

# Stephane M Rombauts

## List of Publications by Year in descending order

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92  
papers

26,145  
citations

34105

52  
h-index

43889

91  
g-index

103  
all docs

103  
docs citations

103  
times ranked

25182  
citing authors

#	ARTICLE	IF	CITATIONS
1	â€Nebbioloâ€™ genome assembly allows surveying the occurrence and functional implications of genomic structural variations in grapevines ( <i>Vitis vinifera</i> L). <i>BMC Genomics</i> , 2022, 23, 159.	2.8	11
2	Flemish soils contain rhizobia partners for Northwestern Europeâ€™ adapted soybean cultivars. <i>Environmental Microbiology</i> , 2022, 24, 3334-3354.	3.8	6
3	The genome of <i>Corydalis</i> reveals the evolution of benzylisoquinoline alkaloid biosynthesis in Ranunculales. <i>Plant Journal</i> , 2022, 111, 217-230.	5.7	19
4	Genomic evidence that a sexually selected trait captures genome-wide variation and facilitates the purging of genetic load. <i>Nature Ecology and Evolution</i> , 2022, 6, 1330-1342.	7.8	8
5	The absence of the caffeine synthase gene is involved in the naturally decaffeinated status of <i>Coffea humblotiana</i> , a wild species from Comoro archipelago. <i>Scientific Reports</i> , 2021, 11, 8119.	3.3	17
6	Transcriptomic analysis of the poultry red mite, <i>Dermanyssus gallinae</i> , across all stages of the lifecycle. <i>BMC Genomics</i> , 2021, 22, 248.	2.8	9
7	RNA viruses in the house dust mite <i>Dermatophagoides pteronyssinus</i> , detection in environmental samples and in commercial allergen extracts used for in vivo diagnosis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 3743-3754.	5.7	1
8	The genome of the extremophile <i>Artemia</i> provides insight into strategies to cope with extreme environments. <i>BMC Genomics</i> , 2021, 22, 635.	2.8	20
9	Rapid protein evolution, organellar reductions, and invasive intronic elements in the marine aerobic parasite dinoflagellate <i>Amoebophrya</i> spp. <i>BMC Biology</i> , 2021, 19, 1.	3.8	135
10	De novo whole-genome assembly and discovery of genes involved in triterpenoid saponin biosynthesis of Vietnamese ginseng ( <i>Panax vietnamensis</i> Ha et Grushv.). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2215-2229.	3.1	3
11	Virus-host coexistence in phytoplankton through the genomic lens. <i>Science Advances</i> , 2020, 6, eaay2587.	10.3	30
12	Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, .	6.0	33
13	A genomic analysis and transcriptomic atlas of gene expression in <i>Psoroptes ovis</i> reveals feeding- and stage-specific patterns of allergen expression. <i>BMC Genomics</i> , 2019, 20, 756.	2.8	14
14	Draft Genome Assembly of the False Spider Mite <i>Brevipalpus yothersi</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
15	Pseudo-chromosomeâ€™length genome assembly of a double haploid â€™Bartlettâ€™ pear ( <i>Pyrus communis</i> L.). <i>GigaScience</i> , 2019, 8, .	6.4	76
16	Identification of salt stress response genes using the <i>Artemia</i> transcriptome. <i>Aquaculture</i> , 2019, 500, 305-314.	3.5	31
17	Draft Genome Assembly of the Sheep Scab Mite, <i>Psoroptes ovis</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	15
18	Draft Genome Assembly of the Poultry Red Mite, <i>Dermanyssus gallinae</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	26

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19	Comparative Time-Scale Gene Expression Analysis Highlights the Infection Processes of Two Amoebophrya Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 2251.	3.5	19
20	The TruSeq™ 3™ sequencing method for high-throughput transcriptomics and gene space refinement in plant genomes. <i>Plant Journal</i> , 2018, 96, 223-232.	3.7	23
21	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	28.9	420
22	Genome Analyses of the Microalga Picochlorum Provide Insights into the Evolution of Thermotolerance in the Green Lineage. <i>Genome Biology and Evolution</i> , 2018, 10, 2347-2365.	2.5	36
23	OMSim: a simulator for optical map data. <i>Bioinformatics</i> , 2017, 33, 2740-2742.	4.1	14
24	Dietary shifts have consequences for the repertoire of allergens produced by the European house dust mite. <i>Medical and Veterinary Entomology</i> , 2017, 31, 272-280.	1.5	9
25	A new version of the grapevine reference genome assembly (12X.v2) and of its annotation (VCost.v3). <i>Genomics Data</i> , 2017, 14, 56-62.	1.3	248
26	Draft Genome Sequences of Two Unclassified Bacteria, <i>Sphingomonas</i> sp. Strains IBVSS1 and IBVSS2, Isolated from Environmental Samples. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
27	Draft Genome Sequences of Two Unclassified Chitinophagaceae Bacteria, IBVUCB1 and IBVUCB2, Isolated from Environmental Samples. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
28	Draft Genome Sequences of Two Unclassified Bacteria, <i>Hydrogenophaga</i> sp. Strains IBVHS1 and IBVHS2, Isolated from Environmental Samples. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
29	Annotation of the Tomato Genome. <i>Compendium of Plant Genomes</i> , 2016, , 159-171.	0.5	0
30	Complex Evolutionary Dynamics of Massively Expanded Chemosensory Receptor Families in an Extreme Generalist Chelicerate Herbivore. <i>Genome Biology and Evolution</i> , 2016, 8, 3323-3339.	2.5	42
31	Jabba: hybrid error correction for long sequencing reads. <i>Algorithms for Molecular Biology</i> , 2016, 11, 10.	1.2	67
32	The grapevine gene nomenclature system. <i>BMC Genomics</i> , 2014, 15, 1077.	2.8	108
33	An improved genome of the model marine alga <i>Ostreococcus tauri</i> unfolds by assessing Illumina de novo assemblies. <i>BMC Genomics</i> , 2014, 15, 1103.	2.8	90
34	Reannotation and extended community resources for the genome of the non-seed plant <i>Physcomitrella patens</i> provide insights into the evolution of plant gene structures and functions. <i>BMC Genomics</i> , 2013, 14, 498.	2.8	170
35	Overview of tomato ( <i>Solanum lycopersicum</i> ) candidate pathogen recognition genes reveals important <i>Solanum</i> R locus dynamics. <i>New Phytologist</i> , 2013, 197, 223-237.	7.3	90
36	Analysis of RNA-Seq Data with TopHat and Cufflinks for Genome-Wide Expression Analysis of Jasmonate-Treated Plants and Plant Cultures. <i>Methods in Molecular Biology</i> , 2013, 1011, 305-315.	0.9	68

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37	CathaCyc, a Metabolic Pathway Database Built from Catharanthus roseus RNA-Seq Data. <i>Plant and Cell Physiology</i> , 2013, 54, 673-685.	3.1	116
38	A link between host plant adaptation and pesticide resistance in the polyphagous spider mite <i>Tetranychus urticae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E113-22.	7.1	347
39	Analysis of the Olive Fruit Fly <i>Bactrocera oleae</i> Transcriptome and Phylogenetic Classification of the Major Detoxification Gene Families. <i>PLoS ONE</i> , 2013, 8, e66533.	2.5	55
40	Gene functionalities and genome structure in <i>Bathycoccus prasinos</i> reflect cellular specializations at the base of the green lineage. <i>Genome Biology</i> , 2012, 13, R74.	9.6	143
41	In silico cloning of genes encoding neuropeptides, neurohormones and their putative G-protein coupled receptors in a spider mite. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 277-295.	2.7	93
42	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
43	The metabolic blueprint of <i>Phaeodactylum tricornutum</i> reveals a eukaryotic Entner-Doudoroff glycolytic pathway. <i>Plant Journal</i> , 2012, 70, 1004-1014.	5.7	124
44	The Medicago genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
45	The genome of <i>Tetranychus urticae</i> reveals herbivorous pest adaptations. <i>Nature</i> , 2011, 479, 487-492.	27.8	897
46	Search for nodulation-related CLE genes in the genome of <i>Glycine max</i> . <i>Journal of Experimental Botany</i> , 2011, 62, 2571-2583.	4.8	30
47	Functional Modules in the <i>Arabidopsis</i> Core Cell Cycle Binary Protein-Protein Interaction Network. <i>Plant Cell</i> , 2010, 22, 1264-1280.	6.6	168
48	Systematic Localization of the <i>Arabidopsis</i> Core Cell Cycle Proteins Reveals Novel Cell Division Complexes. <i>Plant Physiology</i> , 2010, 152, 553-565.	4.8	79
49	AGRONOMICS1: A New Resource for <i>Arabidopsis</i> Transcriptome Profiling. <i>Plant Physiology</i> , 2010, 152, 487-499.	4.8	61
50	CLE Peptides Control <i>Medicago truncatula</i> Nodulation Locally and Systemically. <i>Plant Physiology</i> , 2010, 153, 222-237.	4.8	293
51	A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009, 2, .	2.8	73
52	Systematic analysis of cell cycle gene expression during <i>Arabidopsis</i> development. <i>Plant Journal</i> , 2009, 59, 645-660.	5.7	58
53	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	12.6	591
54	Genome-scale <i>Arabidopsis</i> promoter array identifies targets of the histone acetyltransferase GCN5. <i>Plant Journal</i> , 2008, 56, 493-504.	5.7	120

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55	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	12.6	1,712
56	Seven in Absentia Proteins Affect Plant Growth and Nodulation in <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2008, 148, 369-382.	4.8	52
57	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. <i>Current Bioinformatics</i> , 2008, 3, 87-97.	1.5	102
58	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	7.1	563
59	A Symbiotic Plant Peroxidase Involved in Bacterial Invasion of the Tropical Legume <i>Sesbania rostrata</i> . <i>Plant Physiology</i> , 2007, 144, 717-727.	4.8	33
60	A Molecular Timetable for Apical Bud Formation and Dormancy Induction in Poplar. <i>Plant Cell</i> , 2007, 19, 2370-2390.	6.6	436
61	Comparative Transcriptome Analysis Reveals Common and Specific Tags for Root Hair and Crack-Entry Invasion in <i>Sesbania rostrata</i> . <i>Plant Physiology</i> , 2007, 144, 1878-1889.	4.8	18
62	How many genes are there in plants (and why are they there)?. <i>Current Opinion in Plant Biology</i> , 2007, 10, 199-203.	7.1	115
63	Genome analysis of the smallest free-living eukaryote <i>Ostreococcus tauri</i> unveils many unique features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11647-11652.	7.1	809
64	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	12.6	3,945
65	Aging in Legume Symbiosis. A Molecular View on Nodule Senescence in <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2006, 141, 711-720.	4.8	214
66	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	7.1	286
67	EST data suggest that poplar is an ancient polyploid. <i>New Phytologist</i> , 2005, 167, 165-170.	7.3	128
68	Genome-Wide Analysis of Hydrogen Peroxide-Regulated Gene Expression in <i>Arabidopsis</i> Reveals a High Light-Induced Transcriptional Cluster Involved in Anthocyanin Biosynthesis. <i>Plant Physiology</i> , 2005, 139, 806-821.	4.8	476
69	Starch Division and Partitioning. A Mechanism for Granule Propagation and Maintenance in the Picophytoplanktonic Green Alga <i>Ostreococcus tauri</i> . <i>Plant Physiology</i> , 2004, 136, 3333-3340.	4.8	80
70	GeneFarm, structural and functional annotation of <i>Arabidopsis</i> gene and protein families by a network of experts. <i>Nucleic Acids Research</i> , 2004, 33, D641-D646.	14.5	16
71	Catalase deficiency drastically affects gene expression induced by high light in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2004, 39, 45-58.	5.7	298
72	Annotation of a 95-kb <i>Populus deltoides</i> genomic sequence reveals a disease resistance gene cluster and novel class I and class II transposable elements. <i>Theoretical and Applied Genetics</i> , 2004, 109, 10-22.	3.6	37

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73	Genomewide Structural Annotation and Evolutionary Analysis of the Type I MADS-Box Genes in Plants. <i>Journal of Molecular Evolution</i> , 2003, 56, 573-586.	1.8	109
74	Quantitative cDNA-AFLP analysis for genome-wide expression studies. <i>Molecular Genetics and Genomics</i> , 2003, 269, 173-179.	2.1	133
75	Microarray analysis of E2Fa-DPa-overexpressing plants uncovers a cross-talking genetic network between DNA replication and nitrogen assimilation. <i>Journal of Cell Science</i> , 2003, 116, 4249-4259.	2.0	75
76	Computational Approaches to Identify Promoters and cis-Regulatory Elements in Plant Genomes. <i>Plant Physiology</i> , 2003, 132, 1162-1176.	4.8	158
77	AFLP <i>inSilico</i> , simulating AFLP fingerprints. <i>Bioinformatics</i> , 2003, 19, 776-777.	4.1	42
78	Genome-Wide Analysis of Core Cell Cycle Genes in Arabidopsis. <i>Plant Cell</i> , 2002, 14, 903-916.	6.6	523
79	Transcriptome analysis during cell division in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14825-14830.	7.1	140
80	INCLUSive: INTEgrated Clustering, Upstream sequence retrieval and motif Sampling. <i>Bioinformatics</i> , 2002, 18, 331-332.	4.1	78
81	PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. <i>Nucleic Acids Research</i> , 2002, 30, 325-327.	14.5	4,875
82	A Gibbs Sampling Method to Detect Overrepresented Motifs in the Upstream Regions of Coexpressed Genes. <i>Journal of Computational Biology</i> , 2002, 9, 447-464.	1.6	301
83	Moss transcriptome and beyond. <i>Trends in Plant Science</i> , 2002, 7, 535-538.	8.8	102
84	Identification of novel cyclin-dependent kinases interacting with the CKS1 protein of Arabidopsis1. <i>Journal of Experimental Botany</i> , 2001, 52, 1381-1382.	4.8	30
85	A Gibbs sampling method to detect over-represented motifs in the upstream regions of co-expressed genes. , 2001, , .		22
86	A higher-order background model improves the detection of promoter regulatory elements by Gibbs sampling. <i>Bioinformatics</i> , 2001, 17, 1113-1122.	4.1	344
87	Characterization of two distinct DP-related genes from Arabidopsis thaliana1. <i>FEBS Letters</i> , 2000, 486, 79-87.	2.8	80
88	Gene prediction and gene classes in Arabidopsis thaliana. <i>Journal of Biotechnology</i> , 2000, 78, 293-299.	3.8	13
89	Evaluation of gene prediction software using a genomic data set: application to <O_SSF>Arabidopsis thaliana<C_SSF>sequences. <i>Bioinformatics</i> , 1999, 15, 887-899.	4.1	104
90	PlantCARE, a plant cis-acting regulatory element database. <i>Nucleic Acids Research</i> , 1999, 27, 295-296.	14.5	462

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91	Genome annotation: which tools do we have for it?. <i>Current Opinion in Plant Biology</i> , 1999, 2, 90-95.	7.1	45
92	Evidence for an ancient chromosomal duplication in <i>Arabidopsis thaliana</i> by sequencing and analyzing a 400-kb contig at the <i>APETALA2</i> locus on chromosome 41. <i>FEBS Letters</i> , 1999, 445, 237-245.	2.8	33