Cymon John Cox

List of Publications by Citations

Source: https://exaly.com/author-pdf/4754709/cymon-john-cox-publications-by-citations.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

8,359 85 91 37 h-index g-index citations papers 10,317 91 5.3 5.73 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
85	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009 , 25, 1422-3	7.2	2308
84	Reconstructing the early evolution of Fungi using a six-gene phylogeny. <i>Nature</i> , 2006 , 443, 818-22	50.4	1392
83	Assembling the fungal tree of life: progress, classification, and evolution of subcellular traits. <i>American Journal of Botany</i> , 2004 , 91, 1446-80	2.7	640
82	An archaeal origin of eukaryotes supports only two primary domains of life. <i>Nature</i> , 2013 , 504, 231-6	50.4	353
81	The archaebacterial origin of eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 20356-61	11.5	269
80	The Interrelationships of Land Plants and the Nature of the Ancestral Embryophyte. <i>Current Biology</i> , 2018 , 28, 733-745.e2	6.3	214
79	Moss diversity: A molecular phylogenetic analysis of genera. <i>Phytotaxa</i> , 2010 , 9, 175	0.7	141
78	Three geographically separate domestications of Asian rice. <i>Nature Plants</i> , 2015 , 1, 15164	11.5	138
77	Conflicting phylogenies for early land plants are caused by composition biases among synonymous substitutions. <i>Systematic Biology</i> , 2014 , 63, 272-9	8.4	135
76	A congruent phylogenomic signal places eukaryotes within the Archaea. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012 , 279, 4870-9	4.4	116
75	Extant diversity of bryophytes emerged from successive post-Mesozoic diversification bursts. <i>Nature Communications</i> , 2014 , 5, 5134	17.4	112
74	Phylogenomics provides robust support for a two-domains tree of life. <i>Nature Ecology and Evolution</i> , 2020 , 4, 138-147	12.3	97
73	The primary divisions of life: a phylogenomic approach employing composition-heterogeneous methods. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009 , 364, 2197-207	5.8	95
72	Phylogeny and evolution of medical species of Candida and related taxa: a multigenic analysis. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 5624-35	9.7	94
71	Evolution of the Major Moss Lineages: Phylogenetic Analyses Based on Multiple Gene Sequences and Morphology. <i>Bryologist</i> , 2000 , 103, 187-211	0.7	94
70	Chloroplast Phylogeny of Asplenioid Ferns based on rbcL and trnL-F Spacer Sequences (Polypodiidae, Aspleniaceae) and its Implications for Biogeography. <i>Systematic Botany</i> , 2004 , 29, 260-2	74 ·7	92
69	Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have no roots?. <i>American Journal of Botany</i> , 2003 , 90, 1777-87	2.7	85

(2005-2014)

68	Mitochondrial phylogenomics of early land plants: mitigating the effects of saturation, compositional heterogeneity, and codon-usage bias. <i>Systematic Biology</i> , 2014 , 63, 862-78	8.4	84	
67	Resolution of the ordinal phylogeny of mosses using targeted exons from organellar and nuclear genomes. <i>Nature Communications</i> , 2019 , 10, 1485	17.4	80	
66	Phylogeny and morphological evolution of the amblystegiaceae (Bryopsida). <i>Molecular Phylogenetics and Evolution</i> , 2002 , 23, 1-21	4.1	80	
65	Phylogenetic Relationships among the Mosses Based on Heterogeneous Bayesian Analysis of Multiple Genes from Multiple Genomic Compartments. <i>Systematic Botany</i> , 2004 , 29, 234-250	0.7	75	
64	Phylogenetic Relationships Among the Diplolepideous-alternate Mosses (Bryidae) Inferred from Nuclear and Chloroplast DNA Sequences. <i>Bryologist</i> , 2000 , 103, 224-241	0.7	70	
63	The Bryophyta (Mosses): Systematic and Evolutionary Inferences from an rps4 Gene (cpDNA) Phylogeny. <i>Annals of Botany</i> , 2001 , 87, 191-208	4.1	68	
62	Phylogenetic relationships among the ciliate arthrodontous mosses: Evidence from chloroplast and nuclear DNA sequences. <i>Plant Systematics and Evolution</i> , 1999 , 215, 119-139	1.3	67	
61	Peatmoss (Sphagnum) diversification associated with Miocene Northern Hemisphere climatic cooling?. <i>Molecular Phylogenetics and Evolution</i> , 2010 , 55, 1139-45	4.1	65	
60	Global patterns of moss diversity: taxonomic and molecular inferences. <i>Taxon</i> , 2005 , 54, 337-352	0.8	62	
59	Nuclear protein phylogenies support the monophyly of the three bryophyte groups (Bryophyta Schimp.). <i>New Phytologist</i> , 2019 , 222, 565-575	9.8	58	
58	Disentangling knots of rapid evolution: origin and diversification of the moss order Hypnales. <i>Journal of Bryology</i> , 2012 , 34, 187-211	1.1	53	
57	Analyses of charophyte chloroplast genomes help characterize the ancestral chloroplast genome of land plants. <i>Genome Biology and Evolution</i> , 2014 , 6, 897-911	3.9	52	
56	Circumscription, classification, and (Bryopsida) inferred from nuclear and chloroplast DNA sequence data and morphology taxonomy of Amblystegiaceae. <i>Taxon</i> , 2002 , 51, 115-122	0.8	49	
55	Newly resolved relationships in an early land plant lineage: Bryophyta class Sphagnopsida (peat mosses). <i>American Journal of Botany</i> , 2010 , 97, 1511-31	2.7	45	
54	Organellar phylogenomics of an emerging model system: Sphagnum (peatmoss). <i>Annals of Botany</i> , 2016 , 118, 185-96	4.1	42	
53	Phylogenetically and spatially close marine sponges harbour divergent bacterial communities. <i>PLoS ONE</i> , 2012 , 7, e53029	3.7	39	
52	Genetic structure, reproductive biology and ecology of isolated populations of asplenium csikii (Aspleniaceae, pteridophyta). <i>Heredity</i> , 1999 , 83 (Pt 5), 604-12	3.6	39	
51	Phylogeny, Species Delimitation, and Recombination in Sphagnum Section Acutifolia. <i>Systematic Botany</i> , 2005 , 30, 16-33	0.7	38	

50	Compositional biases among synonymous substitutions cause conflict between gene and protein trees for plastid origins. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1697-709	8.3	37
49	First molecular estimate of cyclostome bryozoan phylogeny confirms extensive homoplasy among skeletal characters used in traditional taxonomy. <i>Molecular Phylogenetics and Evolution</i> , 2009 , 52, 241-	51 ^{4.1}	37
48	Metatranscriptomes reveal functional variation in diatom communities from the Antarctic Peninsula. <i>ISME Journal</i> , 2015 , 9, 2275-89	11.9	36
47	Phylogenetic significance of the rpoA loss in the chloroplast genome of mosses. <i>Taxon</i> , 2005 , 54, 353-3	8 60 .8	36
46	Geographical range in liverworts: does sex really matter?. <i>Journal of Biogeography</i> , 2016 , 43, 627-635	4.1	35
45	Phylogenetic relationships within the moss family Bryaceae based on chloroplast DNA evidence <i>Journal of Bryology</i> , 2003 , 25, 31-40	1.1	35
44	Absence of N-terminal acetyltransferase diversification during evolution of eukaryotic organisms. <i>Scientific Reports</i> , 2016 , 6, 21304	4.9	34
43	Global patterns in peatmoss biodiversity. <i>Molecular Ecology</i> , 2003 , 12, 2553-70	5.7	34
42	Phylogenetic Relationships of Haplolepideous Mosses (Dicranidae) Inferred from rps4 Gene Sequences. <i>Systematic Botany</i> , 2004 , 29, 29-41	0.7	33
41	Distribution and phylogenetic significance of the 71-kb inversion in the plastid genome in Funariidae (Bryophyta). <i>Annals of Botany</i> , 2007 , 99, 747-53	4.1	32
40	Ordinal relationships of pleurocarpous mosses, with special emphasis on the Hookeriales. <i>Systematics and Biodiversity</i> , 2004 , 2, 121-145	1.7	32
39	Phylogenetic Relationships Among Basal-most Arthrodontous Mosses with Special Emphasis on the Evolutionary Significance of the Funariineae. <i>Bryologist</i> , 2000 , 103, 212-223	0.7	32
38	Phylogenetic and biosystematic relationships in four highly disjunct polyploid complexes in the subgenera and in (Aspleniaceae). <i>Organisms Diversity and Evolution</i> , 2002 , 2, 299-311	1.7	31
37	Deep sequencing of Ptilidium (Ptilidiaceae) suggests evolutionary stasis in liverwort plastid genome structure. <i>Plant Ecology and Evolution</i> , 2011 , 144, 29-43	1.6	30
36	Molecular Taxonomic Profiling of Bacterial Communities in a Gilthead Seabream () Hatchery. <i>Frontiers in Microbiology</i> , 2017 , 8, 204	5.7	29
35	Genomic blueprints of sponge-prokaryote symbiosis are shared by low abundant and cultivatable Alphaproteobacteria. <i>Scientific Reports</i> , 2019 , 9, 1999	4.9	29
34	Effects of sample handling and cultivation bias on the specificity of bacterial communities in keratose marine sponges. <i>Frontiers in Microbiology</i> , 2014 , 5, 611	5.7	27
33	A taxonomic reassessment of the Vittiaceae (Hypnales, Bryopsida): evidence from phylogenetic analyses of combined chloroplast and nuclear sequence data. <i>Plant Systematics and Evolution</i> , 2003 , 241, 1-12	1.3	26

(2015-2016)

32	Comparative analysis of zebrafish bone morphogenetic proteins 2, 4 and 16: molecular and evolutionary perspectives. <i>Cellular and Molecular Life Sciences</i> , 2016 , 73, 841-57	10.3	23
31	Land Plant Molecular Phylogenetics: A Review with Comments on Evaluating Incongruence Among Phylogenies. <i>Critical Reviews in Plant Sciences</i> , 2018 , 37, 113-127	5.6	21
30	Optimal data partitioning, multispecies coalescent and Bayesian concordance analyses resolve early divergences of the grape family (Vitaceae). <i>Cladistics</i> , 2018 , 34, 57-77	3.5	20
29	WASABI: an automated sequence processing system for multigene phylogenies. <i>Systematic Biology</i> , 2007 , 56, 523-31	8.4	19
28	Phylogenetic inferences in the dung-moss family Splachnaceae from analyses of cpDNA sequence data and implications for the evolution of entomophily. <i>American Journal of Botany</i> , 2004 , 91, 748-59	2.7	19
27	Evolution of multiple paralogous adenosine kinase genes in the moss genus Hygroamblystegium: phylogenetic implications. <i>Molecular Phylogenetics and Evolution</i> , 2004 , 31, 505-16	4.1	18
26	Divergent and Reticulate Evolution in Closely Related Species of Sphagnum Section Subsecunda. Bryologist, 2005 , 108, 363-376	0.7	18
25	Increased diversification rates follow shifts to bisexuality in liverworts. New Phytologist, 2016, 210, 112	1 ₉ 98	17
24	A 20-state empirical amino-acid substitution model for green plant chloroplasts. <i>Molecular Phylogenetics and Evolution</i> , 2013 , 68, 218-20	4.1	16
23	Phylogenetic Relationships Among Sphagnum Sections: Hemitheca, Isocladus, and Subsecunda. <i>Bryologist</i> , 2004 , 107, 189-196	0.7	15
22	Phylogeny, Character Evolution, and Biogeography of the Gondwanic Moss Family Hypopterygiaceae (Bryophyta). <i>Systematic Botany</i> , 2008 , 33, 21-30	0.7	14
21	Improved phylogeny of brown algae Cystoseira (Fucales) from the Atlantic-Mediterranean region based on mitochondrial sequences. <i>PLoS ONE</i> , 2019 , 14, e0210143	3.7	13
20	Circulating small non-coding RNAs provide new insights into vitamin K nutrition and reproductive physiology in teleost fish. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019 , 1863, 39-51	4	12
19	Multilocus genetic analyses provide insight into speciation and hybridization in aquatic grasses, genusRuppia. <i>Biological Journal of the Linnean Society</i> , 2016 , 117, 177-191	1.9	11
18	Variation in "biodiversity value" of peatmoss species in Sphagnum section Acutifolia (Sphagnaceae). <i>American Journal of Botany</i> , 2005 , 92, 1774-83	2.7	10
17	The mitochondrial phylogeny of land plants shows support for Setaphyta under composition-heterogeneous substitution models. <i>PeerJ</i> , 2020 , 8, e8995	3.1	10
16	A haplotype-resolved draft genome of the European sardine (Sardina pilchardus). <i>GigaScience</i> , 2019 , 8,	7.6	9
15	A transcriptome resource for the copepod Calanus glacialis across a range of culture temperatures. <i>Marine Genomics</i> , 2015 , 23, 27-9	1.9	9

14	The Chloroplast Land Plant Phylogeny: Analyses Employing Better-Fitting Tree- and Site-Heterogeneous Composition Models. <i>Frontiers in Plant Science</i> , 2020 , 11, 1062	6.2	8
13	Phylogenetic Relationships of the Wardiaceae (Musci); Evidence from 18s rRNA and rps4 Gene Sequences. <i>Bryologist</i> , 1999 , 102, 26	0.7	8
12	Diversity of the candidate phylum Poribacteria in the marine sponge Aplysina fulva. <i>Brazilian Journal of Microbiology</i> , 2013 , 44, 329-34	2.2	6
11	Prokaryotic diversity in stream sediments affected by acid mine drainage. Extremophiles, 2020, 24, 809-	849	6
10	Inferring the Deep Past from Molecular Data. Genome Biology and Evolution, 2021, 13,	3.9	6
9	A meta-taxonomic investigation of the prokaryotic diversity of water bodies impacted by acid mine drainage from the SB Domingos mine in southern Portugal. <i>Extremophiles</i> , 2019 , 23, 821-834	3	5
8	Biochemical and molecular responses of the Mediterranean mussel (Mytilus galloprovincialis) to short-term exposure to three commonly prescribed drugs. <i>Marine Environmental Research</i> , 2021 , 168, 105309	3.3	5
7	Multiple domestications of Asian rice. <i>Nature Plants</i> , 2016 , 2, 16037	11.5	5
7	Multiple domestications of Asian rice. <i>Nature Plants</i> , 2016 , 2, 16037 Comparative promoter analysis and its application to the identification of candidate regulatory factors of cartilage-expressed genes. <i>Journal of Applied Ichthyology</i> , 2010 , 26, 245-250	0.9	5
	Comparative promoter analysis and its application to the identification of candidate regulatory		
6	Comparative promoter analysis and its application to the identification of candidate regulatory factors of cartilage-expressed genes. <i>Journal of Applied Ichthyology</i> , 2010 , 26, 245-250 Evolutionary conservation of TFIIH subunits: implications for the use of zebrafish as a model to study TFIIH function and regulation. <i>Comparative Biochemistry and Physiology - B Biochemistry and</i>	0.9	3
6 5	Comparative promoter analysis and its application to the identification of candidate regulatory factors of cartilage-expressed genes. <i>Journal of Applied Ichthyology</i> , 2010 , 26, 245-250 Evolutionary conservation of TFIIH subunits: implications for the use of zebrafish as a model to study TFIIH function and regulation. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2014 , 172-173, 9-20	0.9	3
6 5 4	Comparative promoter analysis and its application to the identification of candidate regulatory factors of cartilage-expressed genes. <i>Journal of Applied Ichthyology</i> , 2010 , 26, 245-250 Evolutionary conservation of TFIIH subunits: implications for the use of zebrafish as a model to study TFIIH function and regulation. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2014 , 172-173, 9-20 A new species of Leskeodon (Daltoniaceae) from Ecuador. <i>Brittonia</i> , 2002 , 54, 178-180 Identification of a fish short-chain dehydrogenase/reductase associated with bone metabolism.	0.9	2