Christina Amory

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/506783/publications.pdf

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		623699	642715
25	649	14	23
papers	citations	h-index	g-index
20	20	20	652
28	28	28	653
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Evidence for frequent and tissue-specific sequence heteroplasmy in human mitochondrial DNA. Mitochondrion, 2015, 20, 82-94.	3.4	83
2	Full mtGenome reference data: Development and characterization of 588 forensic-quality haplotypes representing three U.S. populations. Forensic Science International: Genetics, 2015, 14, 141-155.	3.1	78
3	Evaluation of the precision ID whole MtDNA genome panel for forensic analyses. Forensic Science International: Genetics, 2018, 35, 21-25.	3.1	70
4	Optimized mtDNA Control Region Primer Extension Capture Analysis for Forensically Relevant Samples and Highly Compromised mtDNA of Different Age and Origin. Genes, 2017, 8, 237.	2.4	51
5	Evidence for multi-copy Mega-NUMT <i>s</i> ii) in the human genome. Nucleic Acids Research, 2021, 49, 1517-1531.	14.5	42
6	Evaluation of mitogenome sequence concordance, heteroplasmy detection, and haplogrouping in a worldwide lineage study using the Precision ID mtDNA Whole Genome Panel. Forensic Science International: Genetics, 2019, 42, 244-251.	3.1	37
7	Reprint of: Evaluation of next generation mtGenome sequencing using the Ion Torrent Personal Genome Machine (PGM). Forensic Science International: Genetics, 2013, 7, 632-639.	3.1	33
8	Human settlement history between Sunda and Sahul: a focus on East Timor (Timor-Leste) and the Pleistocenic mtDNA diversity. BMC Genomics, 2015, 16, 70.	2.8	32
9	Evaluation of DNA Extraction Methods Developed for Forensic and Ancient DNA Applications Using Bone Samples of Different Age. Genes, 2021, 12, 146.	2.4	32
10	Developmental Validation of a MPS Workflow with a PCR-Based Short Amplicon Whole Mitochondrial Genome Panel. Genes, 2020, 11, 1345.	2.4	30
11	Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel. Mitochondrion, 2020, 55, 122-133.	3.4	24
12	Helena, the hidden beauty: Resolving the most common West Eurasian mtDNA control region haplotype by massively parallel sequencing an Italian population sample. Forensic Science International: Genetics, 2015, 15, 21-26.	3.1	23
13	SD quantsâ€"Sensitive detection tetraplex-system for nuclear and mitochondrial DNA quantification and degradation inference. Forensic Science International: Genetics, 2019, 42, 39-44.	3.1	23
14	Development of forensic-quality full mtGenome haplotypes: Success rates with low template specimens. Forensic Science International: Genetics, 2014, 10, 73-79.	3.1	18
15	Working towards implementation of whole genome mitochondrial DNA sequencing into routine casework. Forensic Science International: Genetics Supplement Series, 2017, 6, e388-e389.	0.3	14
16	The maternal inheritance of Alto Paran \tilde{A}_i revealed by full mitogenome sequences. Forensic Science International: Genetics, 2019, 39, 66-72.	3.1	13
17	Mitochondrial DNA analysis of a Viking age mass grave in Sweden. Forensic Science International: Genetics, 2019, 42, 268-274.	3.1	10
18	The mitogenome portrait of Umbria in Central Italy as depicted by contemporary inhabitants and pre-Roman remains. Scientific Reports, 2020, 10, 10700.	3.3	9

#	Article	IF	CITATIONS
19	Lack of gene–language correlation due to reciprocal female but directional male admixture in Austronesians and non-Austronesians of East Timor. European Journal of Human Genetics, 2017, 25, 246-252.	2.8	7
20	The lot-to-lot variability in the mitochondrial genome of controls. Forensic Science International: Genetics, 2020, 47, 102298.	3.1	6
21	Mitochondrial DNA Footprints from Western Eurasia in Modern Mongolia. Frontiers in Genetics, 2021, 12, 819337.	2.3	4
22	Helena's Many Daughters: More Mitogenome Diversity behind the Most Common West Eurasian mtDNA Control Region Haplotype in an Extended Italian Population Sample. International Journal of Molecular Sciences, 2022, 23, 6725.	4.1	3
23	Genetic and phylogeographic evidence for Jewish Holocaust victims at the Sobib \tilde{A}^3 r death camp. Genome Biology, 2021, 22, 200.	8.8	2
24	House of the dead-exceptional burials of the Avar period (seventh century AD) in Podersdorf am See (Burgenland/A). Archaeological and Anthropological Sciences, 2020, 12, 1.	1.8	0
25	Post hoc deconvolution of human mitochondrial DNA mixtures by EMMA 2 using fine-tuned Phylotree nomenclature. Computational and Structural Biotechnology Journal, 2022, 20, 3630-3638.	4.1	0