Guan Zhu

List of Publications by Year
in descending order

116 papers	5,076 citations	147801 31 h-index	98798 67 g-index
119 all docs	119 docs citations	119 times ranked	4818 citing authors

#	Article	IF	Citations
1	Complete Genome Sequence of the Apicomplexan, Cryptosporidium parvum. Science, 2004, 304, 441-445.	12.6	877
2	A review of the global burden, novel diagnostics, therapeutics, and vaccine targets for cryptosporidium. Lancet Infectious Diseases, The, 2015, 15, 85-94.	9.1	725
3	Advances in research of fish immune-relevant genes: A comparative overview of innate and adaptive immunity in teleosts. Developmental and Comparative Immunology, 2013, 39, 39-62.	2.3	411
4	Cryptosporidium parvum appears to lack a plastid genome. Microbiology (United Kingdom), 2000, 146, 315-321.	1.8	194
5	Release of Luminal Exosomes Contributes to TLR4-Mediated Epithelial Antimicrobial Defense. PLoS Pathogens, 2013, 9, e1003261.	4.7	159
6	Pyruvate:NADP Oxidoreductase from the Mitochondrion of Euglena gracilis and from the Apicomplexan Cryptosporidium parvum: A Biochemical Relic Linking Pyruvate Metabolism in Mitochondriate and Amitochondriate Protists. Molecular Biology and Evolution, 2001, 18, 710-720.	8.9	121
7	Apicoplast genome of the coccidian Eimeria tenella. Gene, 2003, 321, 39-46.	2.2	119
8	Cryptosporidium parvum: the first protist known to encode a putative polyketide synthase. Gene, 2002, 298, 79-89.	2.2	100
9	Molecular analysis of a Type I fatty acid synthase in Cryptosporidium parvum. Molecular and Biochemical Parasitology, 2000, 105, 253-260.	1.1	83
10	Application of Quantitative Real-Time Reverse Transcription-PCR in Assessing Drug Efficacy against the Intracellular Pathogen Cryptosporidium parvum In Vitro. Antimicrobial Agents and Chemotherapy, 2005, 49, 4437-4442.	3.2	78
11	A Genome-Sequence Survey for Ascogregarina taiwanensis Supports Evolutionary Affiliation but Metabolic Diversity between a Gregarine and Cryptosporidium. Molecular Biology and Evolution, 2010, 27, 235-248.	8.9	78
12	Apical Organelle Discharge by Cryptosporidium parvum Is Temperature, Cytoskeleton, and Intracellular Calcium Dependent and Required for Host Cell Invasion. Infection and Immunity, 2004, 72, 6806-6816.	2.2	77
13	Cryptosporidium parvum invasion of biliary epithelia requires host cell tyrosine phosphorylation of cortactin via c-Src. Gastroenterology, 2003, 125, 216-228.	1.3	75
14	Polyamine biosynthesis in Cryptosporidium parvum and its implications for chemotherapy. Molecular and Biochemical Parasitology, 1997, 88, 35-42.	1.1	62
15	Current Progress in the Fatty Acid Metabolism in Cryptosporidium parvum1. Journal of Eukaryotic Microbiology, 2004, 51, 381-388.	1.7	61
16	Divergent polyamine metabolism in the Apicomplexa. Microbiology (United Kingdom), 2007, 153, 1123-1130.	1.8	60
17	Cryptosporidium: Genomic and biochemical features. Experimental Parasitology, 2010, 124, 2-9.	1.2	60
18	Direct Isolation of DNA from Patient Stools for Polymerase Chain Reaction Detection ofCryptosporidium parvum. Journal of Infectious Diseases, 1998, 177, 1443-1446.	4.0	55

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19	Evolution of Cryptosporidium parvum Lactate Dehydrogenase from Malate Dehydrogenase by a Very Recent Event of Gene Duplication. Molecular Biology and Evolution, 2003, 21, 489-497.	8.9	52
20	Expression and functional characterization of a giant Type I fatty acid synthase (CpFAS1) gene from Cryptosporidium parvum. Molecular and Biochemical Parasitology, 2004, 134, 127-135.	1.1	52
21	Minimizing DNA recombination during long RT-PCR. Journal of Virological Methods, 1998, 76, 139-148.	2.1	49
22	Cryptosporidium Lactate Dehydrogenase Is Associated with the Parasitophorous Vacuole Membrane and Is a Potential Target for Developing Therapeutics. PLoS Pathogens, 2015, 11, e1005250.	4.7	48
23	Transcriptome analysis reveals unique metabolic features in the Cryptosporidium parvum Oocysts associated with environmental survival and stresses. BMC Genomics, 2012, 13, 647.	2.8	46
24	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. Nature Communications, 2016, 7, 12845.	12.8	43
25	The Existing Drug Vorinostat as a New Lead Against Cryptosporidiosis by Targeting the Parasite Histone Deacetylases. Journal of Infectious Diseases, 2018, 217, 1110-1117.	4.0	42
26	Establishment of a continuous in vitro culture of Babesia duncani in human erythrocytes reveals unusually high tolerance to recommended therapies. Journal of Biological Chemistry, 2018, 293, 19974-19981.	3.4	42
27	Molecular analysis of a P-type ATPase from Cryptosporidium parvum1Note: Nucleotide sequence data reported in this paper are available in the EMBL, GenBankâ„¢ and DDJB data bases under the accession number U65981.1. Molecular and Biochemical Parasitology, 1997, 90, 307-316.	1.1	39
28	Functional characterization of a fatty acyl-CoA-binding protein (ACBP) from the apicomplexan Cryptosporidium parvum. Microbiology (United Kingdom), 2006, 152, 2355-2363.	1.8	39
29	Amelioration of Cryptosporidium parvum Infection In Vitro and In Vivo by Targeting Parasite Fatty Acyl-Coenzyme A Synthetases. Journal of Infectious Diseases, 2014, 209, 1279-1287.	4.0	38
30	Quantitative RT-PCR assay for high-throughput screening (HTS) of drugs against the growth of Cryptosporidium parvum in vitro. Frontiers in Microbiology, 2015, 6, 991.	3.5	37
31	Phylogenetic Analyses of Texas Isolates Indicate an Evolving Subtype of the Clade B Feline Immunodeficiency Viruses. Journal of Virology, 2004, 78, 2158-2163.	3.4	34
32	Involvement of Host Cell Integrin Î±2 in Cryptosporidium parvum Infection. Infection and Immunity, 2012, 80, 1753-1758.	2.2	33
33	Annotated draft genome sequences of three species ofCryptosporidium:Cryptosporidium meleagridisisolate UKMEL1,C. baileyiisolate TAMU-09Q1 andC. hominisisolates TU502_2012 and UKH1. Pathogens and Disease, 2016, 74, ftw080.	2.0	33
34	Molecular cloning, phylogenetic analysis and three-dimensional modeling of Cu,Zn superoxide dismutase (CnSOD1) from three varieties of Cryptococcus neoformans. Gene, 2001, 268, 41-51.	2.2	32
35	Cryptosporidium parvum Long-Chain Fatty Acid Elongase. Eukaryotic Cell, 2007, 6, 2018-2028.	3.4	31
36	alpha-Proteobacterial Relationship of Apicomplexan Lactate and Malate Dehydrogenases. Journal of Eukaryotic Microbiology, 2002, 49, 255-261.	1.7	30

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37	Functional Characterization of an Evolutionarily Distinct Phosphopantetheinyl Transferase in the Apicomplexan Cryptosporidium parvum. Eukaryotic Cell, 2005, 4, 1211-1220.	3.4	30
38	Characterization In vitro and In vivo of Resistance to Ionophores in a Strain of Eimeria tenella. Journal of Parasitology, 1992, 78, 1067.	0.7	29
39	Transcriptome Analysis in Chicken Cecal Epithelia upon Infection by Eimeria tenella In Vivo. PLoS ONE, 2013, 8, e64236.	2.5	29
40	Distribution of lethal giant larvae (Lgl) protein in the tegument and negative impact of siRNA-based gene silencing on worm surface structure and egg hatching in Schistosoma japonicum. Parasitology Research, 2014, 113, 1-9.	1.6	29
41	Novel anti-Cryptosporidium activity of known drugs identified by high-throughput screening against parasite fatty acyl-CoA binding protein (ACBP). Journal of Antimicrobial Chemotherapy, 2012, 67, 609-617.	3.0	28
42	Peroxiredoxin 1 (Prx1) is a dual-function enzyme by possessing Cys-independent catalase-like activity. Biochemical Journal, 2017, 474, 1373-1394.	3.7	28
43	Functional characterization of the acyl-[acyl carrier protein] ligase in the Cryptosporidium parvum giant polyketide synthase. International Journal for Parasitology, 2007, 37, 307-316.	3.1	27
44	A Unique Hexokinase in Cryptosporidium parvum, an Apicomplexan Pathogen Lacking the Krebs Cycle and Oxidative Phosphorylation. Protist, 2014, 165, 701-714.	1.5	27
45	Discovery of Novel Anti-cryptosporidial Activities From Natural Products by in vitro High-Throughput Phenotypic Screening. Frontiers in Microbiology, 2019, 10, 1999.	3.5	25
46	New function for Escherichia coli xanthosine phophorylase (xapA): genetic and biochemical evidences on its participation in NAD+ salvage from nicotinamide. BMC Microbiology, 2014, 14, 29.	3.3	24
47	High-Throughput Screening of Drugs Against the Growth of Cryptosporidium parvum In Vitro by qRT-PCR. Methods in Molecular Biology, 2020, 2052, 319-334.	0.9	21
48	Reconstitution of a bacterial/plant polyamine biosynthesis pathway in Saccharomyces cerevisiae. Microbiology (United Kingdom), 1999, 145, 301-307.	1.8	20
49	Discovery of ebselen as an inhibitor of Cryptosporidium parvum glucose-6-phosphate isomerase (CpGPI) by high-throughput screening of existing drugs. International Journal for Parasitology: Drugs and Drug Resistance, 2018, 8, 43-49.	3.4	20
50	Prevalence of intestinal parasites in companion dogs with diarrhea in Beijing, China, and genetic characteristics of Giardia and Cryptosporidium species. Parasitology Research, 2018, 117, 35-43.	1.6	20
51	Differential expression and interaction of transcription co-activator MBF1 with TATA-binding protein (TBP) in the apicomplexan Cryptosporidium parvum. Microbiology (United Kingdom), 2004, 150, 1207-1213.	1.8	19
52	The Protozoan Parasite Cryptosporidium parvum Possesses Two Functionally and Evolutionarily Divergent Replication Protein A Large Subunits. Journal of Biological Chemistry, 2005, 280, 31460-31469.	3.4	19
53	Two distinct oxysterol binding protein-related proteins in the parasitic protist Cryptosporidium parvum (Apicomplexa). Biochemical and Biophysical Research Communications, 2006, 346, 591-599.	2.1	19
54	The reductase domain in a Type I fatty acid synthase from the apicomplexan Cryptosporidium parvum: Restricted substrate preference towards very long chain fatty acyl thioesters. BMC Biochemistry, 2010, 11, 46.	4.4	19

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55	Molecular cloning and differential expression in tissues of a tyrosinase gene in the Pacific oyster Crassostrea gigas. Molecular Biology Reports, 2014, 41, 5403-5411.	2.3	19
56	Differential Gene Expression and Protein Localization of Cryptosporidium parvum Fatty Acylâ€CoA Synthetase Isoforms. Journal of Eukaryotic Microbiology, 2016, 63, 233-246.	1.7	19
57	Cryptosporidium parvumpossesses a short-type replication protein A large subunit that differs from its host. FEMS Microbiology Letters, 1999, 176, 367-372.	1.8	18
58	An apicomplexan ankyrin-repeat histone deacetylase with relatives in photosynthetic eukaryotes. International Journal for Parasitology, 2009, 39, 747-754.	3.1	18
59	Current status and challenges in drug discovery against the globally important zoonotic cryptosporidiosis. Animal Diseases, 2021, 1, .	1.4	18
60	Plant-Type Trehalose Synthetic Pathway in Cryptosporidium and Some Other Apicomplexans. PLoS ONE, 2010, 5, e12593.	2.5	18
61	How Much Does Roxarsone Contribute to Coccidiosis Control in Broilers when Used in Combination with Ionophores?. Journal of Applied Poultry Research, 1992, 1, 172-179.	1.2	17
62	Gene discovery, evolutionary affinity and molecular detection of Oxyspirura petrowi, an eye worm parasite of game birds. BMC Microbiology, 2013, 13, 233.	3.3	17
63	The beta tubulin gene of Eimeria tenella. Molecular and Biochemical Parasitology, 1996, 76, 315-319.	1.1	16
64	Characterization of a heavy metal ATPase from the apicomplexan Cryptosporidium parvum. Gene, 2001, 266, 25-34.	2.2	16
65	Efficacy of S-adenosylhomocysteine hydrolase inhibitors, D-eritadenine and (S)-DHPA, against the growth of Cryptosporidium parvum in vitro. Experimental Parasitology, 2010, 126, 113-116.	1.2	16
66	Intron-containing Î²-tubulin transcripts in Cryptosporidium parvum cultured in vitro. Microbiology (United Kingdom), 2004, 150, 1191-1195.	1.8	14
67	Novel Antiparasitic Activity of the Antifungal Lead Occidiofungin. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	14
68	Computer Program for Calculating the Melting Temperature of Degenerate Oligonucleotides Used in PCR or Hybridization. BioTechniques, 1997, 22, 1158-1160.	1.8	13
69	Cryptosporidium parvum: Functional Complementation of a Parasite Transcriptional Coactivator CpMBF1 in Yeast. Experimental Parasitology, 2000, 96, 195-201.	1.2	13
70	Presence and removal of a contaminating NADH oxidation activity in recombinant maltose-binding protein fusion proteins expressed in Escherichia coli. BioTechniques, 2012, 52, 247-253.	1.8	13
71	Molecular and biochemical characterization of Eimeria tenella hexokinase. Parasitology Research, 2016, 115, 3425-3433.	1.6	13
72	Characterisation of a novel transporter from Cryptosporidium parvum. International Journal for Parasitology, 2002, 32, 877-887.	3.1	12

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73	Heterogeneous expression and functional analysis of two distinct replication protein A large subunits from Cryptosporidium parvum. International Journal for Parasitology, 2002, 32, 1477-1485.	3.1	12
74	Streptococcus troglodytidis sp. nov., isolated from a foot abscess of a chimpanzee (Pan troglodytes). International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 449-453.	1.7	11
75	The MEP pathway in Babesia orientalis apicoplast, a potential target for anti-babesiosis drug development. Parasites and Vectors, 2018, 11, 452.	2.5	11
76	The Action of the Hexokinase Inhibitor 2â€deoxyâ€<scp>d</scp>â€glucose on Cryptosporidium parvum and the Discovery of Activities against the Parasite Hexokinase from Marketed Drugs. Journal of Eukaryotic Microbiology, 2019, 66, 460-468.	1.7	11
77	Cryptosporidium parvum: Polyamine Biosynthesis from Agmatine. Journal of Eukaryotic Microbiology, 1996, 43, 73S-73S.	1.7	10
78	Monophyletic Relationship between Severe Acute Respiratory Syndrome Coronavirus and Group 2 Coronaviruses. Journal of Infectious Diseases, 2004, 189, 1676-1678.	4.0	10
79	Functional characterization of replication protein A2 (RPA2) from Cryptosporidium parvum. Microbiology (United Kingdom), 2004, 150, 1197-1205.	1.8	10
80	A Novel High-Throughput Screening Assay for Putative Antidiabetic Agents through PPARÎ± Interactions. Journal of Biomolecular Screening, 2008, 13, 855-861.	2.6	9
81	Functional characterizations of malonyl-CoA:acyl carrier protein transacylase (MCAT) in Eimeria tenella. Molecular and Biochemical Parasitology, 2012, 184, 20-28.	1.1	9
82	Giardia fatty acyl-CoA synthetases as potential drug targets. Frontiers in Microbiology, 2015, 6, 753.	3.5	9
83	Crystallization of three key glycolytic enzymes of the opportunistic pathogen Cryptosporidium parvum. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1750, 166-172.	2.3	8
84	Differential expression of the two distinct replication protein A subunits from Cryptosporidium parvum. Journal of Cellular Biochemistry, 2008, 104, 2207-2216.	2.6	8
85	Cryptosporidium parvum Elongation Factor 1Î± Participates in the Formation of Base Structure at the Infection Site During Invasion. Journal of Infectious Diseases, 2020, 221, 1816-1825.	4.0	8
86	Discovery of New Microneme Proteins in Cryptosporidium parvum and Implication of the Roles of a Rhomboid Membrane Protein (CpROM1) in Hostâ€“Parasite Interaction. Frontiers in Veterinary Science, 2021, 8, 778560.	2.2	8
87	Amplification of ionophore resistance in a field strain of Eimeria tenella by treating free sporozoites with monensin in vitro. Veterinary Parasitology, 1994, 51, 211-217.	1.8	7
88	Seroprevalence of five parasitic pathogens in pregnant women in ten Caribbean countries. Parasitology Research, 2017, 116, 347-358.	1.6	7
89	A Single-Pass Type I Membrane Protein from the Apicomplexan Parasite Cryptosporidium parvum with Nanomolar Binding Affinity to Host Cell Surface. Microorganisms, 2021, 9, 1015.	3.6	7
90	Unique Tubulin-Based Structures in the Zoonotic Apicomplexan Parasite Cryptosporidium parvum. Microorganisms, 2021, 9, 1921.	3.6	7

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91	Biochemical characterization of enoyl reductase involved in Type II fatty acid synthesis in the intestinal coccidiumEimeria tenella(PhylumApicomplexa). FEMS Microbiology Letters, 2007, 272, 238-244.	1.8	6
92	The apicomplexan Cryptosporidium parvum possesses a single mitochondrialâ€type ferredoxin and ferredoxin:NADP⁺ reductase system. Protein Science, 2010, 19, 2073-2084.	7.6	6
93	Immunocompetent rabbits infected with Cryptosporidium cuniculus as an animal model for anti-cryptosporidial drug testing. International Journal for Parasitology, 2021, , .	3.1	6
94	The mucin-like, secretory type-I transmembrane glycoprotein GP900 in the apicomplexan Cryptosporidium parvum is cleaved in the secretory pathway and likely plays a lubrication role. Parasites and Vectors, 2022, 15, 170.	2.5	6
95	Peptides Associated with Monensin Resistance in Sporozoites of Eimeria tenella (Coccidia). Journal of Parasitology, 1994, 80, 284.	0.7	5
96	Molecular and Biochemical Characterization of a Type II Thioesterase From the Zoonotic Protozoan Parasite Cryptosporidium parvum. Frontiers in Cellular and Infection Microbiology, 2019, 9, 199.	3.9	5
97	Variant proteins associated with ionophore resistance in sporozoites ofEimeria tenella (Coccidia). Zeitschrift FÃ¼r Parasitenkunde (Berlin, Germany), 1993, 79, 480-484.	0.8	4
98	Multiyear Survey of Coccidia, Cryptosporidia, Microsporidia, Histomona, and Hematozoa in Wild Quail in the Rolling Plains Ecoregion of Texas and Oklahoma, USA. Journal of Eukaryotic Microbiology, 2017, 64, 4-17.	1.7	4
99	Cysteine-independent Catalase-like Activity of Vertebrate Peroxiredoxin 1 (Prx1). Journal of Biological Chemistry, 2015, 290, 19942-19955.	3.4	3
100	An old drug as a promising new cure for the hard-to-treat echinococcosis. EBioMedicine, 2020, 55, 102749.	6.1	3
101	OUP accepted manuscript. Journal of Antimicrobial Chemotherapy, 2021, , .	3.0	3
102	Establishment of a Transient and Stable Transfection System for Babesia duncani Using a Homologous Recombination Strategy. Frontiers in Cellular and Infection Microbiology, 2022, 12, 844498.	3.9	3
103	Confocal Laser Scanning Microscopy of Î²-Tubulin and Î±-Actinin in Asexual Stages of Eimeria tenella (Apicomplexa: Eimeriidae) in Cell Culture. Archiv FÃ¼r Protistenkunde, 1995, 145, 112-118.	0.8	2
104	A New Eimeriid (Apicomplexa) Species From Endangered Attwater's Prairie Chickens (Tympanuchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	2
105	Characterization of Host Cell Mutants Significantly Resistant to Cryptosporidium parvum Infection. Journal of Eukaryotic Microbiology, 2017, 64, 843-849.	1.7	2
106	What is your diagnosis? Corneal scrape from a dog. Veterinary Clinical Pathology, 2018, 47, 315-316.	0.7	2
107	The genome of the thin-necked bladder worm Taenia hydatigena reveals evolutionary strategies for helminth survival. Communications Biology, 2021, 4, 1004.	4.4	2
108	Cryptosporidium Metabolism. , 2014, , 361-379.		2

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109	Cryptosporidium Species. , 0, , 271-286.		2
110	A Vavraia-like microsporidium as the cause of deadly infection in threatened and endangered Eurycea salamanders in the United States. Parasites and Vectors, 2019, 12, 108.	2.5	1
111	An improved histone deacetylase (HDAC) assay and its application for highâ€throughput screening of inhibitors against Cryptosporidium parvum enzymes. FASEB Journal, 2008, 22, 791.14.	0.5	1
112	Zoonotic Cryptosporidium Parasites Possess a Unique Carbohydrate-binding Protein (Malectin) that is Absent in other Apicomplexan Lineages. Zoonoses, 2022, 2, .	1.1	1
113	Energy metabolism and carbon flow in Cryptosporidium parvum.. , 2009, , 360-368.		0
114	Silk Fibroin Scaffolds Facilitating the Repair of Rat Abdominal Wall Defect. Journal of Biomaterials and Tissue Engineering, 2016, 6, 665-671.	0.1	0
115	Cryptosporidium. , 2009, , 165-190.		0
116	Implication of Potential Differential Roles of the Two Phosphoglucomutase Isoforms in the Protozoan Parasite Cryptosporidium parvum. Pathogens, 2022, 11, 21.	2.8	0