .	4.8	4
24	Metagenomic analysis of a blood stain from the French revolutionary Jean-Paul Marat (1743–1793). Infection, Genetics and Evolution, 2020, 80, 104209.	2.3	2
25	Salmonella enterica from a soldier from the 1652 siege of Barcelona (Spain) supports historical transatlantic epidemic contacts. IScience, 2021, 24, 103021.	4.1	2
26	Insights from the rescue and breeding management of Cuvier's gazelle ( <i>Gazella cuvieri</i> ) through wholeâ€genome sequencing. Evolutionary Applications, 2022, 15, 351-364.	3.1	2
27	Genomic Analysis of 18th-Century Kazakh Individuals and Their Oral Microbiome. Biology, 2021, 10, 1324.	2.8	2