Arnau Sebé-PedrÃ³s

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. Nature Ecology and Evolution, 2022, 6, 1007-1023.	3.4	26
2	Ectopic activation of GABAB receptors inhibits neurogenesis and metamorphosis in the cnidarian Nematostella vectensis. Nature Ecology and Evolution, 2021, 5, 111-121.	3.4	9
3	ACME dissociation: a versatile cell fixation-dissociation method for single-cell transcriptomics. Genome Biology, 2021, 22, 89.	3.8	39
4	A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity. Cell, 2021, 184, 2973-2987.e18.	13.5	111
5	Orthology Clusters from Gene Trees with <i>Possvm</i> . Molecular Biology and Evolution, 2021, 38, 5204-5208.	3.5	12
6	Evolutionary cell type mapping with single-cell genomics. Trends in Genetics, 2021, 37, 919-932.	2.9	43
7	Tracing the evolutionary history of Ca2+-signaling modulation by human Bcl-2: Insights from the Capsaspora owczarzaki IP3 receptor ortholog. Biochimica Et Biophysica Acta - Molecular Cell Research, 2021, 1868, 119121.	1.9	7
8	A single-cell view on alga-virus interactions reveals sequential transcriptional programs and infection states. Science Advances, 2020, 6, eaba4137.	4.7	55
9	IL18 signaling promotes homing of mature Tregs into the thymus. ELife, 2020, 9, .	2.8	28
10	The Protistan Cellular and Genomic Roots of Animal Multicellularity. Fascinating Life Sciences, 2019, , 15-38.	0.5	0
11	MetaCell: analysis of single-cell RNA-seq data using K-nn graph partitions. Genome Biology, 2019, 20, 206.	3.8	218
12	Origin and evolution of eukaryotic transcription factors. Current Opinion in Genetics and Development, 2019, 58-59, 25-32.	1.5	29
13	Using single-cell transcriptomics to understand functional states and interactions in microbial eukaryotes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190098.	1.8	20
14	Comparative genomic analysis of the â€~pseudofungus' <i>Hyphochytrium catenoides</i> . Open Biology, 2018, 8, 170184.	1.5	31
15	Global transcriptome analysis of the aphelid Paraphelidium tribonemae supports the phagotrophic origin of fungi. Communications Biology, 2018, 1, 231.	2.0	63
16	Cnidarian Cell Type Diversity and Regulation Revealed by Whole-Organism Single-Cell RNA-Seq. Cell, 2018, 173, 1520-1534.e20.	13.5	284
17	Early metazoan cell type diversity and the evolution of multicellular gene regulation. Nature Ecology and Evolution, 2018, 2, 1176-1188.	3.4	226
18	The origin of Metazoa: a unicellular perspective. Nature Reviews Genetics, 2017, 18, 498-512.	7.7	239

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19	Evolution and Classification of the T-Box Transcription Factor Family. Current Topics in Developmental Biology, 2017, 122, 1-26.	1.0	28
20	The Dynamic Regulatory Genome of Capsaspora and the Origin of Animal Multicellularity. Cell, 2016, 165, 1224-1237.	13.5	139
21	High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. Developmental Cell, 2016, 39, 186-197.	3.1	51
22	The Eukaryotic Ancestor Had a Complex Ubiquitin Signaling System of Archaeal Origin. Molecular Biology and Evolution, 2015, 32, 726-739.	3.5	58
23	Tracing the Evolutionary History of Inositol, 1, 4, 5-Trisphosphate Receptor: Insights from Analyses of <i>Capsaspora owczarzaki</i> Ca ²⁺ Release Channel Orthologs. Molecular Biology and Evolution, 2015, 32, 2236-2253.	3.5	44
24	Transcription Factors and the Origin of Animal Multicellularity. Advances in Marine Genomics, 2015, , 379-394.	1.2	12
25	Evolution and Classification of Myosins, a Paneukaryotic Whole-Genome Approach. Genome Biology and Evolution, 2014, 6, 290-305.	1.1	121
26	The Evolution of the GPCR Signaling System in Eukaryotes: Modularity, Conservation, and the Transition to Metazoan Multicellularity. Genome Biology and Evolution, 2014, 6, 606-619.	1.1	145
27	The Capsaspora genome reveals a complex unicellular prehistory of animals. Nature Communications, 2013, 4, 2325.	5.8	244
28	Transcription factor evolution in eukaryotes and the assembly of the regulatory toolkit in multicellular lineages. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4858-66.	3.3	183
29	Early evolution of the T-box transcription factor family. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16050-16055.	3.3	80
30	A Genomic Survey of HECT Ubiquitin Ligases in Eukaryotes Reveals Independent Expansions of the HECT System in Several Lineages. Genome Biology and Evolution, 2013, 5, 833-847.	1.1	35
31	A Broad Genomic Survey Reveals Multiple Origins and Frequent Losses in the Evolution of Respiratory Hemerythrins and Hemocyanins. Genome Biology and Evolution, 2013, 5, 1435-1442.	1.1	26
32	Insights into the Origin of Metazoan Filopodia and Microvilli. Molecular Biology and Evolution, 2013, 30, 2013-2023.	3.5	78
33	Regulated aggregative multicellularity in a close unicellular relative of metazoa. ELife, 2013, 2, e01287.	2.8	139
34	Premetazoan Origin of the Hippo Signaling Pathway. Cell Reports, 2012, 1, 13-20.	2.9	111
35	Unexpected Repertoire of Metazoan Transcription Factors in the Unicellular Holozoan Capsaspora owczarzaki. Molecular Biology and Evolution, 2011, 28, 1241-1254.	3.5	172
36	Ancient origin of the integrin-mediated adhesion and signaling machinery. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10142-10147.	3.3	225

#	Article	IF	CITATIONS
37	Integrin-mediated adhesion complex. Communicative and Integrative Biology, 2010, 3, 475-477.	0.6	33