

Renfu Shao

List of Publications by Year in descending order

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86
papers

4,931
citations

117571

34
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95218

68
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88
docs citations

88
times ranked

5062
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12168-12173.	3.3	482
2	Genomic insights into the Ixodes scapularis tick vector of Lyme disease. Nature Communications, 2016, 7, 10507.	5.8	450
3	The Argasidae, Ixodidae and Nuttalliellidae (Acari: Ixodida) of the world: a list of valid species names. Zootaxa, 2010, 2528, 1.	0.2	421
4	The Highly Rearranged Mitochondrial Genome of the Plague Thrips, Thrips imaginis (Insecta: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 1 rRNA Genes. Molecular Biology and Evolution, 2003, 20, 362-370.	3.5	186
5	Phylogenetic analysis of mitochondrial genome sequences indicates that the cattle tick, Rhipicephalus (Boophilus) microplus, contains a cryptic species. Molecular Phylogenetics and Evolution, 2014, 76, 241-253.	1.2	180
6	Numerous Gene Rearrangements in the Mitochondrial Genome of the Wallaby Louse, Heterodoxus macropus (Phthiraptera). Molecular Biology and Evolution, 2001, 18, 858-865.	3.5	167
7	The single mitochondrial chromosome typical of animals has evolved into 18 minichromosomes in the human body louse, <i>Pediculus humanus</i> . Genome Research, 2009, 19, 904-912.	2.4	155
8	Rates of Gene Rearrangement and Nucleotide Substitution Are Correlated in the Mitochondrial Genomes of Insects. Molecular Biology and Evolution, 2003, 20, 1612-1619.	3.5	145
9	Higher-level phylogeny of paraneopteran insects inferred from mitochondrial genome sequences. Scientific Reports, 2015, 5, 8527.	1.6	140
10	Evolution of Duplicate Control Regions in the Mitochondrial Genomes of Metazoa: A Case Study with Australasian Ixodes Ticks. Molecular Biology and Evolution, 2005, 22, 620-629.	3.5	129
11	Increased Rate of Gene Rearrangement in the Mitochondrial Genomes of Three Orders of Hemipteroid Insects. Molecular Biology and Evolution, 2001, 18, 1828-1832.	3.5	98
12	Molecular phylogeny of soft ticks (Ixodida: Argasidae) inferred from mitochondrial genome and nuclear rRNA sequences. Ticks and Tick-borne Diseases, 2014, 5, 195-207.	1.1	95
13	Phylogenetic analysis of ticks (Acari: Ixodida) using mitochondrial genomes and nuclear rRNA genes indicates that the genus Amblyomma is polyphyletic. Molecular Phylogenetics and Evolution, 2012, 64, 45-55.	1.2	91
14	Evolution of Extensively Fragmented Mitochondrial Genomes in the Lice of Humans. Genome Biology and Evolution, 2012, 4, 1088-1101.	1.1	86
15	Phylogenetic analysis of the mitochondrial genomes and nuclear rRNA genes of ticks reveals a deep phylogenetic structure within the genus Haemaphysalis and further elucidates the polyphyly of the genus Amblyomma with respect to Amblyomma spheonodonti and Amblyomma elaphense. Ticks and Tick-borne Diseases, 2013, 4, 265-274.	1.1	85
16	High-level phylogeny of the Coleoptera inferred with mitochondrial genome sequences. Molecular Phylogenetics and Evolution, 2016, 104, 99-111.	1.2	85
17	Mitochondrial Genome Fragmentation Unites the Parasitic Lice of Eutherian Mammals. Systematic Biology, 2019, 68, 430-440.	2.7	84
18	Applications of nanotechnology for melanoma treatment, diagnosis, and theranostics. International Journal of Nanomedicine, 2013, 8, 2677.	3.3	83

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19	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
20	<scp>PI</scp>3K/Akt</scp>/mTOR</scp> pathway dual inhibitor <scp>BEZ</scp>235 suppresses the stemness of colon cancer stem cells. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2015, 42, 1317-1326.	0.9	76
21	Novel Mitochondrial Gene Content and Gene Arrangement Indicate Illegitimate Inter-mtDNA Recombination in the Chigger Mite, <i>Leptotrombidium pallidum</i> . <i>Journal of Molecular Evolution</i> , 2005, 60, 764-773.	0.8	72
22	Molecular Mechanisms for the Variation of Mitochondrial Gene Content and Gene Arrangement Among Chigger Mites of the Genus <i>Leptotrombidium</i> (Acari: Acariformes). <i>Journal of Molecular Evolution</i> , 2006, 63, 251-261.	0.8	65
23	Activation of PI3K/Akt/mTOR Pathway and Dual Inhibitors of PI3K and mTOR in Endometrial Cancer. <i>Current Medicinal Chemistry</i> , 2014, 21, 3070-3080.	1.2	64
24	The Multipartite Mitochondrial Genome of <i>Liposcelis bostrychophila</i> : Insights into the Evolution of Mitochondrial Genomes in Bilateral Animals. <i>PLoS ONE</i> , 2012, 7, e33973.	1.1	64
25	Phylogenetic and phylogeographic relationships in <i>Ixodes holocyclus</i> and <i>Ixodes cornuatus</i> (Acari: Tj ETQq1 1 0.784314 rgBT /Overlo 871-880.	1.3	63
26	Molecular survey of hard ticks in endemic areas of tick-borne diseases in China. <i>Ticks and Tick-borne Diseases</i> , 2013, 4, 288-296.	1.1	63
27	The phylogenetic position of eriophyoid mites (superfamily Eriophyoidea) in Acariformes inferred from the sequences of mitochondrial genomes and nuclear small subunit (18S) rRNA gene. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 271-282.	1.2	58
28	Molecular Mechanisms of Antipsychotic Drug-Induced Diabetes. <i>Frontiers in Neuroscience</i> , 2017, 11, 643.	1.4	57
29	Nanotechnology in the management of cervical cancer. <i>Reviews in Medical Virology</i> , 2015, 25, 72-83.	3.9	48
30	Fragmented mitochondrial genomes of the rat louse, <i>Polyplax asiatica</i> and <i>Polyplax spinulosa</i> : intra-genus variation in fragmentation pattern and a possible link between the extent of fragmentation and the length of life cycle. <i>BMC Genomics</i> , 2014, 15, 44.	1.2	44
31	Substantial Variation in the Extent of Mitochondrial Genome Fragmentation among Blood-Sucking Lice of Mammals. <i>Genome Biology and Evolution</i> , 2013, 5, 1298-1308.	1.1	42
32	Mitochondrial genome evolution and tRNA truncation in Acariformes mites: new evidence from eriophyoid mites. <i>Scientific Reports</i> , 2016, 6, 18920.	1.6	42
33	Integrative Genome-Scale DNA Methylation Analysis of a Large and Unselected Cohort Reveals 5 Distinct Subtypes of Colorectal Adenocarcinomas. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019, 8, 269-290.	2.3	42
34	Phylogenies from mitochondrial genomes of 120 species of ticks: Insights into the evolution of the families of ticks and of the genus <i>Amblyomma</i> . <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101577.	1.1	38
35	Isolation and genetic characterization of hantaviruses carried by <i>Microtus</i> voles in China. <i>Journal of Medical Virology</i> , 2008, 80, 680-688.	2.5	37
36	Fragmented mitochondrial genomes in two suborders of parasitic lice of eutherian mammals (Anoplura and Rhynchophthirina, Insecta). <i>Scientific Reports</i> , 2015, 5, 17389.	1.6	37

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37	Nuclear (18S-28S rRNA) and mitochondrial genome markers of <i>Carios (Carios) vespertilionis</i> (Argasidae) support <i>Carios Latreille, 1796</i> as a lineage embedded in the <i>Ornithodorinae</i> : re-classification of the <i>Carios sensu Klompen and Oliver (1993)</i> clade into its respective subgenera. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101688.	1.1	37
38	Relationships among the three major lineages of the Acari (Arthropoda:Arachnida) inferred from small subunit rRNA: paraphyly of the Parasitiformes with respect to the Opilioacariformes and relative rates of nucleotide substitution. <i>Invertebrate Systematics</i> , 2005, 19, 383.	0.5	36
39	Rearrangement of mitochondrial tRNA genes in flat bugs (Hemiptera: Aradidae). <i>Scientific Reports</i> , 2016, 6, 25725.	1.6	36
40	Novel insights into mitochondrial gene rearrangement in thrips (Insecta: Thysanoptera) from the grass thrips, <i>Anaphothrips obscurus</i> . <i>Scientific Reports</i> , 2017, 7, 4284.	1.6	34
41	The mitochondrial genome of the chimpanzee louse, <i>Pediculus schaeffi</i> : insights into the process of mitochondrial genome fragmentation in the blood-sucking lice of great apes. <i>BMC Genomics</i> , 2015, 16, 661.	1.2	32
42	Mitochondrial Genomes of Two Barklice, <i>Psococerastis albimaculata</i> and <i>Longivalvus hyalospilus</i> (Psocoptera: Psocomorpha): Contrasting Rates in Mitochondrial Gene Rearrangement between Major Lineages of Psocodea. <i>PLoS ONE</i> , 2013, 8, e61685.	1.1	32
43	Heteroplasmy in the Mitochondrial Genomes of Human Lice and Ticks Revealed by High Throughput Sequencing. <i>PLoS ONE</i> , 2013, 8, e73329.	1.1	32
44	The mitochondrial genomes of sarcoptiform mites: are any transfer RNA genes really lost?. <i>BMC Genomics</i> , 2018, 19, 466.	1.2	29
45	Genetic variations in E6, E7 and the long control region of human papillomavirus type 16 among patients with cervical lesions in Xinjiang, China. <i>Cancer Cell International</i> , 2019, 19, 65.	1.8	29
46	Fragmented mitochondrial genomes are present in both major clades of the blood-sucking lice (suborder Anoplura): evidence from two <i>Hoplopleura</i> rodent lice (family Hoplopleuridae). <i>BMC Genomics</i> , 2014, 15, 751.	1.2	27
47	The Mitochondrial Genome of the Guanaco Louse, <i>Microthoracius praelongiceps</i> : Insights into the Ancestral Mitochondrial Karyotype of Sucking Lice (Anoplura, Insecta). <i>Genome Biology and Evolution</i> , 2017, 9, 431-445.	1.1	27
48	Effective inhibition of colon cancer cell growth with MgAl-layered double hydroxide (LDH) loaded 5-FU and PI3K/mTOR dual inhibitor BEZ-235 through apoptotic pathways. <i>International Journal of Nanomedicine</i> , 2014, 9, 3403.	3.3	26
49	Variation in mitochondrial minichromosome composition between blood-sucking lice of the genus <i>Haematopinus</i> that infest horses and pigs. <i>Parasites and Vectors</i> , 2014, 7, 144.	1.0	26
50	Mitochondrial Phylogenomics yields Strongly Supported Hypotheses for Ascaridomorph Nematodes. <i>Scientific Reports</i> , 2016, 6, 39248.	1.6	26
51	Chimeric mitochondrial minichromosomes of the human body louse, <i>Pediculus humanus</i> : Evidence for homologous and non-homologous recombination. <i>Gene</i> , 2011, 473, 36-43.	1.0	25
52	Mitochondrial genome reorganization characterizes various lineages of mesostigmatid mites (Acari: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	24
53	<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
54	Mitochondrial genome sequencing reveals potential origins of the scabies mite <i>Sarcoptes scabiei</i> infesting two iconic Australian marsupials. <i>BMC Evolutionary Biology</i> , 2017, 17, 233.	3.2	22

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55	The Highly Divergent Mitochondrial Genomes Indicate That the Booklouse, <i>Liposcelis bostrychophila</i> (Psocoptera: Liposcelidae) Is a Cryptic Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1039-1047.	0.8	21
56	Evolution of multipartite mitochondrial genomes in the booklice of the genus <i>Liposcelis</i> (Psocoptera). <i>BMC Genomics</i> , 2014, 15, 861.	1.2	20
57	Mitochondrial genome analysis reveals intraspecific variation within Australian hard tick species. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 677-681.	1.1	18
58	Morphological and molecular characterization of a sexually reproducing colony of the booklouse <i>Liposcelis bostrychophila</i> (Psocodea: Liposcelidae) found in Arizona. <i>Scientific Reports</i> , 2015, 5, 10429.	1.6	17
59	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
60	Down-regulation of the expression of CCAAT/enhancer binding protein β gene in cervical squamous cell carcinoma. <i>BMC Cancer</i> , 2014, 14, 417.	1.1	15
61	Implications of ghrelin and hexarelin in diabetes and diabetes-associated heart diseases. <i>Endocrine</i> , 2015, 49, 307-323.	1.1	14
62	Hexarelin Protects Rodent Pancreatic β -Cells Function from Cytotoxic Effects of Streptozotocin Involving Mitochondrial Signalling Pathways In Vivo and In Vitro. <i>PLoS ONE</i> , 2016, 11, e0149730.	1.1	12
63	The Complete Mitochondrial Genome of the Booklouse, <i>Liposcelis decolor</i> : Insights into Gene Arrangement and Genome Organization within the Genus <i>Liposcelis</i> . <i>PLoS ONE</i> , 2014, 9, e91902.	1.1	12
64	Down-regulation of IFITM1 and its growth inhibitory role in cervical squamous cell carcinoma. <i>Cancer Cell International</i> , 2017, 17, 88.	1.8	11
65	Screening for HPV infection in exfoliated cervical cells of women from different ethnic groups in Yili, Xinjiang, China. <i>Scientific Reports</i> , 2019, 9, 3468.	1.6	10
66	Emerging and well-characterized chlamydial infections detected in a wide range of wild Australian birds. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	9
67	Human pediculosis, a global public health problem. <i>Infectious Diseases of Poverty</i> , 2022, 11, .	1.5	9
68	Methylation in the Promoters of <i>HS3ST2</i> and <i>CCNA1</i> Genes is Associated with Cervical Cancer in Uygur Women in Xinjiang. <i>International Journal of Biological Markers</i> , 2014, 29, 354-362.	0.7	8
69	Variants of human papillomaviruses 16 (HPV16) in Uigur women in Xinjiang, China. <i>Infectious Agents and Cancer</i> , 2016, 11, 44.	1.2	7
70	Frequent tRNA gene translocation towards the boundaries with control regions contributes to the highly dynamic mitochondrial genome organization of the parasitic lice of mammals. <i>BMC Genomics</i> , 2021, 22, 598.	1.2	7
71	Methylation of the RASSF1A gene promoter in Uigur women with cervical squamous cell carcinoma. <i>Tumori</i> , 2009, 95, 76-80.	0.6	7
72	Fragmented mitochondrial genomes of seal lice (family Echinophthiriidae) and gorilla louse (family Tj ETQqO O O rgBT /Overlock 10 Tf 50 2022, 23, 283.	1.2	7

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73	A new species of sucking louse <i>Hoplopleura villosissima</i> n. sp. (Psocodea: Phthiraptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 507 (Psocodea: Phthiraptera: Polyplacidae) from the long-haired rat <i>Rattus villosissimus</i> Waite (Rodentia: Tj ETQq1 1 0.784314 rgBT /Overlock	1.0	5
74	Methylation in the promoter regions of WT1, NKX6-1 and DBC1 genes in cervical cancer tissues of Uygur women in Xinjiang. <i>Genetics and Molecular Biology</i> , 2018, 41, 9-17.	0.6	5
75	Fragmentation in mitochondrial genomes in relation to elevated sequence divergence and extreme rearrangements. <i>BMC Biology</i> , 2022, 20, 7.	1.7	5
76	Reconstruction of mitochondrial genomes from raw sequencing data provides insights on the phylogeny of Ixodes ticks and cautions for species misidentification. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 101832.	1.1	4
77	Description of the female, nymph and larva and mitochondrial genome, and redescription of the male of <i>Ixodes barkeri</i> Barker, 2019 (Acari: Ixodidae), from the short-beaked echidna, <i>Tachyglossus aculeatus</i> , with a consideration of the most suitable subgenus for this tick. <i>Parasites and Vectors</i> , 2022, 15, 117.	1.0	4
78	Rapid host expansion of an introduced parasite, the spiny rat louse <i>Polyplax spinulosa</i> (Psocodea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 508	1.0	8
79	The Value and Clinical Significance of ZNF582 Gene Methylation in the Diagnosis of Cervical Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 403-411.	1.0	3
80	Eight New Species of Sucking Lice (Psocodea: Phthiraptera) From Endemic Murine Rodents in Australia and an Updated Identification Key. <i>Journal of Medical Entomology</i> , 2021, 58, 298-319.	0.9	2
81	Analysis of genetic variation in human papillomavirus type 16 E1 and E2 in women with cervical infection in Xinjiang, China. <i>BMC Medical Genomics</i> , 2021, 14, 268.	0.7	2
82	Rediscovery of <i>Ixodes confusus</i> in Australia with the first description of the male from Australia, a redescription of the female and the mitochondrial (mt) genomes of five species of Ixodes. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 18, 1-11.	0.6	2
83	Possible therapeutic implication of PD-L1/PD-1 axis in endometrial cancer. <i>Journal of Solid Tumors</i> , 2015, 5, .	0.1	1
84	Two New Species of Sucking Lice (Psocodea: Phthiraptera: Hoplopleuridae) from Chestnut Mice, <i>Pseudomys gracilicaudatus</i> and <i>Pseudomys nanus</i> (Rodentia: Muridae), in Australia. <i>Journal of Medical Entomology</i> , 2021, 58, 1157-1165.	0.9	1
85	HPV16 E6 gene polymorphisms and the functions of the mutation site in cervical cancer among Uygur ethnic and Han nationality women in Xinjiang, China. <i>Cancer Cell International</i> , 2022, 22, 94.	1.8	1
86	A new species of sucking louse (Psocodea: Phthiraptera: Anoplura: Hoplopleuridae) from the pale field rat, <i>Rattus tunneyi</i> (Rodentia: Muridae), in Australia. <i>Zootaxa</i> , 2022, 5091, 85-94.	0.2	0