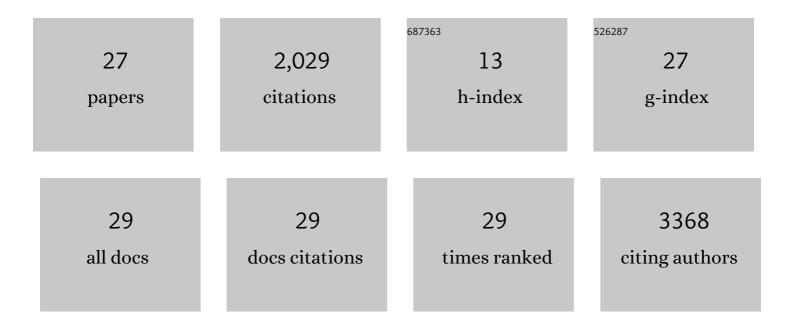
August E Woerner

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6879811/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	27.8	768
2	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	27.8	320
3	Recombination-filtered genomic datasets by information maximization. Bioinformatics, 2007, 23, 1851-1853.	4.1	193
4	The Time Scale of Recombination Rate Evolution in Great Apes. Molecular Biology and Evolution, 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. Nature Genetics, 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. Genome Research, 2016, 26, 291-300.	5.5	87
7	Forensic Human Identification Using Skin Microbiomes. Applied and Environmental Microbiology, 2017, 83, .	3.1	74
8	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. Forensic Science International: Genetics, 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. Molecular Biology and Evolution, 2014, 31, 2267-2282.	8.9	59
10	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. Molecular Biology and Evolution, 2015, 32, 600-612.	8.9	55
11	Forensic human identification with targeted microbiome markers using nearest neighbor classification. Forensic Science International: Genetics, 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. Genetics, 2015, 200, 295-308.	2.9	44
13	Evaluation of the precision ID mtDNA whole genome panel on two massively parallel sequencing systems. Forensic Science International: Genetics, 2018, 36, 213-224.	3.1	35
14	STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. Forensic Science International: Genetics, 2021, 52, 102463.	3.1	16
15	A novel phylogenetic approach for de novo discovery of putative nuclear mitochondrial (pNumt) haplotypes. Forensic Science International: Genetics, 2019, 43, 102146.	3.1	15
16	Evaluation of Promega PowerSeqâ"¢ Auto/Y systems prototype on an admixed sample of Rio de Janeiro, Brazil: Population data, sensitivity, stutter and mixture studies. Forensic Science International: Genetics, 2021, 53, 102516.	3.1	13
17	Compound stutter in D2S1338 and D12S391. Forensic Science International: Genetics, 2019, 39, 50-56.	3.1	9
18	Reducing noise and stutter in short tandem repeat loci with unique molecular identifiers. Forensic Science International: Genetics, 2021, 51, 102459.	3.1	9

AUGUST E WOERNER

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