

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	Tunicates and not cephalochordates are the closest living relatives of vertebrates. <i>Nature</i> , 2006, 439, 965-968.	27.8	1,488
2	Phylogenomics and the reconstruction of the tree of life. <i>Nature Reviews Genetics</i> , 2005, 6, 361-375.	16.3	1,038
3	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
4	Estimating Maximum Likelihood Phylogenies with PhyML. <i>Methods in Molecular Biology</i> , 2009, 537, 113-137.	0.9	771
5	Phylogenomics: the beginning of incongruence?. <i>Trends in Genetics</i> , 2006, 22, 225-231.	6.7	644
6	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
7	MACSE: Multiple Alignment of Coding SEquences Accounting for Frameshifts and Stop Codons. <i>PLoS ONE</i> , 2011, 6, e22594.	2.5	546
8	Comparison of Bayesian and Maximum Likelihood Bootstrap Measures of Phylogenetic Reliability. <i>Molecular Biology and Evolution</i> , 2003, 20, 248-254.	8.9	460
9	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
10	A Large and Consistent Phylogenomic Dataset Supports Sponges as the Sister Group to All Other Animals. <i>Current Biology</i> , 2017, 27, 958-967.	3.9	423
11	Genome-Scale Phylogeny and the Detection of Systematic Biases. <i>Molecular Biology and Evolution</i> , 2004, 21, 1455-1458.	8.9	412
12	MACSE v2: Toolkit for the Alignment of Coding Sequences Accounting for Frameshifts and Stop Codons. <i>Molecular Biology and Evolution</i> , 2018, 35, 2582-2584.	8.9	330
13	Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014, 23, 1301-1317.	3.9	311
14	Phylogenomics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2005, 36, 541-562.	8.3	303
15	The Effects of Captivity on the Mammalian Gut Microbiome. <i>Integrative and Comparative Biology</i> , 2017, 57, 690-704.	2.0	301
16	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
17	Heterotachy and long-branch attraction in phylogenetics. <i>BMC Evolutionary Biology</i> , 2005, 5, 50.	3.2	269
18	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	12.6	251

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19	Phylotranscriptomic consolidation of the jawed vertebrate timetree. <i>Nature Ecology and Evolution</i> , 2017, 1, 1370-1378.	7.8	247
20	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
21	Additional molecular support for the new chordate phylogeny. <i>Genesis</i> , 2008, 46, 592-604.	1.6	207
22	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020, 11, .	4.1	204
23	Minimal ProtoHox cluster inferred from bilaterian and cnidarian Hox complements. <i>Nature</i> , 2006, 442, 684-687.	27.8	177
24	Relaxed Molecular Clock Provides Evidence for Long-Distance Dispersal of <i>Nothofagus</i> (Southern) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	5.6	177
25	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
26	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
27	Shotgun Mitogenomics Provides a Reference Phylogenetic Framework and Timescale for Living Xenarthrans. <i>Molecular Biology and Evolution</i> , 2016, 33, 621-642.	8.9	167
28	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
29	Comment on "Hexapod Origins: Monophyletic or Paraphyletic?". <i>Science</i> , 2003, 301, 1482d-1482.	12.6	143
30	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
31	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
32	A phylogenomic framework and timescale for comparative studies of tunicates. <i>BMC Biology</i> , 2018, 16, 39.	3.8	133
33	OrthoMaM: A database of orthologous genomic markers for placental mammal phylogenetics. <i>BMC Evolutionary Biology</i> , 2007, 7, 241.	3.2	120
34	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
35	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
36	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

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37	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
38	Ancient Mitogenomes Reveal the Evolutionary History and Biogeography of Sloths. <i>Current Biology</i> , 2019, 29, 2031-2042.e6.	3.9	99
39	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
40	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
41	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
42	The phylogenetic affinities of the extinct glyptodonts. <i>Current Biology</i> , 2016, 26, R155-R156.	3.9	83
43	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
44	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
45	Evolution of Proteasome Regulators in Eukaryotes. <i>Genome Biology and Evolution</i> , 2015, 7, 1363-1379.	2.5	77
46	Molecular systematics of armadillos (<i>Xenarthra</i> , <i>Dasyopodidae</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
47	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
48	ANISEED 2015: a digital framework for the comparative developmental biology of ascidians. <i>Nucleic Acids Research</i> , 2016, 44, D808-D818.	14.5	68
49	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
50	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
51	Next-generation sequencing and phylogenetic signal of complete mitochondrial genomes for resolving the evolutionary history of leaf-nosed bats (<i>Phyllostomidae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 728-739.	2.7	55
52	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
53	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
54	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

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55	NEOTROPICAL XENARTHANS: a data set of occurrence of xenarthran species in the Neotropics. <i>Ecology</i> , 2019, 100, e02663.	3.2	54
56	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
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	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> (Xenarthra). <i>Molecular Ecology</i> , 1999, 8, 1743-1748.	3.9	40
59	Accelerated Evolutionary Rate of Housekeeping Genes in Tunicates. <i>Journal of Molecular Evolution</i> , 2010, 71, 153-167.	1.8	40
60	RUNX2 tandem repeats and the evolution of facial length in placental mammals. <i>BMC Evolutionary Biology</i> , 2012, 12, 103.	3.2	35
61	Systematics of hairy armadillos and the taxonomic status of the Andean hairy armadillo (<i>Chaetophractus nationi</i>). <i>Journal of Mammalogy</i> , 2015, 96, 673-689.	1.3	35
62	Convergent Acquisition of Nonembryonic Development in Styelid Ascidiens. <i>Molecular Biology and Evolution</i> , 2018, 35, 1728-1743.	8.9	35
63	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
64	Evolutionary analysis of selective constraints identifies ameloblastin (AMBN) as a potential candidate for amelogenesis imperfecta. <i>BMC Evolutionary Biology</i> , 2015, 15, 148.	3.2	26
65	Thrice better than once: quality control guidelines to validate new mitogenomes. <i>Mitochondrial DNA</i> , 2016, 27, 449-454.	0.6	24
66	In Cold Blood: Compositional Bias and Positive Selection Drive the High Evolutionary Rate of Vampire Bats Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2018, 10, 2218-2239.	2.5	22
67	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
68	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
69	The hidden anatomy of paranasal sinuses reveals biogeographically distinct morphotypes in the nine-banded armadillo (<i>Dasybus novemcinctus</i>). <i>PeerJ</i> , 2017, 5, e3593.	2.0	18
70	PhyloExplorer: a web server to validate, explore and query phylogenetic trees. <i>BMC Evolutionary Biology</i> , 2009, 9, 108.	3.2	16
71	Evolutionary and mechanistic insights into substrate and product accommodation of <i>CTP</i> :phosphocholine cytidyltransferase from <i>Plasmodium falciparum</i> . <i>FEBS Journal</i> , 2013, 280, 3132-3148.	4.7	16
72	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

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73	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
74	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
75	Beyond the carapace: skull shape variation and morphological systematics of long-nosed armadillos (genus <i>Dasybus</i>). <i>PeerJ</i> , 2017, 5, e3650.	2.0	15
76	Naked but Not Hairless: The Pitfalls of Analyses of Molecular Adaptation Based on Few Genome Sequence Comparisons. <i>Genome Biology and Evolution</i> , 2015, 7, 768-774.	2.5	14
77	Genome-Wide Screening of Retroviral Envelope Genes in the Nine-Banded Armadillo (<i>Dasybus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq0 0 0 1.6	3.4	13
78	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
79	Army Ants Trapped by Their Evolutionary History. <i>PLoS Biology</i> , 2003, 1, e37.	5.6	12
80	Ontogenetic and static allometry in the skull and cranial units of nine-banded armadillos (Cingulata): Tj ETQq0 0 0 1.6	1.6	11
81	Aligning Protein-Coding Nucleotide Sequences with MACSE. <i>Methods in Molecular Biology</i> , 2021, 2231, 51-70.	0.9	11
82	Comparative masticatory myology in anteaters and its implications for interpreting morphological convergence in myrmecophagous placentals. <i>PeerJ</i> , 2020, 8, e9690.	2.0	9
83	Genetic structuring in a relictual population of screaming hairy armadillo (<i>Chaetophractus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq0 0 0 1.1	1.1	7
84	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
85	Flexible conservatism in the skull modularity of convergently evolved myrmecophagous placental mammals. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	1.6	6
86	Predicting biotic interactions and their variability in a changing environment. <i>Biology Letters</i> , 2016, 12, 20151073.	2.3	3
87	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
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	2
89	Skull shape variation in extant pangolins (Pholidota: Manidae): allometric patterns and systematic implications. <i>Zoological Journal of the Linnean Society</i> , 0, , .	2.3	1