

# De Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7549203/publications.pdf>

Version: 2024-02-01

15  
papers

179  
citations

1163117

8  
h-index

1199594

12  
g-index

16  
all docs

16  
docs citations

16  
times ranked

241  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Consequences of Long-Term Population Decline in Brown Eared Pheasant. <i>Molecular Biology and Evolution</i> , 2021, 38, 263-273.	8.9	36
2	Population genomic, climatic and anthropogenic evidence suggest the role of human forces in endangerment of green peafowl ( <i>Pavo muticus</i> ). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210073.	2.6	26
3	Was the exposed continental shelf a long-distance colonization route in the ice age? The Southeast Asia origin of Hainan and Taiwan partridges. <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 167-173.	2.7	18
4	Divergence time estimation of Galliformes based on the best gene shopping scheme of ultraconserved elements. <i>Bmc Ecology and Evolution</i> , 2021, 21, 209.	1.6	17
5	Species delimitation in the Chinese bamboo partridge <i>Bambusicola thoracica</i> (Phasianidae; <i>Phasianinae</i> ). <i>Zoologica Scripta</i> , 2014, 43, 562-575.	1.7	15
6	Demographic Histories and Genome-Wide Patterns of Divergence in Incipient Species of Shorebirds. <i>Frontiers in Genetics</i> , 2019, 10, 919.	2.3	14
7	A simple strategy for recovering ultraconserved elements, exons, and introns from low coverage shotgun sequencing of museum specimens: Placement of the partridge genus <i>Tropicoperdix</i> within the galliformes. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 304-314.	2.7	13
8	Revival of the genus <i>Tropicoperdix</i> Blyth 1859 (Phasianidae, Aves) using multilocus sequence data. <i>Zoological Journal of the Linnean Society</i> , 2015, 175, 429-438.	2.3	10
9	Molecular demographic history of the Hainan Peacock Pheasant ( <i>Polyplectron katsumatae</i> ) and its conservation implications. <i>Science Bulletin</i> , 2013, 58, 2185-2190.	1.7	6
10	Genome assembly of the common pheasant <i>Phasianus colchicus</i> , a model for speciation and ecological genomics. <i>Genome Biology and Evolution</i> , 2019, 11, 3326-3331.	2.5	6
11	Comparative analysis of mite genomes reveals positive selection for diet adaptation. <i>Communications Biology</i> , 2021, 4, 668.	4.4	6
12	Characterization of novel microsatellite markers of the Emei Shan Liocichla using restriction site-associated DNA sequencing. <i>Avian Research</i> , 2017, 8, .	1.2	5
13	A pipeline for effectively developing highly polymorphic simple sequence repeats markers based on multi-sample genomic data. <i>Ecology and Evolution</i> , 2022, 12, e8705.	1.9	5
14	Disentangling the evolutionary history and biogeography of hill partridges (Phasianidae, <i>Arborophila</i> ) from low coverage shotgun sequences. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106895.	2.7	2
15	Disentangling the relative roles of geographical and ecological factors in driving genomic variations of a widely distributed bird across a longitudinal gradient. <i>Journal of Avian Biology</i> , 2022, 2022, .	1.2	0