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	Symbiont switching and trophic mode shifts in Orchidaceae. New Phytologist, 2021, 231, 791-800.	7.3	24
2	DBTree:ÂVery large phylogenies in portable databases. Methods in Ecology and Evolution, 2020, 11, 457-463.	5.2	0
3	Ontogeny and Anatomy of the Dimorphic Pitchers of Nepenthes rafflesiana Jack. Plants, 2020, 9, 1603.	3.5	5
4	Organic matter reduces the amount of detectable environmental DNA in freshwater. Ecology and Evolution, 2020, 10, 3647-3654.	1.9	17
5	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	1.6	5
6	outsider: Install and run programs, outside of R, inside of R. Journal of Open Source Software, 2020, 5, 2038.	4.6	0
7	WGS2NCBI - Toolkit for preparing genomes for submission to NCBI. Journal of Open Source Software, 2019, 4, 1364.	4.6	1
8	A roadmap for global synthesis of the plant tree of life. American Journal of Botany, 2018, 105, 614-622.	1.7	38
9	Declines in moth populations stress the need for conserving dark nights. Global Change Biology, 2018, 24, 925-932.	9.5	85
10	Evolutionary dynamics of mycorrhizal symbiosis in land plant diversification. Scientific Reports, 2018, 8, 10698.	3.3	51
11	phylotaR: An Automated Pipeline for Retrieving Orthologous DNA Sequences from GenBank in R. Life, 2018, 8, 20.	2.4	26
12	restez: Create and Query a Local Copy of GenBank in R. Journal of Open Source Software, 2018, 3, 1102.	4.6	4
13	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
14	Algorithmic singleâ€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
15	Ecological determinants of butterfly vulnerability across the European continent. Journal of Insect Conservation, 2017, 21, 439-450.	1.4	32
16	Exploring the evolutionary origin of floral organs of Erycina pusilla, an emerging orchid model system. BMC Evolutionary Biology, 2017, 17, 89.	3.2	52
17	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
18	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

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19	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
20	BioVeL: a virtual laboratory for data analysis and modelling in biodiversity science and ecology. BMC Ecology, 2016, 16, 49.	3.0	45
21	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
22	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
23	Incorporation of an invasive plant into a native insect herbivore food web. PeerJ, 2016, 4, e1954.	2.0	32
24	Integrating and visualizing primary data from prospective and legacy taxonomic literature. Biodiversity Data Journal, 2015, 3, e5063.	0.8	19
25	Emerging semantics to link phenotype and environment. PeerJ, 2015, 3, e1470.	2.0	15
26	Exploring genetic variation in the tomato (*Solanum* section *Lycopersicon*) clade by whole‐genome sequencing. Plant Journal, 2014, 80, 136-148.	5.7	397
27	Multiproxy study of the last meal of a mid-Holocene Oyogos Yar horse, Sakha Republic, Russia. Holocene, 2014, 24, 1288-1296.	1.7	13
28	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
29	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
30	Multiproxy diet analysis of the last meal of an early Holocene Yakutian bison. Journal of Quaternary Science, 2014, 29, 261-268.	2.1	18
31	Enriched biodiversity data as a resource and service. Biodiversity Data Journal, 2014, 2, e1125.	0.8	15
32	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	1.6	26
33	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. BMC Bioinformatics, 2013, 14, 158.	2.6	33
34	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
35	Advancing data reuse in phyloinformatics using an ontology-driven Semantic Web approach. BMC Medical Genomics, 2013, 6, S5.	1.5	5
36	NeXML: Rich, Extensible, and Verifiable Representation of Comparative Data and Metadata. Systematic Biology, 2012, 61, 675-689.	5.6	90

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37	Biogem: an effective tool-based approach for scaling up open source software development in bioinformatics. Bioinformatics, 2012, 28, 1035-1037.	4.1	27
38	Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. BMC Research Notes, 2012, 5, 574.	1.4	42
39	Publishing re-usable phylogenetic trees, in theory and practice. Nature Precedings, 2011, , .	0.1	0
40	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. Journal of Biomedical Semantics, 2011, 2, 4.	1.6	19
41	BIO::Phylo-phyloinformatic analysis using perl. BMC Bioinformatics, 2011, 12, 63.	2.6	44
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	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	1.6	31
44	EvoIO: Community-driven standards for sustainable interoperability. Nature Precedings, 2010, , .	0.1	1
45	Bio::Phylo - Phyloinformatic Analysis Using Perl. Nature Precedings, 2010, , .	0.1	0
46	TreeBASE2: Rise of the Machines. Nature Precedings, 2010, , .	0.1	5
47	The delayed rise of present-day mammals. Nature, 2007, 446, 507-512.	27.8	1,832
48	Estimating the relative order of speciation or coalescence events on a given phylogeny. Evolutionary Bioinformatics, 2007, 2, 285-93.	1.2	2
49	Estimating the Relative Order of Speciation or Coalescence Events on a Given Phylogeny. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	3
50	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
51	Reconstructing Divergence Times for Supertrees. Computational Biology, 2004, , 281-299.	0.2	8
52	Accelerated Likelihood Surface Exploration: The Likelihood Ratchet. Systematic Biology, 2003, 52, 368-373.	5.6	15
53	Hybridization without guilt: gene flow and the biological species concept. Journal of Evolutionary Biology, 2001, 14, 868-869.	1.7	18
54	Community and Code: Nine Lessons from Nine NESCent Hackathons. F1000Research, 0, 6, 786.	1.6	18

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55	Unifying European Biodiversity Informatics (BioUnify). Research Ideas and Outcomes, 0, 2, *e7787*.	1.0	6
56	Community engagement: The â€˜last mileâ€™ challenge for European research e-infrastructures. Research Ideas and Outcomes, 0, 2, e9933.	1.0	6
57	Species Distribution Modelling Using Deep Learning. Biodiversity Information Science and Standards, 0, 3, .	0.0	0