

# Shuyi Zhang

## List of Publications by Year in descending order

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110  
papers

6,141  
citations

109321

35  
h-index

76900

74  
g-index

112  
all docs

112  
docs citations

112  
times ranked

7437  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bats Are Natural Reservoirs of SARS-Like Coronaviruses. <i>Science</i> , 2005, 310, 676-679.	12.6	2,130
2	Review of Bats and SARS. <i>Emerging Infectious Diseases</i> , 2006, 12, 1834-1840.	4.3	375
3	Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases. <i>ISME Journal</i> , 2016, 10, 609-620.	9.8	249
4	Virome Analysis for Identification of Novel Mammalian Viruses in Bat Species from Chinese Provinces. <i>Journal of Virology</i> , 2012, 86, 10999-11012.	3.4	244
5	The evolution of color vision in nocturnal mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8980-8985.	7.1	202
6	Convergent sequence evolution between echolocating bats and dolphins. <i>Current Biology</i> , 2010, 20, R53-R54.	3.9	202
7	Evolutionary Relationships between Bat Coronaviruses and Their Hosts. <i>Emerging Infectious Diseases</i> , 2007, 13, 1526-1532.	4.3	123
8	The hearing gene <i>Prestin</i> reunites echolocating bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13959-13964.	7.1	116
9	Accelerated FoxP2 Evolution in Echolocating Bats. <i>PLoS ONE</i> , 2007, 2, e900.	2.5	103
10	Full-length genome sequences of two SARS-like coronaviruses in horseshoe bats and genetic variation analysis. <i>Journal of General Virology</i> , 2006, 87, 3355-3359.	2.9	96
11	Novel SARS-like Betacoronaviruses in Bats, China, 2011. <i>Emerging Infectious Diseases</i> , 2013, 19, 989-91.	4.3	93
12	MERS-Related Betacoronavirus in <i>Vespertilio superans</i> Bats, China. <i>Emerging Infectious Diseases</i> , 2014, 20, 1260-2.	4.3	90
13	Evolution of the Sweet Taste Receptor Gene <i>Tas1r2</i> in Bats. <i>Molecular Biology and Evolution</i> , 2010, 27, 2642-2650.	8.9	82
14	ORF8-Related Genetic Evidence for Chinese Horseshoe Bats as the Source of Human Severe Acute Respiratory Syndrome Coronavirus. <i>Journal of Infectious Diseases</i> , 2016, 213, 579-583.	4.0	77
15	Discovery of Itraconazole with Broad-Spectrum <i>In Vitro</i> Antienterovirus Activity That Targets Nonstructural Protein 3A. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2654-2665.	3.2	63
16	Adaptive Evolution of 5' <i>HoxD</i> Genes in the Origin and Diversification of the Cetacean Flipper. <i>Molecular Biology and Evolution</i> , 2008, 26, 613-622.	8.9	60
17	PHYLOGENETICS OF SMALL HORSESHOE BATS FROM EAST ASIA BASED ON MITOCHONDRIAL DNA SEQUENCE VARIATION. <i>Journal of Mammalogy</i> , 2006, 87, 1234-1240.	1.3	56
18	Cetaceans on a Molecular Fast Track to Ultrasonic Hearing. <i>Current Biology</i> , 2010, 20, 1834-1839.	3.9	56

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19	Identification of Diverse Bat Alphacoronaviruses and Betacoronaviruses in China Provides New Insights Into the Evolution and Origin of Coronavirus-Related Diseases. <i>Frontiers in Microbiology</i> , 2019, 10, 1900.	3.5	53
20	The Voltage-Gated Potassium Channel Subfamily KQT Member 4 (KCNQ4) Displays Parallel Evolution in Echolocating Bats. <i>Molecular Biology and Evolution</i> , 2012, 29, 1441-1450.	8.9	52
21	Discovery of Retroviral Homologs in Bats: Implications for the Origin of Mammalian Gammaretroviruses. <i>Journal of Virology</i> , 2012, 86, 4288-4293.	3.4	52
22	Rhodopsin Molecular Evolution in Mammals Inhabiting Low Light Environments. <i>PLoS ONE</i> , 2009, 4, e8326.	2.5	51
23	Genomic and Genetic Evidence for the Loss of Umami Taste in Bats. <i>Genome Biology and Evolution</i> , 2012, 4, 73-79.	2.5	51
24	Historical male-mediated introgression in horseshoe bats revealed by multilocus DNA sequence data. <i>Molecular Ecology</i> , 2010, 19, 1352-1366.	3.9	48
25	Identification of diverse groups of endogenous gammaretroviruses in mega- and microbats. <i>Journal of General Virology</i> , 2012, 93, 2037-2045.	2.9	48
26	The two suborders of chiropterans have the canonical heavy-chain immunoglobulin (Ig) gene repertoire of eutherian mammals. <i>Developmental and Comparative Immunology</i> , 2011, 35, 273-284.	2.3	45
27	Enterovirus 71 infection in children with hand, foot, and mouth disease in Shanghai, China: epidemiology, clinical feature and diagnosis. <i>Virology Journal</i> , 2015, 12, 83.	3.4	43
28	Prenatal development supports a single origin of laryngeal echolocation in bats. <i>Nature Ecology and Evolution</i> , 2017, 1, 21.	7.8	43
29	Differential stepwise evolution of SARS coronavirus functional proteins in different host species. <i>BMC Evolutionary Biology</i> , 2009, 9, 52.	3.2	42
30	Widespread Losses of Vomeronasal Signal Transduction in Bats. <i>Molecular Biology and Evolution</i> , 2011, 28, 7-12.	8.9	41
31	Doppler-shift compensation behavior in horseshoe bats revisited: auditory feedback controls both a decrease and an increase in call frequency. <i>Journal of Experimental Biology</i> , 2002, 205, 1607-1616.	1.7	41
32	Dietary analysis confirms that Rickett's big-footed bat ( <i>Myotis ricketti</i> ) is a piscivore. <i>Journal of Zoology</i> , 2003, 261, 245-248.	1.7	40
33	Diet, Echolocation Calls, and Phylogenetic Affinities of the Great Evening Bat ( <i>la io</i> ; <i>Vespertilionidae</i> ): Another Carnivorous Bat. <i>Journal of Mammalogy</i> , 2007, 88, 728-735.	1.3	39
34	Antioxidant Defenses in the Brains of Bats during Hibernation. <i>PLoS ONE</i> , 2016, 11, e0152135.	2.5	39
35	The Genomes of Two Bat Species with Long Constant Frequency Echolocation Calls. <i>Molecular Biology and Evolution</i> , 2017, 34, 20-34.	8.9	38
36	Comparison of Brain Transcriptome of the Greater Horseshoe Bats ( <i>Rhinolophus ferrumequinum</i> ) in Active and Torpid Episodes. <i>PLoS ONE</i> , 2014, 9, e107746.	2.5	37

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37	Progressive Pseudogenization: Vitamin C Synthesis and Its Loss in Bats. <i>Molecular Biology and Evolution</i> , 2011, 28, 1025-1031.	8.9	36
38	Seasonality of matings and births in captive Sichuan golden monkeys ( <i>Rhinopithecus roxellana</i> ). <i>American Journal of Primatology</i> , 2000, 51, 265-269.	1.7	31
39	Discovery of Diverse Rodent and Bat Pestiviruses With Distinct Genomic and Phylogenetic Characteristics in Several Chinese Provinces. <i>Frontiers in Microbiology</i> , 2018, 9, 2562.	3.5	30
40	As Blind as a Bat? Opsin Phylogenetics Illuminates the Evolution of Color Vision in Bats. <i>Molecular Biology and Evolution</i> , 2019, 36, 54-68.	8.9	28
41	Multiple bursts of pancreatic ribonuclease gene duplication in insect-eating bats. <i>Gene</i> , 2013, 526, 112-117.	2.2	27
42	Echolocation Calls, Diet, and Phylogenetic Relationships of Stoliczka's Trident Bat, <i>Aselliscus stoliczkanus</i> (Hipposideridae). <i>Journal of Mammalogy</i> , 2007, 88, 736-744.	1.3	26
43	Historical introgression and the persistence of ghost alleles in the intermediate horseshoe bat ( <i>Rhinolophus affinis</i> ). <i>Molecular Ecology</i> , 2013, 22, 1035-1050.	3.9	26
44	Adaptive Evolution in the Glucose Transporter 4 Gene <i>Slc2a4</i> in Old World Fruit Bats (Family: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462</i> )	2.5	25
45	Comparative inner ear transcriptome analysis between the Rickettsia big-footed bats ( <i>Myotis ricketti</i> ) and the greater short-nosed fruit bats ( <i>Cynopterus sphinx</i> ). <i>BMC Genomics</i> , 2013, 14, 916.	2.8	25
46	Unique expression patterns of multiple key genes associated with the evolution of mammalian flight. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20133133.	2.6	25
47	Comparison of whole embryonic development in the duck ( <i>Anas platyrhynchos</i> ) and goose ( <i>Anser</i> ) <i>Tj ETQq1 1 0.7843 14 rgBT /Overlock 3.4 25</i>	3.4	25
48	Recent Loss of Vitamin C Biosynthesis Ability in Bats. <i>PLoS ONE</i> , 2011, 6, e27114.	2.5	25
49	Multiple Adaptive Losses of Alanine-Glyoxylate Aminotransferase Mitochondrial Targeting in Fruit-Eating Bats. <i>Molecular Biology and Evolution</i> , 2012, 29, 1507-1511.	8.9	23
50	Prestin and high frequency hearing in mammals. <i>Communicative and Integrative Biology</i> , 2011, 4, 236-239.	1.4	22
51	Down but Not Out: The Role of MicroRNAs in Hibernating Bats. <i>PLoS ONE</i> , 2015, 10, e0135064.	2.5	22
52	Circular RNA Profiling Identifies Novel circPPARA that Promotes Intramuscular Fat Deposition in Pigs. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 4123-4137.	5.2	22
53	Evolution of opsin genes reveals a functional role of vision in the echolocating little brown bat ( <i>Myotis lucifugus</i> ). <i>Biochemical Systematics and Ecology</i> , 2009, 37, 154-161.	1.3	20
54	Genetic diversity of coronaviruses in <i>Miniopterus fuliginosus</i> bats. <i>Science China Life Sciences</i> , 2016, 59, 604-614.	4.9	20

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55	Genetic characteristics of H9N2 avian influenza viruses isolated from free-range poultry in Eastern China, in 2014–2015. <i>Poultry Science</i> , 2018, 97, 3793-3800.	3.4	20
56	Molecular signatures and functional analysis of beige adipocytes induced from in vivo intra-abdominal adipocytes. <i>Science Advances</i> , 2018, 4, eaar5319.	10.3	18
57	Differential Expression of Meis2, Mab21l2 and Tbx3 during Limb Development Associated with Diversification of Limb Morphology in Mammals. <i>PLoS ONE</i> , 2014, 9, e106100.	2.5	17
58	Following of Brown Capuchin Monkeys by White Hawks in French Guiana. <i>Condor</i> , 2000, 102, 198-201.	1.6	16
59	Dietary composition and echolocation call design of three sympatric insectivorous bat species from China. <i>Ecological Research</i> , 2008, 23, 113-119.	1.5	16
60	Differential introgression among loci across a hybrid zone of the intermediate horseshoe bat ( <i>Rhinolophus affinis</i> ). <i>BMC Evolutionary Biology</i> , 2014, 14, 154.	3.2	16
61	Identification of Candidate Circular RNAs Underlying Intramuscular Fat Content in the Donkey. <i>Frontiers in Genetics</i> , 2020, 11, 587559.	2.3	16
62	DIETARY CHARACTERISTICS OF MYOTIS RICKETTI IN BEIJING, NORTH CHINA. <i>Journal of Mammalogy</i> , 2006, 87, 339-344.	1.3	15
63	Molecular Data Support an Early Shift to an Intermediate-Light Niche in the Evolution of Mammals. <i>Molecular Biology and Evolution</i> , 2018, 35, 1130-1134.	8.9	15
64	Critical roles of mitochondria in brain activities of torpid <i>Myotis ricketti</i> bats revealed by a proteomic approach. <i>Journal of Proteomics</i> , 2014, 105, 266-284.	2.4	14
65	Prestin Shows Divergent Evolution Between Constant Frequency Echolocating Bats. <i>Journal of Molecular Evolution</i> , 2011, 73, 109-115.	1.8	13
66	Immunohistochemical evidence of cone-based ultraviolet vision in divergent bat species and implications for its evolution. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2012, 161, 398-403.	1.6	12
67	Co-activation of Akt, Nrf2, and NF- $\kappa$ B signals under UPRER in torpid <i>Myotis ricketti</i> bats for survival. <i>Communications Biology</i> , 2020, 3, 658.	4.4	11
68	Unveiling the Biogeography and Potential Functions of the Intestinal Digesta- and Mucosa-Associated Microbiome of Donkeys. <i>Frontiers in Microbiology</i> , 2020, 11, 596882.	3.5	11
69	Adaptive Evolution of the Myo6 Gene in Old World Fruit Bats (Family: Pteropodidae). <i>PLoS ONE</i> , 2013, 8, e62307.	2.5	10
70	Molecular Evolution of the Nuclear Factor (Erythroid-Derived 2)-Like 2 Gene Nrf2 in Old World Fruit Bats (Chiroptera: Pteropodidae). <i>PLoS ONE</i> , 2016, 11, e0146274.	2.5	10
71	Retention and losses of ultraviolet-sensitive visual pigments in bats. <i>Scientific Reports</i> , 2018, 8, 11933.	3.3	10
72	Scotopic rod vision in tetrapods arose from multiple early adaptive shifts in the rate of retinal release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12627-12628.	7.1	10

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73	Independent Losses of Visual Perception Genes <i>Cja10</i> and <i>Rbp3</i> in Echolocating Bats (Order: Tj ETQq1 1 0.784314 rgBT /Overclock 10 T	2.5	9
74	Homocysteine Homeostasis and Betaine-Homocysteine S-Methyltransferase Expression in the Brain of Hibernating Bats. <i>PLoS ONE</i> , 2013, 8, e85632.	2.5	9
75	Heteroplasmy and Ancient Translocation of Mitochondrial DNA to the Nucleus in the Chinese Horseshoe Bat ( <i>Rhinolophus sinicus</i> ) Complex. <i>PLoS ONE</i> , 2014, 9, e98035.	2.5	9
76	Synergy between <i>MC1R</i> and <i>ASIP</i> for coat color in horses ( <i>Equus caballus</i> ). <i>Journal of Animal Science</i> , 2019, 97, 1578-1585.	0.5	9
77	Differences in the gut microbiomes of dogs and wolves: roles of antibiotics and starch. <i>BMC Veterinary Research</i> , 2021, 17, 112.	1.9	9
78	Adaptive Functional Diversification of Lysozyme in Insectivorous Bats. <i>Molecular Biology and Evolution</i> , 2014, 31, 2829-2835.	8.9	8
79	Prolonged treatment with 3-isobutyl-1-methylxanthine improves the efficiency of differentiating 3T3-L1 cells into adipocytes. <i>Analytical Biochemistry</i> , 2016, 507, 18-20.	2.4	8
80	Repetitive transpositions of mitochondrial DNA sequences to the nucleus during the radiation of horseshoe bats ( <i>Rhinolophus</i> , Chiroptera). <i>Gene</i> , 2016, 581, 161-169.	2.2	8
81	Fruit bats as a natural reservoir of zoonotic viruses. <i>Science Bulletin</i> , 2003, 48, 1179-1182.	1.7	7
82	Characteristics of echolocating bats' auditory stereocilia length, compared with other mammals. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 492-496.	1.3	7
83	The Great Roundleaf Bat ( <i>Hipposideros armiger</i> ) as a Good Model for Cold-Induced Browning of Intra-Abdominal White Adipose Tissue. <i>PLoS ONE</i> , 2014, 9, e112495.	2.5	7
84	Phosphoenolpyruvate Carboxykinase 1 Gene ( <i>Pck1</i> ) Displays Parallel Evolution between Old World and New World Fruit Bats. <i>PLoS ONE</i> , 2015, 10, e0118666.	2.5	7
85	Relationship between echolocation frequency and body size in two species of hipposiderid bats. <i>Science Bulletin</i> , 2000, 45, 1587-1590.	1.7	6
86	Adaptive evolution of tight junction protein claudin-14 in echolocating whales. <i>Gene</i> , 2013, 530, 208-214.	2.2	6
87	Relaxed Evolution in the Tyrosine Aminotransferase Gene <i>Tat</i> in Old World Fruit Bats (Chiroptera: Tj ETQq1 1 0.784314 rgBT /Overclock 10 T	2.5	6
88	Parallel Evolution of the Glycogen Synthase 1 (Muscle) Gene <i>Gys1</i> Between Old World and New World Fruit Bats (Order: Chiroptera). <i>Biochemical Genetics</i> , 2014, 52, 443-458.	1.7	6
89	Adaptive Evolution of Feline Coronavirus Genes Based on Selection Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-7.	1.9	6
90	Pooled Sequencing Analysis of Geese ( <i>Anser cygnoides</i> ) Reveals Genomic Variations Associated With Feather Color. <i>Frontiers in Genetics</i> , 2021, 12, 650013.	2.3	6

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91	The Glycogen Synthase 2 Gene ( <i>Gys2</i> ) Displays Parallel Evolution Between Old World and New World Fruit Bats. <i>Journal of Molecular Evolution</i> , 2014, 78, 66-74.	1.8	5
92	Differential introgression suggests candidate beneficial and barrier loci between two parapatric subspecies of Pearson's horseshoe bat <i>Rhinolophus pearsoni</i> . <i>Environmental Epigenetics</i> , 2016, 62, 405-412.	1.8	5
93	Introgression of mitochondrial DNA promoted by natural selection in the Japanese pipistrelle bat ( <i>Pipistrellus abramus</i> ). <i>Genetica</i> , 2014, 142, 483-494.	1.1	4
94	Maintenance of neural activities in torpid <i>Rhinolophus ferrumequinum</i> bats revealed by 2D gel-based proteome analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1004-1019.	2.3	4
95	Accelerated Evolution of Limb-Related Gene <i>Hoxd11</i> in the Common Ancestor of Cetaceans and Ruminants (Cetruminantia). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 515-524.	1.8	4
96	Mucosal Microbiota and Metabolome in the Ileum of Hu Sheep Offered a Low-Grain, Pelleted or Non-pelleted High-Grain Diet. <i>Frontiers in Microbiology</i> , 2021, 12, 718884.	3.5	4
97	Spatial pattern in the foraging group of Sichuan golden monkeys. <i>Science Bulletin</i> , 1999, 44, 1369-1372.	1.7	3
98	Development and characterization of novel microsatellite markers from the Chinese rufous horseshoe bat ( <i>Rhinolophus sinicus</i> ) with cross-species amplification in closely related taxa. <i>Molecular Ecology Resources</i> , 2009, 9, 183-185.	4.8	3
99	Whole Genome Sequencing Reveals Signatures for Artificial Selection for Different Sizes in Japanese Primitive Dog Breeds. <i>Frontiers in Genetics</i> , 2021, 12, 671686.	2.3	3
100	Comparison of Coated and Uncoated Trace Minerals on Growth Performance, Tissue Mineral Deposition, and Intestinal Microbiota in Ducks. <i>Frontiers in Microbiology</i> , 2022, 13, 831945.	3.5	3
101	OB-RL silencing inhibits the thermoregulatory ability of Great Roundleaf Bats ( <i>Hipposideros armiger</i> ). <i>General and Comparative Endocrinology</i> , 2014, 204, 80-87.	1.8	2
102	BGD: A Database of Bat Genomes. <i>PLoS ONE</i> , 2015, 10, e0131296.	2.5	2
103	A missense mutation in <i>ASIP</i> is associated with light point variation in donkeys. <i>Animal Genetics</i> , 2020, 51, 629-629.	1.7	2
104	Parallel Independent Losses of G-Type Lysozyme Genes in Hairless Aquatic Mammals. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	2
105	The complete mitochondrial genome of the king horseshoe bat ( <i>Rhinolophus rex</i> ) using next-generation sequencing and Sanger sequencing. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4545-4546.	0.7	1
106	Parallel Amino Acid Deletions of Prestin Protein in Two Dramatically Divergent Bat Lineages Suggest the Complexity of the Evolution of Echolocation in Bats. <i>Acta Chiropterologica</i> , 2019, 20, 311.	0.6	1
107	Echolocation calls of <i>Myotis frater</i> (Chiroptera: Hipposideridae) during search flight. <i>Science Bulletin</i> , 2000, 45, 1690-1692.	1.7	0
108	A complete mitochondrial genome of the Damaraland mole rat <i>Fukomys damarensis</i> retrieved from the published genome of the brandt's bat <i>Myotis brandtii</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4282-4283.	0.7	0

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109	HUMAN-LIKE MENSTRUAL CYCLE EXHIBITED BY WILD FULVOUS BATS ( <i>Rousettus leschenaultia</i> ). <i>Biology of Reproduction</i> , 2007, 77, 157-157.	2.7	0
110	Adaptive Evolution of the Fox Coronavirus Based on Genome-Wide Sequence Analysis. <i>BioMed Research International</i> , 2022, 2022, 1-8.	1.9	0