Emmanuel J P Douzery

List of Publications by Year
in descending order

99 papers	9,685 citations	31949 53 h-index	39638 94 g-index
102 all docs	102 docs citations	102 times ranked	13315 citing authors

#	Article	IF	Citations
1	ANISEED 2019: 4D exploration of genetic data for an extended range of tunicates. Nucleic Acids Research, 2020, 48, D668-D675.	6.5	30
2	Digging for the spiny rat and hutia phylogeny using a gene capture approach, with the description of a new mammal subfamily. Molecular Phylogenetics and Evolution, 2019, 136, 241-253.	1.2	32
3	OrthoMaM v10: Scaling-Up Orthologous Coding Sequence and Exon Alignments with More than One Hundred Mammalian Genomes. Molecular Biology and Evolution, 2019, 36, 861-862.	3.5	64
4	Convergent Acquisition of Nonembryonic Development in Styelid Ascidians. Molecular Biology and Evolution, 2018, 35, 1728-1743.	3.5	35
5	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. Nucleic Acids Research, 2018, 46, D718-D725.	6.5	90
6	Life-History Traits Evolved Jointly with Climatic Niche and Disturbance Regime in the Genus Leucadendron (Proteaceae). American Naturalist, 2018, 191, 220-234.	1.0	11
7	Salmo macrostigma (Teleostei, Salmonidae): Nothing more than a brown trout (<scp>S.) Tj ETQq1 1 0.784314 rgBT /Overlo	0.7	34
8	A phylogenomic framework and timescale for comparative studies of tunicates. BMC Biology, 2018, 16, 39.	1.7	133
9	MACSE v2: Toolkit for the Alignment of Coding Sequences Accounting for Frameshifts and Stop Codons. Molecular Biology and Evolution, 2018, 35, 2582-2584.	3.5	330
10	Flightless scalyâ€tailed squirrels never learned how to fly: A reappraisal of Anomaluridae phylogeny. Zoologica Scripta, 2018, 47, 404-417.	0.7	12
11	In Cold Blood: Compositional Bias and Positive Selection Drive the High Evolutionary Rate of Vampire Bats Mitochondrial Genomes. Genome Biology and Evolution, 2018, 10, 2218-2239.	1.1	22
12	Mitogenomic phylogeny, diversification, and biogeography of South American spiny rats. Molecular Biology and Evolution, 2017, 34, msw261.	3.5	40
13	Thrice better than once: quality control guidelines to validate new mitogenomes. Mitochondrial DNA, 2016, 27, 449-454.	0.6	24
14	ANISEED 2015: a digital framework for the comparative developmental biology of ascidians. Nucleic Acids Research, 2016, 44, D808-D818.	6.5	68
15	Fast and accurate branch lengths estimation for phylogenomic trees. BMC Bioinformatics, 2016, 17, 23.	1.2	23
16	Projected impacts of climate warming on the functional and phylogenetic components of coastal Mediterranean fish biodiversity. Ecography, 2015, 38, 681-689.	2.1	25
17	A cost-effective straightforward protocol for shotgun Illumina libraries designed to assemble complete mitogenomes from non-model species. Conservation Genetics Resources, 2015, 7, 37-40.	0.4	32
18	Representing taxonomic, phylogenetic and functional diversity: new challenges for <scp>M</scp>editerranean marineâ€protected areas. Diversity and Distributions, 2015, 21, 175-187.	1.9	57

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19	Ascidian Mitogenomics: Comparison of Evolutionary Rates in Closely Related Taxa Provides Evidence of Ongoing Speciation Events. Genome Biology and Evolution, 2014, 6, 591-605.	1.1	39
20	CONVERGENT AND CORRELATED EVOLUTION OF MAJOR LIFE-HISTORY TRAITS IN THE ANGIOSPERM GENUSLEUCADENDRON(PROTEACEAE). Evolution; International Journal of Organic Evolution, 2014, 68, 2775-2792.	1.1	25
21	Developing nuclear DNA phylogenetic markers in the angiosperm genus Leucadendron (Proteaceae): A next-generation sequencing transcriptomic approach. Molecular Phylogenetics and Evolution, 2014, 70, 37-46.	1.2	31
22	Rodents of the Caribbean: origin and diversification of hutias unravelled by next-generation museomics. Biology Letters, 2014, 10, 20140266.	1.0	87
23	OrthoMaM v8: A Database of Orthologous Exons and Coding Sequences for Comparative Genomics in Mammals. Molecular Biology and Evolution, 2014, 31, 1923-1928.	3.5	77
24	Next-generation sequencing and phylogenetic signal of complete mitochondrial genomes for resolving the evolutionary history of leaf-nosed bats (Phyllostomidae). Molecular Phylogenetics and Evolution, 2013, 69, 728-739.	1.2	55
25	Molecular phylogenetic reconstructions identify East Asia as the cradle for the evolution of the cosmopolitan genus Myotis (Mammalia, Chiroptera). Molecular Phylogenetics and Evolution, 2013, 69, 437-449.	1.2	128
26	Less Is More in Mammalian Phylogenomics: AT-Rich Genes Minimize Tree Conflicts and Unravel the Root of Placental Mammals. Molecular Biology and Evolution, 2013, 30, 2134-2144.	3.5	158
27	Diversification of South American spiny rats (Echimyidae): a multigene phylogenetic approach. Zoologica Scripta, 2013, 42, 117-134.	0.7	59
28	Jumping and gliding rodents: Mitogenomic affinities of Pedetidae and Anomaluridae deduced from an RNA-Seq approach. Gene, 2013, 531, 388-397.	1.0	14
29	Genomic Evidence for Large, Long-Lived Ancestors to Placental Mammals. Molecular Biology and Evolution, 2013, 30, 5-13.	3.5	56
30	Deep Sequencing of Mixed Total DNA without Barcodes Allows Efficient Assembly of Highly Plastic Ascidian Mitochondrial Genomes. Genome Biology and Evolution, 2013, 5, 1185-1199.	1.1	56
31	Environment drives high phylogenetic turnover among oceanic bacterial communities. Biology Letters, 2012, 8, 562-566.	1.0	19
32	Efficient Selection of Branch-Specific Models of Sequence Evolution. Molecular Biology and Evolution, 2012, 29, 1861-1874.	3.5	56
33	Molecular phylogenetics unveils the ancient evolutionary origins of the enigmatic fairy armadillos. Molecular Phylogenetics and Evolution, 2012, 62, 673-680.	1.2	90
34	A glimpse on the pattern of rodent diversification: a phylogenetic approach. BMC Evolutionary Biology, 2012, 12, 88.	3.2	390
35	Fast and Robust Characterization of Time-Heterogeneous Sequence Evolutionary Processes Using Substitution Mapping. PLoS ONE, 2012, 7, e33852.	1.1	47
36	A Phylogenetic Perspective on the Evolution of Mediterranean Teleost Fishes. PLoS ONE, 2012, 7, e36443.	1.1	50

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37	Multigenic phylogeny and analysis of tree incongruences in Triticeae (Poaceae). BMC Evolutionary Biology, 2011, 11, 181.	3.2	72
38	MACSE: Multiple Alignment of Coding SEquences Accounting for Frameshifts and Stop Codons. PLoS ONE, 2011, 6, e22594.	1.1	546
39	Protected and Threatened Components of Fish Biodiversity in the Mediterranean Sea. Current Biology, 2011, 21, 1044-1050.	1.8	125
40	Accelerated Evolutionary Rate of Housekeeping Genes in Tunicates. Journal of Molecular Evolution, 2010, 71, 153-167.	0.8	40
41	Contrasting GC-content dynamics across 33 mammalian genomes: Relationship with life-history traits and chromosome sizes. Genome Research, 2010, 20, 1001-1009.	2.4	195
42	S<scp>uper</scp>T<scp>riplets</scp>: a triplet-based supertree approach to phylogenomics. Bioinformatics, 2010, 26, i115-i123.	1.8	51
43	Identification of autophagy genes in Ciona intestinalis: A new experimental model to study autophagy mechanism. Autophagy, 2009, 5, 805-815.	4.3	12
44	A New Malaria Agent in African Hominids. PLoS Pathogens, 2009, 5, e1000446.	2.1	127
45	An updated 18S rRNA phylogeny of tunicates based on mixture and secondary structure models. BMC Evolutionary Biology, 2009, 9, 187.	3.2	133
46	Trypanosoma cruzi: New insights on ecophylogeny and hybridization by multigene sequencing of three nuclear and one maxicircle genes. Experimental Parasitology, 2009, 122, 328-337.	0.5	20
47	Phylogeography and the origin of cassava: New insights from the northern rim of the Amazonian basin. Molecular Phylogenetics and Evolution, 2009, 53, 329-334.	1.2	58
48	Patterns of macroevolution among Primates inferred from a supermatrix of mitochondrial and nuclear DNA. Molecular Phylogenetics and Evolution, 2009, 53, 808-825.	1.2	194
49	Taxonomy, molecular phylogeny and evolution of plant reverse transcribing viruses (family) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 Virology, 2008, 153, 1085-1102.	0.9	41
50	PhySIC_IST: cleaning source trees to infer more informative supertrees. BMC Bioinformatics, 2008, 9, 413.	1.2	42
51	Conserved Features and Evolutionary Shifts of the EDA Signaling Pathway Involved in Vertebrate Skin Appendage Development. Molecular Biology and Evolution, 2008, 25, 912-928.	3.5	42
52	PhySIC: A Veto Supertree Method with Desirable Properties. Systematic Biology, 2007, 56, 798-817.	2.7	49
53	Retroposed Elements and Their Flanking Regions Resolve the Evolutionary History of Xenarthran Mammals (Armadillos, Anteaters, and Sloths). Molecular Biology and Evolution, 2007, 24, 2573-2582.	3.5	82
54	Genetic clustering of Trypanosoma cruzi I lineage evidenced by intergenic miniexon gene sequencing. Infection, Genetics and Evolution, 2007, 7, 587-593.	1.0	64

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55	Molecular evidence for hybridisation between the two living species of South American ratites: potential conservation implications. Conservation Genetics, 2007, 8, 503-507.	0.8	6
56	SDM: A Fast Distance-Based Approach for (Super)Tree Building in Phylogenomics. Systematic Biology, 2006, 55, 740-755.	2.7	69
57	Arrival and Diversification of Caviomorph Rodents and Platyrrhine Primates in South America. Systematic Biology, 2006, 55, 228-244.	2.7	194
58	2. Dating Methods and Corresponding Chronometers in Astrobiology. Earth, Moon and Planets, 2006, 98, 11-38.	0.3	0
59	7. Ancient Fossil Record and Early Evolution (ca.Â3.8 to 0.5ÂGa). Earth, Moon and Planets, 2006, 98, 247-290.	0.3	22
60	Astrocladistics: A Phylogenetic Analysis of Galaxy Evolution I. Character Evolutions and Galaxy Histories. Journal of Classification, 2006, 23, 31-56.	1.2	17
61	The evolutionary radiation of Arvicolinae rodents (voles and lemmings): relative contribution of nuclear and mitochondrial DNA phylogenies. BMC Evolutionary Biology, 2006, 6, 80.	3.2	100
62	Acetylcholinesterase genes within the Diptera: takeover and loss in true flies. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 2595-2604.	1.2	92
63	Ecomorphological diversification among South American spiny rats (Rodentia; Echimyidae): a phylogenetic and chronological approach. Molecular Phylogenetics and Evolution, 2005, 34, 601-615.	1.2	133
64	New DNA data from a transthyretin nuclear intron suggest an Oligocene to Miocene diversification of living South America opossums (Marsupialia: Didelphidae). Molecular Phylogenetics and Evolution, 2005, 35, 363-379.	1.2	61
65	Evolution under domestication: contrasting functional morphology of seedlings in domesticated cassava and its closest wild relatives. New Phytologist, 2005, 166, 305-318.	3.5	60
66	Differentiation in a geographical mosaic of plants coevolving with ants: phylogeny of the Leonardoxa africana complex (Fabaceae: Caesalpinioideae) using amplified fragment length polymorphism markers. Molecular Ecology, 2004, 13, 1157-1171.	2.0	36
67	Influence of Tertiary paleoenvironmental changes on the diversification of South American mammals: a relaxed molecular clock study within xenarthrans. BMC Evolutionary Biology, 2004, 4, 11.	3.2	174
68	Primate phylogeny, evolutionary rate variations, and divergence times: A contribution from the nuclear gene IRBP. American Journal of Physical Anthropology, 2004, 124, 01-16.	2.1	93
69	Rabbits, if anything, are likely Glires. Molecular Phylogenetics and Evolution, 2004, 33, 922-935.	1.2	45
70	The timing of eukaryotic evolution: Does a relaxed molecular clock reconcile proteins and fossils?. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15386-15391.	3.3	566
71	Local Molecular Clocks in Three Nuclear Genes: Divergence Times for Rodents and Other Mammals and Incompatibility Among Fossil Calibrations. Journal of Molecular Evolution, 2003, 57, S201-S213.	0.8	92
72	Genetic variability in MCF-7 sublines: evidence of rapid genomic and RNA expression profile modifications. BMC Cancer, 2003, 3, 13.	1.1	77

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73	Molecular systematics of armadillos (Xenarthra, Dasypodidae): contribution of maximum likelihood and Bayesian analyses of mitochondrial and nuclear genes. Molecular Phylogenetics and Evolution, 2003, 28, 261-275.	1.2	76
74	Molecular estimation of eulipotyphlan divergence times and the evolution of â€œInsectivoraâ€. Molecular Phylogenetics and Evolution, 2003, 28, 285-296.	1.2	77
75	Evidence for genetic exchange and hybridization in Trypanosoma cruzi based on nucleotide sequences and molecular karyotype. Infection, Genetics and Evolution, 2003, 2, 173-183.	1.0	138
76	Comparison of Bayesian and Maximum Likelihood Bootstrap Measures of Phylogenetic Reliability. Molecular Biology and Evolution, 2003, 20, 248-254.	3.5	460
77	Molecular and Morphological Phylogenies of Ruminantia and the Alternative Position of the Moschidae. Systematic Biology, 2003, 52, 206-228.	2.7	224
78	rbcL Phylogeny of the Fern Genus Trichomanes (Hymenophyllaceae), with Special Reference to Neotropical Taxa. International Journal of Plant Sciences, 2003, 164, 753-761.	0.6	52
79	Rodent Phylogeny and a Timescale for the Evolution of Glires: Evidence from an Extensive Taxon Sampling Using Three Nuclear Genes. Molecular Biology and Evolution, 2002, 19, 1053-1065.	3.5	305
80	Molecular Phylogeny of Living Xenarthrans and the Impact of Character and Taxon Sampling on the Placental Tree Rooting. Molecular Biology and Evolution, 2002, 19, 1656-1671.	3.5	214
81	Title is missing!. Journal of Mammalian Evolution, 2002, 9, 225-252.	1.0	53
82	A mitochondrial DNA control region phylogeny of the Cervinae: speciation in Cervus and implications for conservation. Animal Conservation, 2001, 4, 1-11.	1.5	113
83	From the Old World to the New World: A Molecular Chronicle of the Phylogeny and Biogeography of Hystricognath Rodents. Molecular Phylogenetics and Evolution, 2001, 20, 238-251.	1.2	196
84	The evolution of armadillos, anteaters and sloths depicted by nuclear and mitochondrial phylogenies: implications for the status of the enigmatic fossil Eurotamandua. Proceedings of the Royal Society B: Biological Sciences, 2001, 268, 1605-1615.	1.2	137
85	Is the Newly Described Vietnamese Bovid Pseudonovibos spiralis a Chamois (Genus Rupicapra)?. Die Naturwissenschaften, 2000, 87, 122-124.	0.6	15
86	Variance of molecular datings, evolution of rodents and the phylogenetic affinities between Ctenodactylidae and Hystricognathi. Proceedings of the Royal Society B: Biological Sciences, 2000, 267, 393-402.	1.2	117
87	Molecular phylogenetics of Diseae (Orchidaceae): a contribution from nuclear ribosomal ITS sequences. American Journal of Botany, 1999, 86, 887-899.	0.8	190
88	Evolutionary affinities of the enigmatic saola (Pseudoryx nghetinhensis) in the context of the molecular phylogeny of Bovidae. Proceedings of the Royal Society B: Biological Sciences, 1999, 266, 893-900.	1.2	68
89	Armadillos exhibit less genetic polymorphism in North America than in South America: nuclear and mitochondrial data confirm a founder effect in Dasypus novemcinctus (Xenarthra). Molecular Ecology, 1999, 8, 1743-1748.	2.0	40
90	The Tribal Radiation of the Family Bovidae (Artiodactyla) and the Evolution of the Mitochondrial Cytochrome b Gene. Molecular Phylogenetics and Evolution, 1999, 13, 227-243.	1.2	192

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91	Molecular evolution of the nuclear von Willebrand factor gene in mammals and the phylogeny of rodents. Molecular Biology and Evolution, 1999, 16, 577-589.	3.5	95
92	What is a Suiforme (Artiodactyla)?. Molecular Phylogenetics and Evolution, 1998, 9, 528-532.	1.2	17
93	The mitochondrial control region of Cervidae: evolutionary patterns and phylogenetic content. Molecular Biology and Evolution, 1997, 14, 1154-1166.	3.5	171
94	Phylogenetic relationships of artiodactyls and cetaceans as deduced from the comparison of cytochrome b and 12S rRNA mitochondrial sequences. Molecular Biology and Evolution, 1997, 14, 550-559.	3.5	245
95	Interordinal Mammalian Relationships: Evidence for Paenungulate Monophyly Is Provided by Complete Mitochondrial 12S rRNA Sequences. Molecular Phylogenetics and Evolution, 1996, 6, 245-258.	1.2	56
96	Molecular Systematics of Hystricognath Rodents: The Contribution of Sciurognath Mitochondrial 12S rRNA Sequences. Molecular Phylogenetics and Evolution, 1995, 4, 357-360.	1.2	44
97	Testing the generation time hypothesis using DNA/DNA hybridization between artiodactyls. Journal of Evolutionary Biology, 1995, 8, 511-529.	0.8	11
98	Molecular evolution of the mitochondrial 12S rRNA in Ungulata (mammalia). Journal of Molecular Evolution, 1995, 41, 622-36.	0.8	54
99	Molecular Phylogeny of Families Related to Celastrales Based on rbcL 5â€² Flanking Sequences. Molecular Phylogenetics and Evolution, 1994, 3, 27-37.	1.2	89