IÃ±aki Ruiz-Trillo

List of Publications by Year
in descending order

100 papers	6,459 citations	71102 41 h-index	76900 74 g-index

129 all docs	129 docs citations	129 times ranked	5864 citing authors

#	Article	IF	Citations
1	Acoel Flatworms: Earliest Extant Bilaterian Metazoans, Not Members of Platyhelminthes. Science, 1999, 283, 1919-1923.	12.6	427
2	A Phylogenomic Investigation into the Origin of Metazoa. Molecular Biology and Evolution, 2008, 25, 664-672.	8.9	259
3	The Capsaspora genome reveals a complex unicellular prehistory of animals. Nature Communications, 2013, 4, 2325.	12.8	244
4	The origin of Metazoa: a unicellular perspective. Nature Reviews Genetics, 2017, 18, 498-512.	16.3	239
5	A phylogenetic analysis of myosin heavy chain type II sequences corroborates that Acoela and Nemertodermatida are basal bilaterians. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11246-11251.	7.1	229
6	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.	7.1	225
7	The origins of multicellularity: a multi-taxon genome initiative. Trends in Genetics, 2007, 23, 113-118.	6.7	201
8	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.	7.1	183
9	Unexpected Repertoire of Metazoan Transcription Factors in the Unicellular Holozoan Capsaspora owczarzaki. Molecular Biology and Evolution, 2011, 28, 1241-1254.	8.9	172
10	The Nemertodermatida are basal bilaterians and not members of the Platyhelminthes. Zoologica Scripta, 2002, 31, 201-215.	1.7	169
11	Phylogenomics Reveals Convergent Evolution of Lifestyles in Close Relatives of Animals and Fungi. Current Biology, 2015, 25, 2404-2410.	3.9	169
12	The others: our biased perspective of eukaryotic genomes. Trends in Ecology and Evolution, 2014, 29, 252-259.	8.7	167
13	Phylogenetic Relationships within the Opisthokonta Based on Phylogenomic Analyses of Conserved Single-Copy Protein Domains. Molecular Biology and Evolution, 2012, 29, 531-544.	8.9	166
14	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.	2.5	145
15	Regulated aggregative multicellularity in a close unicellular relative of metazoa. ELife, 2013, 2, e01287.	6.0	139
16	The Dynamic Regulatory Genome of Capsaspora and the Origin of Animal Multicellularity. Cell, 2016, 165, 1224-1237.	28.9	139
17	Evolution and Classification of Myosins, a Paneukaryotic Whole-Genome Approach. Genome Biology and Evolution, 2014, 6, 290-305.	2.5	121
18	Dynamics of genomic innovation in the unicellular ancestry of animals. ELife, 2017, 6, .	6.0	121

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19	Premetazoan Origin of the Hippo Signaling Pathway. Cell Reports, 2012, 1, 13-20.	6.4	111
20	Sterol and genomic analyses validate the sponge biomarker hypothesis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2684-2689.	7.1	110
21	Genomic Survey of Premetazoans Shows Deep Conservation of Cytoplasmic Tyrosine Kinases and Multiple Radiations of Receptor Tyrosine Kinases. Science Signaling, 2012, 5, ra35.	3.6	108
22	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. Nature Methods, 2020, 17, 481-494.	19.0	97
23	Alternative Methods for Concatenation of Core Genes Indicate a Lack of Resolution in Deep Nodes of the Prokaryotic Phylogeny. Molecular Biology and Evolution, 2007, 25, 83-91.	8.9	96
24	Mitochondrial genome data support the basal position of Acoelomorpha and the polyphyly of the Platyhelminthes. Molecular Phylogenetics and Evolution, 2004, 33, 321-332.	2.7	92
25	Evolution of the MAGUK protein gene family in premetazoan lineages. BMC Evolutionary Biology, 2010, 10, 93.	3.2	91
26	Molecular Phylogeny of Unikonts: New Insights into the Position of Apusomonads and Ancyromonads and the Internal Relationships of Opisthokonts. Protist, 2013, 164, 2-12.	1.5	91
27	Origin and evolution of lysyl oxidases. Scientific Reports, 2015, 5, 10568.	3.3	86
28	Capsaspora owczarzaki is an independent opisthokont lineage. Current Biology, 2004, 14, R946-R947.	3.9	82
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.	7.1	80
30	Insights into the Origin of Metazoan Filopodia and Microvilli. Molecular Biology and Evolution, 2013, 30, 2013-2023.	8.9	78
31	Development of ichthyosporeans sheds light on the origin of metazoan multicellularity. Developmental Biology, 2013, 377, 284-292.	2.0	73
32	The origin of animals: an ancestral reconstruction of the unicellular-to-multicellular transition. Open Biology, 2021, 11, 200359.	3.6	67
33	Environmental Survey Meta-analysis Reveals Hidden Diversity among Unicellular Opisthokonts. Molecular Biology and Evolution, 2013, 30, 802-805.	8.9	64
34	Insights into the Evolutionary Origin and Genome Architecture of the Unicellular Opisthokonts Capsaspora owczarzaki and Sphaeroforma arctica. Journal of Eukaryotic Microbiology, 2006, 53, 379-384.	1.7	61
35	Origin of exon skipping-rich transcriptomes in animals driven by evolution of gene architecture. Genome Biology, 2018, 19, 135.	8.8	61
36	Premetazoan Ancestry of the Mycâ€“Max Network. Molecular Biology and Evolution, 2011, 28, 2961-2971.	8.9	59

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37	Complex transcriptional regulation and independent evolution of fungal-like traits in a relative of animals. ELife, 2015, 4, e08904.	6.0	59
38	The Eukaryotic Ancestor Had a Complex Ubiquitin Signaling System of Archaeal Origin. Molecular Biology and Evolution, 2015, 32, 726-739.	8.9	58
39	Losing Complexity: The Role of Simplification in Macroevolution. Trends in Ecology and Evolution, 2016, 31, 608-621.	8.7	55
40	Diversity and distribution of unicellular opisthokonts along the <scp>E</scp>uropean coast analysed using highâ€throughput sequencing. Environmental Microbiology, 2015, 17, 3195-3207.	3.8	52
41	High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. Developmental Cell, 2016, 39, 186-197.	7.0	51
42	Novel roles of plant RETINOBLASTOMA-RELATED (RBR) protein in cell proliferation and asymmetric cell division. Journal of Experimental Botany, 2014, 65, 2657-2666.	4.8	49
43	Codon adaptation to tRNAs with Inosine modification at position 34 is widespread among Eukaryotes and present in two Bacterial phyla. RNA Biology, 2018, 15, 500-507.	3.1	49
44	Tracing the Evolutionary History of Inositol, 1, 4, 5-Trisphosphate Receptor: Insights from Analyses ofCapsaspora owczarzakiCa²⁺Release Channel Orthologs. Molecular Biology and Evolution, 2015, 32, 2236-2253.	8.9	44
45	Concepts of the last eukaryotic common ancestor. Nature Ecology and Evolution, 2019, 3, 338-344.	7.8	44
46	Unicellular Origin of the Animal MicroRNA Machinery. Current Biology, 2018, 28, 3288-3295.e5.	3.9	42
47	A robust molecular phylogeny of the Tricladida (Platyhelminthes: Seriata) with a discussion on morphological synapomorphies. Proceedings of the Royal Society B: Biological Sciences, 1998, 265, 631-640.	2.6	41
48	Earliest Holozoan Expansion of Phosphotyrosine Signaling. Molecular Biology and Evolution, 2014, 31, 517-528.	8.9	41
49	A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. ELife, 2019, 8, .	6.0	41
50	Sawyeria marylandensis (Heterolobosea) Has a Hydrogenosome with Novel Metabolic Properties. Eukaryotic Cell, 2010, 9, 1913-1924.	3.4	40
51	Reconstruction of protein domain evolution using single-cell amplified genomes of uncultured choanoflagellates sheds light on the origin of animals. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190088.	4.0	36
52	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.	2.5	35
53	Metabarcoding analysis on European coastal samples reveals new molecular metazoan diversity. Scientific Reports, 2018, 8, 9106.	3.3	34
54	The Expansion of Inosine at the Wobble Position of tRNAs, and Its Role in the Evolution of Proteomes. Molecular Biology and Evolution, 2019, 36, 650-662.	8.9	34

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55	Integrin-mediated adhesion complex. Communicative and Integrative Biology, 2010, 3, 475-477.	1.4	33
56	Transfection of Capsaspora owczarzaki, a close unicellular relative of animals. Development (Cambridge), 2018, 145, .	2.5	33
57	The Evolutionary History of Lysine Biosynthesis Pathways Within Eukaryotes. Journal of Molecular Evolution, 2009, 69, 240-248.	1.8	32
58	Evolution and Classification of the T-Box Transcription Factor Family. Current Topics in Developmental Biology, 2017, 122, 1-26.	2.2	28
59	Decoupling of Nuclear Division Cycles and Cell Size during the Coenocytic Growth of the Ichthyosporean Sphaeroforma arctica. Current Biology, 2018, 28, 1964-1969.e2.	3.9	27
60	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.	2.5	26
61	Acoelomorpha: earliest branching bilaterians or deuterostomes?. Organisms Diversity and Evolution, 2016, 16, 391-399.	1.6	26
62	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. Nature Ecology and Evolution, 2022, 6, 1007-1023.	7.8	26
63	Reticulate evolution in eukaryotes: Origin and evolution of the nitrate assimilation pathway. PLoS Genetics, 2019, 15, e1007986.	3.5	21
64	Parvularia atlantis gen. et sp. nov., a Nucleariid Filose Amoeba (Holomycota, Opisthokonta). Journal of Eukaryotic Microbiology, 2018, 65, 170-179.	1.7	21
65	Capsaspora owczarzaki. Current Biology, 2017, 27, R829-R830.	3.9	20
66	Novel Diversity of Deeply Branching Holomycota and Unicellular Holozoans Revealed by Metabarcoding in Middle ParanÃ¡ River, Argentina. Frontiers in Ecology and Evolution, 2018, 6, .	2.2	20
67	Integrin-Mediated Adhesion in the Unicellular Holozoan Capsaspora owczarzaki. Current Biology, 2020, 30, 4270-4275.e4.	3.9	20
68	Lack of Csk-Mediated Negative Regulation in a Unicellular Src Kinase. Biochemistry, 2012, 51, 8267-8277.	2.5	19
69	Evaluation of single-cell genomics to address evolutionary questions using three SAGs of the choanoflagellate Monosiga brevicollis. Scientific Reports, 2017, 7, 11025.	3.3	19
70	The Diversity of Mitochondrion-Related Organelles Amongst Eukaryotic Microbes. , 2007, , 239-275.		17
71	Hidden diversity of Acoelomorpha revealed through metabarcoding. Biology Letters, 2016, 12, 20160674.	2.3	17
72	Towards understanding the origin of animal development. Development (Cambridge), 2020, 147, .	2.5	17

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73	Regulation of sedimentation rate shapes the evolution of multicellularity in a close unicellular relative of animals. PLoS Biology, 2022, 20, e3001551.	5.6	14
74	Stable transfection in protist Corallochytrium limacisporum identifies novel cellular features among unicellular animals relatives. Current Biology, 2021, 31, 4104-4110.e5.	3.9	13
75	The Mysterious Evolutionary Origin for the GNE Gene and the Root of Bilateria. Molecular Biology and Evolution, 2011, 28, 2987-2991.	8.9	11
76	Expression Atlas of the Deubiquitinating Enzymes in the Adult Mouse Retina, Their Evolutionary Diversification and Phenotypic Roles. PLoS ONE, 2016, 11, e0150364.	2.5	10
77	Sterol metabolism in the filasterean Capsaspora owczarzaki has features that resemble both fungi and animals. Open Biology, 2016, 6, 160029.	3.6	9
78	Gene Similarity Networks Unveil a Potential Novel Unicellular Group Closely Related to Animals from the Tara Oceans Expedition. Genome Biology and Evolution, 2020, 12, 1664-1678.	2.5	9
79	Origin Recognition Complex (ORC) Evolution Is Influenced by Global Gene Duplication/Loss Patterns in Eukaryotic Genomes. Genome Biology and Evolution, 2020, 12, 3878-3889.	2.5	9
80	Antifungal and antiprotozoal green amino acid-based rhamnolipids: Mode of action, antibiofilm efficiency and selective activity against resistant Candida spp. strains and Acanthamoeba castellanii. Colloids and Surfaces B: Biointerfaces, 2020, 193, 111148.	5.0	8
81	Cell cycle transcriptomics of Capsaspora provides insights into the evolution of cyclin-CDK machinery. PLoS Genetics, 2020, 16, e1008584.	3.5	8
82	Phylogenomic Evidence for a Myxococcal Contribution to the Mitochondrial Fatty Acid Beta-Oxidation. PLoS ONE, 2011, 6, e21989.	2.5	7
83	Revision of the Capsaspora genome using read mating information adjusts the view on premetazoan genome. Development Growth and Differentiation, 2019, 61, 34-42.	1.5	7
84	Revisiting the phylogenetic position of Caullerya mesnili (Ichthyosporea), a common Daphnia parasite, based on 22 protein-coding genes. Molecular Phylogenetics and Evolution, 2020, 151, 106891.	2.7	7
85	Rel/NF-ÎºB Transcription Factors Emerged at the Onset of Opisthokonts. Genome Biology and Evolution, 2022, 14, .	2.5	7
86	Evolution of a histone variant involved in compartmental regulation of NAD metabolism. Nature Structural and Molecular Biology, 2021, 28, 1009-1019.	8.2	7
87	Characterization of a group I Nme protein of Capsaspora owczarzakiâ€”a close unicellular relative of animals. Laboratory Investigation, 2018, 98, 304-314.	3.7	6
88	A global metabarcoding analysis expands molecular diversity of Platyhelminthes and reveals novel early-branching clades. Biology Letters, 2019, 15, 20190182.	2.3	6
89	Txikispora philomaios n. sp., n. g., a microâ€eukaryotic pathogen of amphipods, reveals parasitism and hidden diversity in Class Filasterea. Journal of Eukaryotic Microbiology, 2022, 69, e12875.	1.7	6
90	Observations on aGeocentrophorasp. (Lecithoepitheliata) flatworm from forest soils in Nova Scotia. Journal of Natural History, 2006, 40, 1381-1387.	0.5	5

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91	Filastereans and Ichthyosporeans: Models to Understand the Origin of Metazoan Multicellularity. Advances in Marine Genomics, 2015, , 117-128.	1.2	5
92	A genomic survey shows that the haloarchaeal type tyrosyl tRNA synthetase is not a synapomorphy of opisthokonts. European Journal of Protistology, 2012, 48, 89-93.	1.5	4
93	A Unicellular Relative of Animals Generates an Epithelium-Like Cell Layer by Actomyosin-dependent Cellularization. SSRN Electronic Journal, 0, , .	0.4	3
94	Forward genetics for back-in-time questions. ELife, 2014, 3, .	6.0	1
95	New genomes, new taxa and deep questions in the eukaryotic tree of life: a meeting report on the EMBO comparative genomics conference. EvoDevo, 2011, 2, 22.	3.2	0
96	Discovering the biology behind the organism while developing genetic tools for Corallochytrium limacisporum. Access Microbiology, 2019, 1, .	0.5	0
97	Title is missing!. , 2020, 16, e1008584.		0
98	Title is missing!. , 2020, 16, e1008584.		0
99	Title is missing!. , 2020, 16, e1008584.		0
100	Title is missing!. , 2020, 16, e1008584.		0