Iñaki Ruiz-Trillo

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/740419/publications.pdf

Version: 2024-02-01

100 papers 6,459 citations

71102 41 h-index 76900 74 g-index

129 all docs

129 docs citations

times ranked

129

5864 citing authors

#	Article	IF	CITATIONS
1	<i>Txikispora philomaios</i> i> 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
2	Rel/NF-l $^{\circ}$ B Transcription Factors Emerged at the Onset of Opisthokonts. Genome Biology and Evolution, 2022, 14, .	2.5	7
3	Regulation of sedimentation rate shapes the evolution of multicellularity in a close unicellular relative of animals. PLoS Biology, 2022, 20, e3001551.	5.6	14
4	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. Nature Ecology and Evolution, 2022, 6, 1007-1023.	7.8	26
5	The origin of animals: an ancestral reconstruction of the unicellular-to-multicellular transition. Open Biology, 2021, 11, 200359.	3.6	67
6	Stable transfection in protist Corallochytrium limacisporum identifies novel cellular features among unicellular animals relatives. Current Biology, 2021, 31, 4104-4110.e5.	3.9	13
7	Evolution of a histone variant involved in compartmental regulation of NAD metabolism. Nature Structural and Molecular Biology, 2021, 28, 1009-1019.	8.2	7
8	Towards understanding the origin of animal development. Development (Cambridge), 2020, 147, .	2.5	17
9	Integrin-Mediated Adhesion in the Unicellular Holozoan Capsaspora owczarzaki. Current Biology, 2020, 30, 4270-4275.e4.	3.9	20
10	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
11	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
12	Gene Similarity Networks Unveil a Potential Novel Unicellular Group Closely Related to Animals from the <i>Tara</i> Oceans Expedition. Genome Biology and Evolution, 2020, 12, 1664-1678.	2.5	9
13	Cell cycle transcriptomics of Capsaspora provides insights into the evolution of cyclin-CDK machinery. PLoS Genetics, 2020, 16, e1008584.	3.5	8
14	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. Nature Methods, 2020, 17, 481-494.	19.0	97
15	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
16	Title is missing!. , 2020, 16, e1008584.		0
17	Title is missing!. , 2020, 16, e1008584.		0
18	Title is missing!. , 2020, 16, e1008584.		0

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19	Title is missing!. , 2020, 16, e1008584.		O
20	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
21	A global metabarcoding analysis expands molecular diversity of Platyhelminthes and reveals novel early-branching clades. Biology Letters, 2019, 15, 20190182.	2.3	6
22	Reticulate evolution in eukaryotes: Origin and evolution of the nitrate assimilation pathway. PLoS Genetics, 2019, 15, e1007986.	3 . 5	21
23	Concepts of the last eukaryotic common ancestor. Nature Ecology and Evolution, 2019, 3, 338-344.	7.8	44
24	Revision of the <i>Capsaspora</i> genome using read mating information adjusts the view on premetazoan genome. Development Growth and Differentiation, 2019, 61, 34-42.	1.5	7
25	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
26	A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. ELife, $2019,8,.$	6.0	41
27	Discovering the biology behind the organism while developing genetic tools for Corallochytrium limacisporum. Access Microbiology, 2019, 1, .	0.5	0
28	Characterization of a group I Nme protein of Capsaspora owczarzaki—a close unicellular relative of animals. Laboratory Investigation, 2018, 98, 304-314.	3.7	6
29	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
30	Novel Diversity of Deeply Branching Holomycota and Unicellular Holozoans Revealed by Metabarcoding in Middle Paran \tilde{A}_i River, Argentina. Frontiers in Ecology and Evolution, 2018, 6, .	2.2	20
31	Origin of exon skipping-rich transcriptomes in animals driven by evolution of gene architecture. Genome Biology, 2018, 19, 135.	8.8	61
32	Unicellular Origin of the Animal MicroRNA Machinery. Current Biology, 2018, 28, 3288-3295.e5.	3.9	42
33	Transfection of <i>Capsaspora owczarzaki</i> , a close unicellular relative of animals. Development (Cambridge), 2018, 145, .	2.5	33
34	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
35	Metabarcoding analysis on European coastal samples reveals new molecular metazoan diversity. Scientific Reports, 2018, 8, 9106.	3.3	34
36	<i>Parvularia atlantis</i> gen. et sp. nov., a Nucleariid Filose Amoeba (Holomycota, Opisthokonta). Journal of Eukaryotic Microbiology, 2018, 65, 170-179.	1.7	21

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37	The origin of Metazoa: a unicellular perspective. Nature Reviews Genetics, 2017, 18, 498-512.	16.3	239
38	Evolution and Classification of the T-Box Transcription Factor Family. Current Topics in Developmental Biology, 2017, 122, 1-26.	2.2	28
39	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
40	Capsaspora owczarzaki. Current Biology, 2017, 27, R829-R830.	3.9	20
41	Dynamics of genomic innovation in the unicellular ancestry of animals. ELife, 2017, 6, .	6.0	121
42	The Dynamic Regulatory Genome of Capsaspora and the Origin of Animal Multicellularity. Cell, 2016, 165, 1224-1237.	28.9	139
43	Losing Complexity: The Role of Simplification in Macroevolution. Trends in Ecology and Evolution, 2016, 31, 608-621.	8.7	55
44	Sterol metabolism in the filasterean <i>Capsaspora owczarzaki</i> has features that resemble both fungi and animals. Open Biology, 2016, 6, 160029.	3.6	9
45	High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. Developmental Cell, 2016, 39, 186-197.	7.0	51
46	Hidden diversity of Acoelomorpha revealed through metabarcoding. Biology Letters, 2016, 12, 20160674.	2.3	17
47	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
48	Acoelomorpha: earliest branching bilaterians or deuterostomes?. Organisms Diversity and Evolution, 2016, 16, 391-399.	1.6	26
49			
49	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
50		2.5	10 58
	Diversification and Phenotypic Roles. PLoS ONE, 2016, 11, e0150364. The Eukaryotic Ancestor Had a Complex Ubiquitin Signaling System of Archaeal Origin. Molecular		
50	Diversification and Phenotypic Roles. PLoS ONE, 2016, 11, e0150364. The Eukaryotic Ancestor Had a Complex Ubiquitin Signaling System of Archaeal Origin. Molecular Biology and Evolution, 2015, 32, 726-739. Diversity and distribution of unicellular opisthokonts along the <scp>E</scp> uropean coast analysed	8.9	58
50 51	Diversification and Phenotypic Roles. PLoS ONE, 2016, 11, e0150364. The Eukaryotic Ancestor Had a Complex Ubiquitin Signaling System of Archaeal Origin. Molecular Biology and Evolution, 2015, 32, 726-739. Diversity and distribution of unicellular opisthokonts along the ⟨scp⟩E⟨/scp⟩uropean coast analysed using highâ€throughput sequencing. Environmental Microbiology, 2015, 17, 3195-3207.	8.9 3.8	58 52

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55	Filastereans and Ichthyosporeans: Models to Understand the Origin of Metazoan Multicellularity. Advances in Marine Genomics, 2015, , 117-128.	1.2	5
56	Complex transcriptional regulation and independent evolution of fungal-like traits in a relative of animals. ELife, 2015, 4, e08904.	6.0	59
57	Evolution and Classification of Myosins, a Paneukaryotic Whole-Genome Approach. Genome Biology and Evolution, 2014, 6, 290-305.	2.5	121
58	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
59	The others: our biased perspective of eukaryotic genomes. Trends in Ecology and Evolution, 2014, 29, 252-259.	8.7	167
60	Earliest Holozoan Expansion of Phosphotyrosine Signaling. Molecular Biology and Evolution, 2014, 31, 517-528.	8.9	41
61	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
62	Forward genetics for back-in-time questions. ELife, 2014, 3, .	6.0	1
63	The Capsaspora genome reveals a complex unicellular prehistory of animals. Nature Communications, 2013, 4, 2325.	12.8	244
64	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
65	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
66	Development of ichthyosporeans sheds light on the origin of metazoan multicellularity. Developmental Biology, 2013, 377, 284-292.	2.0	73
67	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
68	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
69	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
70	Environmental Survey Meta-analysis Reveals Hidden Diversity among Unicellular Opisthokonts. Molecular Biology and Evolution, 2013, 30, 802-805.	8.9	64
71	Insights into the Origin of Metazoan Filopodia and Microvilli. Molecular Biology and Evolution, 2013, 30, 2013-2023.	8.9	78
72	Regulated aggregative multicellularity in a close unicellular relative of metazoa. ELife, 2013, 2, e01287.	6.0	139

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73	Premetazoan Origin of the Hippo Signaling Pathway. Cell Reports, 2012, 1, 13-20.	6.4	111
74	Lack of Csk-Mediated Negative Regulation in a Unicellular Src Kinase. Biochemistry, 2012, 51, 8267-8277.	2.5	19
75	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
76	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
77	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
78	Phylogenomic Evidence for a Myxococcal Contribution to the Mitochondrial Fatty Acid Beta-Oxidation. PLoS ONE, 2011, 6, e21989.	2.5	7
79	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
80	The Mysterious Evolutionary Origin for the GNE Gene and the Root of Bilateria. Molecular Biology and Evolution, 2011, 28, 2987-2991.	8.9	11
81	Premetazoan Ancestry of the Myc–Max Network. Molecular Biology and Evolution, 2011, 28, 2961-2971.	8.9	59
82	Unexpected Repertoire of Metazoan Transcription Factors in the Unicellular Holozoan Capsaspora owczarzaki. Molecular Biology and Evolution, 2011, 28, 1241-1254.	8.9	172
83	Evolution of the MAGUK protein gene family in premetazoan lineages. BMC Evolutionary Biology, 2010, 10, 93.	3.2	91
84	Sawyeria marylandensis (Heterolobosea) Has a Hydrogenosome with Novel Metabolic Properties. Eukaryotic Cell, 2010, 9, 1913-1924.	3.4	40
85	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
86	Integrin-mediated adhesion complex. Communicative and Integrative Biology, 2010, 3, 475-477.	1.4	33
87	The Evolutionary History of Lysine Biosynthesis Pathways Within Eukaryotes. Journal of Molecular Evolution, 2009, 69, 240-248.	1.8	32
88	A Phylogenomic Investigation into the Origin of Metazoa. Molecular Biology and Evolution, 2008, 25, 664-672.	8.9	259
89	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
90	The Diversity of Mitochondrion-Related Organelles Amongst Eukaryotic Microbes., 2007,, 239-275.		17

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91	The origins of multicellularity: a multi-taxon genome initiative. Trends in Genetics, 2007, 23, 113-118.	6.7	201
92	Observations on aGeocentrophorasp. (Lecithoepitheliata) flatworm from forest soils in Nova Scotia. Journal of Natural History, 2006, 40, 1381-1387.	0.5	5
93	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
94	Capsaspora owczarzaki is an independent opisthokont lineage. Current Biology, 2004, 14, R946-R947.	3.9	82
95	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
96	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
97	The Nemertodermatida are basal bilaterians and not members of the Platyhelminthes. Zoologica Scripta, 2002, 31, 201-215.	1.7	169
98	Acoel Flatworms: Earliest Extant Bilaterian Metazoans, Not Members of Platyhelminthes. Science, 1999, 283, 1919-1923.	12.6	427
99	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
100	A Unicellular Relative of Animals Generates an Epithelium-Like Cell Layer by Actomyosin-dependent Cellularization. SSRN Electronic Journal, 0, , .	0.4	3