August E Woerner

List of Publications by Year in descending order

27	2,029	687220	526166
papers	citations	13	27
		h-index	g-index

29	29	29	3368
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	ProSynAR: a reference aware read merger. Bioinformatics, 2022, 38, 2052-2053.	1.8	2
2	skater: an R package for SNP-based kinship analysis, testing, and evaluation. F1000Research, 2022, 11, 18.	0.8	5
3	Determining Informative Microbial Single Nucleotide Polymorphisms for Human Identification. Applied and Environmental Microbiology, 2022, 88, e0005222.	1.4	5
4	Techniques for estimating genetically variable peptides and semi-continuous likelihoods from massively parallel sequencing data. Forensic Science International: Genetics, 2022, 59, 102719.	1.6	2
5	mixIndependR: a R package for statistical independence testing of loci in database of multi-locus genotypes. BMC Bioinformatics, 2021, 22, 12.	1.2	1
6	Reducing noise and stutter in short tandem repeat loci with unique molecular identifiers. Forensic Science International: Genetics, 2021, 51, 102459.	1.6	9
7	STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. Forensic Science International: Genetics, 2021, 52, 102463.	1.6	16
8	Evaluation of Promega PowerSeq™ 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.	1.6	13
9	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.	1.4	8
10	MMDIT: A tool for the deconvolution and interpretation of mitochondrial DNA mixtures. Forensic Science International: Genetics, 2021, 55, 102568.	1.6	4
11	ProDerAl: reference position dependent alignment. Bioinformatics, 2021, 37, 2479-2480.	1.8	3
12	A novel phylogenetic approach for de novo discovery of putative nuclear mitochondrial (pNumt) haplotypes. Forensic Science International: Genetics, 2019, 43, 102146.	1.6	15
13	Compound stutter in D2S1338 and D12S391. Forensic Science International: Genetics, 2019, 39, 50-56.	1.6	9
14	Forensic human identification with targeted microbiome markers using nearest neighbor classification. Forensic Science International: Genetics, 2019, 38, 130-139.	1.6	45
15	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. Forensic Science International: Genetics, 2018, 32, 50-61.	1.6	69
16	Evaluation of the precision ID mtDNA whole genome panel on two massively parallel sequencing systems. Forensic Science International: Genetics, 2018, 36, 213-224.	1.6	35
17	The Role of Phylogenetically Conserved Elements in Shaping Patterns of Human Genomic Diversity. Molecular Biology and Evolution, 2018, 35, 2284-2295.	3.5	5
18	Forensic Human Identification Using Skin Microbiomes. Applied and Environmental Microbiology, 2017, 83, .	1.4	74

#	Article	IF	Citations
19	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.	2.4	87
20	The Time Scale of Recombination Rate Evolution in Great Apes. Molecular Biology and Evolution, 2016, 33, 928-945.	3.5	92
21	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. Molecular Biology and Evolution, 2015, 32, 600-612.	3.5	55
22	Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach. Genetics, 2015, 200, 295-308.	1.2	44
23	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320
24	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.	3.5	59
25	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768
26	The ratio of human X chromosome to autosome diversity is positively correlated with genetic distance from genes. Nature Genetics, 2010, 42, 830-831.	9.4	90
27	Recombination-filtered genomic datasets by information maximization. Bioinformatics, 2007, 23, 1851-1853.	1.8	193