Rutger A Vos

List of Publications by Year
in descending order

57 papers	4,178 citations	257450 24 h-index	197818 49 g-index
78 all docs	78 docs citations	78 times ranked	6977 citing authors

#	Article	IF	Citations
1	The delayed rise of present-day mammals. Nature, 2007, 446, 507-512.	27.8	1,832
2	The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20651-20656.	7.1	412
3	Exploring genetic variation in the tomato (<i>Solanum</i> section <i>Lycopersicon</i>) clade by whole‐genome sequencing. Plant Journal, 2014, 80, 136-148.	5.7	397
4	Species-Level Para- and Polyphyly in DNA Barcode Gene Trees: Strong Operational Bias in European Lepidoptera. Systematic Biology, 2016, 65, 1024-1040.	5.6	160
5	NeXML: Rich, Extensible, and Verifiable Representation of Comparative Data and Metadata. Systematic Biology, 2012, 61, 675-689.	5.6	90
6	Algorithmic single‐locus species delimitation: effects of sampling effort, variation and nonmonophyly in four methods and 1870 species of beetles. Molecular Ecology Resources, 2017, 17, 393-404.	4.8	88
7	Declines in moth populations stress the need for conserving dark nights. Global Change Biology, 2018, 24, 925-932.	9.5	85
8	Exploring the evolutionary origin of floral organs of Erycina pusilla, an emerging orchid model system. BMC Evolutionary Biology, 2017, 17, 89.	3.2	52
9	Evolutionary dynamics of mycorrhizal symbiosis in land plant diversification. Scientific Reports, 2018, 8, 10698.	3.3	51
10	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. Journal of Biomedical Semantics, 2014, 5, 5.	1.6	47
11	BioVeL: a virtual laboratory for data analysis and modelling in biodiversity science and ecology. BMC Ecology, 2016, 16, 49.	3.0	45
12	BIO::Phylo-phyloinformatic analysis using perl. BMC Bioinformatics, 2011, 12, 63.	2.6	44
13	Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. BMC Research Notes, 2012, 5, 574.	1.4	42
14	Toward a Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages, and Relationships of Taxa. Systematic Biology, 2017, 66, syw066.	5.6	42
15	A roadmap for global synthesis of the plant tree of life. American Journal of Botany, 2018, 105, 614-622.	1.7	38
16	The flora phenotype ontology (FLOPO): tool for integrating morphological traits and phenotypes of vascular plants. Journal of Biomedical Semantics, 2016, 7, 65.	1.6	34
17	Scalariform-to-simple transition in vessel perforation plates triggered by differences in climate during the evolution of Adoxaceae. Annals of Botany, 2016, 118, 1043-1056.	2.9	34
18	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. BMC Bioinformatics, 2013, 14, 158.	2.6	33

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19	The HTS barcode checker pipeline, a tool for automated detection of illegally traded species from high-throughput sequencing data. BMC Bioinformatics, 2014, 15, 44.	2.6	32
20	Ecological determinants of butterfly vulnerability across the European continent. Journal of Insect Conservation, 2017, 21, 439-450.	1.4	32
21	Incorporation of an invasive plant into a native insect herbivore food web. PeerJ, 2016, 4, e1954.	2.0	32
22	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	1.6	31
23	Biogem: an effective tool-based approach for scaling up open source software development in bioinformatics. Bioinformatics, 2012, 28, 1035-1037.	4.1	27
24	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	1.6	26
25	phylotaR: An Automated Pipeline for Retrieving Orthologous DNA Sequences from GenBank in R. Life, 2018, 8, 20.	2.4	26
26	Symbiont switching and trophic mode shifts in Orchidaceae. New Phytologist, 2021, 231, 791-800.	7.3	24
27	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. Journal of Biomedical Semantics, 2011, 2, 4.	1.6	19
28	Integrating and visualizing primary data from prospective and legacy taxonomic literature. Biodiversity Data Journal, 2015, 3, e5063.	0.8	19
29	Phylogenetic analysis of niche divergence reveals distinct evolutionary histories and climate change implications for tropical carnivorous pitcher plants. Diversity and Distributions, 2016, 22, 97-110.	4.1	19
30	Hybridization without guilt: gene flow and the biological species concept. Journal of Evolutionary Biology, 2001, 14, 868-869.	1.7	18
31	Multiproxy diet analysis of the last meal of an early Holocene Yakutian bison. Journal of Quaternary Science, 2014, 29, 261-268.	2.1	18
32	Community and Code: Nine Lessons from Nine NESCent Hackathons. F1000Research, 0, 6, 786.	1.6	18
33	Organic matter reduces the amount of detectable environmental DNA in freshwater. Ecology and Evolution, 2020, 10, 3647-3654.	1.9	17
34	Accelerated Likelihood Surface Exploration: The Likelihood Ratchet. Systematic Biology, 2003, 52, 368-373.	5.6	15
35	Enriched biodiversity data as a resource and service. Biodiversity Data Journal, 2014, 2, e1125.	0.8	15
36	Emerging semantics to link phenotype and environment. PeerJ, 2015, 3, e1470.	2.0	15

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37	Multiproxy study of the last meal of a mid-Holocene Oyogos Yar horse, Sakha Republic, Russia. Holocene, 2014, 24, 1288-1296.	1.7	13
38	Reconstructing Divergence Times for Supertrees. Computational Biology, 2004, , 281-299.	0.2	8
39	Western flower thrips (Thysanoptera: Thripidae) preference for thrips-damaged leaves over fresh leaves enables uptake of symbiotic gut bacteria. European Journal of Entomology, 2006, 103, 779-786.	1.2	7
40	Unifying European Biodiversity Informatics (BioUnify). Research Ideas and Outcomes, 0, 2, e7787.	1.0	6
41	Community engagement: The 'last mile' challenge for European research e-infrastructures. Research Ideas and Outcomes, 0, 2, e9933.	1.0	6
42	Evolution of embryonic developmental period in the marine bird families Alcidae and Spheniscidae: roles for nutrition and predation?. BMC Evolutionary Biology, 2010, 10, 179.	3.2	5
43	TreeBASE2: Rise of the Machines. Nature Precedings, 2010, , .	0.1	5
44	Advancing data reuse in phyloinformatics using an ontology-driven Semantic Web approach. BMC Medical Genomics, 2013, 6, S5.	1.5	5
45	Ontogeny and Anatomy of the Dimorphic Pitchers of Nepenthes rafflesiana Jack. Plants, 2020, 9, 1603.	3.5	5
46	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	1.6	5
47	restez: Create and Query a Local Copy of GenBank in R. Journal of Open Source Software, 2018, 3, 1102.	4.6	4
48	Estimating the Relative Order of Speciation or Coalescence Events on a Given Phylogeny. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	3
49	RNeXML: a package for reading and writing richly annotated phylogenetic, character and trait data in r. Methods in Ecology and Evolution, 2016, 7, 352-357.	5.2	2
50	Estimating the relative order of speciation or coalescence events on a given phylogeny. Evolutionary Bioinformatics, 2007, 2, 285-93.	1.2	2
51	EvoIO: Community-driven standards for sustainable interoperability. Nature Precedings, 2010, , .	0.1	1
52	WGS2NCBI - Toolkit for preparing genomes for submission to NCBI. Journal of Open Source Software, 2019, 4, 1364.	4.6	1
53	Bio::Phylo - Phyloinformatic Analysis Using Perl. Nature Precedings, 2010, , .	0.1	0
54	Publishing re-usable phylogenetic trees, in theory and practice. Nature Precedings, 2011, , .	0.1	0

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55	DBTree:ÂVery large phylogenies in portable databases. Methods in Ecology and Evolution, 2020, 11, 457-463.	5.2	0
56	Species Distribution Modelling Using Deep Learning. Biodiversity Information Science and Standards, 0, 3, .	0.0	0
57	outsider: Install and run programs, outside of R, inside of R. Journal of Open Source Software, 2020, 5, 2038.	4.6	0