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List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

2,029
citations

687363

13
h-index

526287

27
g-index

29
all docs

29
docs citations

29
times ranked

3368
citing authors

#	ARTICLE	IF	CITATIONS
1	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
2	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320
3	Recombination-filtered genomic datasets by information maximization. <i>Bioinformatics</i> , 2007, 23, 1851-1853.	4.1	193
4	The Time Scale of Recombination Rate Evolution in Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 928-945.	8.9	92
5	The ratio of human X chromosome to autosome diversity is positively correlated with genetic distance from genes. <i>Nature Genetics</i> , 2010, 42, 830-831.	21.4	90
6	Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. <i>Genome Research</i> , 2016, 26, 291-300.	5.5	87
7	Forensic Human Identification Using Skin Microbiomes. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	74
8	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018, 32, 50-61.	3.1	69
9	Evidence for Increased Levels of Positive and Negative Selection on the X Chromosome versus Autosomes in Humans. <i>Molecular Biology and Evolution</i> , 2014, 31, 2267-2282.	8.9	59
10	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. <i>Molecular Biology and Evolution</i> , 2015, 32, 600-612.	8.9	55
11	Forensic human identification with targeted microbiome markers using nearest neighbor classification. <i>Forensic Science International: Genetics</i> , 2019, 38, 130-139.	3.1	45
12	Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach. <i>Genetics</i> , 2015, 200, 295-308.	2.9	44
13	Evaluation of the precision ID mtDNA whole genome panel on two massively parallel sequencing systems. <i>Forensic Science International: Genetics</i> , 2018, 36, 213-224.	3.1	35
14	STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. <i>Forensic Science International: Genetics</i> , 2021, 52, 102463.	3.1	16
15	A novel phylogenetic approach for de novo discovery of putative nuclear mitochondrial (pNumt) haplotypes. <i>Forensic Science International: Genetics</i> , 2019, 43, 102146.	3.1	15
16	Evaluation of Promega PowerSeq [®] , [®] Auto/Y systems prototype on an admixed sample of Rio de Janeiro, Brazil: Population data, sensitivity, stutter and mixture studies. <i>Forensic Science International: Genetics</i> , 2021, 53, 102516.	3.1	13
17	Compound stutter in D2S1338 and D12S391. <i>Forensic Science International: Genetics</i> , 2019, 39, 50-56.	3.1	9
18	Reducing noise and stutter in short tandem repeat loci with unique molecular identifiers. <i>Forensic Science International: Genetics</i> , 2021, 51, 102459.	3.1	9

#	ARTICLE	IF	CITATIONS
19	Population Informative Markers Selected Using Wright's Fixation Index and Machine Learning Improves Human Identification Using the Skin Microbiome. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0120821.	3.1	8
20	The Role of Phylogenetically Conserved Elements in Shaping Patterns of Human Genomic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 2284-2295.	8.9	5
21	skater: an R package for SNP-based kinship analysis, testing, and evaluation. <i>F1000Research</i> , 2022, 11, 18.	1.6	5
22	Determining Informative Microbial Single Nucleotide Polymorphisms for Human Identification. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0005222.	3.1	5
23	MMDIT: A tool for the deconvolution and interpretation of mitochondrial DNA mixtures. <i>Forensic Science International: Genetics</i> , 2021, 55, 102568.	3.1	4
24	ProDerAl: reference position dependent alignment. <i>Bioinformatics</i> , 2021, 37, 2479-2480.	4.1	3
25	ProSynAR: a reference aware read merger. <i>Bioinformatics</i> , 2022, 38, 2052-2053.	4.1	2
26	Techniques for estimating genetically variable peptides and semi-continuous likelihoods from massively parallel sequencing data. <i>Forensic Science International: Genetics</i> , 2022, 59, 102719.	3.1	2
27	mixIndependR: a R package for statistical independence testing of loci in database of multi-locus genotypes. <i>BMC Bioinformatics</i> , 2021, 22, 12.	2.6	1