

Vincent Segura

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

3,436
citations

279798

23
h-index

233421

45
g-index

51
all docs

51
docs citations

51
times ranked

5162
citing authors

#	ARTICLE	IF	CITATIONS
1	Tree architecture, light interception and water-use related traits are controlled by different genomic regions in an apple tree core collection. <i>New Phytologist</i> , 2022, 234, 209-226.	7.3	5
2	Across-population genomic prediction in grapevine opens up promising prospects for breeding. <i>Horticulture Research</i> , 2022, 9, .	6.3	9
3	Genomic Signatures of a Major Adaptive Event in the Pathogenic Fungus <i>Melampsora larici-populina</i> . <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	9
4	Phenomic Selection: A New and Efficient Alternative to Genomic Selection. <i>Methods in Molecular Biology</i> , 2022, 2467, 397-420.	0.9	13
5	eQTLs are key players in the integration of genomic and transcriptomic data for phenotype prediction. <i>BMC Genomics</i> , 2022, 23, .	2.8	3
6	RNAi suppression of DNA methylation affects the drought stress response and genome integrity in transgenic poplar. <i>New Phytologist</i> , 2021, 232, 80-97.	7.3	31
7	Favorable Conditions for Genomic Evaluation to Outperform Classical Pedigree Evaluation Highlighted by a Proof-of-Concept Study in Poplar. <i>Frontiers in Plant Science</i> , 2020, 11, 581954.	3.6	18
8	Gene expression predictions and networks in natural populations supports the omnigenic theory. <i>BMC Genomics</i> , 2020, 21, 416.	2.8	26
9	Assessment of resistance to xylem cavitation in cordilleran cypress using near-infrared spectroscopy. <i>Forest Ecology and Management</i> , 2020, 462, 117943.	3.2	3
10	Native-source climate determines the Douglas-fir potential of adaptation to drought. <i>Forest Ecology and Management</i> , 2019, 444, 9-20.	3.2	24
11	Changes in the epigenome and transcriptome of the poplar shoot apical meristem in response to water availability affect preferentially hormone pathways. <i>Journal of Experimental Botany</i> , 2018, 69, 537-551.	4.8	52
12	Accuracy of RNAseq based SNP discovery and genotyping in <i>Populus nigra</i> . <i>BMC Genomics</i> , 2018, 19, 909.	2.8	27
13	Epigenetics in Forest Trees. <i>Advances in Botanical Research</i> , 2018, 88, 387-453.	1.1	37
14	Narrow-sense heritability and PST estimates of DNA methylation in three <i>Populus nigra</i> L. populations under contrasting water availability. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	15
15	Phenomic Selection Is a Low-Cost and High-Throughput Method Based on Indirect Predictions: Proof of Concept on Wheat and Poplar. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3961-3972.	1.8	114
16	Winter-dormant shoot apical meristem in poplar trees shows environmental epigenetic memory. <i>Journal of Experimental Botany</i> , 2018, 69, 4821-4837.	4.8	52
17	Identification of major loci and genomic regions controlling acid and volatile content in tomato fruit: implications for flavor improvement. <i>New Phytologist</i> , 2017, 215, 624-641.	7.3	65
18	Near-infrared spectroscopy enables the genetic analysis of chemical properties in a large set of wood samples from <i>Populus nigra</i> (L.) natural populations. <i>Industrial Crops and Products</i> , 2017, 107, 159-171.	5.2	30

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19	New resources for genetic studies in <i>Populus nigra</i> : genome-wide SNP discovery and development of a 12k Infinium array. <i>Molecular Ecology Resources</i> , 2016, 16, 1023-1036.	4.8	48
20	Prediction of Stilbene Content from Heartwood Increment Cores of Scots Pine Using near Infrared Spectroscopy Methodology. <i>Journal of Near Infrared Spectroscopy</i> , 2016, 24, 517-528.	1.5	4
21	Association mapping reveals the genetic architecture of tomato response to water deficit: focus on major fruit quality traits. <i>Journal of Experimental Botany</i> , 2016, 67, 6413-6430.	4.8	65
22	Forest tree genomics: 10 achievements from the past 10 years and future prospects. <i>Annals of Forest Science</i> , 2016, 73, 77-103.	2.0	91
23	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. <i>Genetics</i> , 2014, 198, 1717-1734.	2.9	89
24	Genome-Wide Association in Tomato Reveals 44 Candidate Loci for Fruit Metabolic Traits. <i>Plant Physiology</i> , 2014, 165, 1120-1132.	4.8	187
25	Genome-Wide Prediction Methods in Highly Diverse and Heterozygous Species: Proof-of-Concept through Simulation in Grapevine. <i>PLoS ONE</i> , 2014, 9, e110436.	2.5	37
26	GWAPP: A Web Application for Genome-Wide Association Mapping in Arabidopsis. <i>Plant Cell</i> , 2013, 24, 4793-4805.	6.6	162
27	The Use of Combining Ability Analysis to Identify Elite Parents for <i>Artemisia annua</i> F1 Hybrid Production. <i>PLoS ONE</i> , 2013, 8, e61989.	2.5	56
28	Annealing of magnetic nanoparticles for their encapsulation into microcarriers guided by vascular magnetic resonance navigation. <i>Journal of Nanoparticle Research</i> , 2012, 14, 1.	1.9	6
29	A mixed-model approach for genome-wide association studies of correlated traits in structured populations. <i>Nature Genetics</i> , 2012, 44, 1066-1071.	21.4	380
30	An efficient multi-locus mixed-model approach for genome-wide association studies in structured populations. <i>Nature Genetics</i> , 2012, 44, 825-830.	21.4	884
31	GENETIC ANALYSIS AND QTL DETECTION FOR BIENNIAL BEARING IN APPLE. <i>Acta Horticulturae</i> , 2012, , 65-72.	0.2	1
32	Transposon-induced gene activation as a mechanism generating cluster shape somatic variation in grapevine. <i>Plant Journal</i> , 2010, 61, 545-557.	5.7	116
33	The Genetic Map of <i>Artemisia annua</i> L. Identifies Loci Affecting Yield of the Antimalarial Drug Artemisinin. <i>Science</i> , 2010, 327, 328-331.	12.6	325
34	QTL ANALYSIS FOR LEAF GAS EXCHANGE IN AN APPLE PROGENY GROWN UNDER ATMOSPHERIC CONSTRAINTS. <i>Acta Horticulturae</i> , 2009, , 369-374.	0.2	10
35	Dissecting apple tree architecture into genetic, ontogenetic and environmental effects: QTL mapping. <i>Tree Genetics and Genomes</i> , 2009, 5, 165-179.	1.6	48
36	EXPLORING THE GENETIC DETERMINISMS OF ARCHITECTURAL AND FUNCTIONAL TRAITS IN AN APPLE PROGENY. <i>Acta Horticulturae</i> , 2009, , 311-318.	0.2	2

#	ARTICLE	IF	CITATIONS
37	QTL ANALYSIS FOR GROWTH AND BRANCHING TRAITS ANNUALLY ASSESSED ALONG THE TRUNK OF THREE-YEAR-OLD APPLE HYBRIDS. Acta Horticulturae, 2009, , 669-674.	0.2	1
38	Comparison of tree architecture using tree edit distances: application to 2-year-old apple hybrids. Euphytica, 2008, 161, 155-164.	1.2	9
39	Dissecting apple tree architecture into genetic, ontogenetic and environmental effects: mixed linear modelling of repeated spatial and temporal measures. New Phytologist, 2008, 178, 302-314.	7.3	76
40	LAMINA: a tool for rapid quantification of leaf size and shape parameters. BMC Plant Biology, 2008, 8, 82.	3.6	181
41	PHENOTYPING APPLE PROGENY FOR ECOPHYSIOLOGICAL TRAITS: HOW AND WHAT FOR?. Acta Horticulturae, 2008, , 151-158.	0.2	9
42	Wide range QTL analysis for complex architectural traits in a 1-year-old apple progeny. Genome, 2007, 50, 159-171.	2.0	61
43	The effect of genotype, location and their interaction on early growth and branching in apricot trees. Journal of Horticultural Science and Biotechnology, 2006, 81, 189-198.	1.9	7
44	Phenotyping progenies for complex architectural traits: a strategy for 1-year-old apple trees (Malus x Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	39