

Ferdinand MarlÃ©taz

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

3,294
citations

279701

23
h-index

315616

38
g-index

51
all docs

51
docs citations

51
times ranked

4502
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.	13.7	564
2	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 820-830.	3.4	250
3	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	13.7	224
4	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015, 527, 459-465.	13.7	217
5	A New Spiralian Phylogeny Places the Enigmatic Arrow Worms among Gnathiferans. <i>Current Biology</i> , 2019, 29, 312-318.e3.	1.8	201
6	Evolution of the ARF Gene Family in Land Plants: Old Domains, New Tricks. <i>Molecular Biology and Evolution</i> , 2013, 30, 45-56.	3.5	196
7	Multigene Phylogeny of the Green Lineage Reveals the Origin and Diversification of Land Plants. <i>Current Biology</i> , 2010, 20, 2217-2222.	1.8	178
8	Retinoic acid signaling and the evolution of chordates. <i>International Journal of Biological Sciences</i> , 2006, 2, 38-47.	2.6	136
9	Chaetognath phylogenomics: a protostome with deuterostome-like development. <i>Current Biology</i> , 2006, 16, R577-R578.	1.8	129
10	A single three-dimensional chromatin compartment in amphioxus indicates a stepwise evolution of vertebrate Hox bimodal regulation. <i>Nature Genetics</i> , 2016, 48, 336-341.	9.4	113
11	Retinoic acid signaling in development: Tissue-specific functions and evolutionary origins. <i>Genesis</i> , 2008, 46, 640-656.	0.8	112
12	New genes from old: asymmetric divergence of gene duplicates and the evolution of development. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20150480.	1.8	90
13	Deeply conserved synteny and the evolution of metazoan chromosomes. <i>Science Advances</i> , 2022, 8, eabi5884.	4.7	81
14	Conservation, Duplication, and Divergence of Five Opsin Genes in Insect Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 579-587.	1.1	77
15	Chaetognath transcriptome reveals ancestral and unique features among bilaterians. <i>Genome Biology</i> , 2008, 9, R94.	13.9	67
16	Ancient Expansion of the Hox Cluster in Lepidoptera Generated Four Homeobox Genes Implicated in Extra-Embryonic Tissue Formation. <i>PLoS Genetics</i> , 2014, 10, e1004698.	1.5	58
17	Structural shifts of aldehyde dehydrogenase enzymes were instrumental for the early evolution of retinoid-dependent axial patterning in metazoans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 226-231.	3.3	57
18	Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. <i>Nature Communications</i> , 2020, 11, 2631.	5.8	57

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19	Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021, 5, 231-242.	3.4	51
20	DrosoPhyla: Resources for Drosophilid Phylogeny and Systematics. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	45
21	Evolutionary origin and functional divergence of totipotent cell homeobox genes in eutherian mammals. <i>BMC Biology</i> , 2016, 14, 45.	1.7	37
22	Unravelling spiral cleavage. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	31
23	Genome sequence of a diabetes-prone rodent reveals a mutation hotspot around the ParaHox gene cluster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7677-7682.	3.3	30
24	Draft genome assemblies and predicted microRNA complements of the intertidal lophotrochozoans <i>Patella vulgata</i> (Mollusca, Patellogastropoda) and <i>Spirobranchus (Pomatoceros) lamarcki</i> (Annelida,) Tj ETQq0 0 OqBT /Overhock 10 TF		
25	The origin and diversification of pteropods precede past perturbations in the Earth's carbon cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25609-25617.	3.3	25
26	<i>De novo</i> genome assembly and <i>in natura</i> epigenomics reveal salinity-induced DNA methylation in the mangrove tree <i>Bruguiera gymnorhiza</i> . <i>New Phytologist</i> , 2022, 233, 2094-2110.	3.5	25
27	Time-calibrated molecular phylogeny of pteropods. <i>PLoS ONE</i> , 2017, 12, e0177325.	1.1	24
28	Phylogenomics illuminates the evolution of bobtail and bottletail squid (order Sepiolida). <i>Communications Biology</i> , 2021, 4, 819.	2.0	24
29	Extreme Mitogenomic Variation in Natural Populations of Chaetognaths. <i>Genome Biology and Evolution</i> , 2017, 9, 1374-1384.	1.1	21
30	Careful with understudied phyla: The case of chaetognath. <i>BMC Evolutionary Biology</i> , 2008, 8, 251.	3.2	13
31	Novel genomic resources for shelled pteropods: a draft genome and target capture probes for <i>Limacina bulimoides</i> , tested for cross-species relevance. <i>BMC Genomics</i> , 2020, 21, 11.	1.2	13
32	Cdx ParaHox genes acquired distinct developmental roles after gene duplication in vertebrate evolution. <i>BMC Biology</i> , 2015, 13, 56.	1.7	12
33	Evolution and biomineralization of pteropod shells. <i>Journal of Structural Biology</i> , 2021, 213, 107779.	1.3	11
34	Evidence from oyster suggests an ancient role for Pdx in regulating insulin gene expression in animals. <i>Nature Communications</i> , 2021, 12, 3117.	5.8	10
35	New bobtail squid (Sepiolidae: Sepiolinae) from the Ryukyu islands revealed by molecular and morphological analysis. <i>Communications Biology</i> , 2019, 2, 465.	2.0	9
36	Discovery and Classification of Homeobox Genes in Animal Genomes. <i>Methods in Molecular Biology</i> , 2014, 1196, 3-18.	0.4	4

#	ARTICLE	IF	CITATIONS
37	High Level of Structural Polymorphism Driven by Mobile Elements in the Hox Genomic Region of the Chaetognath <i>Spadella cephaloptera</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 665-667.	1.1	3
38	Zoology: Worming into the Origin of Bilaterians. <i>Current Biology</i> , 2019, 29, R577-R579.	1.8	3
39	Phylogeny of Animals: Genomes Have a Lot to Say. , 2010, , 119-141.		0