

Robert W Li

List of Publications by Year in descending order

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97
papers

3,503
citations

126708

33
h-index

155451

55
g-index

99
all docs

99
docs citations

99
times ranked

4500
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of the rumen microbiota of pre-ruminant calves using metagenomic tools. <i>Environmental Microbiology</i> , 2012, 14, 129-139.	1.8	311
2	Alterations in the Porcine Colon Microbiota Induced by the Gastrointestinal Nematode <i>Trichuris suis</i> . <i>Infection and Immunity</i> , 2012, 80, 2150-2157.	1.0	208
3	Worm Burden-Dependent Disruption of the Porcine Colon Microbiota by <i>Trichuris suis</i> Infection. <i>PLoS ONE</i> , 2012, 7, e35470.	1.1	138
4	The effect of helminth infection on the microbial composition and structure of the caprine abomasal microbiome. <i>Scientific Reports</i> , 2016, 6, 20606.	1.6	129
5	Gene expression in bovine rumen epithelium during weaning identifies molecular regulators of rumen development and growth. <i>Functional and Integrative Genomics</i> , 2013, 13, 133-142.	1.4	118
6	Perturbation Dynamics of the Rumen Microbiota in Response to Exogenous Butyrate. <i>PLoS ONE</i> , 2012, 7, e29392.	1.1	103
7	Butyrate induces profound changes in gene expression related to multiple signal pathways in bovine kidney epithelial cells. <i>BMC Genomics</i> , 2006, 7, 234.	1.2	91
8	The Bacterial Community Composition of the Bovine Rumen Detected Using Pyrosequencing of 16S rRNA Genes. <i>Metagenomics (Cairo, Egypt)</i> , 2012, 1, 1-11.	1.2	91
9	A Previously Uncharacterized, Nonphotosynthetic Member of the Chromatiaceae Is the Primary CO ₂ -Fixing Constituent in a Self-Regenerating Biocathode. <i>Applied and Environmental Microbiology</i> , 2015, 81, 699-712.	1.4	89
10	Mastitis associated transcriptomic disruptions in cattle. <i>Veterinary Immunology and Immunopathology</i> , 2010, 138, 267-279.	0.5	79
11	The valproic acid rat model of autism presents with gut bacterial dysbiosis similar to that in human autism. <i>Molecular Autism</i> , 2018, 9, 61.	2.6	74
12	Metagenome Plasticity of the Bovine Abomasal Microbiota in Immune Animals in Response to <i>Ostertagia Ostertagi</i> Infection. <i>PLoS ONE</i> , 2011, 6, e24417.	1.1	71
13	Possible mechanisms of host resistance to <i>Haemonchus contortus</i> infection in sheep breeds native to the Canary Islands. <i>Scientific Reports</i> , 2016, 6, 26200.	1.6	70
14	Mechanistic insights into the attenuation of intestinal inflammation and modulation of the gut microbiome by krill oil using in vitro and in vivo models. <i>Microbiome</i> , 2020, 8, 83.	4.9	70
15	Suppression of Aflatoxin Biosynthesis in <i>Aspergillus flavus</i> by 2-Phenylethanol Is Associated with Stimulated Growth and Decreased Degradation of Branched-Chain Amino Acids. <i>Toxins</i> , 2015, 7, 3887-3902.	1.5	69
16	Characterization of the abomasal transcriptome for mechanisms of resistance to gastrointestinal nematodes in cattle. <i>Veterinary Research</i> , 2011, 42, 114.	1.1	66
17	Integrated metagenomic and metaproteomic analyses of marine biofilm communities. <i>Biofouling</i> , 2014, 30, 1211-1223.	0.8	66
18	Neogargarotetraose protects mice against intense exercise-induced fatigue damage by modulating gut microbial composition and function. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1600585.	1.5	63

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19	Lowbush Wild Blueberries have the Potential to Modify Gut Microbiota and Xenobiotic Metabolism in the Rat Colon. <i>PLoS ONE</i> , 2013, 8, e67497.	1.1	63
20	Identification of estrogen-responsive genes in the parenchyma and fat pad of the bovine mammary gland by microarray analysis. <i>Physiological Genomics</i> , 2006, 27, 42-53.	1.0	61
21	Pathway analysis identifies perturbation of genetic networks induced by butyrate in a bovine kidney epithelial cell line. <i>Functional and Integrative Genomics</i> , 2007, 7, 193-205.	1.4	58
22	Genome-wide ChIP-seq mapping and analysis reveal butyrate-induced acetylation of H3K9 and H3K27 correlated with transcription activity in bovine cells. <i>Functional and Integrative Genomics</i> , 2012, 12, 119-130.	1.4	55
23	Genome wide analysis of the bovine mucin genes and their gastrointestinal transcription profile. <i>BMC Genomics</i> , 2011, 12, 140.	1.2	54
24	Chondroitin sulfate disaccharides modified the structure and function of the murine gut microbiome under healthy and stressed conditions. <i>Scientific Reports</i> , 2017, 7, 6783.	1.6	52
25	Quantification of Transcriptome Responses of the Rumen Epithelium to Butyrate Infusion using RNA-seq Technology. <i>Gene Regulation and Systems Biology</i> , 2012, 6, GRSB.S9687.	2.3	51
26	Infection with the gastrointestinal nematode <i>Ostertagia ostertagi</i> in cattle affects mucus biosynthesis in the abomasum. <i>Veterinary Research</i> , 2011, 42, 61.	1.1	49
27	Identification of <i>bla</i> _{OXA-51-like} , <i>bla</i> _{OXA-58} , <i>bla</i> _{DIM-1} , and <i>bla</i> _{VIM} Carbapenemase Genes in Hospital Enterobacteriaceae Isolates from Sierra Leone. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2435-2438.	1.8	47
28	Food-grade carrageenans and their implications in health and disease. <i>Comprehensive Reviews in Food Science and Food Safety</i> , 2021, 20, 3918-3936.	5.9	46
29	Transcriptome Characterization by RNA-seq Unravels the Mechanisms of Butyrate-Induced Epigenomic Regulation in Bovine Cells. <i>PLoS ONE</i> , 2012, 7, e36940.	1.1	44
30	Local inflammation as a possible mechanism of resistance to gastrointestinal nematodes in Angus heifers. <i>Veterinary Parasitology</i> , 2007, 145, 100-107.	0.7	42
31	A temporal shift in regulatory networks and pathways in the bovine small intestine during <i>Cooperia oncophora</i> infection. <i>International Journal for Parasitology</i> , 2009, 39, 813-824.	1.3	40
32	Transcriptome analysis revealed anti-obesity effects of the Sodium Alginate in high-fat diet -induced obese mice. <i>International Journal of Biological Macromolecules</i> , 2018, 115, 861-870.	3.6	39
33	Canonical pathways and networks regulated by estrogen in the bovine mammary gland. <i>Functional and Integrative Genomics</i> , 2008, 8, 55-68.	1.4	36
34	Polymannuronic acid prevents dopaminergic neuronal loss via brain-gut-microbiota axis in Parkinson's disease model. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 994-1005.	3.6	34
35	Inhibition of Tumor Growth by Dietary Indole-3-Carbinol in a Prostate Cancer Xenograft Model May Be Associated with Disrupted Gut Microbial Interactions. <i>Nutrients</i> , 2019, 11, 467.	1.7	33
36	Astaxanthin n-Octanoic Acid Diester Ameliorates Insulin Resistance and Modulates Gut Microbiota in High-Fat and High-Sucrose Diet-Fed Mice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2149.	1.8	33

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37	Method Development for Metaproteomic Analyses of Marine Biofilms. <i>Analytical Chemistry</i> , 2012, 84, 4006-4013.	3.2	32
38	Transcriptome analysis unraveled potential mechanisms of resistance to <i>Haemonchus contortus</i> infection in Merino sheep populations bred for parasite resistance. <i>Veterinary Research</i> , 2019, 50, 7.	1.1	28
39	<i>Ascaris suum</i> infection was associated with a worm-independent reduction in microbial diversity and altered metabolic potential in the porcine gut microbiome. <i>International Journal for Parasitology</i> , 2019, 49, 247-256.	1.3	27
40	Cytoskeleton remodeling and alterations in smooth muscle contractility in the bovine jejunum during nematode infection. <i>Functional and Integrative Genomics</i> , 2012, 12, 35-44.	1.4	26
41	Mucin biosynthesis in the bovine goblet cell induced by <i>Cooperia oncophora</i> infection. <i>Veterinary Parasitology</i> , 2009, 165, 281-289.	0.7	25
42	<i>Aspergillus flavus</i> aswA, a gene homolog of <i>Aspergillus nidulans</i> oefC, regulates sclerotial development and biosynthesis of sclerotium-associated secondary metabolites. <i>Fungal Genetics and Biology</i> , 2017, 104, 29-37.	0.9	23
43	Interleukin-17 receptor A (IL-17RA) as a central regulator of the protective immune response against <i>Giardia</i> . <i>Scientific Reports</i> , 2017, 7, 8520.	1.6	23
44	Transcriptomic Analysis of Persistent Infection with Foot-and-Mouth Disease Virus in Cattle Suggests Impairment of Apoptosis and Cell-Mediated Immunity in the Nasopharynx. <i>PLoS ONE</i> , 2016, 11, e0162750.	1.1	23
45	Malvidin 3- β -Glucoside Modulated Gut Microbial Dysbiosis and Global Metabolome Disrupted in a Murine Colitis Model Induced by Dextran Sulfate Sodium. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1900455.	1.5	21
46	Effects of <i>Eimeria maxima</i> and <i>Clostridium perfringens</i> infections on cecal microbial composition and the possible correlation with body weight gain in broiler chickens. <i>Research in Veterinary Science</i> , 2020, 132, 142-149.	0.9	21
47	Effects of Differences in Resistant Starch Content of Rice on Intestinal Microbial Composition. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 8017-8027.	2.4	21
48	Microarray Analysis of the Intestinal Host Response in <i>Giardia duodenalis</i> Assemblage E Infected Calves. <i>PLoS ONE</i> , 2012, 7, e40985.	1.1	21
49	Butyrate Induced Cell Cycle Arrest in Bovine Cells through Targeting Gene Expression Relevant to DNA Replication Apparatus. <i>Gene Regulation and Systems Biology</i> , 2008, 2, GRSB.S465.	2.3	20
50	Characterization of the longissimus lumborum transcriptome response to adding propionate to the diet of growing Angus beef steers. <i>Physiological Genomics</i> , 2012, 44, 543-550.	1.0	20
51	Localized complement activation in the development of protective immunity against <i>Ostertagia ostertagi</i> infections in cattle. <i>Veterinary Parasitology</i> , 2010, 174, 247-256.	0.7	19
52	The vitamin D receptor and inducible nitric oxide synthase associated pathways in acquired resistance to <i>Cooperia oncophora</i> infection in cattle. <i>Veterinary Research</i> , 2011, 42, 48.	1.1	19
53	Granule Exocytosis of Granulysin and Granzyme B as a Potential Key Mechanism in Vaccine-Induced Immunity in Cattle against the Nematode <i>Ostertagia ostertagi</i> . <i>Infection and Immunity</i> , 2013, 81, 1798-1809.	1.0	19
54	Comparison of the Transcriptomes of Long-Term Label Retaining-Cells and Control Cells Microdissected from Mammary Epithelium: An Initial Study to Characterize Potential Stem/Progenitor Cells. <i>Frontiers in Oncology</i> , 2013, 3, 21.	1.3	19

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55	Transcriptomic Sequencing Reveals a Set of Unique Genes Activated by Butyrate-Induced Histone Modification. <i>Gene Regulation and Systems Biology</i> , 2016, 10, GRSB.S35607.	2.3	18
56	Characterization of a Lytic Bacteriophage as an Antimicrobial Agent for Biocontrol of Shiga Toxin-Producing <i>Escherichia coli</i> O145 Strains. <i>Antibiotics</i> , 2019, 8, 74.	1.5	18
57	Genistein Reduces the Risk of Local Mammary Cancer Recurrence and Ameliorates Alterations in the Gut Microbiota in the Offspring of Obese Dams. <i>Nutrients</i> , 2021, 13, 201.	1.7	18
58	Chimeric classical swine fever (CSF)-Japanese encephalitis (JE) viral replicon as a non-transmissible vaccine candidate against CSF and JE infections. <i>Virus Research</i> , 2012, 165, 61-70.	1.1	17
59	Transcriptomic Profile of Whole Blood Cells from Elderly Subjects Fed Probiotic Bacteria <i>Lactobacillus rhamnosus</i> GG ATCC 53103 (LGG) in a Phase I Open Label Study. <i>PLoS ONE</i> , 2016, 11, e0147426.	1.1	16
60	A new paraprobiotic-based treatment for control of <i>Haemonchus contortus</i> in sheep. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2020, 14, 230-236.	1.4	16
61	Selection of internal reference genes for normalization of reverse transcription quantitative polymerase chain reaction (RT-qPCR) analysis in the rumen epithelium. <i>PLoS ONE</i> , 2017, 12, e0172674.	1.1	15
62	Microbial Co-Occurrence Patterns and Keystone Species in the Gut Microbial Community of Mice in Response to Stress and Chondroitin Sulfate Disaccharide. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2130.	1.8	15
63	Diet-induced changes in bacterial communities in the jejunum and their associations with bile acids in Angus beef cattle. <i>Animal Microbiome</i> , 2020, 2, 33.	1.5	14
64	Alternative Splicing Regulated by Butyrate in Bovine Epithelial Cells. <i>PLoS ONE</i> , 2012, 7, e39182.	1.1	13
65	Metagenomic Insights into the RDX-Degrading Potential of the Ovine Rumen Microbiome. <i>PLoS ONE</i> , 2014, 9, e110505.	1.1	13
66	Exploring the host transcriptome for mechanisms underlying protective immunity and resistance to nematode infections in ruminants. <i>Veterinary Parasitology</i> , 2012, 190, 1-11.	0.7	12
67	Transcriptomic alterations in human prostate cancer cell LNCaP tumor xenograft modulated by dietary phenethyl isothiocyanate. <i>Molecular Carcinogenesis</i> , 2013, 52, 426-437.	1.3	12
68	Transcriptomic Impacts of Rumen Epithelium Induced by Butyrate Infusion in Dairy Cattle in Dry Period. <i>Gene Regulation and Systems Biology</i> , 2018, 12, 117762501877479.	2.3	12
69	Temporal Dynamic Methods for Bulk RNA-Seq Time Series Data. <i>Genes</i> , 2021, 12, 352.	1.0	12
70	Web-based bioinformatics workflows for end-to-end RNA-seq data computation and analysis in agricultural animal species. <i>BMC Genomics</i> , 2016, 17, 761.	1.2	11
71	Molecular and metabolomic changes in the proximal colon of pigs infected with <i>Trichuris suis</i> . <i>Scientific Reports</i> , 2020, 10, 12853.	1.6	10
72	Absorbability of Astaxanthin Was Much Lower in Obese Mice Than in Normal Mice. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 11161-11169.	2.4	10

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73	Gut microbial signatures associated with moxidectin treatment efficacy of <i>Haemonchus contortus</i> in infected goats. <i>Veterinary Microbiology</i> , 2020, 242, 108607.	0.8	9
74	<i>Escherichia coli</i> O-Antigen Gene Clusters of Serogroups O62, O68, O131, O140, O142, and O163: DNA Sequences and Similarity between O62 and O68, and PCR-Based Serogrouping. <i>Biosensors</i> , 2015, 5, 51-68.	2.3	8
75	Transcriptomic analysis reveals effects of fucoxanthin on intestinal glucose transport. <i>Journal of Functional Foods</i> , 2018, 49, 205-213.	1.6	8
76	An inactivated bacterium (paraprobiotic) expressing <i>Bacillus thuringiensis</i> Cry5B as a therapeutic for <i>Ascaris</i> and <i>Parascaris</i> spp. infections in large animals. <i>One Health</i> , 2021, 12, 100241.	1.5	8
77	Butyrate Induced IGF2 Activation Correlated with Distinct Chromatin Signatures Due to Histone Modification. <i>Gene Regulation and Systems Biology</i> , 2013, 7, GRSB.S11243.	2.3	7
78	Bioinformatic Dissecting of TP53 Regulation Pathway Underlying Butyrate-induced Histone Modification in Epigenetic Regulation. <i>Genetics & Epigenetics</i> , 2014, 6, GEG.S14176.	2.5	7
79	Molecular and Microbial Signatures Predictive of Prebiotic Action of Neogargarotetraose in a Dextran Sulfate Sodium-Induced Murine Colitis Model. <i>Microorganisms</i> , 2020, 8, 995.	1.6	7
80	Splice variants and regulatory networks associated with host resistance to the intestinal worm <i>Cooperia oncophora</i> in cattle. <i>Veterinary Parasitology</i> , 2015, 211, 241-250.	0.7	6
81	Triacylglycerol Rich in Docosahexaenoic Acid Regulated Appetite via the Mediation of Leptin and Intestinal Epithelial Functions in High-Fat, High-Sugar Diet-Fed Mice. <i>Journal of Nutritional Biochemistry</i> , 2021, 99, 108856.	1.9	6
82	Alpha-Tocopherol Alters Transcription Activities that Modulates Tumor Necrosis Factor Alpha (TNF- α) Induced Inflammatory Response in Bovine Cells. <i>Gene Regulation and Systems Biology</i> , 2012, 6, GRSB.S8303.	2.3	5
83	Rumen Metagenomics. , 2015, , 223-245.		5
84	Microbial Composition and Co-occurrence Patterns in the Gut Microbial Community of Normal and Obese Mice in Response to Astaxanthin. <i>Frontiers in Microbiology</i> , 2021, 12, 671271.	1.5	5
85	Temporal dynamics in meta longitudinal RNA-Seq data. <i>Scientific Reports</i> , 2019, 9, 763.	1.6	4
86	<i>Neospora caninum</i> : Comparative gene expression profiling of <i>Neospora caninum</i> wild type and a temperature sensitive clone. <i>Experimental Parasitology</i> , 2011, 129, 346-354.	0.5	3
87	Complete Genome Sequence of <i>Escherichia coli</i> Phage ν B_EcoS Sa179lw, Isolated from Surface Water in a Produce-Growing Area in Northern California. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
88	Complete Genome Sequence of <i>Escherichia coli</i> Phage ν B_EcoM Sa157lw, Isolated from Surface Water Collected in Salinas, California. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
89	Gut Microbial Composition in Mice Fed Different Amount of Rice Resistant Starch (P21-031-19). <i>Current Developments in Nutrition</i> , 2019, 3, nzz041.P21-031-19.	0.1	2
90	Transcriptome analysis reveals the protective role of fructo-oligosaccharide in colonic mucosal barriers in exercise-induced stressed mice. <i>Food and Function</i> , 2021, 12, 4484-4495.	2.1	2

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91	Lowbush blueberries, <i>Vaccinium angustifolium</i> , modulate the functional potential of nutrient utilization and DNA maintenance mechanisms in the rat proximal colon microbiota. <i>Functional Foods in Health and Disease</i> , 2012, 2, 228.	0.3	2
92	Assembly and Analysis of Changes in Transcriptomes of Dairy Cattle Rumen Epithelia during Lactation and Dry Periods. <i>Agricultural Sciences</i> , 2018, 09, 619-638.	0.2	1
93	The improvement effect of astaxanthin-loaded emulsions on obesity is better than that of astaxanthin in the oil phase. <i>Food and Function</i> , 2022, 13, 3720-3731.	2.1	1
94	Large-Scale Meta-Longitudinal Microbiome Data with a Known Batch Factor. <i>Genes</i> , 2022, 13, 392.	1.0	1
95	Transcriptomic Analysis of LNCaP Tumor Xenograft to Elucidate the Components and Mechanisms Contributed by Tumor Environment as Targets for Dietary Prostate Cancer Prevention Studies. <i>Nutrients</i> , 2021, 13, 1000.	1.7	0
96	Cytochrome P450 Induction and Gene Expression in Channel Catfish (<i>Ictalurus punctatus</i>) Following Wastewater Treatment Plant Effluent Exposure in Field and Laboratory Settings. <i>Journal of Environmental Protection</i> , 2010, 01, 362-373.	0.3	0
97	Microbial Co-occurrence Patterns and Keystone Species in the Gut Microbial Community of Mice in Response to Stress and Chondroitin Sulfate Disaccharide. <i>FASEB Journal</i> , 2019, 33, lb300.	0.2	0