

# Guo-Hua Liu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6431741/publications.pdf>

Version: 2024-02-01

106  
papers

2,246  
citations

236612

25  
h-index

276539

41  
g-index

114  
all docs

114  
docs citations

114  
times ranked

1746  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbiome analysis of the midguts of different developmental stages of <i>Argas persicus</i> in China. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 101868.	1.1	4
2	Metagenomics of the midgut microbiome of <i>Rhipicephalus microplus</i> from China. <i>Parasites and Vectors</i> , 2022, 15, 48.	1.0	10
3	Comparative analyses of the mitochondrial genomes of the cattle tick <i>Rhipicephalus microplus</i> clades A and B from China. <i>Parasitology Research</i> , 2022, 121, 1789-1797.	0.6	2
4	Comparative analyses of the fragmented mitochondrial genomes of wild pig louse <i>Haematopinus apri</i> from China and Japan. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 18, 25-29.	0.6	2
5	Identification of a new species of <i>Ixodes</i> Latreille, 1795 (Acari: Ixodidae), parasite of hog badgers (Carnivora: Mustelidae) in China. <i>Medical and Veterinary Entomology</i> , 2022, , .	0.7	0
6	Human pediculosis, a global public health problem. <i>Infectious Diseases of Poverty</i> , 2022, 11, .	1.5	9
7	Mitochondrial phylogenomics provides insights into the taxonomy and phylogeny of fleas. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	8
8	Global profiling of lncRNAs-miRNAs-mRNAs reveals differential expression of coding genes and non-coding RNAs in the lung of beagle dogs at different stages of <i>Toxocara canis</i> infection. <i>International Journal for Parasitology</i> , 2021, 51, 49-61.	1.3	13
9	Proteomic alterations in the plasma of Beagle dogs induced by <i>Toxocara canis</i> infection. <i>Journal of Proteomics</i> , 2021, 232, 104049.	1.2	6
10	Seroprevalence, Risk Factors, and Genotypes of <i>Toxoplasma gondii</i> in Free-Range Chickens Intended for Human Consumption in China. <i>Foodborne Pathogens and Disease</i> , 2021, 18, 253-259.	0.8	2
11	Molecular Detection of <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> in Domestic Ducks in Hunan Province, China. <i>Frontiers in Veterinary Science</i> , 2021, 8, 649603.	0.9	1
12	Highly rearranged mitochondrial genome in <i>Falcolipeurus</i> lice (Phthiraptera: Philopteridae) from endangered eagles. <i>Parasites and Vectors</i> , 2021, 14, 269.	1.0	6
13	<i>Dipylidium caninum</i> draft genome - a new resource for comparative genomic and genetic explorations of flatworms. <i>Genomics</i> , 2021, 113, 1272-1280.	1.3	8
14	The complete mitochondrial genome sequences of the cat flea <i>Ctenocephalides felis felis</i> (Siphonaptera: Pulicidae) support the hypothesis that <i>C. felis</i> isolates from China and USA were the same <i>C. f. felis</i> subspecies. <i>Acta Tropica</i> , 2021, 217, 105880.	0.9	8
15	Characterization of the complete mitochondrial genome of the swine kidney worm <i>Stephanurus dentatus</i> (Nematoda: Syngamidae) and phylogenetic implications. <i>Veterinary Parasitology</i> , 2021, 295, 109475.	0.7	4
16	The complete mitochondrial genome of capillariid nematodes ( <i>Eucoleus annulatus</i> ): A novel gene arrangement and phylogenetic implications. <i>Veterinary Parasitology</i> , 2021, 296, 109476.	0.7	6
17	Molecular Investigation of Zoonotic Intestinal Protozoa in Pet Dogs and Cats in Yunnan Province, Southwestern China. <i>Pathogens</i> , 2021, 10, 1107.	1.2	8
18	Characterization of the complete mitochondrial genomes of six horseflies (Diptera: Tabanidae). <i>Infection, Genetics and Evolution</i> , 2021, 95, 105054.	1.0	9

#	ARTICLE	IF	CITATIONS
19	Mitochondrial genome evidence suggests <i>Cooperia</i> sp. from China may represent a distinct species from <i>Cooperia oncophora</i> from Australia. <i>Parasitology International</i> , 2020, 75, 102001.	0.6	3
20	First report of <i>Neospora caninum</i> infection in pigs in China. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 29-32.	1.3	12
21	Novel genotypes and multilocus genotypes of <i>Enterocytozoon bieneusi</i> in two wild rat species in China: potential for zoonotic transmission. <i>Parasitology Research</i> , 2020, 119, 283-290.	0.6	15
22	Variation of mitochondrial minichromosome composition in <i>Hoplopleura</i> lice (Phthiraptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 T	1.0	12
23	Fragmented mitochondrial genomes evolved in opposite directions between closely related macaque louse <i>Pedicinus obtusus</i> and colobus louse <i>Pedicinus badii</i> . <i>Genomics</i> , 2020, 112, 4924-4933.	1.3	17
24	Human gnathostomiasis: a neglected food-borne zoonosis. <i>Parasites and Vectors</i> , 2020, 13, 616.	1.0	31
25	Epidemiology of <i>Toxocara</i> spp. in dogs and cats in mainland China, 2000â€“2019. <i>Advances in Parasitology</i> , 2020, 109, 843-860.	1.4	7
26	Microbiome analysis of the saliva and midgut from partially or fully engorged female adult <i>Dermacentor silvarum</i> ticks in China. <i>Experimental and Applied Acarology</i> , 2020, 80, 543-558.	0.7	13
27	<i>Toxocara</i> and the promises it holds for medicine and veterinary medicine. <i>Advances in Parasitology</i> , 2020, 109, 89-108.	1.4	25
28	Characterization of the complete mitochondrial genome of the echinostome <i>Echinostoma miyagawai</i> and phylogenetic implications. <i>Parasitology Research</i> , 2019, 118, 3091-3097.	0.6	13
29	Molecular Detection and Genotyping of <i>Toxoplasma gondii</i> in Edward's Long-Tailed Rats ( <i>Leopoldamys edwardsi</i> ). <i>Foodborne Pathogens and Disease</i> , 2019, 16, 539-542.	0.8	7
30	Seroprevalence and Risk Factors of <i>Toxoplasma gondii</i> Infection in Growth Stages of Pigs in Hunan Province, Subtropical China. <i>Vector-Borne and Zoonotic Diseases</i> , 2019, 19, 945-949.	0.6	8
31	Identification of <i>Cryptosporidium viatorum</i> XVa subtype family in two wild rat species in China. <i>Parasites and Vectors</i> , 2019, 12, 502.	1.0	14
32	The Complete Mitochondrial Genome of the Caecal Fluke of Poultry, <i>Postharmostomum commutatum</i> , as the First Representative from the Superfamily Brachylaimoidea. <i>Frontiers in Genetics</i> , 2019, 10, 1037.	1.1	13
33	Serum metabolomic alterations in Beagle dogs experimentally infected with <i>Toxocara canis</i> . <i>Parasites and Vectors</i> , 2019, 12, 447.	1.0	32
34	Molecular detection of <i>Neospora caninum</i> from naturally infected four passeriforme birds in China. <i>Acta Tropica</i> , 2019, 197, 105044.	0.9	4
35	Comparative analysis of mitochondrial DNA datasets indicates that <i>Toxascaris leonina</i> represents a species complex. <i>Parasites and Vectors</i> , 2019, 12, 194.	1.0	19
36	Mitochondrial Gene Heterogeneity and Population Genetics of <i>Haemaphysalis longicornis</i> (Acari: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	5

#	ARTICLE	IF	CITATIONS
37	Mitochondrial Genome Fragmentation Unites the Parasitic Lice of Eutherian Mammals. <i>Systematic Biology</i> , 2019, 68, 430-440.	2.7	84
38	Molecular Prevalence and Genetic Characterization of <i>Toxoplasma gondii</i> in Wild Birds in Hunan Province, China. <i>Vector-Borne and Zoonotic Diseases</i> , 2019, 19, 378-383.	0.6	2
39	Veterinary parasitology teaching in China in the 21st century – Challenges, opportunities and perspectives. <i>Veterinary Parasitology</i> , 2018, 252, 70-73.	0.7	3
40	Seroprevalence and Risk Factors of <i>Chlamydia abortus</i> Infection in Goats in Hunan Province, Subtropical China. <i>Vector-Borne and Zoonotic Diseases</i> , 2018, 18, 500-503.	0.6	9
41	Proteomics analysis of faecal proteins in the tick <i>Haemaphysalis flava</i> . <i>Parasites and Vectors</i> , 2018, 11, 89.	1.0	7
42	Molecular characterization of hard tick <i>Haemaphysalis longicornis</i> from China by sequences of the internal transcribed spacers of ribosomal DNA. <i>Experimental and Applied Acarology</i> , 2018, 74, 171-176.	0.7	6
43	Genetic analysis of <i>Toxocara cati</i> (Nematoda: Ascarididae) from Guangdong province, subtropical China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 132-135.	0.7	10
44	Characterization of the complete mitochondrial genome of <i>Marshallagia marshalli</i> and phylogenetic implications for the superfamily Trichostrongyloidea. <i>Parasitology Research</i> , 2018, 117, 307-313.	0.6	7
45	Molecular Detection and Genotyping of <i>Toxoplasma gondii</i> in Pigs for Human Consumption in Hunan Province, China. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 809-813.	0.8	5
46	Comparative analyses of the mitochondrial genome of the sheep ked <i>Melophagus ovinus</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2677-2683.	0.6	10
47	Toxocarasis: a silent threat with a progressive public health impact. <i>Infectious Diseases of Poverty</i> , 2018, 7, 59.	1.5	134
48	<i>Enterocytozoon bienersi</i> in Minks ( <i>Neovison vison</i> ) in Northern China: A Public Health Concern. <i>Frontiers in Microbiology</i> , 2018, 9, 1221.	1.5	13
49	First Report of <i>Ixodes nipponensis</i> Infection in Goats in China. <i>Vector-Borne and Zoonotic Diseases</i> , 2018, 18, 575-578.	0.6	5
50	Sequence variation in three mitochondrial genes among <i>Gasterophilus intestinalis</i> isolates from two distinct regions in China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 37-40.	0.7	2
51	Genetic variation in mitochondrial genes of the tick <i>Haemaphysalis flava</i> collected from wild hedgehogs in China. <i>Experimental and Applied Acarology</i> , 2017, 71, 131-137.	0.7	6
52	PCR denaturing gradient gel electrophoresis as a useful method to identify of intestinal bacteria flora in <i>Haemaphysalis flava</i> ticks. <i>Acta Parasitologica</i> , 2017, 62, 269-272.	0.4	4
53	De novo transcriptome sequencing and analysis of the juvenile and adult stages of <i>Fasciola gigantica</i> . <i>Infection, Genetics and Evolution</i> , 2017, 51, 33-40.	1.0	18
54	Complete mitochondrial genomes of <i>Gnathostoma nipponicum</i> and <i>Gnathostoma</i> sp., and their comparison with other <i>Gnathostoma</i> species. <i>Infection, Genetics and Evolution</i> , 2017, 48, 109-115.	1.0	8

#	ARTICLE	IF	CITATIONS
55	Complete mitochondrial genomes of <i>Triodontophorus serratus</i> and <i>Triodontophorus nipponicus</i> , and their comparison with <i>Triodontophorus brevicauda</i> . <i>Experimental Parasitology</i> , 2017, 181, 88-93.	0.5	10
56	<i>Fasciolopsis buski</i> (Digenea: Fasciolidae) from China and India may represent distinct taxa based on mitochondrial and nuclear ribosomal DNA sequences. <i>Parasites and Vectors</i> , 2017, 10, 101.	1.0	30
57	Microbial population analysis of the midgut of <i>Melophagus ovinus</i> via high-throughput sequencing. <i>Parasites and Vectors</i> , 2017, 10, 382.	1.0	19
58	Complete mitochondrial genome of the giant liver fluke <i>Fascioloides magna</i> (Digenea: Fasciolidae) and its comparison with selected trematodes. <i>Parasites and Vectors</i> , 2016, 9, 429.	1.0	21
59	Seroprevalence of <i>Toxoplasma gondii</i> in goats in Hunan province, China. <i>Parasite</i> , 2016, 23, 44.	0.8	15
60	Mitochondrial Phylogenomics yields Strongly Supported Hypotheses for Ascaridomorph Nematodes. <i>Scientific Reports</i> , 2016, 6, 39248.	1.6	26
61	The complete mitochondrial genomes of <i>Gnathostoma doloresi</i> from China and Japan. <i>Parasitology Research</i> , 2016, 115, 4013-4020.	0.6	10
62	Mitochondrial genomes of <i>Heterakis gallinae</i> and <i>Heterakis beramporia</i> support that they belong to the infraorder Ascaridomorpha. <i>Infection, Genetics and Evolution</i> , 2016, 40, 228-235.	1.0	25
63	The complete mitochondrial genome of the dwarf tapeworm <i>Hymenolepis nana</i> a neglected zoonotic helminth. <i>Parasitology Research</i> , 2016, 115, 1253-1262.	0.6	21
64	Genetic variability among <i>Hymenolepis nana</i> isolates from different geographical regions in China revealed by sequence analysis of three mitochondrial genes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4646-4650.	0.7	5
65	The complete mitochondrial genome of <i>Gasterophilus intestinalis</i> , the first representative of the family Gasterophilidae. <i>Parasitology Research</i> , 2016, 115, 2573-2579.	0.6	10
66	The complete mitochondrial genome of <i>Metorchis orientalis</i> (Trematoda: Opisthorchiidae): Comparison with other closely related species and phylogenetic implications. <i>Infection, Genetics and Evolution</i> , 2016, 39, 45-50.	1.0	37
67	Mitochondrial genome of <i>Ogmocotyle sikae</i> and implications for phylogenetic studies of the Notocotylidae trematodes. <i>Infection, Genetics and Evolution</i> , 2016, 37, 208-214.	1.0	15
68	The complete mitochondrial genome of rabbit pinworm <i>Passalurus ambiguus</i> : genome characterization and phylogenetic analysis. <i>Parasitology Research</i> , 2016, 115, 423-429.	0.6	12
69	Sequencing and characterization of the complete mitochondrial genome from the pancreatic fluke <i>Eurytrema pancreaticum</i> (Trematoda: Dicrocoeliidae). <i>Gene</i> , 2016, 576, 160-165.	1.0	32
70	<i>Gnathostoma spinigerum</i> Mitochondrial Genome Sequence: a Novel Gene Arrangement and its Phylogenetic Position within the Class Chromadorea. <i>Scientific Reports</i> , 2015, 5, 12691.	1.6	22
71	The complete mitochondrial genome of <i>Pseudoterranova azarasi</i> and comparative analysis with other anisakid nematodes. <i>Infection, Genetics and Evolution</i> , 2015, 33, 293-298.	1.0	18
72	The complete mitochondrial genome of the gullet worm <i>Gongylonema pulchrum</i> : gene content, arrangement, composition and phylogenetic implications. <i>Parasites and Vectors</i> , 2015, 8, 100.	1.0	20

#	ARTICLE	IF	CITATIONS
73	Mitochondrial and nuclear ribosomal DNA dataset supports that <i>Paramphistomum leydeni</i> (Trematoda: Digenea) is a distinct rumen fluke species. <i>Parasites and Vectors</i> , 2015, 8, 201.	1.0	24
74	The complete mitochondrial genome sequence of <i>Eimeria magna</i> (Apicomplexa: Coccidia). <i>Mitochondrial DNA</i> , 2015, 26, 714-715.	0.6	13
75	The complete mitochondrial genomes of five <i>Eimeria</i> species infecting domestic rabbits. <i>Experimental Parasitology</i> , 2015, 159, 67-71.	0.5	12
76	The complete mitochondrial genome of <i>Strongylus equinus</i> (Chromadorea: Strongylidae): Comparison with other closely related species and phylogenetic analyses. <i>Experimental Parasitology</i> , 2015, 159, 94-99.	0.5	16
77	Seroprevalence of <i>Toxoplasma gondii</i> infection in Sows in Hunan Province, China. <i>Scientific World Journal</i> , The, 2014, 2014, 1-4.	0.8	2
78	Prevalence of <i>Sarcoptes scabiei</i> infection in Pet Dogs in Southern China. <i>Scientific World Journal</i> , The, 2014, 2014, 1-3.	0.8	3
79	High seroprevalence of <i>Chlamydia</i> infection in sows in Hunan province, subtropical China. <i>Tropical Animal Health and Production</i> , 2014, 46, 701-704.	0.5	8
80	The complete mitochondrial genome of <i>Toxascaris leonina</i> : Comparison with other closely related species and phylogenetic implications. <i>Infection, Genetics and Evolution</i> , 2014, 21, 329-333.	1.0	27
81	<i>Dicrocoelium chinensis</i> and <i>Dicrocoelium dendriticum</i> (Trematoda: Digenea) are distinct lancet fluke species based on mitochondrial and nuclear ribosomal DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 325-331.	1.2	47
82	Characterization of the complete mitochondrial genomes of <i>Nematodirus oiratianus</i> and <i>Nematodirus spathiger</i> of small ruminants. <i>Parasites and Vectors</i> , 2014, 7, 319.	1.0	15
83	The complete mitochondrial genome of the scab mite <i>Psoroptes cuniculi</i> (Arthropoda: Arachnida) provides insights into Acari phylogeny. <i>Parasites and Vectors</i> , 2014, 7, 340.	1.0	37
84	Complete mitochondrial genomes of the "intermediate form" of <i>Fasciola</i> and <i>Fasciola gigantica</i> , and their comparison with <i>F. hepatica</i> . <i>Parasites and Vectors</i> , 2014, 7, 150.	1.0	80
85	<i>Chabertia erschowi</i> (Nematoda) is a distinct species based on nuclear ribosomal DNA sequences and mitochondrial DNA sequences. <i>Parasites and Vectors</i> , 2014, 7, 44.	1.0	24
86	Comparative analyses of the complete mitochondrial genomes of the two ruminant hookworms <i>Bunostomum trigonocephalum</i> and <i>Bunostomum phlebotomum</i> . <i>Gene</i> , 2014, 541, 92-100.	1.0	29
87	Characterization of the complete mitochondrial genome of <i>Spirocerca lupi</i> : sequence, gene organization and phylogenetic implications. <i>Parasites and Vectors</i> , 2013, 6, 45.	1.0	35
88	Sequence variation in four mitochondrial genes among sibling species within <i>Contraecaecum rudolphii sensu lato</i> . <i>Molecular and Cellular Probes</i> , 2013, 27, 145-148.	0.9	9
89	The complete mitochondrial genomes of three parasitic nematodes of birds: a unique gene order and insights into nematode phylogeny. <i>BMC Genomics</i> , 2013, 14, 414.	1.2	76
90	The complete mitochondrial genomes of <i>Oesophagostomum asperum</i> and <i>Oesophagostomum columbianum</i> in small ruminants. <i>Infection, Genetics and Evolution</i> , 2013, 19, 205-211.	1.0	15

#	ARTICLE	IF	CITATIONS
91	Mitochondrial Genome of the Eyeworm, <i>Thelazia callipaeda</i> (Nematoda: Spirurida), as the First Representative from the Family Thelaziidae. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2029.	1.3	36
92	Complete Mitochondrial Genome Sequence Data Provides Genetic Evidence That the Brown Dog Tick <i>Rhipicephalus sanguineus</i> (Acari: Ixodidae) Represents a Species Complex. <i>International Journal of Biological Sciences</i> , 2013, 9, 361-369.	2.6	90
93	Mitochondrial and Nuclear Ribosomal DNA Evidence Supports the Existence of a New <i>Trichuris</i> Species in the Endangered François's Leaf-Monkey. <i>PLoS ONE</i> , 2013, 8, e66249.	1.1	40
94	Clear Genetic Distinctiveness between Human- and Pig-Derived <i>Trichuris</i> Based on Analyses of Mitochondrial Datasets. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1539.	1.3	98
95	RT-PCR test for detecting porcine sapovirus in weanling piglets in Hunan Province, China. <i>Tropical Animal Health and Production</i> , 2012, 44, 1335-1339.	0.5	17
96	The complete mitochondrial genome sequence of <i>Eimeria mitis</i> (Apicomplexa: Coccidia). <i>Mitochondrial DNA</i> , 2012, 23, 341-343.	0.6	21
97	Comparative analyses of the complete mitochondrial genomes of <i>Ascaris lumbricoides</i> and <i>Ascaris suum</i> from humans and pigs. <i>Gene</i> , 2012, 492, 110-116.	1.0	124
98	Characterization of the complete mitochondrial genomes of two whipworms <i>Trichuris ovis</i> and <i>Trichuris discolor</i> (Nematoda: Trichuridae). <i>Infection, Genetics and Evolution</i> , 2012, 12, 1635-1641.	1.0	54
99	Characterization of the Complete Mitochondrial Genome Sequence of <i>Spirometra erinaceieuropaei</i> (Cestoda: Diphylobothriidae) from China. <i>International Journal of Biological Sciences</i> , 2012, 8, 640-649.	2.6	34
100	<i>Contraecaecum rudolphii</i> B: Gene content, arrangement and composition of its complete mitochondrial genome compared with <i>Anisakis simplex</i> s.l.. <i>Experimental Parasitology</i> , 2012, 130, 135-140.	0.5	23
101	<i>Oesophagostomum dentatum</i> and <i>Oesophagostomum quadrispinulatum</i> : Characterization of the complete mitochondrial genome sequences of the two pig nodule worms. <i>Experimental Parasitology</i> , 2012, 131, 1-7.	0.5	32
102	Seroprevalence of porcine cytomegalovirus and sapovirus infection in pigs in Hunan province, China. <i>Archives of Virology</i> , 2012, 157, 521-524.	0.9	11
103	The Complete Mitochondrial Genome of <i>Galba perversa</i> (Gastropoda: Mollusca), an Intermediate Host Snail of <i>Fasciola</i> spp. <i>PLoS ONE</i> , 2012, 7, e42172.	1.1	33
104	Characterization of the complete mitochondrial genomes of five <i>Eimeria</i> species from domestic chickens. <i>Gene</i> , 2011, 480, 28-33.	1.0	60
105	The complete mitochondrial genomes of three cestode species of <i>Taenia</i> infecting animals and humans. <i>Molecular Biology Reports</i> , 2011, 38, 2249-2256.	1.0	62
106	Comparative Mitochondrial Genomic Analysis Robustly Supported That Cat Tapeworm <i>Hydatigera taeniaeformis</i> (Platyhelminthes: Cestoda) Represents a Species Complex. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2