

# Pragathi Belagola Shridhar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5479314/publications.pdf>

Version: 2024-02-01

27  
papers

361  
citations

933447

10  
h-index

794594

19  
g-index

27  
all docs

27  
docs citations

27  
times ranked

306  
citing authors

#	ARTICLE	IF	CITATIONS
1	Summer and Winter Prevalence of Shiga Toxinâ€“Producing <i>Escherichia coli</i> (STEC) O26, O45, O103, O111, O121, O145, and O157 in Feces of Feedlot Cattle. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 726-732.	1.8	75
2	A Comparison of Culture- and PCR-Based Methods to Detect Six Major Non-O157 Serogroups of Shiga Toxin-Producing <i>Escherichia coli</i> in Cattle Feces. <i>PLoS ONE</i> , 2015, 10, e0135446.	2.5	53
3	Shiga Toxin Subtypes of Non-O157 <i>Escherichia coli</i> Serogroups Isolated from Cattle Feces. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 121.	3.9	38
4	A Four-Plex Real-Time PCR Assay, Based on <i>rfbE</i> , <i>stx1</i> , <i>stx2</i> , and <i>eae</i> Genes, for the Detection and Quantification of Shiga Toxinâ€“Producing <i>Escherichia coli</i> O157 in Cattle Feces. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 787-794.	1.8	29
5	Feedlot- and Pen-Level Prevalence of Enterohemorrhagic <i>Escherichia coli</i> in Feces of Commercial Feedlot Cattle in Two Major U.S. Cattle Feeding Areas. <i>Foodborne Pathogens and Disease</i> , 2017, 14, 309-317.	1.8	23
6	<i>Escherichia coli</i> O104 in Feedlot Cattle Feces: Prevalence, Isolation and Characterization. <i>PLoS ONE</i> , 2016, 11, e0152101.	2.5	22
7	Multiplex PCR Assays for the Detection of One Hundred and Thirty Seven Serogroups of Shiga Toxin-Producing <i>Escherichia coli</i> Associated With Cattle. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 378.	3.9	18
8	Genetic Analysis of Virulence Potential of <i>Escherichia coli</i> O104 Serotypes Isolated From Cattle Feces Using Whole Genome Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 341.	3.5	16
9	Comparative genomics reveals differences in mobile virulence genes of <i>Escherichia coli</i> O103 pathotypes of bovine fecal origin. <i>PLoS ONE</i> , 2018, 13, e0191362.	2.5	15
10	Whole genome sequence analyses-based assessment of virulence potential and antimicrobial susceptibilities and resistance of <i>Enterococcus faecium</i> strains isolated from commercial swine and cattle probiotic products. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	14
11	Pooling of Immunomagnetic Separation Beads Does Not Affect Detection Sensitivity of Six Major Serogroups of Shiga Toxinâ€“Producing <i>Escherichia coli</i> in Cattle Feces. <i>Journal of Food Protection</i> , 2016, 79, 59-65.	1.7	11
12	Quantification of Bacteria Indicative of Fecal and Environmental Contamination from Hides to Carcasses. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 844-855.	1.8	9
13	Identification, Shiga toxin subtypes and prevalence of minor serogroups of Shiga toxin-producing <i>Escherichia coli</i> in feedlot cattle feces. <i>Scientific Reports</i> , 2021, 11, 8601.	3.3	8
14	Detection and Quantification of Seven Major Serogroups of Shiga Toxinâ€“Producing <i>Escherichia coli</i> on Hides of Cull Dairy, Cull Beef, and Fed Beef Cattle at Slaughterâ€“. <i>Journal of Food Protection</i> , 2018, 81, 1236-1244.	1.7	7
15	Analysis of virulence potential of <i>Escherichia coli</i> O145 isolated from cattle feces and hide samples based on whole genome sequencing. <i>PLoS ONE</i> , 2019, 14, e0225057.	2.5	5
16	Associations Between Season, Processing Plant, and Hide Cleanliness Scores with Prevalence and Concentration of Major Shiga Toxinâ€“Producing <i>Escherichia coli</i> on Beef Cattle Hides. <i>Foodborne Pathogens and Disease</i> , 2020, 17, 611-619.	1.8	5
17	Validation and Application of a Real-Time PCR Assay Based on the CRISPR Array for Serotype-Specific Detection and Quantification of Enterohemorrhagic <i>Escherichia coli</i> O157:H7 in Cattle Feces. <i>Journal of Food Protection</i> , 2018, 81, 1157-1164.	1.7	4
18	Bayesian estimation of sensitivity and specificity of culture- and PCR-based methods for the detection of six major non-O157 <i>Escherichia coli</i> serogroups in cattle feces. <i>Preventive Veterinary Medicine</i> , 2018, 161, 90-99.	1.9	4

#	ARTICLE	IF	CITATIONS
19	DNA Microarray-Based Genomic Characterization of the Pathotypes of Escherichia coli O26, O45, O103, O111, and O145 Isolated from Feces of Feedlot Cattle. <i>Journal of Food Protection</i> , 2019, 82, 395-404.	1.7	4
20	Draft Genome Sequences of Salmonella enterica subsp. diarizonae Serotype Illb_61:l,v:1,5,(7) Strains Isolated from Wheat Grains. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
21	Draft Genome Sequences of Enteropathogenic Escherichia coli O103 Strains Isolated from Feces of Feedlot Cattle. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
22	Draft Genome Sequences of Escherichia coli O104 Strains of Bovine and Human Origin. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
23	Draft Genome Sequences of Enterohemorrhagic Escherichia coli O103:H2 Strains Isolated from Feces of Feedlot Cattle. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
24	Title is missing!. , 2019, 14, e0225057.		0
25	Title is missing!. , 2019, 14, e0225057.		0
26	Title is missing!. , 2019, 14, e0225057.		0
27	Title is missing!. , 2019, 14, e0225057.		0