

Vincent Ranwez

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

4,763
citations

159585
30
h-index

114465
63
g-index

69
all docs

69
docs citations

69
times ranked

7065
citing authors

#	ARTICLE	IF	CITATIONS
1	A new versatile primer set targeting a short fragment of the mitochondrial COI region for metabarcoding metazoan diversity: application for characterizing coral reef fish gut contents. <i>Frontiers in Zoology</i> , 2013, 10, 34.	2.0	955
2	MACSE: Multiple Alignment of Coding SEquences Accounting for Frameshifts and Stop Codons. <i>PLoS ONE</i> , 2011, 6, e22594.	2.5	546
3	MACSE v2: Toolkit for the Alignment of Coding Sequences Accounting for Frameshifts and Stop Codons. <i>Molecular Biology and Evolution</i> , 2018, 35, 2582-2584.	8.9	330
4	Contrasting GC-content dynamics across 33 mammalian genomes: Relationship with life-history traits and chromosome sizes. <i>Genome Research</i> , 2010, 20, 1001-1009.	5.5	195
5	Sequencing of the smallest Apicomplexan genome from the human pathogen <i>Babesia microti</i> . <i>Nucleic Acids Research</i> , 2012, 40, 9102-9114.	14.5	179
6	GC-biased gene conversion promotes the fixation of deleterious amino acid changes in primates. <i>Trends in Genetics</i> , 2009, 25, 1-5.	6.7	167
7	Less Is More in Mammalian Phylogenomics: AT-Rich Genes Minimize Tree Conflicts and Unravel the Root of Placental Mammals. <i>Molecular Biology and Evolution</i> , 2013, 30, 2134-2144.	8.9	158
8	Reference-free transcriptome assembly in non-model animals from next-generation sequencing data. <i>Molecular Ecology Resources</i> , 2012, 12, 834-845.	4.8	142
9	Multiple molecular evidences for a living mammalian fossil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7495-7499.	7.1	141
10	Models, algorithms and programs for phylogeny reconciliation. <i>Briefings in Bioinformatics</i> , 2011, 12, 392-400.	6.5	132
11	Origin and Diversity of Plant Receptor-Like Kinases. <i>Annual Review of Plant Biology</i> , 2020, 71, 131-156.	18.7	130
12	OrthoMaM: A database of orthologous genomic markers for placental mammal phylogenetics. <i>BMC Evolutionary Biology</i> , 2007, 7, 241.	3.2	120
13	Bio++: a set of C++ libraries for sequence analysis, phylogenetics, molecular evolution and population genetics. <i>BMC Bioinformatics</i> , 2006, 7, 188.	2.6	101
14	Quartet-Based Phylogenetic Inference: Improvements and Limits. <i>Molecular Biology and Evolution</i> , 2001, 18, 1103-1116.	8.9	93
15	Pervasive hybridizations in the history of wheat relatives. <i>Science Advances</i> , 2019, 5, eaav9188.	10.3	79
16	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
17	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
18	Multigenic phylogeny and analysis of tree incongruences in Triticeae (Poaceae). <i>BMC Evolutionary Biology</i> , 2011, 11, 181.	3.2	72

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19	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
20	Improvement of Distance-Based Phylogenetic Methods by a Local Maximum Likelihood Approach Using Triplets. <i>Molecular Biology and Evolution</i> , 2002, 19, 1952-1963.	8.9	63
21	Efficient Selection of Branch-Specific Models of Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 1861-1874.	8.9	56
22	Genomic Evidence for Large, Long-Lived Ancestors to Placental Mammals. <i>Molecular Biology and Evolution</i> , 2013, 30, 5-13.	8.9	56
23	Order independent homotopic thinning for binary and grey tone anchored skeletons. <i>Pattern Recognition Letters</i> , 2002, 23, 687-702.	4.2	52
24	S^{uper}T^{riplets}: a triplet-based supertree approach to phylogenomics. <i>Bioinformatics</i> , 2010, 26, i115-i123.	4.1	51
25	<i>Plant Defensin type 1</i> (<i>^{PDF}1</i>): protein promiscuity and expression variation within the <i>Arabidopsis</i> genus shed light on zinc tolerance acquisition in <i>Arabidopsis halleri</i>. <i>New Phytologist</i> , 2013, 200, 820-833.	7.3	50
26	Pitfalls in supermatrix phylogenomics. <i>European Journal of Taxonomy</i> , 2017, , .	0.6	50
27	PhySIC: A Veto Supertree Method with Desirable Properties. <i>Systematic Biology</i> , 2007, 56, 798-817.	5.6	49
28	Fast and Robust Characterization of Time-Heterogeneous Sequence Evolutionary Processes Using Substitution Mapping. <i>PLoS ONE</i> , 2012, 7, e33852.	2.5	47
29	PhySIC_IST: cleaning source trees to infer more informative supertrees. <i>BMC Bioinformatics</i> , 2008, 9, 413.	2.6	42
30	REPRESENTING A SET OF RECONCILIATIONS IN A COMPACT WAY. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1250025.	0.8	41
31	Impact of recurrent gene duplication on adaptation of plant genomes. <i>BMC Plant Biology</i> , 2014, 14, 151.	3.6	32
32	Genotyping by Sequencing Using Specific Allelic Capture to Build a High-Density Genetic Map of Durum Wheat. <i>PLoS ONE</i> , 2016, 11, e0154609.	2.5	30
33	Inferring incomplete lineage sorting, duplications, transfers and losses with reconciliations. <i>Journal of Theoretical Biology</i> , 2017, 432, 1-13.	1.7	30
34	An information theoretic approach to improve semantic similarity assessments across multiple ontologies. <i>Information Sciences</i> , 2014, 283, 197-210.	6.9	27
35	User centered and ontology based information retrieval system for life sciences. <i>BMC Bioinformatics</i> , 2012, 13, S4.	2.6	26
36	Reconciliation and local gene tree rearrangement can be of mutual profit. <i>Algorithms for Molecular Biology</i> , 2013, 8, 12.	1.2	25

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37	Evolutionary tinkering of the expression of PDF1s suggests their joint effect on zinc tolerance and the response to pathogen attack. <i>Frontiers in Plant Science</i> , 2014, 5, 70.	3.6	25
38	Support Measures to Estimate the Reliability of Evolutionary Events Predicted by Reconciliation Methods. <i>PLoS ONE</i> , 2013, 8, e73667.	2.5	22
39	Genotyping by sequencing transcriptomes in an evolutionary pre-breeding durum wheat population. <i>Molecular Breeding</i> , 2014, 34, 1531-1548.	2.1	20
40	The genetic map comparator: a user-friendly application to display and compare genetic maps. <i>Bioinformatics</i> , 2017, 33, 1387-1388.	4.1	17
41	PhyloExplorer: a web server to validate, explore and query phylogenetic trees. <i>BMC Evolutionary Biology</i> , 2009, 9, 108.	3.2	16
42	Building species trees from larger parts of phylogenomic databases. <i>Information and Computation</i> , 2011, 209, 590-605.	0.7	16
43	Disentangling homeologous contigs in allo-tetraploid assembly: application to durum wheat. <i>BMC Bioinformatics</i> , 2013, 14, S15.	2.6	13
44	Ontological Distance Measures for Information Visualisation on Conceptual Maps. <i>Lecture Notes in Computer Science</i> , 2006, , 1050-1061.	1.3	13
45	Aligning Protein-Coding Nucleotide Sequences with MACSE. <i>Methods in Molecular Biology</i> , 2021, 2231, 51-70.	0.9	11
46	How Ontology Based Information Retrieval Systems May Benefit from Lexical Text Analysis. <i>Theory and Applications of Natural Language Processing</i> , 2013, , 209-231.	0.3	10
47	A fast method for calculating reliable event supports in tree reconciliations via Pareto optimality. <i>BMC Bioinformatics</i> , 2015, 16, 384.	2.6	10
48	Domestication reduces alternative splicing expression variations in sorghum. <i>PLoS ONE</i> , 2017, 12, e0183454.	2.5	10
49	Accounting for Gene Tree Uncertainties Improves Gene Trees and Reconciliation Inference. <i>Lecture Notes in Computer Science</i> , 2012, , 123-134.	1.3	9
50	Exploring the space of gene/species reconciliations with transfers. <i>Journal of Mathematical Biology</i> , 2015, 71, 1179-1209.	1.9	9
51	Order Independent Homotopic Thinning. <i>Lecture Notes in Computer Science</i> , 1999, , 337-346.	1.3	9
52	From Gene Trees to Species Trees through a Supertree Approach. <i>Lecture Notes in Computer Science</i> , 2009, , 702-714.	1.3	9
53	Subontology Extraction Using Hyponym and Hypernym Closure on is-a Directed Acyclic Graphs. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2012, 24, 2288-2300.	5.7	8
54	Is diversity optimization always suitable? Toward a better understanding of diversity within recommendation approaches. <i>Information Processing and Management</i> , 2021, 58, 102721.	8.6	8

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55	A new comprehensive annotation of leucine-rich repeat-containing receptors in rice. <i>Plant Journal</i> , 2021, 108, 492-508.	5.7	7
56	Epistatic determinism of durum wheat resistance to the wheat spindle streak mosaic virus. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1491-1505.	3.6	6
57	Reconciliation-based detection of co-evolving gene families. <i>BMC Bioinformatics</i> , 2013, 14, 332.	2.6	4
58	USI: a fast and accurate approach for conceptual document annotation. <i>BMC Bioinformatics</i> , 2015, 16, 83.	2.6	4
59	Two Simple and Efficient Algorithms to Compute the SP-Score Objective Function of a Multiple Sequence Alignment. <i>PLoS ONE</i> , 2016, 11, e0160043.	2.5	4
60	Fast and reliable inference of semantic clusters. <i>Knowledge-Based Systems</i> , 2016, 111, 133-143.	7.1	3
61	Post-hoc recommendation explanations through an efficient exploitation of the DBpedia category hierarchy. <i>Knowledge-Based Systems</i> , 2022, 245, 108560.	7.1	3
62	Erratum to "GC-biased gene conversion promotes the fixation of deleterious amino acid changes in primates" [Trends in Genetics 25 (2009) 1-5]. <i>Trends in Genetics</i> , 2009, 25, 287.	6.7	2
63	Inferring gene duplications, transfers and losses can be done in a discrete framework. <i>Journal of Mathematical Biology</i> , 2016, 72, 1811-1844.	1.9	2
64	Evolution of flowering time in a selfing annual plant: Roles of adaptation and genetic drift. <i>Ecology and Evolution</i> , 2022, 12, e8555.	1.9	2
65	Efficient algorithms for Longest Common Subsequence of two bucket orders to speed up pairwise genetic map comparison. <i>PLoS ONE</i> , 2018, 13, e0208838.	2.5	0
66	EBCR: Empirical Bayes concordance ratio method to improve similarity measurement in memory-based collaborative filtering. <i>PLoS ONE</i> , 2021, 16, e0255929.	2.5	0