

# Gregory Harhay

## List of Publications by Year in descending order

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53  
papers

2,805  
citations

304743

22  
h-index

175258

52  
g-index

73  
all docs

73  
docs citations

73  
times ranked

4345  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid estimation of <i>Salmonella enterica</i> contamination level in ground beef – Application of the time-to-positivity method using a combination of molecular detection and direct plating. <i>Food Microbiology</i> , 2021, 93, 103615.	4.2	3
2	A Conserved <i>Histophilus somni</i> 23S Intervening Sequence Yields Functional, Fragmented 23S rRNA. <i>Microbiology Spectrum</i> , 2021, 9, e0143121.	3.0	1
3	Complete Genome Sequence of a <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Fresno Isolate Recovered from a Bovine Lymph Node. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
4	A Computational Method to Quantify the Effects of Slipped Strand Mispairing on Bacterial Tetranucleotide Repeats. <i>Scientific Reports</i> , 2019, 9, 18087.	3.3	5
5	Complete Closed Genome Sequences of Three <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Dublin Strains Isolated from Cattle at Harvest. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	2
6	Closed Genome Sequences and Antibigrams of 16 <i>Pasteurella multocida</i> Isolates from Bovine Respiratory Disease Complex Cases and Apparently Healthy Controls. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	2
7	Comparative genomics of <i>Salmonella enterica</i> serovar Montevideo reveals lineage-specific gene differences that may influence ecological niche association. <i>Microbial Genomics</i> , 2018, 4, .	2.0	19
8	Comparison of the diagnostic performance of bacterial culture of nasopharyngeal swab and bronchoalveolar lavage fluid samples obtained from calves with bovine respiratory disease. <i>American Journal of Veterinary Research</i> , 2017, 78, 350-358.	0.6	21
9	Genome Sequence of the Thermotolerant Foodborne Pathogen <i>Salmonella enterica</i> Serovar Senftenberg ATCC 43845 and Phylogenetic Analysis of Loci Encoding Increased Protein Quality Control Mechanisms. <i>MSystems</i> , 2017, 2, .	3.8	25
10	Closed Genome Sequences of Seven <i>Histophilus somni</i> Isolates from Beef Calves with Bovine Respiratory Disease Complex. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
11	Genomic signatures of <i>Mannheimia haemolytica</i> that associate with the lungs of cattle with respiratory disease, an integrative conjugative element, and antibiotic resistance genes. <i>BMC Genomics</i> , 2016, 17, 982.	2.8	46
12	Observations on macrolide resistance and susceptibility testing performance in field isolates collected from clinical bovine respiratory disease cases. <i>Veterinary Microbiology</i> , 2016, 192, 186-193.	1.9	13
13	Resolving <i>Bovine viral diarrhea virus</i> subtypes from persistently infected U.S. beef calves with complete genome sequence. <i>Journal of Veterinary Diagnostic Investigation</i> , 2016, 28, 519-528.	1.1	31
14	Complete, Closed Genome Sequences of 10 <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Typhimurium Strains Isolated from Human and Bovine Sources. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
15	Complete and Closed Genome Sequences of 10 <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Anatum Isolates from Human and Bovine Sources. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
16	Complete Closed Genome Sequences of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotypes Anatum, Montevideo, Typhimurium, and Newport, Isolated from Beef, Cattle, and Humans. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
17	Comparative Methylome Analysis of the Occasional Ruminant Respiratory Pathogen <i>Bibersteinia trehalosi</i> . <i>PLoS ONE</i> , 2016, 11, e0161499.	2.5	6
18	Full-Length Coding Sequences for 12 Bovine Viral Diarrhea Virus Isolates from Persistently Infected Cattle in a Feedyard in Kansas. <i>Genome Announcements</i> , 2015, 3, .	0.8	9

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19	Complete Closed Genome Sequences of a Mannheimia haemolytica Serotype A1 Leukotoxin Deletion Mutant and Its Wild-Type Parent Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
20	Evolutionary characterization of pig interferon-inducible transmembrane gene family and member expression dynamics in tracheobronchial lymph nodes of pigs infected with swine respiratory disease viruses. <i>Veterinary Immunology and Immunopathology</i> , 2014, 159, 180-191.	1.2	19
21	Complete Closed Genome Sequences of Three Bibersteinia trehalosi Nasopharyngeal Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
22	Complete Closed Genome Sequences of Four Mannheimia varigena Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
23	Small ruminant lentivirus genetic subgroups associate with sheep TMEM154 genotypes. <i>Veterinary Research</i> , 2013, 44, 64.	3.0	19
24	Complete Closed Genome Sequences of Mannheimia haemolytica Serotypes A1 and A6, Isolated from Cattle. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
25	Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , 2013, 14, R101.	9.6	378
26	Effects of TMEM154 haplotypes 1 and 3 on susceptibility to ovine progressive pneumonia virus following natural exposure in sheep <sup>1,2,3</sup> . <i>Journal of Animal Science</i> , 2013, 91, 5114-5121.	0.5	27
27	Genetic Testing for TMEM154 Mutations Associated with Lentivirus Susceptibility in Sheep. <i>PLoS ONE</i> , 2013, 8, e55490.	2.5	28
28	Reactomes of Porcine Alveolar Macrophages Infected with Porcine Reproductive and Respiratory Syndrome Virus. <i>PLoS ONE</i> , 2013, 8, e59229.	2.5	33
29	Phylogeny of Shiga Toxin-Producing Escherichia coli O157 Isolated from Cattle and Clinically Ill Humans. <i>Molecular Biology and Evolution</i> , 2012, 29, 2047-2062.	8.9	53
30	Reduced Lentivirus Susceptibility in Sheep with TMEM154 Mutations. <i>PLoS Genetics</i> , 2012, 8, e1002467.	3.5	78
31	Comparison of bacterial communities in faeces of beef cattle fed diets containing corn and wet distillers' grain with solubles. <i>Letters in Applied Microbiology</i> , 2012, 55, 109-114.	2.2	39
32	Next-Generation Sequencing of the Porcine Skeletal Muscle Transcriptome for Computational Prediction of MicroRNA Gene Targets. <i>PLoS ONE</i> , 2012, 7, e42039.	2.5	7
33	Bacterial Community Analysis of Beef Cattle Feedlots Reveals That Pen Surface Is Distinct from Feces. <i>Foodborne Pathogens and Disease</i> , 2011, 8, 647-649.	1.8	23
34	Virulence-associated and antibiotic resistance genes of microbial populations in cattle feces analyzed using a metagenomic approach. <i>Journal of Microbiological Methods</i> , 2011, 84, 278-282.	1.6	103
35	In-Depth Global Analysis of Transcript Abundance Levels in Porcine Alveolar Macrophages Following Infection with Porcine Reproductive and Respiratory Syndrome Virus. <i>Advances in Virology</i> , 2010, 2010, 1-12.	1.1	12
36	Animal-to-Animal Variation in Fecal Microbial Diversity among Beef Cattle. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4858-4862.	3.1	146

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37	An atlas of bovine gene expression reveals novel distinctive tissue characteristics and evidence for improving genome annotation. <i>Genome Biology</i> , 2010, 11, R102.	8.8	46
38	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
39	Prevalence of the prion protein gene E211K variant in U.S. cattle. <i>BMC Veterinary Research</i> , 2008, 4, 25.	1.9	46
40	A sequencing strategy for identifying variation throughout the prion gene of BSE-affected cattle. <i>BMC Research Notes</i> , 2008, 1, 32.	1.4	2
41	Prion gene haplotypes of U.S. cattle. <i>BMC Genetics</i> , 2006, 7, 51.	2.7	36
42	Characterization of 954 bovine full-CDS cDNA sequences. <i>BMC Genomics</i> , 2005, 6, 166.	2.8	26
43	Linkage mapping bovine EST-based SNP. <i>BMC Genomics</i> , 2005, 6, 74.	2.8	58
44	Identification of genetic markers for fat deposition and meat tenderness on bovine chromosome 5: Development of a low-density single nucleotide polymorphism map <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2005, 83, 2280-2288.	0.5	31
45	Use of bovine single nucleotide polymorphism markers to verify sample tracking in beef processing. <i>Journal of the American Veterinary Medical Association</i> , 2005, 226, 1311-1314.	0.5	46
46	Integrating linkage and radiation hybrid mapping data for bovine chromosome 15. <i>BMC Genomics</i> , 2004, 5, 77.	2.8	14
47	Positional candidate gene selection from livestock EST databases using Gene Ontology. <i>Bioinformatics</i> , 2003, 19, 249-255.	4.1	19
48	Weaving a computing fabric. <i>IEEE Internet Computing</i> , 2002, 6, 88-91.	3.3	4
49	Selection and use of SNP markers for animal identification and paternity analysis in U.S. beef cattle. <i>Mammalian Genome</i> , 2002, 13, 272-281.	2.2	199
50	The Effect of Correlation of Inhomogeneous Environmental Shifts on Raman Depolarization Ratio Dispersion. <i>Journal of Physical Chemistry A</i> , 2000, 104, 681-684.	2.5	3
51	HYDROGEN-DEUTERIUM EXCHANGE AND ULTRAVIOLET RESONANCE RAMAN SPECTROSCOPY OF BACTERIA IN A COMPLEX FOOD MATRIX <sup>1</sup> . <i>Journal of Rapid Methods and Automation in Microbiology</i> , 1999, 7, 25-38.	0.4	6
52	Quantitative resonance Raman spectroscopy of N-acetylpyrrolidine in aqueous solution. <i>The Journal of Physical Chemistry</i> , 1993, 97, 8158-8164.	2.9	11
53	Ultraviolet resonance Raman study of proline isomerization. <i>The Journal of Physical Chemistry</i> , 1991, 95, 3511-3513.	2.9	13