

# Tracy L Nicholson

## List of Publications by Year in descending order

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65  
papers

1,823  
citations

257450

24  
h-index

289244

40  
g-index

66  
all docs

66  
docs citations

66  
times ranked

1863  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Stage-Specific Gene Regulation during the Developmental Cycle of <i>Chlamydia trachomatis</i> . <i>Journal of Bacteriology</i> , 2003, 185, 3179-3189.	2.2	192
2	Genomic sequence and virulence comparison of four Type 2 porcine reproductive and respiratory syndrome virus strains. <i>Virus Research</i> , 2012, 169, 212-221.	2.2	128
3	Experimental infection of United States swine with a Chinese highly pathogenic strain of porcine reproductive and respiratory syndrome virus. <i>Virology</i> , 2013, 435, 372-384.	2.4	98
4	Role of fimbriae as antigens and intestinal colonization factors of <i>Salmonella</i> serovars. <i>FEMS Microbiology Letters</i> , 2001, 201, 121-125.	1.8	85
5	Acquisition and loss of virulence-associated factors during genome evolution and speciation in three clades of <i>Bordetella</i> species. <i>BMC Genomics</i> , 2016, 17, 767.	2.8	70
6	Influenza virus coinfection with <i>Bordetella bronchiseptica</i> enhances bacterial colonization and host responses exacerbating pulmonary lesions. <i>Microbial Pathogenesis</i> , 2010, 49, 237-245.	2.9	69
7	Pipeline for amplifying and analyzing amplicons of the V1-V3 region of the 16S rRNA gene. <i>BMC Research Notes</i> , 2016, 9, 380.	1.4	61
8	Contribution of <i>Bordetella bronchiseptica</i> Filamentous Hemagglutinin and Pertactin to Respiratory Disease in Swine. <i>Infection and Immunity</i> , 2009, 77, 2136-2146.	2.2	48
9	Microarray-based genomic surveying of gene polymorphisms in <i>Chlamydia trachomatis</i> . <i>Genome Biology</i> , 2004, 5, R42.	9.6	44
10	Role of the Type III Secretion System in a Hypervirulent Lineage of <i>Bordetella bronchiseptica</i> . <i>Infection and Immunity</i> , 2009, 77, 3969-3977.	2.2	44
11	Replacement of Adenylate Cyclase Toxin in a Lineage of <i>Bordetella bronchiseptica</i> . <i>Journal of Bacteriology</i> , 2008, 190, 5502-5511.	2.2	43
12	Transcriptome Profiling Reveals Stage-Specific Production and Requirement of Flagella during Biofilm Development in <i>Bordetella bronchiseptica</i> . <i>PLoS ONE</i> , 2012, 7, e49166.	2.5	43
13	Virulence, Transmission, and Heterologous Protection of Four Isolates of <i>Haemophilus parasuis</i> . <i>Vaccine Journal</i> , 2013, 20, 1466-1472.	3.1	40
14	Comparative Prevalence of Immune Evasion Complex Genes Associated with $\beta$ -Hemolysin Converting Bacteriophages in MRSA ST5 Isolates from Swine, Swine Facilities, Humans with Swine Contact, and Humans with No Swine Contact. <i>PLoS ONE</i> , 2015, 10, e0142832.	2.5	40
15	Construction and validation of a first-generation <i>Bordetella bronchiseptica</i> long-oligonucleotide microarray by transcriptional profiling the Bvg regulon. <i>BMC Genomics</i> , 2007, 8, 220.	2.8	39
16	The <i>Bordetella bronchiseptica</i> Type III Secretion System Is Required for Persistence and Disease Severity but Not Transmission in Swine. <i>Infection and Immunity</i> , 2014, 82, 1092-1103.	2.2	38
17	Virulence and Draft Genome Sequence Overview of Multiple Strains of the Swine Pathogen <i>Haemophilus parasuis</i> . <i>PLoS ONE</i> , 2014, 9, e103787.	2.5	37
18	The Presence of Alpha Interferon at the Time of Infection Alters the Innate and Adaptive Immune Responses to Porcine Reproductive and Respiratory Syndrome Virus. <i>Vaccine Journal</i> , 2012, 19, 508-514.	3.1	34

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19	Zinc Resistance within Swine-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates in the United States Is Associated with Multilocus Sequence Type Lineage. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	33
20	Characterization and Comparative Analysis of the Genes Encoding <i>Haemophilus parasuis</i> Outer Membrane Proteins P2 and P5. <i>Journal of Bacteriology</i> , 2009, 191, 5988-6002.	2.2	32
21	<i>Bordetella pertussis</i> transmission: Graphical Abstract Figure.. <i>Pathogens and Disease</i> , 2015, 73, ftv068.	2.0	32
22	Identification of a CO2 Responsive Regulon in <i>Bordetella</i> . <i>PLoS ONE</i> , 2012, 7, e47635.	2.5	31
23	<i>Chlamydia trachomatis</i> Lacks an Adaptive Response to Changes in Carbon Source Availability. <i>Infection and Immunity</i> , 2004, 72, 4286-4289.	2.2	28
24	Microarray and Functional Analysis of Growth Phase-Dependent Gene Regulation in <i>Bordetella bronchiseptica</i> . <i>Infection and Immunity</i> , 2009, 77, 4221-4231.	2.2	28
25	Single Nucleotide Polymorphism Analysis Indicates Genetic Distinction and Reduced Diversity of Swine-Associated Methicillin Resistant <i>Staphylococcus aureus</i> (MRSA) ST5 Isolates Compared to Clinical MRSA ST5 Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 2078.	3.5	28
26	Phenotypic Modulation of the Virulent Bvg Phase Is Not Required for Pathogenesis and Transmission of <i>Bordetella bronchiseptica</i> in Swine. <i>Infection and Immunity</i> , 2012, 80, 1025-1036.	2.2	26
27	Comparative Analyses of a Cystic Fibrosis Isolate of <i>Bordetella bronchiseptica</i> Reveal Differences in Important Pathogenic Phenotypes. <i>Infection and Immunity</i> , 2014, 82, 1627-1637.	2.2	26
28	<i>Salmonella enterica</i> Serotype Typhimurium Elicits Cross-Immunity against a <i>Salmonella enterica</i> Serotype Enteritidis Strain Expressing LP Fimbriae from the lac Promoter. <i>Infection and Immunity</i> , 2001, 69, 204-212.	2.2	25
29	Comparison of Asian porcine high fever disease isolates of porcine reproductive and respiratory syndrome virus to United States isolates for their ability to cause disease and secondary bacterial infection in swine. <i>Veterinary Microbiology</i> , 2017, 203, 6-17.	1.9	25
30	Subinhibitory Concentrations of Amoxicillin, Lincomycin, and Oxytetracycline Commonly Used to Treat Swine Increase <i>Streptococcus suis</i> Biofilm Formation. <i>Frontiers in Microbiology</i> , 2018, 9, 2707.	3.5	25
31	Misidentification of <i>Bordetella bronchiseptica</i> as <i>Bordetella pertussis</i> using a newly described real-time PCR targeting the pertactin gene. <i>Journal of Medical Microbiology</i> , 2007, 56, 1608-1610.	1.8	21
32	Utility of a Panviral Microarray for Detection of Swine Respiratory Viruses in Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1542-1548.	3.9	21
33	Interferon alpha inhibits replication of a live-attenuated porcine reproductive and respiratory syndrome virus vaccine preventing development of an adaptive immune response in swine. <i>Veterinary Microbiology</i> , 2017, 212, 48-51.	1.9	21
34	Evidence for Horizontal Gene Transfer of Two Antigenically Distinct O Antigens in <i>Bordetella bronchiseptica</i> . <i>Infection and Immunity</i> , 2009, 77, 3249-3257.	2.2	20
35	Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> (LA-MRSA) Isolates of Swine Origin Form Robust Biofilms. <i>PLoS ONE</i> , 2013, 8, e73376.	2.5	20
36	Draft Genome Sequences of 63 Swine-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 5 Isolates from the United States. <i>Genome Announcements</i> , 2017, 5, .	0.8	19

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37	Blood or Serum Exposure Induce Global Transcriptional Changes, Altered Antigenic Profile, and Increased Cytotoxicity by Classical <i>Bordetellae</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1969.	3.5	17
38	Use of Proteins Identified through a Functional Genomic Screen To Develop a Protein Subunit Vaccine That Provides Significant Protection against Virulent <i>Streptococcus suis</i> in Pigs. <i>Infection and Immunity</i> , 2018, 86, .	2.2	16
39	Draft Genome Sequences of 14 <i>Staphylococcus aureus</i> Sequence Type 5 Isolates from California, USA. <i>Genome Announcements</i> , 2017, 5, .	0.8	14
40	Antimicrobial Resistance Distribution Differs Among Methicillin Resistant <i>Staphylococcus aureus</i> Sequence Type (ST) 5 Isolates From Health Care and Agricultural Sources. <i>Frontiers in Microbiology</i> , 2018, 9, 2102.	3.5	13
41	Draft Genome Sequences of One Methicillin-Sensitive and Seven Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 5 Isolates Obtained in California. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
42	Draft Genome Sequences of 50 Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 5 Isolates Obtained from a U.S. Hospital. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
43	Draft Genome Sequences of Nine Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 5 Isolates from Humans with Long-Term Swine Contact. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
44	Draft Genome Sequences of Nine Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 5 Isolates Obtained from Humans after Short-Term Swine Contact. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
45	The <i>Bordetella</i> Bps Polysaccharide Is Required for Biofilm Formation and Enhances Survival in the Lower Respiratory Tract of Swine. <i>Infection and Immunity</i> , 2017, 85, .	2.2	11
46	Comparison of Adjuvanted-Whole Inactivated Virus and Live-Attenuated Virus Vaccines against Challenge with Contemporary, Antigenically Distinct H3N2 Influenza A Viruses. <i>Journal of Virology</i> , 2018, 92, .	3.4	11
47	Comparative Virulence and Genomic Analysis of <i>Streptococcus suis</i> Isolates. <i>Frontiers in Microbiology</i> , 2020, 11, 620843.	3.5	11
48	Evaluation of Specificity of BP3385 for <i>Bordetella pertussis</i> Detection. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3334-3337.	3.9	10
49	Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type (ST) 5 Isolates from Health Care and Agricultural Sources Adhere Equivalently to Human Keratinocytes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	9
50	Draft Genome Sequence of the <i>Bordetella bronchiseptica</i> Swine Isolate KM22. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
51	Draft Genome Sequences of Nine <i>Streptococcus suis</i> Strains Isolated in the United States. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
52	Comparative genomic and methylome analysis of non-virulent D74 and virulent Nagasaki <i>Haemophilus parasuis</i> isolates. <i>PLoS ONE</i> , 2018, 13, e0205700.	2.5	6
53	Evaluation of the recombinant proteins RlpB and VacJ as a vaccine for protection against <i>Glaesserella parasuis</i> in pigs. <i>BMC Veterinary Research</i> , 2020, 16, 167.	1.9	5
54	Comparative genomic analysis of the swine pathogen <i>Bordetella bronchiseptica</i> strain KM22. <i>Veterinary Microbiology</i> , 2016, 182, 87-94.	1.9	4

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55	Complete Genome Sequence of <i>Bordetella bronchiseptica</i> Strain KM22. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
56	Porcine TLR3 characterization and expression in response to influenza virus and <i>Bordetella bronchiseptica</i> . <i>Veterinary Immunology and Immunopathology</i> , 2011, 142, 57-63.	1.2	3
57	Complete Genome Sequence of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398 Isolated from Swine in the United States. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
58	Complete Genome Sequence of a Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 5 Isolate from the United States. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
59	Editorial: Spotting the Future. <i>Sexually Transmitted Diseases</i> , 2002, 29, 789-791.	1.7	1
60	Comparison of ribotyping and sequence-based typing for discriminating among isolates of <i>Bordetella bronchiseptica</i> . <i>Journal of Microbiological Methods</i> , 2016, 129, 117-126.	1.6	1
61	Complete Genome Sequences of Two <i>Staphylococcus aureus</i> Sequence Type 5 Isolates from California, USA. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
62	Draft Genome Sequences of 14 Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398 Isolates from Swine Farms in the United States. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
63	Complete Genome Sequence of <i>Escherichia coli</i> Antibiotic-Resistant Isolate AR Bank #0349. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
64	Complete Genome Sequence of <i>Escherichia coli</i> Antibiotic Resistance Isolate Bank Number 0346. <i>Microbiology Resource Announcements</i> , 2021, 10, e0030521.	0.6	0
65	Microarray-Based Approach for Genome-Wide Survey of Nucleotide Polymorphisms. <i>Methods in Molecular Biology</i> , 2007, 396, 267-279.	0.9	0