

Mary K Kuhner

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

2,593
citations

516561

16
h-index

395590

33
g-index

35
all docs

35
docs citations

35
times ranked

3597
citing authors

#	ARTICLE	IF	CITATIONS
1	Somatic whole genome dynamics of precancer in Barrett's esophagus reveals features associated with disease progression. <i>Nature Communications</i> , 2022, 13, 2300.	5.8	13
2	Within-patient phylogenetic reconstruction reveals early events in Barrett's Esophagus. <i>Evolutionary Applications</i> , 2021, 14, 399-415.	1.5	2
3	Who are the elephants living in the hybridization zone? How genetics may guide conservation to better protect endangered elephants. <i>Global Ecology and Conservation</i> , 2021, 32, e01917.	1.0	5
4	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020, 183, 197-210.e32.	13.5	141
5	CNValidator: validating somatic copy-number inference. <i>Bioinformatics</i> , 2019, 35, 2660-2662.	1.8	2
6	Evolution of Barrett's esophagus through space and time at single-crypt and whole-biopsy levels. <i>Nature Communications</i> , 2018, 9, 794.	5.8	47
7	A Consensus Method for Ancestral Recombination Graphs. <i>Journal of Molecular Evolution</i> , 2017, 84, 129-138.	0.8	0
8	Limitations of the Driver/Passenger Model in Cancer Prevention. <i>Cancer Prevention Research</i> , 2016, 9, 335-338.	0.7	7
9	Bulk Genotyping of Biopsies Can Create Spurious Evidence for Heterogeneity in Mutation Content. <i>PLoS Computational Biology</i> , 2016, 12, e1004413.	1.5	21
10	Assessing Differences Between Ancestral Recombination Graphs. <i>Journal of Molecular Evolution</i> , 2015, 80, 258-264.	0.8	1
11	Assessment of Esophageal Adenocarcinoma Risk Using Somatic Chromosome Alterations in Longitudinal Samples in Barrett's Esophagus. <i>Cancer Prevention Research</i> , 2015, 8, 845-856.	0.7	44
12	Practical Performance of Tree Comparison Metrics. <i>Systematic Biology</i> , 2015, 64, 205-214.	2.7	65
13	Correcting for Sequencing Error in Maximum Likelihood Phylogeny Inference. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2545-2552.	0.8	10
14	Joint Inference of Identity by Descent Along Multiple Chromosomes from Population Samples. <i>Journal of Computational Biology</i> , 2014, 21, 185-200.	0.8	5
15	Temporal and Spatial Evolution of Somatic Chromosomal Alterations: A Case-Cohort Study of Barrett's Esophagus. <i>Cancer Prevention Research</i> , 2014, 7, 114-127.	0.7	135
16	Bayesian Inference of Local Trees Along Chromosomes by the Sequential Markov Coalescent. <i>Journal of Molecular Evolution</i> , 2014, 78, 279-292.	0.8	8
17	NSAIDs Modulate Clonal Evolution in Barrett's Esophagus. <i>PLoS Genetics</i> , 2013, 9, e1003553.	1.5	59
18	Correcting Coalescent Analyses for Panel-Based SNP Ascertainment. <i>Genetics</i> , 2013, 193, 1185-1196.	1.2	7

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19	GraphML specializations to codify ancestral recombinant graphs. <i>Frontiers in Genetics</i> , 2013, 4, 146.	1.1	8
20	Signatures of High-Altitude Adaptation in the Major Hemoglobin of Five Species of Andean Dabbling Ducks. <i>American Naturalist</i> , 2009, 174, 631-650.	1.0	50
21	Gene Flow in the Face of Countervailing Selection: Adaptation to High-Altitude Hypoxia in the β Hemoglobin Subunit of Yellow-Billed Pintails in the Andes. <i>Molecular Biology and Evolution</i> , 2009, 26, 815-827.	3.5	70
22	The limits of fine-scale mapping. <i>Genetic Epidemiology</i> , 2009, 33, 344-356.	0.6	6
23	Coalescent genealogy samplers: windows into population history. <i>Trends in Ecology and Evolution</i> , 2009, 24, 86-93.	4.2	249
24	Comparing Likelihood and Bayesian Coalescent Estimation of Population Parameters. <i>Genetics</i> , 2007, 175, 155-165.	1.2	78
25	LAMARC 2.0: maximum likelihood and Bayesian estimation of population parameters. <i>Bioinformatics</i> , 2006, 22, 768-770.	1.8	572
26	Robustness of Coalescent Estimators to Between-Lineage Mutation Rate Variation. <i>Molecular Biology and Evolution</i> , 2006, 23, 2355-2360.	3.5	6
27	Sampling among haplotype resolutions in a coalescent-based genealogy sampler. <i>Genetic Epidemiology</i> , 2000, 19, S15-S21.	0.6	17
28	Usefulness of Single Nucleotide Polymorphism Data for Estimating Population Parameters. <i>Genetics</i> , 2000, 156, 439-447.	1.2	126
29	Maximum Likelihood Estimation of Recombination Rates From Population Data. <i>Genetics</i> , 2000, 156, 1393-1401.	1.2	189
30	Maximum Likelihood Estimation of Population Growth Rates Based on the Coalescent. <i>Genetics</i> , 1998, 149, 429-434.	1.2	554
31	Genetic exchange in the evolution of the human MHC class II loci. <i>Tissue Antigens</i> , 1992, 39, 209-215.	1.0	13
32	Gene conversion in the evolution of the human and chimpanzee MHC class I loci. <i>Tissue Antigens</i> , 1991, 38, 152-164.	1.0	50
33	DNA sequences of mouse H-2 and Qa genes. <i>Immunogenetics</i> , 1989, 30, 458-464.	1.2	29
34	Clues to IDDM pathogenesis from genetic and serological traits in multiply affected families. <i>Genetic Epidemiology</i> , 1989, 6, 117-122.	0.6	4