Scott A Jackson

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Analysis of the Molecular Diversity Among Cronobacter Species Isolated From Filth Flies Using Targeted PCR, Pan Genomic DNA Microarray, and Whole Genome Sequencing Analyses. Frontiers in Microbiology, 2020, 11, 561204.	3.5	17
2	Current explorations of nutrition and the gut microbiome: a comprehensive evaluation of the review literature. Nutrition Reviews, 2020, 78, 798-812.	5.8	71
3	Performing Skin Microbiome Research: A Method to the Madness. Journal of Investigative Dermatology, 2017, 137, 561-568.	0.7	164
4	Use of a Pan–Genomic DNA Microarray in Determination of the Phylogenetic Relatedness among Cronobacter spp. and Its Use as a Data Mining Tool to Understand Cronobacter Biology. Microarrays (Basel, Switzerland), 2017, 6, 6.	1.4	6
5	FDA Escherichia coli Identification (FDA-ECID) Microarray: a Pangenome Molecular Toolbox for Serotyping, Virulence Profiling, Molecular Epidemiology, and Phylogeny. Applied and Environmental Microbiology, 2016, 82, 3384-3394.	3.1	25
6	PEPR: pipelines for evaluating prokaryotic references. Analytical and Bioanalytical Chemistry, 2016, 408, 2975-2983.	3.7	5
7	Development of a Custom-Designed, Pan Genomic DNA Microarray to Characterize Strain-Level Diversity among Cronobacter spp Frontiers in Pediatrics, 2015, 3, 36.	1.9	26
8	Genomic Evidence Reveals Numerous Salmonella enterica Serovar Newport Reintroduction Events in Suwannee Watershed Irrigation Ponds. Applied and Environmental Microbiology, 2015, 81, 8243-8253.	3.1	19
9	Novel Microarray Design for Molecular Serotyping of Shiga Toxin-Producing Escherichia coli Strains Isolated from Fresh Produce. Applied and Environmental Microbiology, 2014, 80, 4677-4682.	3.1	40
10	Pan-genome analysis of the emerging foodborne pathogen Cronobacter spp. suggests a species-level bidirectional divergence driven by niche adaptation. BMC Genomics, 2013, 14, 366.	2.8	78
11	Rapid Genomic-Scale Analysis of Escherichia coli O104:H4 by Using High-Resolution Alternative Methods to Next-Generation Sequencing. Applied and Environmental Microbiology, 2012, 78, 1601-1605.	3.1	22
12	High Density Microarray Analysis Reveals New Insights into Genetic Footprints of Listeria monocytogenes Strains Involved in Listeriosis Outbreaks. PLoS ONE, 2012, 7, e32896.	2.5	31
13	Investigating the global genomic diversity of Escherichia coli using a multi-genome DNA microarray platform with novel gene prediction strategies. BMC Genomics, 2011, 12, 349.	2.8	47
14	A Microarray Based Approach for the Identification of Common Foodborne Viruses. The Open Virology Journal, 2009, 3, 7-20.	1.8	27
15	Optical maps distinguish individual strains of Escherichia coli O157â€:â€H7. Microbiology (United) Tj ETQq	1 1 9.7843	14 rgBT /Ove
16	Interrogating genomic diversity of E. coli O157:H7 using DNA tiling arrays. Forensic Science International, 2007, 168, 183-199.	2.2	36
17	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	17.5	1,927
18	Self-splicing of a group I intron reveals partitioning of native and misfolded RNA populations in yeast. Rna. 2006, 12, 2149-2159.	3.5	29

SCOTT A JACKSON

#	Article	IF	CITATIONS
19	Exploring Genotypic and Phenotypic Diversity of Microbes Using Microarray Approaches. Toxicology Mechanisms and Methods, 2006, 16, 121-128.	2.7	7
20	Chips and SNPs, Bugs and Thugs: A Molecular Sleuthing Perspective. Journal of Food Protection, 2005, 68, 1271-1284.	1.7	26
21	Molecular applications for identifying microbial pathogens in the post-9/11 era. Expert Review of Molecular Diagnostics, 2005, 5, 431-445.	3.1	27
22	Distribution of rRNA Introns in the Three-dimensional Structure of the Ribosome. Journal of Molecular Biology, 2002, 323, 35-52.	4.2	58