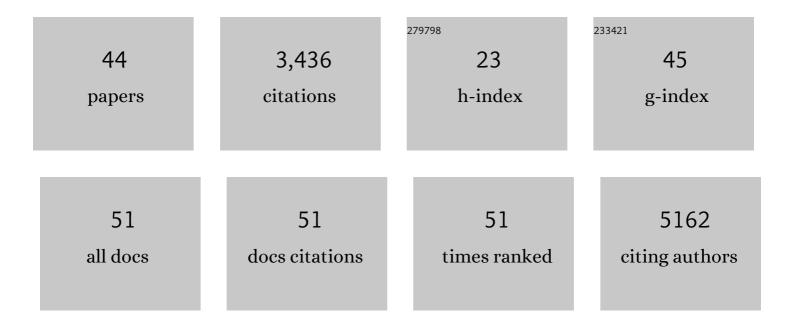
Vincent Segura

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	An efficient multi-locus mixed-model approach for genome-wide association studies in structured populations. Nature Genetics, 2012, 44, 825-830.	21.4	884
2	A mixed-model approach for genome-wide association studies of correlated traits in structured populations. Nature Genetics, 2012, 44, 1066-1071.	21.4	380
3	The Genetic Map of <i>Artemisia annua</i> L. Identifies Loci Affecting Yield of the Antimalarial Drug Artemisinin. Science, 2010, 327, 328-331.	12.6	325
4	Genome-Wide Association in Tomato Reveals 44 Candidate Loci for Fruit Metabolic Traits Â. Plant Physiology, 2014, 165, 1120-1132.	4.8	187
5	LAMINA: a tool for rapid quantification of leaf size and shape parameters. BMC Plant Biology, 2008, 8, 82.	3.6	181
6	GWAPP: A Web Application for Genome-Wide Association Mapping in Arabidopsis Â. Plant Cell, 2013, 24, 4793-4805.	6.6	162
7	Transposon-induced gene activation as a mechanism generating cluster shape somatic variation in grapevine. Plant Journal, 2010, 61, 545-557.	5.7	116
8	Phenomic Selection Is a Low-Cost and High-Throughput Method Based on Indirect Predictions: Proof of Concept on Wheat and Poplar. G3: Genes, Genomes, Genetics, 2018, 8, 3961-3972.	1.8	114
9	Forest tree genomics: 10 achievements from the past 10Âyears and future prospects. Annals of Forest Science, 2016, 73, 77-103.	2.0	91
10	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. Genetics, 2014, 198, 1717-1734.	2.9	89
11	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
12	Association mapping reveals the genetic architecture of tomato response to water deficit: focus on major fruit quality traits. Journal of Experimental Botany, 2016, 67, 6413-6430.	4.8	65
13	Identification of major loci and genomic regions controlling acid and volatile content in tomato fruit: implications for flavor improvement. New Phytologist, 2017, 215, 624-641.	7.3	65
14	Wide range QTL analysis for complex architectural traits in a 1-year-old apple progeny. Genome, 2007, 50, 159-171.	2.0	61
15	The Use of Combining Ability Analysis to Identify Elite Parents for Artemisia annua F1 Hybrid Production. PLoS ONE, 2013, 8, e61989.	2.5	56
16	Changes in the epigenome and transcriptome of the poplar shoot apical meristem in response to water availability affect preferentially hormone pathways. Journal of Experimental Botany, 2018, 69, 537-551.	4.8	52
17	Winter-dormant shoot apical meristem in poplar trees shows environmental epigenetic memory. Journal of Experimental Botany, 2018, 69, 4821-4837.	4.8	52
18	Dissecting apple tree architecture into genetic, ontogenetic and environmental effects: QTL mapping. Tree Genetics and Genomes, 2009, 5, 165-179.	1.6	48

#	Article	IF	CITATIONS
19	New resources for genetic studies in <i>Populus nigra</i> : genomeâ€wide <scp>SNP</scp> discovery and development of a 12k Infinium array. Molecular Ecology Resources, 2016, 16, 1023-1036.	4.8	48
20	Phenotyping progenies for complex architectural traits: a strategy for 1-year-old apple trees (Malus x) Tj ETQq0 C	0 0 1 gBT /O	verlock 10 Tf

21	Epigenetics in Forest Trees. Advances in Botanical Research, 2018, 88, 387-453.	1.1	37
22	Genome-Wide Prediction Methods in Highly Diverse and Heterozygous Species: Proof-of-Concept through Simulation in Grapevine. PLoS ONE, 2014, 9, e110436.	2.5	37
23	RNAi suppression of DNA methylation affects the drought stress response and genome integrity in transgenic poplar. New Phytologist, 2021, 232, 80-97.	7.3	31
24	Near-infrared spectroscopy enables the genetic analysis of chemical properties in a large set of wood samples from Populus nigra (L.) natural populations. Industrial Crops and Products, 2017, 107, 159-171.	5.2	30
25	Accuracy of RNAseq based SNP discovery and genotyping in Populusnigra. BMC Genomics, 2018, 19, 909.	2.8	27
26	Gene expression predictions and networks in natural populations supports the omnigenic theory. BMC Genomics, 2020, 21, 416.	2.8	26
27	Native-source climate determines the Douglas-fir potential of adaptation to drought. Forest Ecology and Management, 2019, 444, 9-20.	3.2	24
28	Favorable Conditions for Genomic Evaluation to Outperform Classical Pedigree Evaluation Highlighted by a Proof-of-Concept Study in Poplar. Frontiers in Plant Science, 2020, 11, 581954.	3.6	18
29	Narrow-sense heritability and PST estimates of DNA methylation in three Populus nigra L. populations under contrasting water availability. Tree Genetics and Genomes, 2018, 14, 1.	1.6	15
30	Phenomic Selection: A New and Efficient Alternative to Genomic Selection. Methods in Molecular Biology, 2022, 2467, 397-420.	0.9	13
31	QTL ANALYSIS FOR LEAF GAS EXCHANGE IN AN APPLE PROGENY GROWN UNDER ATMOSPHERIC CONSTRAINTS. Acta Horticulturae, 2009, , 369-374.	0.2	10
32	Comparison of tree architecture using tree edit distances: application to 2-year-old apple hybrids. Euphytica, 2008, 161, 155-164.	1.2	9
33	PHENOTYPING APPLE PROGENY FOR ECOPHYSIOLOGICAL TRAITS: HOW AND WHAT FOR?. Acta Horticulturae, 2008, , 151-158.	0.2	9
34	Across-population genomic prediction in grapevine opens up promising prospects for breeding. Horticulture Research, 2022, 9, .	6.3	9
35	Genomic Signatures of a Major Adaptive Event in the Pathogenic Fungus <i>Melampsora larici-populina</i> . Genome Biology and Evolution, 2022, 14, .	2.5	9
36	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

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#	Article	IF	CITATIONS
37	Annealing of magnetic nanoparticles for their encapsulation into microcarriers guided by vascular magnetic resonance navigation. Journal of Nanoparticle Research, 2012, 14, 1.	1.9	6
38	Tree architecture, light interception and waterâ€use related traits are controlled by different genomic regions in an apple tree core collection. New Phytologist, 2022, 234, 209-226.	7.3	5
39	Prediction of Stilbene Content from Heartwood Increment Cores of Scots Pine Using near Infrared Spectroscopy Methodology. Journal of Near Infrared Spectroscopy, 2016, 24, 517-528.	1.5	4
40	Assessment of resistance to xylem cavitation in cordilleran cypress using near-infrared spectroscopy. Forest Ecology and Management, 2020, 462, 117943.	3.2	3
41	eQTLs are key players in the integration of genomic and transcriptomic data for phenotype prediction. BMC Genomics, 2022, 23, .	2.8	3
42	EXPLORING THE GENETIC DETERMINISMS OF ARCHITECTURAL AND FUNCTIONAL TRAITS IN AN APPLE PROGENY. Acta Horticulturae, 2009, , 311-318.	0.2	2
43	GENETIC ANALYSIS AND QTL DETECTION FOR BIENNIAL BEARING IN APPLE. Acta Horticulturae, 2012, , 65-72.	0.2	1
44	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