Pallavi Singh

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Variability in the Occupancy of Escherichia coli O157 Integration Sites by Shiga Toxin-Encoding Prophages. Toxins, 2021, 13, 433.	3.4	7
2	Characterizing the Cattle Gut Microbiome in Farms with a High and Low Prevalence of Shiga Toxin Producing Escherichia coli. Microorganisms, 2021, 9, 1737.	3.6	8
3	A Nonhemolytic Group B Streptococcus Strain Exhibits Hypervirulence. Journal of Infectious Diseases, 2018, 217, 983-987.	4.0	18
4	Intestinal Microbial Community Dynamics of White-Tailed Deer (Odocoileus virginianus) in an Agroecosystem. Microbial Ecology, 2017, 74, 496-506.	2.8	37
5	Microbial Ecology: Where are we now?. Postdoc Journal, 2016, 4, 3-17.	0.4	23
6	Antimicrobial Susceptibility Profiles of Human Campylobacter jejuni Isolates and Association with Phylogenetic Lineages. Frontiers in Microbiology, 2016, 7, 589.	3.5	48
7	Factors Associated with Shiga Toxin-Producing Escherichia coli Shedding by Dairy and Beef Cattle. Applied and Environmental Microbiology, 2016, 82, 5049-5056.	3.1	55
8	Draft Genome Sequence of an Invasive Streptococcus agalactiae Isolate Lacking Pigmentation. Genome Announcements, 2016, 4, .	0.8	9
9	Impact of age and sex on the composition and abundance of the intestinal microbiota in individuals with and without enteric infections. Annals of Epidemiology, 2016, 26, 380-385.	1.9	47
10	High prevalence of clade 8 Escherichia coli O157:H7 isolated from retail meat and butcher shop environment. Infection, Genetics and Evolution, 2016, 45, 1-5.	2.3	5
11	Intestinal microbial communities associated with acute enteric infections and disease recovery. Microbiome, 2015, 3, 45.	11.1	151
12	Draft Genome Sequence of a Diarrheagenic Morganella morganii Isolate. Genome Announcements, 2015, 3, .	0.8	3
13	Characterization of enteropathogenic and Shiga toxin-producing Escherichia coli in cattle and deer in a shared agroecosystem. Frontiers in Cellular and Infection Microbiology, 2015, 5, 29.	3.9	43
14	Clade 8 and Clade 6 Strains of Escherichia coli O157:H7 from Cattle in Argentina have Hypervirulent-Like Phenotypes. PLoS ONE, 2015, 10, e0127710.	2.5	39
15	Pilus distribution among lineages of group b streptococcus: an evolutionary and clinical perspective. BMC Microbiology, 2014, 14, 159.	3.3	58
16	Comparative analysis of Campylobacter populations within individual market-age broilers using fla gene typing method. Poultry Science, 2013, 92, 2135-2144.	3.4	9
17	Massively parallel sequencing of enriched target amplicons for high-resolution genotyping of Salmonella serovars. Molecular and Cellular Probes, 2013, 27, 80-85.	2.1	11
18	Influence of penicillin on microbial diversity of the cecal microbiota in broiler chickens. Poultry Science, 2013, 92, 272-276.	3.4	102

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19	Whole-Genome Shotgun Sequencing of a Colonizing Multilocus Sequence Type 17 Streptococcus agalactiae Strain. Journal of Bacteriology, 2012, 194, 6005-6005.	2.2	8
20	Multilocus sequence typing of Salmonella strains by high-throughput sequencing of selectively amplified target genes. Journal of Microbiological Methods, 2012, 88, 127-133.	1.6	17
21	Target-Enrichment Through Amplification of Hairpin-Ligated Universal Targets for Next-Generation Sequencing Analysis. Methods in Molecular Biology, 2011, 733, 267-278.	0.9	2