

Davide Pisani

List of Publications by Year in descending order

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Version: 2024-02-01

103
papers

9,166
citations

44069

48
h-index

45317

90
g-index

111
all docs

111
docs citations

111
times ranked

8682
citing authors

#	ARTICLE	IF	CITATIONS
1	The Ediacaran origin of Ecdysozoa: integrating fossil and phylogenomic data. <i>Journal of the Geological Society</i> , 2022, 179, .	2.1	21
2	Integrated phylogenomics and fossil data illuminate the evolution of beetles. <i>Royal Society Open Science</i> , 2022, 9, 211771.	2.4	117
3	MicroRNAs as Indicators into the Causes and Consequences of Whole-Genome Duplication Events. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	17
4	Eukaryogenesis and oxygen in Earth history. <i>Nature Ecology and Evolution</i> , 2022, 6, 520-532.	7.8	48
5	Empirical distributions of homoplasy in morphological data. <i>Palaeontology</i> , 2021, 64, 505-518.	2.2	9
6	Diversification dynamics of total-, stem-, and crown-groups are compatible with molecular clock estimates of divergence times. <i>Science Advances</i> , 2021, 7, .	10.3	7
7	Phylogenomics of Opsin Genes in Diptera Reveals Lineage-Specific Events and Contrasting Evolutionary Dynamics in <i>Anopheles</i> and <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	16
8	New Tardigrade Opsins and Differential Expression Analyses Show Ontogenic Variation in Light Perception. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	2
9	Phylogenetic sampling affects evolutionary patterns of morphological disparity. <i>Palaeontology</i> , 2021, 64, 765-787.	2.2	6
10	Evolution and dispersal of snakes across the Cretaceous-Paleogene mass extinction. <i>Nature Communications</i> , 2021, 12, 5335.	12.8	13
11	The evolution of insect biodiversity. <i>Current Biology</i> , 2021, 31, R1299-R1311.	3.9	39
12	Eye-Transcriptome and Genome-Wide Sequencing for Scolecophidia: Implications for Inferring the Visual System of the Ancestral Snake. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	8
13	The impact of fossil stratigraphic ranges on tip-calibration, and the accuracy and precision of divergence time estimates. <i>Palaeontology</i> , 2020, 63, 67-83.	2.2	25
14	Performance of A Priori and A Posteriori Calibration Strategies in Divergence Time Estimation. <i>Genome Biology and Evolution</i> , 2020, 12, 1087-1098.	2.5	9
15	Mitochondrial genomes illuminate the evolutionary history of the Western honey bee (<i>Apis mellifera</i>). <i>Scientific Reports</i> , 2020, 10, 14515.	3.3	32
16	Spectral Diversification and Trans-Species Allelic Polymorphism during the Land-to-Sea Transition in Snakes. <i>Current Biology</i> , 2020, 30, 2608-2615.e4.	3.9	20
17	A Cambrian-Ordovician Terrestrialization of Arachnids. <i>Frontiers in Genetics</i> , 2020, 11, 182.	2.3	43
18	Data curation and modeling of compositional heterogeneity in insect phylogenomics: A case study of the phylogeny of Dytiscoidea (Coleoptera: Adephega). <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106782.	2.7	23

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19	Sensory Neuroscience: A Taste for Light and the Origin of Animal Vision. <i>Current Biology</i> , 2020, 30, R773-R775.	3.9	7
20	A Novel Approach to Investigate the Effect of Tree Reconstruction Artifacts in Single-Gene Analysis Clarifies Opsin Evolution in Nonbilaterian Metazoans. <i>Genome Biology and Evolution</i> , 2020, 12, 3906-3916.	2.5	17
21	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	6.4	37
22	Integrated phylogenomic and fossil evidence of stick and leaf insects (Phasmatodea) reveal a Permian–Triassic co-origination with insectivores. <i>Royal Society Open Science</i> , 2020, 7, 201689.	2.4	25
23	<p>Fleas are parasitic scorpionflies</p>. <i>Palaeoentomology</i> , 2020, 3, 641-653.	1.0	17
24	Probabilistic methods outperform parsimony in the phylogenetic analysis of data simulated without a probabilistic model. <i>Palaeontology</i> , 2019, 62, 1-17.	2.2	44
25	Pancrustacean Evolution Illuminated by Taxon-Rich Genomic-Scale Data Sets with an Expanded Remipede Sampling. <i>Genome Biology and Evolution</i> , 2019, 11, 2055-2070.	2.5	76
26	The Role of Homology and Orthology in the Phylogenomic Analysis of Metazoan Gene Content. <i>Molecular Biology and Evolution</i> , 2019, 36, 643-649.	8.9	44
27	Increasing species sampling in chelicerate genomic-scale datasets provides support for monophyly of Acari and Arachnida. <i>Nature Communications</i> , 2019, 10, 2295.	12.8	90
28	Inadvertent Paralog Inclusion Drives Artifactual Topologies and Timetree Estimates in Phylogenomics. <i>Molecular Biology and Evolution</i> , 2019, 36, 1344-1356.	8.9	56
29	Cambrian Sessile, Suspension Feeding Stem-Group Ctenophores and Evolution of the Comb Jelly Body Plan. <i>Current Biology</i> , 2019, 29, 1112-1125.e2.	3.9	58
30	Exploring the evolution and terrestrialization of scorpions (Arachnida: Scorpiones) with rocks and clocks. <i>Organisms Diversity and Evolution</i> , 2019, 19, 71-86.	1.6	33
31	Empirical realism of simulated data is more important than the model used to generate it: a reply to Goloboff <i>et al</i>.. <i>Palaeontology</i> , 2018, 61, 631-635.	2.2	29
32	The Interrelationships of Land Plants and the Nature of the Ancestral Embryophyte. <i>Current Biology</i> , 2018, 28, 733-745.e2.	3.9	398
33	Probabilistic methods surpass parsimony when assessing clade support in phylogenetic analyses of discrete morphological data. <i>Palaeontology</i> , 2018, 61, 105-118.	2.2	61
34	Molecular palaeontology illuminates the evolution of ecdysozoan vision. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, .	2.6	25
35	Well-Annotated microRNAs Do Not Evidence Pervasive miRNA Loss. <i>Genome Biology and Evolution</i> , 2018, 10, 1457-1470.	2.5	41
36	Integrated genomic and fossil evidence illuminates life's early evolution and eukaryote origin. <i>Nature Ecology and Evolution</i> , 2018, 2, 1556-1562.	7.8	274

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37	Homeobox Gene Duplication and Divergence in Arachnids. <i>Molecular Biology and Evolution</i> , 2018, 35, 2240-2253.	8.9	66
38	Uncertain-tree: discriminating among competing approaches to the phylogenetic analysis of phenotype data. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162290.	2.6	114
39	Molecular clocks indicate turnover and diversification of modern coleoid cephalopods during the Mesozoic Marine Revolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162818.	2.6	86
40	RelTime Rates Collapse to a Strict Clock When Estimating the Timeline of Animal Diversification. <i>Genome Biology and Evolution</i> , 2017, 9, 1320-1328.	2.5	25
41	Parsimony and maximum-likelihood phylogenetic analyses of morphology do not generally integrate uncertainty in inferring evolutionary history: a response to Brown <i>et al.</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171636.	2.6	19
42	Early photosynthetic eukaryotes inhabited low-salinity habitats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7737-E7745.	7.1	244
43	Reply to Nakov <i>et al.</i> : Model choice requires biological insight when studying the ancestral habitat of photosynthetic eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10608-E10609.	7.1	9
44	Improved Modeling of Compositional Heterogeneity Supports Sponges as Sister to All Other Animals. <i>Current Biology</i> , 2017, 27, 3864-3870.e4.	3.9	244
45	Estimation of phylogenetic divergence times in Panagrolaimidae and other nematodes using relaxed molecular clocks calibrated with insect and crustacean fossils. <i>Nematology</i> , 2017, 19, 899-913.	0.6	6
46	Bayesian methods outperform parsimony but at the expense of precision in the estimation of phylogeny from discrete morphological data. <i>Biology Letters</i> , 2016, 12, 20160081.	2.3	160
47	The Evolution of Olfactory Gene Families in <i>Drosophila</i> and the Genomic Basis of chemical-Ecological Adaptation in <i>Drosophila suzukii</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2297-2311.	2.5	76
48	A molecular palaeobiological exploration of arthropod terrestrialization. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150133.	4.0	131
49	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 330-344.	2.5	195
50	Reply to Halanych <i>et al.</i> : Ctenophore misplacement is corroborated by independent datasets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E948-9.	7.1	14
51	Implementing and testing Bayesian and maximum-likelihood supertree methods in phylogenetics. <i>Royal Society Open Science</i> , 2015, 2, 140436.	2.4	49
52	Anhydrobiosis and Freezing-Tolerance: Adaptations That Facilitate the Establishment of Panagrolaimus Nematodes in Polar Habitats. <i>PLoS ONE</i> , 2015, 10, e0116084.	2.5	28
53	Concatabominations: Identifying Unstable Taxa in Morphological Phylogenetics using a Heuristic Extension to Safe Taxonomic Reduction. <i>Systematic Biology</i> , 2015, 64, 137-143.	5.6	37
54	Biogeography of worm lizards (Amphisbaenia) driven by end-Cretaceous mass extinction. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20143034.	2.6	52

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55	The ring of life hypothesis for eukaryote origins is supported by multiple kinds of data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140323.	4.0	19
56	Horizontal gene flow from Eubacteria to Archaeobacteria and what it means for our understanding of eukaryogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140337.	4.0	23
57	Genomic data do not support comb jellies as the sister group to all other animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15402-15407.	7.1	286
58	Animal Evolution: Only Rocks Can Set the Clock. <i>Current Biology</i> , 2015, 25, R1079-R1081.	3.9	13
59	The Comb Jelly Opsins and the Origins of Animal Phototransduction. <i>Genome Biology and Evolution</i> , 2014, 6, 1964-1971.	2.5	62
60	Evolutionary relationships of the Critically Endangered frog <i>Ericabatrachus baleensis</i> Largen, 1991 with notes on incorporating previously unsampled taxa into large-scale phylogenetic analyses. <i>BMC Evolutionary Biology</i> , 2014, 14, 44.	3.2	9
61	A Pluralistic Account of Homology: Adapting the Models to the Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 501-516.	8.9	37
62	The hybrid nature of the Eukaryota and a consilient view of life on Earth. <i>Nature Reviews Microbiology</i> , 2014, 12, 449-455.	28.6	124
63	The Shape of Modern Tree Reconstruction Methods. <i>Systematic Biology</i> , 2014, 63, 436-441.	5.6	9
64	L.U.St: a tool for approximated maximum likelihood supertree reconstruction. <i>BMC Bioinformatics</i> , 2014, 15, 183.	2.6	14
65	Toward consilience in reptile phylogeny: miRNAs support an archosaur, not lepidosaur, affinity for turtles. <i>Evolution & Development</i> , 2014, 16, 189-196.	2.0	106
66	Molecular Timetrees Reveal a Cambrian Colonization of Land and a New Scenario for Ecdysozoan Evolution. <i>Current Biology</i> , 2013, 23, 392-398.	3.9	322
67	Serine Codon-Usage Bias in Deep Phylogenomics: Pancrustacean Relationships as a Case Study. <i>Systematic Biology</i> , 2013, 62, 121-133.	5.6	124
68	Heterogeneous Models Place the Root of the Placental Mammal Phylogeny. <i>Molecular Biology and Evolution</i> , 2013, 30, 2145-2156.	8.9	115
69	miRNAs: Small Genes with Big Potential in Metazoan Phylogenetics. <i>Molecular Biology and Evolution</i> , 2013, 30, 2369-2382.	8.9	118
70	Linking Genomics and Ecology to Investigate the Complex Evolution of an Invasive <i>Drosophila</i> Pest. <i>Genome Biology and Evolution</i> , 2013, 5, 745-757.	2.5	138
71	Reconstruction of Family-Level Phylogenetic Relationships within Demospongiae (Porifera) Using Nuclear Encoded Housekeeping Genes. <i>PLoS ONE</i> , 2013, 8, e50437.	2.5	47
72	An Overview of Arthropod Genomics, Mitogenomics, and the Evolutionary Origins of the Arthropod Proteome. , 2013, , 41-61.		10

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73	Metazoan opsin evolution reveals a simple route to animal vision. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18868-18872.	7.1	168
74	Resolving phylogenetic signal from noise when divergence is rapid: A new look at the old problem of echinoderm class relationships. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 27-34.	2.7	70
75	A congruent solution to arthropod phylogeny: phylogenomics, microRNAs and morphology support monophyletic Mandibulata. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 298-306.	2.6	227
76	MicroRNAs and phylogenomics resolve the relationships of Tardigrada and suggest that velvet worms are the sister group of Arthropoda. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15920-15924.	7.1	212
77	The Cambrian Conundrum: Early Divergence and Later Ecological Success in the Early History of Animals. <i>Science</i> , 2011, 334, 1091-1097.	12.6	1,055
78	Molecular paleobiological insights into the origin of the Brachiopoda. <i>Evolution & Development</i> , 2011, 13, 290-303.	2.0	55
79	The public goods hypothesis for the evolution of life on Earth. <i>Biology Direct</i> , 2011, 6, 41.	4.6	74
80	Ecdysozoan Mitogenomics: Evidence for a Common Origin of the Legged Invertebrates, the Panarthropoda. <i>Genome Biology and Evolution</i> , 2010, 2, 425-440.	2.5	154
81	Deep Genomic-Scale Analyses of the Metazoa Reject Coelomata: Evidence from Single- and Multigene Families Analyzed Under a Supertree and Supermatrix Paradigm. <i>Genome Biology and Evolution</i> , 2010, 2, 310-324.	2.5	51
82	Deconstructing the tree of life. <i>Trends in Ecology and Evolution</i> , 2009, 24, 184-185.	8.7	0
83	Phylogenetic-Signal Dissection of Nuclear Housekeeping Genes Supports the Paraphyly of Sponges and the Monophyly of Eumetazoa. <i>Molecular Biology and Evolution</i> , 2009, 26, 2261-2274.	8.9	158
84	The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. , 2009, , 15-23.		0
85	The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1435-1443.	4.0	286
86	The prokaryotic tree of life: past, present and future?. <i>Trends in Ecology and Evolution</i> , 2008, 23, 276-281.	8.7	82
87	Dinosaurs and the Cretaceous Terrestrial Revolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 2483-2490.	2.6	274
88	Investigating Stagnation in Morphological Phylogenetics Using Consensus Data. <i>Systematic Biology</i> , 2007, 56, 125-129.	5.6	14
89	Properties of Supertree Methods in the Consensus Setting. <i>Systematic Biology</i> , 2007, 56, 330-337.	5.6	41
90	Paradigm for Life. <i>Science</i> , 2007, 318, 1390-1391.	12.6	17

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91	A supertree of Temnospondyli: cladogenetic patterns in the most species-rich group of early tetrapods. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 3087-3095.	2.6	68
92	Supertrees Disentangle the Chimerical Origin of Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1752-1760.	8.9	157
93	Relative time scales reveal multiple origins of parallel disjunct distributions of African caecilian amphibians. <i>Biology Letters</i> , 2007, 3, 505-508.	2.3	59
94	Congruence of Morphological and Molecular Phylogenies. <i>Acta Biotheoretica</i> , 2007, 55, 269-281.	1.5	80
95	Molecular evidence for dim-light vision in the last common ancestor of the vertebrates. <i>Current Biology</i> , 2006, 16, R318-R319.	3.9	39
96	Testing the Molecular Clock: Molecular and Paleontological Estimates of Divergence Times in the Echinoidea (Echinodermata). <i>Molecular Biology and Evolution</i> , 2006, 23, 1832-1851.	8.9	188
97	The Shape of Supertrees to Come: Tree Shape Related Properties of Fourteen Supertree Methods. <i>Systematic Biology</i> , 2005, 54, 419-431.	5.6	88
98	Measuring Support and Finding Unsupported Relationships in Supertrees. <i>Systematic Biology</i> , 2005, 54, 823-831.	5.6	70
99	Identifying and Removing Fast-Evolving Sites Using Compatibility Analysis: An Example from the Arthropoda. <i>Systematic Biology</i> , 2004, 53, 978-989.	5.6	101
100	The colonization of land by animals: molecular phylogeny and divergence times among arthropods. <i>BMC Biology</i> , 2004, 2, 1.	3.8	239
101	Some Desiderata for Liberal Supertrees. <i>Computational Biology</i> , 2004, , 227-246.	0.2	35
102	A genus-level supertree of the Dinosauria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 915-921.	2.6	67
103	Matrix Representation with Parsimony, Taxonomic Congruence, and Total Evidence. <i>Systematic Biology</i> , 2002, 51, 151-155.	5.6	85