

Celine Scornavacca

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

3,809
citations

257450

24
h-index

233421

45
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54
all docs

54
docs citations

54
times ranked

6017
citing authors

#	ARTICLE	IF	CITATIONS
1	Dendroscope 3: An Interactive Tool for Rooted Phylogenetic Trees and Networks. <i>Systematic Biology</i> , 2012, 61, 1061-1067.	5.6	1,438
2	A Survey of Combinatorial Methods for Phylogenetic Networks. <i>Genome Biology and Evolution</i> , 2011, 3, 23-35.	2.5	165
3	Bio++: Efficient Extensible Libraries and Tools for Computational Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2013, 30, 1745-1750.	8.9	163
4	ASTRAL-Pro: Quartet-Based Species-Tree Inference despite Paralogy. <i>Molecular Biology and Evolution</i> , 2020, 37, 3292-3307.	8.9	116
5	ecceTERA: comprehensive gene tree-species tree reconciliation using parsimony. <i>Bioinformatics</i> , 2016, 32, 2056-2058.	4.1	98
6	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. <i>Nucleic Acids Research</i> , 2018, 46, D718-D725.	14.5	90
7	Incomplete Lineage Sorting in Mammalian Phylogenomics. <i>Systematic Biology</i> , 2017, 66, syw082.	5.6	88
8	Tanglegrams for rooted phylogenetic trees and networks. <i>Bioinformatics</i> , 2011, 27, i248-i256.	4.1	86
9	Pervasive hybridizations in the history of wheat relatives. <i>Science Advances</i> , 2019, 5, eaav9188.	10.3	79
10	An Efficient Algorithm for Gene/Species Trees Parsimonious Reconciliation with Losses, Duplications and Transfers. <i>Lecture Notes in Computer Science</i> , 2010, , 93-108.	1.3	78
11	OrthoMaM v8: A Database of Orthologous Exons and Coding Sequences for Comparative Genomics in Mammals. <i>Molecular Biology and Evolution</i> , 2014, 31, 1923-1928.	8.9	77
12	Multigenic phylogeny and analysis of tree incongruences in Triticeae (Poaceae). <i>BMC Evolutionary Biology</i> , 2011, 11, 181.	3.2	72
13	ANISEED 2015: a digital framework for the comparative developmental biology of ascidians. <i>Nucleic Acids Research</i> , 2016, 44, D808-D818.	14.5	68
14	Reconstructible Phylogenetic Networks: Do Not Distinguish the Indistinguishable. <i>PLoS Computational Biology</i> , 2015, 11, e1004135.	3.2	65
15	Whole Genome Shotgun Phylogenomics Resolves the Pattern and Timing of Swallowtail Butterfly Evolution. <i>Systematic Biology</i> , 2020, 69, 38-60.	5.6	65
16	OrthoMaM v10: Scaling-Up Orthologous Coding Sequence and Exon Alignments with More than One Hundred Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 861-862.	8.9	64
17	Fast computation of minimum hybridization networks. <i>Bioinformatics</i> , 2012, 28, 191-197.	4.1	56
18	Island songbirds as windows into evolution in small populations. <i>Current Biology</i> , 2021, 31, 1303-1310.e4.	3.9	56

#	ARTICLE	IF	CITATIONS
19	PhySIC: A Veto Supertree Method with Desirable Properties. <i>Systematic Biology</i> , 2007, 56, 798-817.	5.6	49
20	Joint amalgamation of most parsimonious reconciled gene trees. <i>Bioinformatics</i> , 2015, 31, 841-848.	4.1	44
21	PhySIC_IST: cleaning source trees to infer more informative supertrees. <i>BMC Bioinformatics</i> , 2008, 9, 413.	2.6	42
22	REPRESENTING A SET OF RECONCILIATIONS IN A COMPACT WAY. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1250025.	0.8	41
23	Exploring the Solution Space of Sorting by Reversals, with Experiments and an Application to Evolution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 348-356.	3.0	36
24	DeCoSTAR: Reconstructing the Ancestral Organization of Genes or Genomes Using Reconciled Phylogenies. <i>Genome Biology and Evolution</i> , 2017, 9, 1312-1319.	2.5	32
25	Deep Ancestral Introgression Shapes Evolutionary History of Dragonflies and Damselflies. <i>Systematic Biology</i> , 2022, 71, 526-546.	5.6	32
26	Fast and accurate branch lengths estimation for phylogenomic trees. <i>BMC Bioinformatics</i> , 2016, 17, 23.	2.6	23
27	Reconstructing Phylogenetic Level-1 Networks from Nondense Binet and Trinet Sets. <i>Algorithmica</i> , 2017, 77, 173-200.	1.3	23
28	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.1	22
29	Cycle Killer...Qu'est-ce que c'est? On the Comparative Approximability of Hybridization Number and Directed Feedback Vertex Set. <i>SIAM Journal on Discrete Mathematics</i> , 2012, 26, 1635-1656.	0.8	18
30	On the Weighted Quartet Consensus problem. <i>Theoretical Computer Science</i> , 2019, 769, 1-17.	0.9	18
31	On Computing the Maximum Parsimony Score of a Phylogenetic Network. <i>SIAM Journal on Discrete Mathematics</i> , 2015, 29, 559-585.	0.8	17
32	Constructing Minimal Phylogenetic Networks from Softwired Clusters is Fixed Parameter Tractable. <i>Algorithmica</i> , 2014, 68, 886-915.	1.3	16
33	Rearrangement moves on rooted phylogenetic networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005611.	3.2	15
34	High-quality carnivoran genomes from roadkill samples enable comparative species delineation in aardwolf and bat-eared fox. <i>ELife</i> , 2021, 10, .	6.0	15
35	The Solution Space of Sorting by Reversals. , 2007, , 293-304.		13
36	A bird's white-eye view on avian sex chromosome evolution. , 0, 1, .		13

#	ARTICLE	IF	CITATIONS
37	NetRAX: accurate and fast maximum likelihood phylogenetic network inference. <i>Bioinformatics</i> , 2022, 38, 3725-3733.	4.1	13
38	On the inference of complex phylogenetic networks by Markov Chain Monte-Carlo. <i>PLoS Computational Biology</i> , 2021, 17, e1008380.	3.2	12
39	Improved Maximum Parsimony Models for Phylogenetic Networks. <i>Systematic Biology</i> , 2018, 67, 518-542.	5.6	10
40	A practical approximation algorithm for solving massive instances of hybridization number for binary and nonbinary trees. <i>BMC Bioinformatics</i> , 2014, 15, 127.	2.6	9
41	The Multilocus Multispecies Coalescent: A Flexible New Model of Gene Family Evolution. <i>Systematic Biology</i> , 2021, 70, 822-837.	5.6	9
42	From Gene Trees to Species Trees through a Supertree Approach. <i>Lecture Notes in Computer Science</i> , 2009, , 702-714.	1.3	9
43	Do Branch Lengths Help to Locate a Tree in a Phylogenetic Network?. <i>Bulletin of Mathematical Biology</i> , 2016, 78, 1773-1795.	1.9	8
44	A First Step Toward Computing All Hybridization Networks For Two Rooted Binary Phylogenetic Trees. <i>Journal of Computational Biology</i> , 2012, 19, 1227-1242.	1.6	7
45	Generation of Binary Tree-Child phylogenetic networks. <i>PLoS Computational Biology</i> , 2019, 15, e1007347.	3.2	7
46	A Practical Approximation Algorithm for Solving Massive Instances of Hybridization Number. <i>Lecture Notes in Computer Science</i> , 2012, , 430-440.	1.3	1