

Jianfa Bai

List of Publications by Year in descending order

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Version: 2024-02-01

126
papers

4,169
citations

126907

33
h-index

128289

60
g-index

131
all docs

131
docs citations

131
times ranked

4960
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of multiplex real-time PCR assays for differential detection of capripoxvirus, parapoxvirus and foot-and-mouth disease virus. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 1326-1337.	3.0	1
2	Molecular detection of SARS-CoV-2 strains and differentiation of Delta variant strains. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 2879-2889.	3.0	25
3	Development of a real-time PCR assay for detection and differentiation of <i>Mycoplasma ovipneumoniae</i> and a novel respiratory-associated <i>Mycoplasma</i> species in domestic sheep and goats. <i>Transboundary and Emerging Diseases</i> , 2022, , .	3.0	4
4	Molecular detection of SARS-CoV-2 and differentiation of Omicron and Delta variant strains. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	14
5	53 Evaluating the Efficacy of Boot Baths with Wet and Dry Disinfectants for Porcine Epidemic Diarrhea Virus and Porcine Reproductive and Respiratory Syndrome Virus. <i>Journal of Animal Science</i> , 2022, 100, 17-18.	0.5	0
6	PSV-5 Effects of Benzoic Acid and an Essential Oils Blend on Detection of Swine Viruses in Inoculated Swine Feed and Premix. <i>Journal of Animal Science</i> , 2022, 100, 193-194.	0.5	0
7	Assessment of porcine Rotavirus-associated virome variations in pigs with enteric disease. <i>Veterinary Microbiology</i> , 2022, 270, 109447.	1.9	4
8	Development of a three-panel multiplex real-time PCR assay for simultaneous detection of nine canine respiratory pathogens. <i>Journal of Microbiological Methods</i> , 2022, 199, 106528.	1.6	8
9	Development of a real-time RT-qPCR assay for the detection of porcine respirovirus 1. <i>Journal of Virological Methods</i> , 2021, 289, 114040.	2.1	9
10	Development of a bead-based assay for detection and differentiation of field strains and four vaccine strains of type 2 porcine reproductive and respiratory syndrome virus (PRRSV) in the USA. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 1414-1423.	3.0	7
11	Genetic diversity and prevalence of Atypical Porcine Pestivirus in the Midwest of US swine herds during 2016–2018. <i>Transboundary and Emerging Diseases</i> , 2021, , .	3.0	5
12	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
13	Diversity and seasonality of host-seeking ticks in a periurban environment in the Central Midwest (USA). <i>PLoS ONE</i> , 2021, 16, e0250272.	2.5	5
14	Whole-genome classification of rotavirus C and genetic diversity of porcine strains in the USA. <i>Journal of General Virology</i> , 2021, 102, .	2.9	6
15	High-resolution melting curve FRET-PCR rapidly identifies SARS-CoV-2 mutations. <i>Journal of Medical Virology</i> , 2021, 93, 5588-5593.	5.0	13
16	Universal Peptide Hydrogel for Scalable Physiological Formation and Bioprinting of 3D Spheroids from Human Induced Pluripotent Stem Cells. <i>Advanced Functional Materials</i> , 2021, 31, 2104046.	14.9	13
17	Surveillance of Host-Seeking Ticks in the Flint Hills Region (USA) and Associations with Environmental Determinants. <i>Parasitologia</i> , 2021, 1, 137-147.	1.3	5
18	Development of a quantitative real time RT-PCR assay for sensitive and rapid detection of emerging Atypical Porcine Pestivirus associated with congenital tremor in pigs. <i>Journal of Virological Methods</i> , 2021, 296, 114220.	2.1	6

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19	Near-Complete Genome of SARS-CoV-2 Delta (AY.3) Variant Identified in a Dog in Kansas, USA. <i>Viruses</i> , 2021, 13, 2104.	3.3	18
20	Feed Mitigant Efficacy for Control of Porcine Epidemic Diarrhea Virus and Porcine Reproductive and Respiratory Syndrome Virus when Inoculated Alone or Together in Feed. <i>Kansas Agricultural Experiment Station Research Reports</i> , 2021, 7, .	0.0	0
21	Effect of Benzoic Acid and Essential Oil Blends on Viral Load in Swine Feed and Vitamin Premix. <i>Kansas Agricultural Experiment Station Research Reports</i> , 2021, 7, .	0.0	0
22	Identification of the SARS-CoV-2 Delta variant C22995A using a high-resolution melting curve RT-FRET-PCR. <i>Emerging Microbes and Infections</i> , 2021, , 1-11.	6.5	6
23	Evaluating the Impact of Presence of Organic Matter on Environmental Samples and Sample Processing Technique on RNA Detection of PEDV. <i>Kansas Agricultural Experiment Station Research Reports</i> , 2021, 7, .	0.0	0
24	Quantification of Semi-Truck Cab Decontamination. <i>Kansas Agricultural Experiment Station Research Reports</i> , 2021, 7, .	0.0	0
25	The United States Swine Pathogen Database: integrating veterinary diagnostic laboratory sequence data to monitor emerging pathogens of swine. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	5
26	Feed Mitigant Efficacy for Control of Porcine Epidemic Diarrhea Virus and Porcine Reproductive and Respiratory Syndrome Virus when Inoculated Alone or Together in Feed. <i>Kansas Agricultural Experiment Station Research Reports</i> , 2021, 7, .	0.0	0
27	Effect of Benzoic Acid and Essential Oil Blends on Viral Load in Swine Feed and Vitamin Premix. <i>Kansas Agricultural Experiment Station Research Reports</i> , 2021, 7, .	0.0	0
28	Development and evaluation of multiplex real-time RT-qPCR assays for the detection and differentiation of foot-and-mouth disease virus and Seneca Valley virus 1. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 604-616.	3.0	16
29	Single-Cell-Based Digital PCR Detection and Association of Shiga Toxin-Producing <i>Escherichia coli</i> Serogroups and Major Virulence Genes. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	4
30	Inhibition monitoring in veterinary molecular testing. <i>Journal of Veterinary Diagnostic Investigation</i> , 2020, 32, 758-766.	1.1	7
31	Assessing the effects of medium-chain fatty acids and fat sources on PEDV infectivity. <i>Translational Animal Science</i> , 2020, 4, 1051-1059.	1.1	23
32	Genetic diversity and prevalence of porcine circovirus type 3 (PCV3) and type 2 (PCV2) in the Midwest of the USA during 2016–2018. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 1284-1294.	3.0	84
33	Suggested guidelines for validation of real-time PCR assays in veterinary diagnostic laboratories. <i>Journal of Veterinary Diagnostic Investigation</i> , 2020, 32, 802-814.	1.1	23
34	Development of a differential multiplex real-time PCR assay for porcine circovirus type 2 (PCV2) genotypes PCV2a, PCV2b and PCV2d. <i>Journal of Virological Methods</i> , 2020, 286, 113971.	2.1	4
35	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
36	Polymerase Chain Reaction-Based Prevalence of Serogroups of <i>Escherichia coli</i> Known to Carry Shiga Toxin Genes in Feces of Finisher Pigs. <i>Foodborne Pathogens and Disease</i> , 2020, 17, 782-791.	1.8	3

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37	Development of a nested PCR assay for detection of <i>Streptococcus equi</i> subspecies <i>equi</i> in clinical equine specimens and comparison with a qPCR assay. <i>Journal of Microbiological Methods</i> , 2020, 172, 105887.	1.6	7
38	Guidelines for Sanger sequencing and molecular assay monitoring. <i>Journal of Veterinary Diagnostic Investigation</i> , 2020, 32, 767-775.	1.1	81
39	Impact of added copper, alone or in combination with chlortetracycline, on growth performance and antimicrobial resistance of fecal enterococci of weaned piglets. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	10
40	Development of a real-time PCR assay for detection of African swine fever virus with an endogenous internal control. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2446-2454.	3.0	47
41	Effects of medium chain fatty acids as a mitigation or prevention strategy against porcine epidemic diarrhea virus in swine feed. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	13
42	72 Young Scholar Presentation: Use of medium chain fatty acids as mitigation or prevention strategies against pathogens in swine feed. <i>Journal of Animal Science</i> , 2020, 98, 59-60.	0.5	0
43	Seasonal Presence of <i>Salmonella</i> spp., <i>Salmonella</i> Typhimurium and Its Monophasic Variant Serotype I 4,[5],12:i:-, in Selected United States Swine Feed Mills. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 276-281.	1.8	15
44	Development of a multiplex real-time RT-PCR assay for simultaneous detection and differentiation of influenza A, B, C, and D viruses. <i>Diagnostic Microbiology and Infectious Disease</i> , 2019, 95, 59-66.	1.8	7
45	The Role of miRNAs in Zearalenone-Promotion of TM3 Cell Proliferation. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 1517.	2.6	7
46	A multiplex real-time PCR assay for the detection and differentiation of the newly emerged porcine circovirus type 3 and continuously evolving type 2 strains in the United States. <i>Journal of Virological Methods</i> , 2019, 269, 7-12.	2.1	17
47	DNA Microarray-Based Genomic Characterization of the Pathotypes of <i>Escherichia coli</i> 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
48	Effects of zearalenone and its derivatives on the synthesis and secretion of mammalian sex steroid hormones: A review. <i>Food and Chemical Toxicology</i> , 2019, 126, 262-276.	3.6	76
49	A multiplex real-time PCR assay for the detection and differentiation of five bovine pinkeye pathogens. <i>Journal of Microbiological Methods</i> , 2019, 160, 87-92.	1.6	20
50	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
51	Identification of BVDV2b and 2c subgenotypes in the United States: Genetic and antigenic characterization. <i>Virology</i> , 2019, 528, 19-29.	2.4	32
52	Determining the impact of commercial feed additives as potential porcine epidemic diarrhea virus mitigation strategies as determined by polymerase chain reaction analysis and bioassay ¹ . <i>Translational Animal Science</i> , 2019, 3, 93-102.	1.1	13
53	Zearalenone altered the cytoskeletal structure via ER stress- autophagy- oxidative stress pathway in mouse TM4 Sertoli cells. <i>Scientific Reports</i> , 2018, 8, 3320.	3.3	58
54	Comparison data of a two-target real-time PCR assay with and without an internal control in detecting <i>Salmonella enterica</i> from cattle lymph nodes. <i>Data in Brief</i> , 2018, 18, 1819-1824.	1.0	2

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55	A multiplex real-time PCR assay, based on <i>inv A</i> and <i>pag C</i> genes, for the detection and quantification of <i>Salmonella enterica</i> from cattle lymph nodes. <i>Journal of Microbiological Methods</i> , 2018, 148, 110-116.	1.6	34
56	Molecular detection and characterization of transient bovine viral diarrhea virus (BVDV) infections in cattle commingled with ten BVDV persistently infected cattle. <i>Journal of Veterinary Diagnostic Investigation</i> , 2018, 30, 413-422.	1.1	7
57	Complete Genome Sequence of an Influenza C Virus Strain Identified from a Sick Calf in the United States. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	8
58	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
59	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
60	Influenza C Virus in Cattle with Respiratory Disease, United States, 2016–2018. <i>Emerging Infectious Diseases</i> , 2018, 24, 1926-1929.	4.3	27
61	Evaluation of the effects of flushing feed manufacturing equipment with chemically treated rice hulls on porcine epidemic diarrhea virus cross-contamination during feed manufacturing ¹ . <i>Journal of Animal Science</i> , 2018, 96, 4149-4158.	0.5	27
62	Whole Genome Classification and Phylogenetic Analyses of Rotavirus B strains from the United States. <i>Pathogens</i> , 2018, 7, 44.	2.8	13
63	Zearalenone Promotes Cell Proliferation or Causes Cell Death?. <i>Toxins</i> , 2018, 10, 184.	3.4	65
64	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
65	Feed batch sequencing to decrease the risk of porcine epidemic diarrhea virus (PEDV) cross-contamination during feed manufacturing ¹ . <i>Journal of Animal Science</i> , 2018, 96, 4562-4570.	0.5	29
66	DNA microarray-based assessment of virulence potential of Shiga toxin gene-carrying <i>Escherichia coli</i> O104:H7 isolated from feedlot cattle feces. <i>PLoS ONE</i> , 2018, 13, e0196490.	2.5	9
67	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
68	Draft Genome Sequences of Enteropathogenic <i>Escherichia coli</i> O103 Strains Isolated from Feces of Feedlot Cattle. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
69	Bayesian estimation of true prevalence, sensitivity and specificity of three diagnostic tests for detection of <i>Escherichia coli</i> O157 in cattle feces. <i>Preventive Veterinary Medicine</i> , 2017, 148, 21-27.	1.9	9
70	Draft Genome Sequences of <i>Escherichia coli</i> O104 Strains of Bovine and Human Origin. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
71	Genotyping <i>Brucella canis</i> isolates using a highly discriminatory multilocus variable-number tandem-repeat analysis (MLVA) assay. <i>Scientific Reports</i> , 2017, 7, 1067.	3.3	13
72	Development of a novel real-time RT-PCR assay to detect Seneca Valley virus-1 associated with emerging cases of vesicular disease in pigs. <i>Journal of Virological Methods</i> , 2017, 239, 34-37.	2.1	32

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73	The non-host pathogen <i>Puccinia triticina</i> elicits an active transcriptional response in rice. <i>European Journal of Plant Pathology</i> , 2017, 147, 553-569.	1.7	1
74	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
75	Characterizing the rapid spread of porcine epidemic diarrhea virus (PEDV) through an animal food manufacturing facility. <i>PLoS ONE</i> , 2017, 12, e0187309.	2.5	26
76	Draft Genome Sequences of Enterohemorrhagic <i>Escherichia coli</i> O103:H2 Strains Isolated from Feces of Feedlot Cattle. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
77	Spiral Plating Method To Quantify the Six Major Non-O157 <i>Escherichia coli</i> Serogroups in Cattle Feces. <i>Journal of Food Protection</i> , 2017, 80, 848-856.	1.7	6
78	Elimination of Porcine Epidemic Diarrhea Virus in an Animal Feed Manufacturing Facility. <i>PLoS ONE</i> , 2017, 12, e0169612.	2.5	34
79	Development of 11-Plex MOL-PCR Assay for the Rapid Screening of Samples for Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 92.	3.9	8
80	<i>Escherichia coli</i> O104 in Feedlot Cattle Feces: Prevalence, Isolation and Characterization. <i>PLoS ONE</i> , 2016, 11, e0152101.	2.5	22
81	Tissue localization, shedding, virus carriage, antibody response, and aerosol transmission of <i>Porcine epidemic diarrhea virus</i> following inoculation of 4-week-old feeder pigs. <i>Journal of Veterinary Diagnostic Investigation</i> , 2016, 28, 671-678.	1.1	36
82	A multiplex real-time PCR panel assay for simultaneous detection and differentiation of 12 common swine viruses. <i>Journal of Virological Methods</i> , 2016, 236, 258-265.	2.1	28
83	Construction and characterization of a full-length cDNA infectious clone of emerging porcine Senecavirus A. <i>Virology</i> , 2016, 497, 111-124.	2.4	44
84	Experimental infection of conventional nursing pigs and their dams with <i>Porcine deltacoronavirus</i> . <i>Journal of Veterinary Diagnostic Investigation</i> , 2016, 28, 486-497.	1.1	24
85	Pigs immunized with a novel E2 subunit vaccine are protected from subgenotype heterologous classical swine fever virus challenge. <i>BMC Veterinary Research</i> , 2016, 12, 197.	1.9	43
86	Mutations in a Highly Conserved Motif of nsp1 ² Protein Attenuate the Innate Immune Suppression Function of Porcine Reproductive and Respiratory Syndrome Virus. <i>Journal of Virology</i> , 2016, 90, 3584-3599.	3.4	34
87	Multiplex Quantitative PCR Assays for the Detection and Quantification of the Six Major Non-O157 <i>Escherichia coli</i> Serogroups in Cattle Feces. <i>Journal of Food Protection</i> , 2016, 79, 66-74.	1.7	22
88	First Molecular Characterization of Bovine Leukemia Virus Infections in the Caribbean. <i>PLoS ONE</i> , 2016, 11, e0168379.	2.5	15
89	Pathogenicity and Transmissibility of Novel Reassortant H3N2 Influenza Viruses with 2009 Pandemic H1N1 Genes in Pigs. <i>Journal of Virology</i> , 2015, 89, 2831-2841.	3.4	36
90	Effects of chlortetracycline and copper supplementation on the prevalence, distribution, and quantity of antimicrobial resistance genes in the fecal metagenome of weaned pigs. <i>Preventive Veterinary Medicine</i> , 2015, 119, 179-189.	1.9	30

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91	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 Toxin-Producing <i>Escherichia coli</i> O157 in Cattle Feces. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 787-794.	1.8	29
92	Comparing Real-Time and Conventional PCR to Culture-Based Methods for Detecting and Quantifying <i>Escherichia coli</i> O157 in Cattle Feces. <i>Journal of Food Protection</i> , 2014, 77, 314-319.	1.7	12
93	Effects of chlortetracycline and copper supplementation on antimicrobial resistance of fecal <i>Escherichia coli</i> from weaned pigs. <i>Preventive Veterinary Medicine</i> , 2014, 114, 231-246.	1.9	58
94	<i>Escherichia coli</i> O26 in Feedlot Cattle: Fecal Prevalence, Isolation, Characterization, and Effects of an <i>E. coli</i> O157 Vaccine and a Direct-Fed Microbial. <i>Foodborne Pathogens and Disease</i> , 2014, 11, 186-193.	1.8	27
95	Impact of treatment strategies on cephalosporin and tetracycline resistance gene quantities in the bovine fecal metagenome. <i>Scientific Reports</i> , 2014, 4, 5100.	3.3	40
96	Prevalence of Shiga Toxin-Producing <i>Escherichia coli</i> and Associated Virulence Genes in Feces of Commercial Feedlot Cattle. <i>Foodborne Pathogens and Disease</i> , 2013, 10, 835-841.	1.8	47
97	Detection of <i>Escherichia coli</i> O104 in the Feces of Feedlot Cattle by a Multiplex PCR Assay Designed To Target Major Genetic Traits of the Virulent Hybrid Strain Responsible for the 2011 German Outbreak. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3522-3525.	3.1	28
98	Prevalence of <i>Escherichia coli</i> O-Types and Shiga Toxin Genes in Fecal Samples from Feedlot Cattle. <i>Foodborne Pathogens and Disease</i> , 2013, 10, 392-396.	1.8	27
99	Effects of Ceftiofur and Chlortetracycline Treatment Strategies on Antimicrobial Susceptibility and on tet(A), tet(B), and blaCMY-2 Resistance Genes among <i>E. coli</i> Isolated from the Feces of Feedlot Cattle. <i>PLoS ONE</i> , 2013, 8, e80575.	2.5	58
100	Applicability of a Multiplex PCR to Detect the Seven Major Shiga Toxin-Producing <i>Escherichia coli</i> Based on Genes That Code for Serogroup-Specific O-Antigens and Major Virulence Factors in Cattle Feces. <i>Foodborne Pathogens and Disease</i> , 2012, 9, 541-548.	1.8	88
101	Evaluation of a Multiplex Real-Time Polymerase Chain Reaction for the Quantification of <i>Escherichia coli</i> O157 in Cattle Feces. <i>Foodborne Pathogens and Disease</i> , 2012, 9, 79-85.	1.8	21
102	Characterization of reference genes for quantitative real-time PCR analysis in various tissues of <i>Anoectochilus roxburghii</i> . <i>Molecular Biology Reports</i> , 2012, 39, 5905-5912.	2.3	23
103	Applicability of a multiplex PCR to detect O26, O45, O103, O111, O121, O145, and O157 serogroups of <i>Escherichia coli</i> in cattle feces. <i>Veterinary Microbiology</i> , 2012, 156, 381-388.	1.9	84
104	Characterization of a New Disease Syndrome Associated with Porcine Circovirus Type 2 in Previously Vaccinated Herds. <i>Journal of Clinical Microbiology</i> , 2011, 49, 2012-2016.	3.9	36
105	Aphid Feeding Activates Expression of a Transcriptome of Oxylipin-based Defense Signals in Wheat Involved in Resistance to Herbivory. <i>Journal of Chemical Ecology</i> , 2010, 36, 260-276.	1.8	86
106	A benefit of high temperature: increased effectiveness of a rice bacterial blight disease resistance gene. <i>New Phytologist</i> , 2010, 185, 568-576.	7.3	108
107	Variation in gene expression of <i>Andropogon gerardii</i> in response to altered environmental conditions associated with climate change. <i>Journal of Ecology</i> , 2010, 98, 374-383.	4.0	29
108	Bovine Abortion Associated with <i>Nocardia farcinica</i> . <i>Journal of Veterinary Diagnostic Investigation</i> , 2010, 22, 108-111.	1.1	9

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109	Diagnostic microarray for human and animal bacterial diseases and their virulence and antimicrobial resistance genes. <i>Journal of Microbiological Methods</i> , 2010, 80, 223-230.	1.6	18
110	A multiplex PCR procedure for the detection of six major virulence genes in <i>Escherichia coli</i> O157:H7. <i>Journal of Microbiological Methods</i> , 2010, 82, 85-89.	1.6	117
111	Nonadditive Expression of Homoeologous Genes Is Established Upon Polyploidization in Hexaploid Wheat. <i>Genetics</i> , 2009, 181, 1147-1157.	2.9	151
112	Detection of genomic deletions in rice using oligonucleotide microarrays. <i>BMC Genomics</i> , 2009, 10, 129.	2.8	36
113	Determination of internal control for gene expression studies in equine tissues and cell culture using quantitative RT-PCR. <i>Veterinary Immunology and Immunopathology</i> , 2009, 130, 114-119.	1.2	27
114	A co-printed oligomer to enhance reliability of spotted microarrays. <i>Journal of Microbiological Methods</i> , 2009, 77, 261-266.	1.6	9
115	<i>Tsn1</i> -Mediated Host Responses to ToxA from <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1056-1068.	2.6	40
116	Gene Expression Patterns in Near Isogenic Lines for Wheat Rust Resistance Gene <i>Lr34/Yr18</i> . <i>Phytopathology</i> , 2007, 97, 1083-1093.	2.2	81
117	Ecological genomics: making the leap from model systems in the lab to native populations in the field. <i>Frontiers in Ecology and the Environment</i> , 2007, 5, 19-24.	4.0	43
118	Gene Expression of Different Wheat Genotypes During Attack by Virulent and Avirulent Hessian Fly (<i>Mayetiola destructor</i>) Larvae. <i>Journal of Chemical Ecology</i> , 2007, 33, 2171-2194.	1.8	105
119	Cloning and characterization of protease inhibitor-like cDNAs from the Hessian fly <i>mayetiola destructor</i> (SAY). <i>Insect Molecular Biology</i> , 2006, 15, 485-496.	2.0	5
120	Expression patterns of three heat shock protein 70 genes among developmental stages of the red flour beetle, <i>Tribolium castaneum</i> (Coleoptera: Tenebrionidae). <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2005, 141, 247-256.	1.8	116
121	Molecular characterization of the <i>avrXa7</i> locus from <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> field isolates. <i>Physiological and Molecular Plant Pathology</i> , 2004, 64, 145-153.	2.5	11
122	The <i>avrXo1</i> Gene from the Rice Pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> Confers a Nonhost Defense Reaction on Maize with Resistance Gene <i>Rxo1</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 771-779.	2.6	97
123	Diversity in Nucleotide Binding Site-Leucine-Rich Repeat Genes in Cereals. <i>Genome Research</i> , 2002, 12, 1871-1884.	5.5	292
124	PATHOGENFITNESSPENALTY AS APREDICTOR OFDURABILITY OFDISEASERESISTANCEGENES. <i>Annual Review of Phytopathology</i> , 2001, 39, 187-224.	7.8	308
125	Predicting durability of a disease resistance gene based on an assessment of the fitness loss and epidemiological consequences of avirulence gene mutation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 13500-13505.	7.1	243
126	<i>Xanthomonas oryzae</i> pv. <i>Oryzae</i> Avirulence Genes Contribute Differently and Specifically to Pathogen Aggressiveness. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 1322-1329.	2.6	143