Vincent Ranwez

List of Publications by Year
in descending order

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	Evolution of flowering time in a selfing annual plant: Roles of adaptation and genetic drift. Ecology and Evolution, 2022, 12, e8555.	1.9	2
2	Post-hoc recommendation explanations through an efficient exploitation of the DBpedia category hierarchy. Knowledge-Based Systems, 2022, 245, 108560.	7.1	3
3	EBCR: Empirical Bayes concordance ratio method to improve similarity measurement in memory-based collaborative filtering. PLoS ONE, 2021, 16, e0255929.	2.5	0
4	A new comprehensive annotation of leucineâ€rich repeatâ€containing receptors in rice. Plant Journal, 2021, 108, 492-508.	5.7	7
5	Is diversity optimization always suitable? Toward a better understanding of diversity within recommendation approaches. Information Processing and Management, 2021, 58, 102721.	8.6	8
6	Aligning Protein-Coding Nucleotide Sequences with MACSE. Methods in Molecular Biology, 2021, 2231, 51-70.	0.9	11
7	Origin and Diversity of Plant Receptor-Like Kinases. Annual Review of Plant Biology, 2020, 71, 131-156.	18.7	130
8	Pervasive hybridizations in the history of wheat relatives. Science Advances, 2019, 5, eaav9188.	10.3	79
9	OrthoMaM v10: Scaling-Up Orthologous Coding Sequence and Exon Alignments with More than One Hundred Mammalian Genomes. Molecular Biology and Evolution, 2019, 36, 861-862.	8.9	64
10	Efficient algorithms for Longest Common Subsequence of two bucket orders to speed up pairwise genetic map comparison. PLoS ONE, 2018, 13, e0208838.	2.5	0
11	MACSE v2: Toolkit for the Alignment of Coding Sequences Accounting for Frameshifts and Stop Codons. Molecular Biology and Evolution, 2018, 35, 2582-2584.	8.9	330
12	The genetic map comparator: a user-friendly application to display and compare genetic maps. Bioinformatics, 2017, 33, 1387-1388.	4.1	17
13	Inferring incomplete lineage sorting, duplications, transfers and losses with reconciliations. Journal of Theoretical Biology, 2017, 432, 1-13.	1.7	30
14	Epistatic determinism of durum wheat resistance to the wheat spindle streak mosaic virus. Theoretical and Applied Genetics, 2017, 130, 1491-1505.	3.6	6
15	Domestication reduces alternative splicing expression variations in sorghum. PLoS ONE, 2017, 12, e0183454.	2.5	10
16	Pitfalls in supermatrix phylogenomics. European Journal of Taxonomy, 2017, , .	0.6	50
17	Genotyping by Sequencing Using Specific Allelic Capture to Build a High-Density Genetic Map of Durum Wheat. PLoS ONE, 2016, 11, e0154609.	2.5	30
18	Two Simple and Efficient Algorithms to Compute the SP-Score Objective Function of a Multiple Sequence Alignment. PLoS ONE, 2016, 11, e0160043.	2.5	4

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19	Fast and reliable inference of semantic clusters. Knowledge-Based Systems, 2016, 111, 133-143.	7.1	3
20	Inferring gene duplications, transfers and losses can be done in a discrete framework. Journal of Mathematical Biology, 2016, 72, 1811-1844.	1.9	2
21	A fast method for calculating reliable event supports in tree reconciliations via Pareto optimality. BMC Bioinformatics, 2015, 16, 384.	2.6	10
22	Exploring the space of gene/species reconciliations with transfers. Journal of Mathematical Biology, 2015, 71, 1179-1209.	1.9	9
23	USI: a fast and accurate approach for conceptual document annotation. BMC Bioinformatics, 2015, 16, 83.	2.6	4
24	Evolutionary tinkering of the expression of PDF1s suggests their joint effect on zinc tolerance and the response to pathogen attack. Frontiers in Plant Science, 2014, 5, 70.	3.6	25
25	Genotyping by sequencing transcriptomes in an evolutionary pre-breeding durum wheat population. Molecular Breeding, 2014, 34, 1531-1548.	2.1	20
26	Impact of recurrent gene duplication on adaptation of plant genomes. BMC Plant Biology, 2014, 14, 151.	3.6	32
27	An information theoretic approach to improve semantic similarity assessments across multiple ontologies. Information Sciences, 2014, 283, 197-210.	6.9	27
28	OrthoMaM v8: A Database of Orthologous Exons and Coding Sequences for Comparative Genomics in Mammals. Molecular Biology and Evolution, 2014, 31, 1923-1928.	8.9	77
29	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. Frontiers in Zoology, 2013, 10, 34.	2.0	955
30	*Plant Defensin type 1* (*PDF1*): protein promiscuity and expression variation within the *Arabidopsis* genus shed light on zinc tolerance acquisition in *Arabidopsis halleri*. New Phytologist, 2013, 200, 820-833.	7.3	50
31	Disentangling homeologous contigs in allo-tetraploid assembly: application to durum wheat. BMC Bioinformatics, 2013, 14, S15.	2.6	13
32	Less Is More in Mammalian Phylogenomics: AT-Rich Genes Minimize Tree Conflicts and Unravel the Root of Placental Mammals. Molecular Biology and Evolution, 2013, 30, 2134-2144.	8.9	158
33	Reconciliation-based detection of co-evolving gene families. BMC Bioinformatics, 2013, 14, 332.	2.6	4
34	REPRESENTING A SET OF RECONCILIATIONS IN A COMPACT WAY. Journal of Bioinformatics and Computational Biology, 2013, 11, 1250025.	0.8	41
35	Reconciliation and local gene tree rearrangement can be of mutual profit. Algorithms for Molecular Biology, 2013, 8, 12.	1.2	25
36	Genomic Evidence for Large, Long-Lived Ancestors to Placental Mammals. Molecular Biology and Evolution, 2013, 30, 5-13.	8.9	56

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37	How Ontology Based Information Retrieval Systems May Benefit from Lexical Text Analysis. Theory and Applications of Natural Language Processing, 2013, , 209-231.	0.3	10
38	Support Measures to Estimate the Reliability of Evolutionary Events Predicted by Reconciliation Methods. PLoS ONE, 2013, 8, e73667.	2.5	22
39	User centered and ontology based information retrieval system for life sciences. BMC Bioinformatics, 2012, 13, S4.	2.6	26
40	Efficient Selection of Branch-Specific Models of Sequence Evolution. Molecular Biology and Evolution, 2012, 29, 1861-1874.	8.9	56
41	Sequencing of the smallest Apicomplexan genome from the human pathogen Babesia microtiâ€. Nucleic Acids Research, 2012, 40, 9102-9114.	14.5	179
42	Subontology Extraction Using Hyponym and Hypernym Closure on is-a Directed Acyclic Graphs. IEEE Transactions on Knowledge and Data Engineering, 2012, 24, 2288-2300.	5.7	8
43	Accounting for Gene Tree Uncertainties Improves Gene Trees and Reconciliation Inference. Lecture Notes in Computer Science, 2012, , 123-134.	1.3	9
44	Fast and Robust Characterization of Time-Heterogeneous Sequence Evolutionary Processes Using Substitution Mapping. PLoS ONE, 2012, 7, e33852.	2.5	47
45	Referenceâ€free transcriptome assembly in nonâ€model animals from nextâ€generation sequencing data. Molecular Ecology Resources, 2012, 12, 834-845.	4.8	142
46	Multigenic phylogeny and analysis of tree incongruences in Triticeae (Poaceae). BMC Evolutionary Biology, 2011, 11, 181.	3.2	72
47	MACSE: Multiple Alignment of Coding SEquences Accounting for Frameshifts and Stop Codons. PLoS ONE, 2011, 6, e22594.	2.5	546
48	Building species trees from larger parts of phylogenomic databases. Information and Computation, 2011, 209, 590-605.	0.7	16
49	Models, algorithms and programs for phylogeny reconciliation. Briefings in Bioinformatics, 2011, 12, 392-400.	6.5	132
50	Contrasting GC-content dynamics across 33 mammalian genomes: Relationship with life-history traits and chromosome sizes. Genome Research, 2010, 20, 1001-1009.	5.5	195
51	S<scp>uper</scp>T<scp>riplets</scp>: a triplet-based supertree approach to phylogenomics. Bioinformatics, 2010, 26, i115-i123.	4.1	51
52	An Efficient Algorithm for Gene/Species Trees Parsimonious Reconciliation with Losses, Duplications and Transfers. Lecture Notes in Computer Science, 2010, , 93-108.	1.3	78
53	GC-biased gene conversion promotes the fixation of deleterious amino acid changes in primates. Trends in Genetics, 2009, 25, 1-5.	6.7	167
54	Erratum to â€œGC-biased gene conversion promotes the fixation of deleterious amino acid changes in primatesâ€•[Trends in Genetics 25 (2009) 1â€"5]. Trends in Genetics, 2009, 25, 287.	6.7	2

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55	PhyloExplorer: a web server to validate, explore and query phylogenetic trees. BMC Evolutionary Biology, 2009, 9, 108.	3.2	16
56	From Gene Trees to Species Trees through a Supertree Approach. Lecture Notes in Computer Science, 2009, , 702-714.	1.3	9
57	PhySIC_IST: cleaning source trees to infer more informative supertrees. BMC Bioinformatics, 2008, 9, 413.	2.6	42
58	Multiple molecular evidences for a living mammalian fossil. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7495-7499.	7.1	141
59	PhySIC: A Veto Supertree Method with Desirable Properties. Systematic Biology, 2007, 56, 798-817.	5.6	49
60	OrthoMaM: A database of orthologous genomic markers for placental mammal phylogenetics. BMC Evolutionary Biology, 2007, 7, 241.	3.2	120
61	Bio++: a set of C++ libraries for sequence analysis, phylogenetics, molecular evolution and population genetics. BMC Bioinformatics, 2006, 7, 188.	2.6	101
62	Ontological Distance Measures for Information Visualisation on Conceptual Maps. Lecture Notes in Computer Science, 2006, , 1050-1061.	1.3	13
63	Improvement of Distance-Based Phylogenetic Methods by a Local Maximum Likelihood Approach Using Triplets. Molecular Biology and Evolution, 2002, 19, 1952-1963.	8.9	63
64	Order independent homotopic thinning for binary and grey tone anchored skeletons. Pattern Recognition Letters, 2002, 23, 687-702.	4.2	52
65	Quartet-Based Phylogenetic Inference: Improvements and Limits. Molecular Biology and Evolution, 2001, 18, 1103-1116.	8.9	93
66	Order Independent Homotopic Thinning. Lecture Notes in Computer Science, 1999, , 337-346.	1.3	9