

Alexandre Hassanin

List of Publications by Year in descending order

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92
papers

6,706
citations

101496

36
h-index

64755

79
g-index

102
all docs

102
docs citations

102
times ranked

7702
citing authors

#	ARTICLE	IF	CITATIONS
1	Fruit bats as reservoirs of Ebola virus. <i>Nature</i> , 2005, 438, 575-576.	13.7	1,320
2	Bats host major mammalian paramyxoviruses. <i>Nature Communications</i> , 2012, 3, 796.	5.8	546
3	Pattern and timing of diversification of Cetartiodactyla (Mammalia, Laurasiatheria), as revealed by a comprehensive analysis of mitochondrial genomes. <i>Comptes Rendus - Biologies</i> , 2012, 335, 32-50.	0.1	448
4	Evidence for Multiple Reversals of Asymmetric Mutational Constraints during the Evolution of the Mitochondrial Genome of Metazoa, and Consequences for Phylogenetic Inferences. <i>Systematic Biology</i> , 2005, 54, 277-298.	2.7	375
5	Phylogeny of Arthropoda inferred from mitochondrial sequences: Strategies for limiting the misleading effects of multiple changes in pattern and rates of substitution. <i>Molecular Phylogenetics and Evolution</i> , 2006, 38, 100-116.	1.2	245
6	Mitochondrial and nuclear phylogenies of Cervidae (Mammalia, Ruminantia): Systematics, morphology, and biogeography. <i>Molecular Phylogenetics and Evolution</i> , 2006, 40, 101-117.	1.2	229
7	Molecular and Morphological Phylogenies of Ruminantia and the Alternative Position of the Moschidae. <i>Systematic Biology</i> , 2003, 52, 206-228.	2.7	224
8	The Tribal Radiation of the Family Bovidae (Artiodactyla) and the Evolution of the Mitochondrial Cytochrome b Gene. <i>Molecular Phylogenetics and Evolution</i> , 1999, 13, 227-243.	1.2	192
9	Phylogenetic Analysis of Invertebrate Lysozymes and the Evolution of Lysozyme Function. <i>Journal of Molecular Evolution</i> , 2002, 54, 652-664.	0.8	192
10	Evolution of the Mitochondrial Genome in Mammals Living at High Altitude: New Insights from a Study of the Tribe Caprini (Bovidae, Antilopinae). <i>Journal of Molecular Evolution</i> , 2009, 68, 293-310.	0.8	174
11	A novel SARS-CoV-2 related coronavirus in bats from Cambodia. <i>Nature Communications</i> , 2021, 12, 6563.	5.8	127
12	Captured retroviral envelope syncytin gene associated with the unique placental structure of higher ruminants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E828-37.	3.3	123
13	The "evolutionary signal"™ of homoplasy in protein-coding gene sequences and its consequences for a priori weighting in phylogeny. <i>Comptes Rendus De L'Académie Des Sciences Série 3, Sciences De La Vie</i> , 1998, 321, 611-620.	0.8	111
14	Molecular phylogeny of the tribe Bovini (Bovidae, Bovinae) and the taxonomic status of the Kouprey, <i>Bos sauveli</i> Urbain 1937. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 896-907.	1.2	104
15	Isolates of Zaire ebolavirus from wild apes reveal genetic lineage and recombinants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17123-17127.	3.3	102
16	Evolutionary origins of hepatitis A virus in small mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15190-15195.	3.3	99
17	Title is missing!. <i>Journal of Mammalian Evolution</i> , 1998, 5, 217-236.	1.0	96
18	Molecular phylogenetics unveils the ancient evolutionary origins of the enigmatic fairy armadillos. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 673-680.	1.2	90

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19	Phylogenetic relationships within the Laridae (Charadriiformes: Aves) inferred from mitochondrial markers. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 686-699.	1.2	89
20	Hybrid origin of the Pliocene ancestor of wild goats. <i>Molecular Phylogenetics and Evolution</i> , 2006, 41, 395-404.	1.2	82
21	MADS-Box Genes in <i>Ginkgo biloba</i> and the Evolution of the AGAMOUS Family. <i>Molecular Biology and Evolution</i> , 2003, 20, 842-854.	3.5	75
22	Molecular evidence for the polyphyly of the genus <i>Hemitragus</i> (Mammalia, Bovidae). <i>Molecular Phylogenetics and Evolution</i> , 2005, 36, 154-168.	1.2	73
23	Combining multiple autosomal introns for studying shallow phylogeny and taxonomy of Laurasiatherian mammals: Application to the tribe Bovini (Cetartiodactyla, Bovidae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 766-775.	1.2	71
24	Molecular phylogeny of caprines (Bovidae, Antilopinae): the question of their origin and diversification during the Miocene. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2005, 43, 49-60.	0.6	69
25	Evolutionary affinities of the enigmatic saola (<i>Pseudoryx nghetinhensis</i>) in the context of the molecular phylogeny of Bovidae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 893-900.	1.2	68
26	Multiple host-switching of Haemosporidia parasites in bats. <i>Malaria Journal</i> , 2007, 6, 157.	0.8	59
27	Comparisons between mitochondrial genomes of domestic goat (<i>Capra hircus</i>) reveal the presence of numts and multiple sequencing errors. <i>Mitochondrial DNA</i> , 2010, 21, 68-76.	0.6	56
28	Genetic diversity of coronaviruses in bats in Lao PDR and Cambodia. <i>Infection, Genetics and Evolution</i> , 2017, 48, 10-18.	1.0	56
29	DNA barcoding of African fruit bats (Mammalia, Pteropodidae). The mitochondrial genome does not provide a reliable discrimination between <i>Epomophorus agambianus</i> and <i>Micropteropus pusillus</i> . <i>Comptes Rendus - Biologies</i> , 2011, 334, 544-554.	0.1	55
30	Nucleotide Composition of CO1 Sequences in Chelicerata (Arthropoda): Detecting New Mitogenomic Rearrangements. <i>Journal of Molecular Evolution</i> , 2012, 74, 81-95.	0.8	54
31	The comparative phylogeography of fruit bats of the tribe Scotonycterini (Chiroptera, Pteropodidae) reveals cryptic species diversity related to African Pleistocene forest refugia. <i>Comptes Rendus - Biologies</i> , 2015, 338, 197-211.	0.1	53
32	The role of Pleistocene glaciations in shaping the evolution of polar and brown bears. Evidence from a critical review of mitochondrial and nuclear genome analyses. <i>Comptes Rendus - Biologies</i> , 2015, 338, 494-501.	0.1	52
33	Molecular systematics and phylogeography of the tribe Myonycterini (Mammalia, Pteropodidae) inferred from mitochondrial and nuclear markers. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 126-137.	1.2	48
34	Mitochondrial DNA variability in <i>Giraffa camelopardalis</i> : consequences for taxonomy, phylogeography and conservation of giraffes in West and central Africa. <i>Comptes Rendus - Biologies</i> , 2007, 330, 265-274.	0.1	43
35	Studying sources of incongruence in arthropod molecular phylogenies: Sea spiders (Pycnogonida) as a case study. <i>Comptes Rendus - Biologies</i> , 2010, 333, 438-453.	0.1	43
36	Evolutionary history of Carnivora (Mammalia, Laurasiatheria) inferred from mitochondrial genomes. <i>PLoS ONE</i> , 2021, 16, e0240770.	1.1	43

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37	Improving biodiversity assessment of anuran amphibians using DNA barcoding of tadpoles. Case studies from Southeast Asia. <i>Comptes Rendus - Biologies</i> , 2015, 338, 351-361.	0.1	40
38	Comparison of mitochondrial genome sequences of pangolins (Mammalia, Pholidota). <i>Comptes Rendus - Biologies</i> , 2015, 338, 260-265.	0.1	38
39	A comparative approach for species delimitation based on multiple methods of multi-locus DNA sequence analysis: A case study of the genus <i>Giraffa</i> (Mammalia, Cetartiodactyla). <i>PLoS ONE</i> , 2020, 15, e0217956.	1.1	37
40	Resolving a zoological mystery: the kouprey is a real species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 2849-2855.	1.2	36
41	Phylogenetic position of the saola (<i>Pseudoryx nghetinhensis</i>); inferred from cytogenetic analysis of eleven species of Bovidae. <i>Cytogenetic and Genome Research</i> , 2008, 122, 41-54.	0.6	32
42	Chromosome evolution in the subtribe Bovina (Mammalia, Bovidae): The karyotype of the Cambodian banteng (<i>Bos javanicus birmanicus</i>) suggests that Robertsonian translocations are related to interspecific hybridization. <i>Chromosome Research</i> , 2008, 16, 1107-1118.	1.0	29
43	SuperTRI: A new approach based on branch support analyses of multiple independent data sets for assessing reliability of phylogenetic inferences. <i>Comptes Rendus - Biologies</i> , 2009, 332, 832-847.	0.1	27
44	Evolution of the recombination signal sequences in the Ig heavy-chain variable region locus of mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 11415-11420.	3.3	25
45	Comparative phylogeography of African fruit bats (Chiroptera, Pteropodidae) provide new insights into the outbreak of Ebola virus disease in West Africa, 2014–2016. <i>Comptes Rendus - Biologies</i> , 2016, 339, 517-528.	0.1	22
46	Multilocus phylogeny and species delimitation within the genus <i>Glauconycteris</i> (Chiroptera, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Democratic Republic of the Congo. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 1-22.	0.6	22
47	Inferring the ecological niche of bat viruses closely related to SARS-CoV-2 using phylogeographic analyses of <i>Rhinolophus</i> species. <i>Scientific Reports</i> , 2021, 11, 14276.	1.6	22
48	Covid-19: natural or anthropic origin?. <i>Mammalia</i> , 2021, 85, 1-7.	0.3	22
49	Genetic variability of <i>Austropotamobius italicus</i> in the Marches region: implications for conservation. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2010, 20, 261-268.	0.9	21
50	Phylogeny, biogeography and character evolution in the tribe Desmodieae (Fabaceae: Papilionoideae), with special emphasis on the New Caledonian endemic genera. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 108-121.	1.2	19
51	What is the taxonomic status of the Cambodian banteng and does it have close genetic links with the kouprey?. <i>Journal of Zoology</i> , 2007, 271, 246-252.	0.8	18
52	A paradox revealed: karyotype evolution in the four-horned antelope occurs by tandem fusion (Mammalia, Bovidae, <i>Tetracerus quadricornis</i>). <i>Chromosome Research</i> , 2010, 18, 277-286.	1.0	18
53	Diversity of bat astroviruses in Lao PDR and Cambodia. <i>Infection, Genetics and Evolution</i> , 2017, 47, 41-50.	1.0	18
54	Highly rearranged mitochondrial genome in <i>Nycteria</i> parasites (Haemosporidia) from bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9834-9839.	3.3	17

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55	Phylogeny of African fruit bats (Chiroptera, Pteropodidae) based on complete mitochondrial genomes. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1395-1410.	0.6	17
56	Contamination and chimerism are perpetuating the legend of the snake-eating cow with twisted horns (<i>Pseudonovibos spiralis</i>). A case study of the pitfalls of ancient DNA. <i>Molecular Phylogenetics and Evolution</i> , 2003, 27, 545-548.	1.2	16
57	Is the Newly Described Vietnamese Bovid <i>Pseudonovibos spiralis</i> a Chamois (Genus <i>Rupicapra</i>)?. <i>Die Naturwissenschaften</i> , 2000, 87, 122-124.	0.6	15
58	Early expression of two TdT isoforms in the hematopoietic system of the Mexican axolotl. <i>Immunogenetics</i> , 2004, 56, 204-13.	1.2	15
59	Chromosome painting and molecular dating indicate a low rate of chromosomal evolution in golden moles (Mammalia, Chrysochloridae). <i>Chromosome Research</i> , 2006, 14, 793-803.	1.0	15
60	Description of a new bat species of the tribe Scotonycterini (Chiroptera, Pteropodidae) from southwestern Cameroon. <i>Comptes Rendus - Biologies</i> , 2014, 337, 134-42.	0.1	15
61	Taxonomic and phylogenetic signals in bovine cheek teeth: Towards new biosystematic markers to explore the history of wild and domestic cattle. <i>Journal of Archaeological Science</i> , 2019, 109, 104993.	1.2	14
62	150-million-year-old sea spiders (Pycnogonida: Pantopoda) of Solnhofen. <i>Journal of Systematic Palaeontology</i> , 2019, 17, 1927-1938.	0.6	14
63	Evidence from DNA that the mysterious "linh duong" (<i>Pseudonovibos spiralis</i>) is not a new bovid. <i>Comptes Rendus De L'Académie Des Sciences Série 3, Sciences De La Vie</i> , 2001, 324, 71-80.	0.8	12
64	Has the kouprey (<i>Bos sauveli</i> Urbain, 1937) been domesticated in Cambodia?. <i>Comptes Rendus - Biologies</i> , 2006, 329, 124-135.	0.1	12
65	Ancient specimens and DNA contamination: a case study from the 12S rRNA gene sequence of the "Linh Duong" bovid (<i>Pseudonovibos spiralis</i>). <i>Die Naturwissenschaften</i> , 2002, 89, 107-110.	0.6	10
66	Multi-locus phylogeny of the tribe Tragelaphini (Mammalia, Bovidae) and species delimitation in bushbuck: Evidence for chromosomal speciation mediated by interspecific hybridization. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 96-105.	1.2	10
67	The enigmatic new Indochinese bovid, <i>Pseudonovibos spiralis</i> : an extraordinary forgery. <i>Comptes Rendus De L'Académie Des Sciences Série 3, Sciences De La Vie</i> , 2001, 324, 81-86.	0.8	9
68	Integrative taxonomy of the <i>Rhinolophus macrotis</i> complex (Chiroptera, Rhinolophidae) in Vietnam and nearby regions. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 177-198.	0.6	9
69	Biodiversity and phylogeny of Ammotheidae (Arthropoda: Pycnogonida). <i>European Journal of Taxonomy</i> , 2017, , .	0.6	9
70	New insights into the systematics of Malagasy mongoose-like carnivorans (Carnivora, Eupleridae,) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 and Evolutionary Research</i> , 2017, 55, 250-264.	0.6	8
71	Debate on the authenticity of <i>Pseudonovibos spiralis</i> as a new species of wild bovid from Vietnam and Cambodia. <i>Journal of Zoology</i> , 2001, 255, 437-444.	0.8	7
72	The complete mitochondrial genome of the Spotted Linsang, <i>Prionodon pardicolor</i> , the first representative from the family Prionodontidae (Mammalia, Carnivora). <i>Mitochondrial DNA</i> , 2016, 27, 912-913.	0.6	7

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73	Echolocation Calls and Flight Behaviour of the Elusive Pied Butterfly Bat (<i>Glauconycteris superba</i>), and New Data on Its Morphology and Ecology. <i>Acta Chiropterologica</i> , 2016, 18, 477.	0.2	7
74	The genome of the lowland anoa (<i>Bubalus depressicornis</i>) illuminates the origin of river and swamp buffalo. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107170.	1.2	7
75	Comparative phylogeography of bamboo bats of the genus <i>Tylonycteris</i> (Chiroptera, Vespertilionidae) in Southeast Asia. <i>European Journal of Taxonomy</i> , 2017, , .	0.6	7
76	Genomic Bootstrap Barcodes and Their Application to Study the Evolution of Sarbecoviruses. <i>Viruses</i> , 2022, 14, 440.	1.5	7
77	Sequence analysis of the myosin regulatory light chain gene of the vestimentiferan <i>Riftia pachyptila</i> . <i>Gene</i> , 2001, 263, 141-149.	1.0	6
78	Description of a new species of <i>Neoromicia</i> (Chiroptera: Vespertilionidae) from southern Africa: A name for "N. cf. melckorum". <i>Zootaxa</i> , 2017, 4236, 351.	0.2	6
79	First insights into past biodiversity of giraffes based on mitochondrial sequences from museum specimens. <i>European Journal of Taxonomy</i> , 2020, , .	0.6	6
80	Systematic and evolution of Bovini. , 0, , 7-20.		5
81	Four times more species of sea spiders (Arthropoda: Pycnogonida) in Martinique Island (Lesser Tj ETQq1 1 0.784314 rgBT / Overlock 0.3 5		
82	The complete mitochondrial genome of the African palm civet, <i>Nandinia binotata</i> , the only representative of the family Nandiniidae (Mammalia, Carnivora). <i>Mitochondrial DNA</i> , 2016, 27, 904-905.	0.6	4
83	The complete mitochondrial genome of the boky-boky, <i>Mungotictis decemlineata</i> , the first representative of the Malagasy carnivores (Mammalia, Carnivora, Eupleridae). <i>Mitochondrial DNA</i> , 2016, 27, 908-909.	0.6	4
84	The complete mitochondrial genome of the Servaline Genet, <i>Genetta servalina</i> , the first representative from the family Viverridae (Mammalia, Carnivora). <i>Mitochondrial DNA</i> , 2016, 27, 906-907.	0.6	3
85	Haplotype diversity in the mitochondrial genome of the Egyptian river buffalo (<i>Bubalus bubalis</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 145-147.	0.2	3
86	Integrative taxonomy and biogeography of Asian yellow house bats (Vespertilionidae: <i>Scotophilus</i>) in the Indomalayan Region. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 772-795.	0.6	2
87	Presence of Recombinant Bat Coronavirus GCCDC1 in Cambodian Bats. <i>Viruses</i> , 2022, 14, 176.	1.5	2
88	Évolution des séquences « signal de recombinaison » dans le locus de la région variable de la chaîne lourde des immunoglobulines. <i>Medecine/Sciences</i> , 2001, 17, 1168-1175.	0.0	1
89	First records of <i>Murina lorelieae</i> (Chiroptera: Vespertilionidae) from Vietnam. <i>Mammalia</i> , 2014, .	0.3	1
90	Molecular systematics and biogeography of the Hemigalinae civets (Mammalia, Carnivora). <i>European Journal of Taxonomy</i> , 2017, , .	0.6	1

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91	Variation in synonymous nucleotide composition among genomes of sarbecoviruses and consequences for the origin of COVID-19. <i>Gene</i> , 2022, 835, 146641.	1.0	1
92	Kouprey Bos sauveli A. Urbain, 1937. , 0, , 231-239.		0