

Ganwu Li

List of Publications by Year in descending order

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304368

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times ranked

2344
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#	ARTICLE	IF	CITATIONS
1	Avian pathogenic, uropathogenic, and newborn meningitis-causing <i>Escherichia coli</i> : How closely related are they?. <i>International Journal of Medical Microbiology</i> , 2007, 297, 163-176.	1.5	449
2	Avian-Pathogenic <i>Escherichia coli</i> Strains Are Similar to Neonatal Meningitis <i>E. coli</i> Strains and Are Able To Cause Meningitis in the Rat Model of Human Disease. <i>Infection and Immunity</i> , 2010, 78, 3412-3419.	1.0	172
3	Identification of Genes Required for Avian <i>Escherichia coli</i> Septicemia by Signature-Tagged Mutagenesis. <i>Infection and Immunity</i> , 2005, 73, 2818-2827.	1.0	112
4	Full-Length Genome Sequence of Porcine Deltacoronavirus Strain USA/IA/2014/8734. <i>Genome Announcements</i> , 2014, 2, .	0.8	104
5	Pathogenesis comparison between the United States porcine epidemic diarrhoea virus prototype and S-INDEL-variant strains in conventional neonatal piglets. <i>Journal of General Virology</i> , 2016, 97, 1107-1121.	1.3	78
6	A Novel Two-Component Signaling System Facilitates Uropathogenic <i>Escherichia coli</i> 's Ability to Exploit Abundant Host Metabolites. <i>PLoS Pathogens</i> , 2013, 9, e1003428.	2.1	71
7	High-throughput whole genome sequencing of <i>Porcine reproductive and respiratory syndrome virus</i> from cell culture materials and clinical specimens using next-generation sequencing technology. <i>Journal of Veterinary Diagnostic Investigation</i> , 2017, 29, 41-50.	0.5	70
8	Phylogenetics, Genomic Recombination, and NSP2 Polymorphic Patterns of Porcine Reproductive and Respiratory Syndrome Virus in China and the United States in 2014–2018. <i>Journal of Virology</i> , 2020, 94, .	1.5	69
9	Metagenomic analysis of the RNA fraction of the fecal virome indicates high diversity in pigs infected by porcine endemic diarrhea virus in the United States. <i>Virology Journal</i> , 2018, 15, 95.	1.4	57
10	FNR Regulates Expression of Important Virulence Factors Contributing to Pathogenicity of Uropathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2014, 82, 5086-5098.	1.0	51
11	Transcriptome Analysis of Avian Pathogenic <i>Escherichia coli</i> O1 in Chicken Serum Reveals Adaptive Responses to Systemic Infection. <i>Infection and Immunity</i> , 2011, 79, 1951-1960.	1.0	47
12	Isolation of PCV3 from Perinatal and Reproductive Cases of PCV3-Associated Disease and In Vivo Characterization of PCV3 Replication in CD/CD Growing Pigs. <i>Viruses</i> , 2020, 12, 219.	1.5	46
13	Recombination between Vaccine and Field Strains of Porcine Reproductive and Respiratory Syndrome Virus. <i>Emerging Infectious Diseases</i> , 2019, 25, 2335-2337.	2.0	42
14	ArcA Controls Metabolism, Chemotaxis, and Motility Contributing to the Pathogenicity of Avian Pathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2015, 83, 3545-3554.	1.0	41
15	AatA Is a Novel Autotransporter and Virulence Factor of Avian Pathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2010, 78, 898-906.	1.0	40
16	Detection of live attenuated influenza vaccine virus and evidence of reassortment in the U.S. swine population. <i>Journal of Veterinary Diagnostic Investigation</i> , 2020, 32, 301-311.	0.5	39
17	Full-Length Genome Sequences of Senecavirus A from Recent Idiopathic Vesicular Disease Outbreaks in U.S. Swine. <i>Genome Announcements</i> , 2015, 3, .	0.8	37
18	The emergence of novel sparrow deltacoronaviruses in the United States more closely related to porcine deltacoronaviruses than sparrow deltacoronavirus HKU17. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-4.	3.0	33

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19	Evaluation of serological cross-reactivity and cross-neutralization between the United States porcine epidemic diarrhea virus prototype and S-INDEL-variant strains. <i>BMC Veterinary Research</i> , 2016, 12, 70.	0.7	31
20	Characterization of a yjjQ mutant of avian pathogenic <i>Escherichia coli</i> (APEC). <i>Microbiology (United Kingdom)</i> , 2016, 156, 1000-1007.	0.7	30
21	Genetic characterization of <i>Streptococcus equi</i> subspecies <i>zooepidemicus</i> associated with high swine mortality in the United States. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2797-2808.	1.3	28
22	Genotypes and Antimicrobial Susceptibility Profiles of Hemolytic <i>Escherichia coli</i> from Diarrheic Piglets. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 94-103.	0.8	24
23	Detection, isolation, and in vitro characterization of porcine parainfluenza virus type 1 isolated from respiratory diagnostic specimens in swine. <i>Veterinary Microbiology</i> , 2019, 228, 219-225.	0.8	23
24	Extraintestinal pathogenic <i>Escherichia coli</i> increase extracytoplasmic polysaccharide biosynthesis for serum resistance in response to bloodstream signals. <i>Molecular Microbiology</i> , 2018, 110, 689-706.	1.2	21
25	Role of enterotoxigenic <i>Escherichia coli</i> prophage in spreading antibiotic resistance in a porcine-derived environment. <i>Environmental Microbiology</i> , 2020, 22, 4974-4984.	1.8	21
26	Complete Genome Sequences of Two Novel Human-Like H3N2 Influenza A Viruses, A/Swine/Oklahoma/65980/2017 (H3N2) and A/Swine/Oklahoma/65260/2017 (H3N2), Detected in Swine in the United States. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	20
27	Proteome response of an extraintestinal pathogenic <i>Escherichia coli</i> strain with zoonotic potential to human and chicken sera. <i>Journal of Proteomics</i> , 2012, 75, 4853-4862.	1.2	19
28	Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. <i>Veterinary Microbiology</i> , 2017, 207, 267-279.	0.8	17
29	Complete Coding Genome Sequence of a Novel Porcine Reproductive and Respiratory Syndrome Virus 2 Restriction Fragment Length Polymorphism 1-4-4 Lineage 1C Variant Identified in Iowa, USA. <i>Microbiology Resource Announcements</i> , 2021, 10, e0044821.	0.3	16
30	Genome Sequence of Chinese Porcine Parvovirus Strain PPV2010. <i>Journal of Virology</i> , 2012, 86, 2379-2379.	1.5	15
31	FNR Regulates the Expression of Important Virulence Factors Contributing to the Pathogenicity of Avian Pathogenic <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 265.	1.8	14
32	Identification of porcine epidemic diarrhea virus variant with a large spike gene deletion from a clinical swine sample in the United States. <i>Virus Genes</i> , 2018, 54, 323-327.	0.7	14
33	O-specific polysaccharide confers lysozyme resistance to extraintestinal pathogenic <i>Escherichia coli</i> . <i>Virulence</i> , 2018, 9, 666-680.	1.8	14
34	Genetically divergent porcine sapovirus identified in pigs, United States. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 18-28.	1.3	14
35	Cases of high mortality in cull sows and feeder pigs associated with <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> septicemia. <i>Journal of Veterinary Diagnostic Investigation</i> , 2020, 32, 565-571.	0.5	14
36	Identification of a Ruminant Origin Group B Rotavirus Associated with Diarrhea Outbreaks in Foals. <i>Viruses</i> , 2021, 13, 1330.	1.5	14

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37	Genetic Characterization of ExPEC-Like Virulence Plasmids among a Subset of NMEC. <i>PLoS ONE</i> , 2016, 11, e0147757.	1.1	14
38	Novel Avian Pathogenic <i>Escherichia coli</i> Genes Responsible for Adhesion to Chicken and Human Cell Lines. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	13
39	Whole-genome analysis of <i>Klebsiella pneumoniae</i> from bovine mastitis milk in the U.S.. <i>Environmental Microbiology</i> , 2022, 24, 1183-1199.	1.8	13
40	Complete Genome Sequence of Porcine Sapelovirus Strain USA/IA33375/2015 Identified in the United States. <i>Genome Announcements</i> , 2016, 4, .	0.8	12
41	Identification of Host Adaptation Genes in Extraintestinal Pathogenic <i>Escherichia coli</i> during Infection in Different Hosts. <i>Infection and Immunity</i> , 2019, 87, .	1.0	12
42	GroEL Protein (Heat Shock Protein 60) of <i>Mycoplasma gallisepticum</i> Induces Apoptosis in Host Cells by Interacting with Annexin A2. <i>Infection and Immunity</i> , 2019, 87, .	1.0	12
43	A previously uncharacterized two-component signaling system in uropathogenic <i>Escherichia coli</i> coordinates protection against host-derived oxidative stress with activation of hemolysin-mediated host cell pyroptosis. <i>PLoS Pathogens</i> , 2021, 17, e1010005.	2.1	12
44	A novel small RNA Bmsr1 enhances virulence in <i>Brucella melitensis</i> M28. <i>Veterinary Microbiology</i> , 2018, 223, 1-8.	0.8	11
45	Genetic diversity of porcine reproductive and respiratory syndrome virus 1 in the United States of America from 2010 to 2018. <i>Veterinary Microbiology</i> , 2019, 239, 108486.	0.8	11
46	Detection and genetic characterization of porcine pegivirus in pigs in the United States. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 618-626.	1.3	10
47	Detection and genomic characterization of new avian-like hepatitis E virus in a sparrow in the United States. <i>Archives of Virology</i> , 2018, 163, 2861-2864.	0.9	10
48	Uropathogenic <i>Escherichia coli</i> preferentially utilize metabolites in urine for nucleotide biosynthesis through salvage pathways. <i>International Journal of Medical Microbiology</i> , 2018, 308, 990-999.	1.5	10
49	Novel siadenovirus infection in a cockatiel with chronic liver disease. <i>Virus Research</i> , 2019, 263, 164-168.	1.1	10
50	Transcriptomic profile analysis of brain inferior colliculus following acute hydrogen sulfide exposure. <i>Toxicology</i> , 2020, 430, 152345.	2.0	10
51	The Twin-Arginine Translocation System Is Important for Stress Resistance and Virulence of <i>Brucella melitensis</i> . <i>Infection and Immunity</i> , 2020, 88, .	1.0	10
52	<i>Streptococcus suis</i> Serotype 2 Infection Causes Host Immunomodulation through Induction of Thymic Atrophy. <i>Infection and Immunity</i> , 2020, 88, .	1.0	10
53	Whole genome sequencing analysis of avian pathogenic <i>Escherichia coli</i> from China. <i>Veterinary Microbiology</i> , 2021, 259, 109158.	0.8	10
54	tkt1, located on a novel pathogenicity island, is prevalent in avian and human extraintestinal pathogenic <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2012, 12, 51.	1.3	8

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55	Complete Genome Sequence of the Neonatal Meningitis-Causing <i>Escherichia coli</i> Strain NMEC O18. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
56	Complete Genome Sequence of <i>Porcine respirovirus 1</i> Strain USA/MN2589ONS/2016, Isolated in the United States. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
57	<i>Mycoplasma hyopneumoniae</i> Inhibits Porcine Beta-Defensin 2 Production by Blocking the Unfolded Protein Response To Facilitate Epithelial Adhesion and Infection. <i>Infection and Immunity</i> , 2020, 88, .	1.0	8
58	An Extracytoplasmic Function Sigma/Anti-Sigma Factor System Regulates Hypochlorous Acid Resistance and Impacts Expression of the Type IV Secretion System in <i>Brucella melitensis</i> . <i>Journal of Bacteriology</i> , 2021, 203, e0012721.	1.0	8
59	Monoclonal antibodies against Stx1B subunit of <i>Escherichia coli</i> O157:H7 distinguish the bacterium from other bacteria. <i>Letters in Applied Microbiology</i> , 2010, 51, 499-503.	1.0	7
60	Cyclooxygenase-2 Inhibition Reduces Autophagy of Macrophages Enhancing Extraintestinal Pathogenic <i>Escherichia coli</i> Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 708.	1.5	7
61	Characterization of Shiga toxin-producing <i>Escherichia coli</i> isolated from Cattle and Sheep in Xinjiang province, China, using whole-genome sequencing. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 413-422.	1.3	7
62	Response characteristics of nirS-type denitrifier <i>Paracoccus denitrificans</i> under florfenicol stress. <i>Ecotoxicology and Environmental Safety</i> , 2021, 219, 112355.	2.9	7
63	Origin and Dissemination of Antimicrobial Resistance among Uropathogenic <i>Escherichia coli</i> . <i>Microbiology Spectrum</i> , 2015, 3, .	1.2	6
64	Intrahost Selection Pressure Drives Equine Arteritis Virus Evolution during Persistent Infection in the Stallion Reproductive Tract. <i>Journal of Virology</i> , 2019, 93, .	1.5	6
65	Silibinin attenuates <i>Streptococcus suis</i> serotype 2 virulence by targeting suilysin. <i>Journal of Applied Microbiology</i> , 2019, 126, 435-442.	1.4	6
66	Citrate utilization under anaerobic environment in <i>Escherichia coli</i> is under direct control of Fnr and indirect control of ArcA and Fnr via CitA-CitB system. <i>Environmental Microbiology</i> , 2021, 23, 1496-1509.	1.8	6
67	Implementing a user-friendly format to analyze PRRSV next-generation sequencing results and associating breeding herd production performance with number of PRRSV strains and recombination events. <i>Transboundary and Emerging Diseases</i> , 2022, .	1.3	6
68	Complete Genome Sequence of the Avian-Pathogenic <i>Escherichia coli</i> Strain APEC O18. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
69	Development of a triplex real-time RT-PCR assay for detection and differentiation of three US genotypes of porcine hemagglutinating encephalomyelitis virus. <i>Journal of Virological Methods</i> , 2019, 269, 13-17.	1.0	5
70	Characterization of a 2016-2017 Human Seasonal H3 Influenza A Virus Spillover Now Endemic to U.S. Swine. <i>MSphere</i> , 2022, 7, e0080921.	1.3	5
71	Genomic Analysis of <i>Escherichia coli</i> Longitudinally Isolated from Broiler Breeder Flocks after the Application of an Autogenous Vaccine. <i>Microorganisms</i> , 2022, 10, 377.	1.6	5
72	Molecular Characterization of the Major Open Reading Frames (ORFs) and Enhancer Elements From Four Geographically Distinct North American Equine Infectious Anemia Virus (EIAV) Isolates. <i>Journal of Equine Veterinary Science</i> , 2020, 85, 102852.	0.4	4

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73	Genetic characterization of porcine sapoviruses identified from pigs during a diarrhoea outbreak in Iowa, 2019. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 1246-1255.	1.3	4
74	High Genetic Diversity of Porcine Sapovirus From Diarrheic Piglets in Yunnan Province, China. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
75	Complete Genome Sequence of Noncytopathic Bovine Viral Diarrhea Virus 1 Contaminating a High-Passage RK-13 Cell Line. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
76	Characterization of PRRSV in clinical samples and the corresponding cell culture isolates. <i>Transboundary and Emerging Diseases</i> , 0, , .	1.3	3
77	Genomic Sequence of a Swine Pasivirus Type 1 Strain Identified in U.S. Swine. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
78	Interâ€šerotype reassortment among epizootic haemorrhagic disease viruses in the United States. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 1809-1820.	1.3	2
79	Proteomics Investigation of the Time Course Responses of RAW264.7 Macrophages to Infections With the Wild-Type and Twin-Arginine Translocation Mutant Strains of <i>Brucella melitensis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 679571.	1.8	2
80	Comparison of Antimicrobial Resistance Profiles in <i>Salmonella</i> spp. from Swine Upon Arrival and Postslaughter at the Abattoir. <i>Microbial Drug Resistance</i> , 2021, 27, 1144-1154.	0.9	2
81	MDA5 attenuate autophagy in chicken embryo fibroblasts infected with IBDV. <i>British Poultry Science</i> , 2022, 63, 154-163.	0.8	2
82	Case Report and Genomic Characterization of a Novel Porcine Nodavirus in the United States. <i>Viruses</i> , 2021, 13, 73.	1.5	2
83	<i>Salmonella enterica</i> serovar Brandenburg abortions in dairy cattle. <i>Journal of Veterinary Diagnostic Investigation</i> , 2022, 34, 864-869.	0.5	2
84	Origin and Dissemination of Antimicrobial Resistance among Uropathogenic<i> Escherichia coli</i>. , 0, , 179-205.		1
85	Genomic Sequence of a Megrivirus Strain Identified in Laying Hens in Brazil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
86	Bis â€šmolybdopterin guanine dinucleotide modulates hemolysin expression under anaerobiosis and contributes to fitness in vivo in uropathogenic <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2021, 116, 1216-1231.	1.2	1
87	Transcriptomic and Metabolomic Profiling Reveals That KguR Broadly Impacts the Physiology of Uropathogenic <i>Escherichia coli</i> Under in vivo Relevant Conditions. <i>Frontiers in Microbiology</i> , 2021, 12, 793391.	1.5	1
88	Mode of action and structural modelling of the interaction of formononetin with suilysin. <i>Journal of Applied Microbiology</i> , 2021, 131, 2010-2018.	1.4	0
89	Near-Complete Genome Sequence of GI-17 Lineage Infectious Bronchitis Virus, Circulating in Iowa. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0