

Sebastian Proost

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

6,932
citations

236612

25
h-index

288905

40
g-index

47
all docs

47
docs citations

47
times ranked

9746
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the domesticated apple (<i>Malus domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	9.4	1,891
2	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	13.7	1,166
3	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	9.4	413
4	Growth-Regulating Factors (GRFs): A Small Transcription Factor Family with Important Functions in Plant Biology. <i>Molecular Plant</i> , 2015, 8, 998-1010.	3.9	343
5	PLAZA 3.0: an access point for plant comparative genomics. <i>Nucleic Acids Research</i> , 2015, 43, D974-D981.	6.5	329
6	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
7	The flowering world: a tale of duplications. <i>Trends in Plant Science</i> , 2009, 14, 680-688.	4.3	277
8	PLAZA: A Comparative Genomics Resource to Study Gene and Genome Evolution in Plants. <i>Plant Cell</i> , 2010, 21, 3718-3731.	3.1	243
9	Dissecting Plant Genomes with the PLAZA Comparative Genomics Platform. <i>Plant Physiology</i> , 2012, 158, 590-600.	2.3	238
10	i-ADHoRe 3.0: fast and sensitive detection of genomic homology in extremely large data sets. <i>Nucleic Acids Research</i> , 2012, 40, e11-e11.	6.5	192
11	FLOWERING LOCUS C in monocots and the tandem origin of angiosperm-specific MADS-box genes. <i>Nature Communications</i> , 2013, 4, 2280.	5.8	142
12	Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. <i>Molecular Biology and Evolution</i> , 2012, 29, 3793-3806.	3.5	127
13	Predicting protein-protein interactions in <i>Arabidopsis thaliana</i> through integration of orthology, gene ontology and co-expression. <i>BMC Genomics</i> , 2009, 10, 288.	1.2	120
14	TRAPID: an efficient online tool for the functional and comparative analysis of de novo RNA-Seq transcriptomes. <i>Genome Biology</i> , 2013, 14, R134.	13.9	108
15	Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in <i>Brachypodium distachyon</i> . <i>New Phytologist</i> , 2017, 215, 1009-1025.	3.5	108
16	Phylogenomic analysis of gene co-expression networks reveals the evolution of functional modules. <i>Plant Journal</i> , 2017, 90, 447-465.	2.8	97
17	Beyond Genomics: Studying Evolution with Gene Coexpression Networks. <i>Trends in Plant Science</i> , 2017, 22, 298-307.	4.3	96
18	Reversal of senescence by N resupply to N-starved <i>Arabidopsis thaliana</i> : transcriptomic and metabolomic consequences. <i>Journal of Experimental Botany</i> , 2014, 65, 3975-3992.	2.4	94

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19	Journey through the past: 150 million years of plant genome evolution. <i>Plant Journal</i> , 2011, 66, 58-65.	2.8	91
20	CoNekT: an open-source framework for comparative genomic and transcriptomic network analyses. <i>Nucleic Acids Research</i> , 2018, 46, W133-W140.	6.5	81
21	Comparative transcriptomic analysis reveals conserved programmes underpinning organogenesis and reproduction in land plants. <i>Nature Plants</i> , 2021, 7, 1143-1159.	4.7	61
22	Kingdom-wide comparison reveals the evolution of diurnal gene expression in Archaeplastida. <i>Nature Communications</i> , 2019, 10, 737.	5.8	52
23	PlaNet: Comparative Co-Expression Network Analyses for Plants. <i>Methods in Molecular Biology</i> , 2017, 1533, 213-227.	0.4	42
24	Novel allelic variants in <i>ACD6</i> cause hybrid necrosis in local collection of <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2017, 213, 900-915.	3.5	40
25	LSTrAP: efficiently combining RNA sequencing data into co-expression networks. <i>BMC Bioinformatics</i> , 2017, 18, 444.	1.2	35
26	Multi-tissue integration of transcriptomic and specialized metabolite profiling provides tools for assessing the common bean (<i>Phaseolus vulgaris</i>) metabolome. <i>Plant Journal</i> , 2019, 97, 1132-1153.	2.8	33
27	Tools of the trade: studying molecular networks in plants. <i>Current Opinion in Plant Biology</i> , 2016, 30, 143-150.	3.5	31
28	Topology of the redox network during induction of photosynthesis as revealed by time-resolved proteomics in tobacco. <i>Science Advances</i> , 2021, 7, eabi8307.	4.7	27
29	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. <i>Bioinformatics</i> , 2011, 27, 749-756.	1.8	24
30	Appropriate Thiamin Pyrophosphate Levels Are Required for Acclimation to Changes in Photoperiod. <i>Plant Physiology</i> , 2019, 180, 185-197.	2.3	24
31	Kingdom-wide analysis of the evolution of the plant type III polyketide synthase superfamily. <i>Plant Physiology</i> , 2021, 185, 857-875.	2.3	20
32	The Effect of γ -Glucan Prebiotic on Kidney Function, Uremic Toxins and Gut Microbiome in Stage 3 to 5 Chronic Kidney Disease (CKD) Predialysis Participants: A Randomized Controlled Trial. <i>Nutrients</i> , 2022, 14, 805.	1.7	18
33	PhytoNet: comparative co-expression network analyses across phytoplankton and land plants. <i>Nucleic Acids Research</i> , 2018, 46, W76-W83.	6.5	16
34	Transcriptomics of manually isolated <i>Amborella trichopoda</i> egg apparatus cells. <i>Plant Reproduction</i> , 2019, 32, 15-27.	1.3	16
35	A novel seed plants gene regulates oxidative stress tolerance in <i>Arabidopsis thaliana</i> . <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 705-718.	2.4	11
36	<i>AtRsgA</i> from <i>Arabidopsis thaliana</i> is important for maturation of the small subunit of the chloroplast ribosome. <i>Plant Journal</i> , 2018, 96, 404-420.	2.8	9

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37	The effect of oral iron supplementation on the gut microbiota, gut inflammation, and iron status in iron-depleted South African school-age children with virally suppressed HIV and without HIV. <i>European Journal of Nutrition</i> , 2022, 61, 2067-2078.	1.8	3
38	High-energy-level metabolism and transport occur at the transition from closed to open flowers. <i>Plant Physiology</i> , 2022, 190, 319-339.	2.3	2