

Frédéric Delsuc

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

14,599
citations

36303

51
h-index

48315

88
g-index

105
all docs

105
docs citations

105
times ranked

15998
citing authors

#	ARTICLE	IF	CITATIONS
1	Flexible conservatism in the skull modularity of convergently evolved myrmecophagous placental mammals. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	1.6	6
2	High-quality carnivoran genomes from roadkill samples enable comparative species delineation in aardwolf and bat-eared fox. <i>ELife</i> , 2021, 10, .	6.0	15
3	Aligning Protein-Coding Nucleotide Sequences with MACSE. <i>Methods in Molecular Biology</i> , 2021, 2231, 51-70.	0.9	11
4	Ontogenetic and static allometry in the skull and cranial units of nine-banded armadillos (Cingulata): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 673-698.	1.6	11
5	The role of the Neotropics as a source of world tetrapod biodiversity. <i>Global Ecology and Biogeography</i> , 2020, 29, 1565-1578.	5.8	15
6	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020, 11, .	4.1	204
7	MitoFinder: Efficient automated large-scale extraction of mitogenomic data in target enrichment phylogenomics. <i>Molecular Ecology Resources</i> , 2020, 20, 892-905.	4.8	785
8	Comparative masticatory myology in anteaters and its implications for interpreting morphological convergence in myrmecophagous placentals. <i>PeerJ</i> , 2020, 8, e9690.	2.0	9
9	Odontogenic ameloblast-associated (ODAM) is inactivated in toothless/enamelless placental mammals and toothed whales. <i>BMC Evolutionary Biology</i> , 2019, 19, 31.	3.2	22
10	Ancient Mitogenomes Reveal the Evolutionary History and Biogeography of Sloths. <i>Current Biology</i> , 2019, 29, 2031-2042.e6.	3.9	99
11	NEOTROPICAL XENARTHTRANS: a data set of occurrence of xenarthran species in the Neotropics. <i>Ecology</i> , 2019, 100, e02663.	3.2	54
12	OrthoMaM v10: Scaling-Up Orthologous Coding Sequence and Exon Alignments with More than One Hundred Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 861-862.	8.9	64
13	Evolutionary Tinkering of the Mandibular Canal Linked to Convergent Regression of Teeth in Placental Mammals. <i>Current Biology</i> , 2019, 29, 468-475.e3.	3.9	13
14	Convergent Acquisition of Nonembryonic Development in Styelid Ascidiars. <i>Molecular Biology and Evolution</i> , 2018, 35, 1728-1743.	8.9	35
15	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. <i>Nucleic Acids Research</i> , 2018, 46, D718-D725.	14.5	90
16	Resolving the phylogenetic position of Darwin's extinct ground sloth (<i>Mylodon darwini</i>) using mitogenomic and nuclear exon data. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180214.	2.6	16
17	Chitinase genes (<i>CHIA</i> s) provide genomic footprints of a post-Cretaceous dietary radiation in placental mammals. <i>Science Advances</i> , 2018, 4, eaar6478.	10.3	55
18	A phylogenomic framework and timescale for comparative studies of tunicates. <i>BMC Biology</i> , 2018, 16, 39.	3.8	133

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37	A cost-effective straightforward protocol for shotgun Illumina libraries designed to assemble complete mitogenomes from non-model species. <i>Conservation Genetics Resources</i> , 2015, 7, 37-40.	0.8	32
38	Genome skimming by shotgun sequencing helps resolve the phylogeny of a pantropical tree family. <i>Molecular Ecology Resources</i> , 2014, 14, 966-975.	4.8	102
39	Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014, 23, 1301-1317.	3.9	311
40	OrthoMaM v8: A Database of Orthologous Exons and Coding Sequences for Comparative Genomics in Mammals. <i>Molecular Biology and Evolution</i> , 2014, 31, 1923-1928.	8.9	77
41	Next-generation sequencing and phylogenetic signal of complete mitochondrial genomes for resolving the evolutionary history of leaf-nosed bats (Phyllostomidae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 728-739.	2.7	55
42	Less Is More in Mammalian Phylogenomics: AT-Rich Genes Minimize Tree Conflicts and Unravel the Root of Placental Mammals. <i>Molecular Biology and Evolution</i> , 2013, 30, 2134-2144.	8.9	158
43	Evolutionary and mechanistic insights into substrate and product accommodation of <sc>CTP</sc>:phosphocholine cytidyltransferase from <i><sc>P</sc>lasmodium falciparum</i>. <i>FEBS Journal</i> , 2013, 280, 3132-3148.	4.7	16
44	Deep Sequencing of Mixed Total DNA without Barcodes Allows Efficient Assembly of Highly Plastic Ascidian Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2013, 5, 1185-1199.	2.5	56
45	Fossil Rhabdoviral Sequences Integrated into Arthropod Genomes: Ontogeny, Evolution, and Potential Functionality. <i>Molecular Biology and Evolution</i> , 2012, 29, 381-390.	8.9	100
46	Molecular phylogenetics unveils the ancient evolutionary origins of the enigmatic fairy armadillos. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 673-680.	2.7	90
47	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.	0.2	448
48	Evolutionary and Functional Analyses of the Interaction between the Myeloid Restriction Factor SAMHD1 and the Lentiviral Vpx Protein. <i>Cell Host and Microbe</i> , 2012, 11, 205-217.	11.0	169
49	RUNX2 tandem repeats and the evolution of facial length in placental mammals. <i>BMC Evolutionary Biology</i> , 2012, 12, 103.	3.2	35
50	Phylogenomic analyses support the position of turtles as the sister group of birds and crocodiles (Archosauria). <i>BMC Biology</i> , 2012, 10, 65.	3.8	296
51	JOINT RECONSTRUCTION OF DIVERGENCE TIMES AND LIFE-HISTORY EVOLUTION IN PLACENTAL MAMMALS USING A PHYLOGENETIC COVARIANCE MODEL. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1773-1787.	2.3	71
52	MACSE: Multiple Alignment of Coding SEquences Accounting for Frameshifts and Stop Codons. <i>PLoS ONE</i> , 2011, 6, e22594.	2.5	546
53	Phylogenetic analyses of mitochondrial and nuclear data in haematophagous flies support the paraphyly of the genus <i>Stomoxys</i> (Diptera: Muscidae). <i>Infection, Genetics and Evolution</i> , 2011, 11, 663-670.	2.3	21
54	Diversification of <i>Wolbachia</i> Endosymbiont in the <i>Culex pipiens</i> Mosquito. <i>Molecular Biology and Evolution</i> , 2011, 28, 2761-2772.	8.9	114

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55	Accelerated Evolutionary Rate of Housekeeping Genes in Tunicates. <i>Journal of Molecular Evolution</i> , 2010, 71, 153-167.	1.8	40
56	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	12.6	251
57	IS LEPROSY SPREADING AMONG NINE-BANDED ARMADILLOS IN THE SOUTHEASTERN UNITED STATES?. <i>Journal of Wildlife Diseases</i> , 2009, 45, 144-152.	0.8	41
58	PhyloExplorer: a web server to validate, explore and query phylogenetic trees. <i>BMC Evolutionary Biology</i> , 2009, 9, 108.	3.2	16
59	An updated 18S rRNA phylogeny of tunicates based on mixture and secondary structure models. <i>BMC Evolutionary Biology</i> , 2009, 9, 187.	3.2	133
60	Tunicate mitogenomics and phylogenetics: peculiarities of the <i>Herdmania momus</i> mitochondrial genome and support for the new chordate phylogeny. <i>BMC Genomics</i> , 2009, 10, 534.	2.8	54
61	Estimating Maximum Likelihood Phylogenies with PhyML. <i>Methods in Molecular Biology</i> , 2009, 537, 113-137.	0.9	771
62	Additional molecular support for the new chordate phylogeny. <i>Genesis</i> , 2008, 46, 592-604.	1.6	207
63	Conserved Features and Evolutionary Shifts of the EDA Signaling Pathway Involved in Vertebrate Skin Appendage Development. <i>Molecular Biology and Evolution</i> , 2008, 25, 912-928.	8.9	42
64	Retroposed Elements and Their Flanking Regions Resolve the Evolutionary History of Xenarthran Mammals (Armadillos, Anteaters, and Sloths). <i>Molecular Biology and Evolution</i> , 2007, 24, 2573-2582.	8.9	82
65	Resolving the root of the avian mitogenomic tree by breaking up long branches. <i>Molecular Phylogenetics and Evolution</i> , 2007, 42, 1-13.	2.7	116
66	OrthoMaM: A database of orthologous genomic markers for placental mammal phylogenetics. <i>BMC Evolutionary Biology</i> , 2007, 7, 241.	3.2	120
67	Molecular evidence for hybridisation between the two living species of South American ratites: potential conservation implications. <i>Conservation Genetics</i> , 2007, 8, 503-507.	1.5	6
68	Minimal ProtoHox cluster inferred from bilaterian and cnidarian Hox complements. <i>Nature</i> , 2006, 442, 684-687.	27.8	177
69	Tunicates and not cephalochordates are the closest living relatives of vertebrates. <i>Nature</i> , 2006, 439, 965-968.	27.8	1,488
70	Phylogenomics: the beginning of incongruence?. <i>Trends in Genetics</i> , 2006, 22, 225-231.	6.7	644
71	Heterotachy and long-branch attraction in phylogenetics. <i>BMC Evolutionary Biology</i> , 2005, 5, 50.	3.2	269
72	Visualizing Conflicting Evolutionary Hypotheses in Large Collections of Trees: Using Consensus Networks to Study the Origins of Placentals and Hexapods. <i>Systematic Biology</i> , 2005, 54, 66-76.	5.6	54

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73	Phylogenomics and the reconstruction of the tree of life. <i>Nature Reviews Genetics</i> , 2005, 6, 361-375.	16.3	1,038
74	Phylogenomics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2005, 36, 541-562.	8.3	303
75	Relaxed Molecular Clock Provides Evidence for Long-Distance Dispersal of <i>Nothofagus</i> (Southern) Tj ETQq1 1 0.784314 rgBT /Overlo 5.6 177	5.6	177
76	Genome-Scale Phylogeny and the Detection of Systematic Biases. <i>Molecular Biology and Evolution</i> , 2004, 21, 1455-1458.	8.9	412
77	Influence of Tertiary paleoenvironmental changes on the diversification of South American mammals: a relaxed molecular clock study within xenarthrans. <i>BMC Evolutionary Biology</i> , 2004, 4, 11.	3.2	174
78	The timing of eukaryotic evolution: Does a relaxed molecular clock reconcile proteins and fossils?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15386-15391.	7.1	566
79	Comment on "Hexapod Origins: Monophyletic or Paraphyletic?". <i>Science</i> , 2003, 301, 1482d-1482.	12.6	143
80	Local Molecular Clocks in Three Nuclear Genes: Divergence Times for Rodents and Other Mammals and Incompatibility Among Fossil Calibrations. <i>Journal of Molecular Evolution</i> , 2003, 57, S201-S213.	1.8	92
81	Molecular systematics of armadillos (<i>Xenarthra</i> , <i>Dasypodidae</i>): contribution of maximum likelihood and Bayesian analyses of mitochondrial and nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 261-275.	2.7	76
82	Comparison of Bayesian and Maximum Likelihood Bootstrap Measures of Phylogenetic Reliability. <i>Molecular Biology and Evolution</i> , 2003, 20, 248-254.	8.9	460
83	Army Ants Trapped by Their Evolutionary History. <i>PLoS Biology</i> , 2003, 1, e37.	5.6	12
84	Molecular Phylogeny of Living Xenarthrans and the Impact of Character and Taxon Sampling on the Placental Tree Rooting. <i>Molecular Biology and Evolution</i> , 2002, 19, 1656-1671.	8.9	214
85	The evolution of armadillos, anteaters and sloths depicted by nuclear and mitochondrial phylogenies: implications for the status of the enigmatic fossil <i>Eurotamandua</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001, 268, 1605-1615.	2.6	137
86	Armadillos exhibit less genetic polymorphism in North America than in South America: nuclear and mitochondrial data confirm a founder effect in <i>Dasybus novemcinctus</i> (<i>Xenarthra</i>). <i>Molecular Ecology</i> , 1999, 8, 1743-1748.	3.9	40
87	Skull shape variation in extant pangolins (<i>Pholidota</i> : <i>Manidae</i>): allometric patterns and systematic implications. <i>Zoological Journal of the Linnean Society</i> , 0, , .	2.3	1
88	Genomic evidence for the parallel regression of melatonin synthesis and signaling pathways in placental mammals. <i>Open Research Europe</i> , 0, 1, 75.	2.0	3
89	Genomic evidence for the parallel regression of melatonin synthesis and signaling pathways in placental mammals. <i>Open Research Europe</i> , 0, 1, 75.	2.0	2