

Marie-Anne Van Sluys

List of Publications by Year in descending order

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107
papers

9,582
citations

57758

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93
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all docs

111
docs citations

111
times ranked

9146
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of the genomes of two <i>Xanthomonas</i> pathogens with differing host specificities. <i>Nature</i> , 2002, 417, 459-463.	27.8	1,074
2	The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> . <i>Nature</i> , 2000, 406, 151-157.	27.8	827
3	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	7.1	652
4	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	21.4	463
5	Pathogenomics of <i>Xanthomonas</i> : understanding bacterium-plant interactions. <i>Nature Reviews Microbiology</i> , 2011, 9, 344-355.	28.6	428
6	Comparative Genomics of Two <i>Leptospira interrogans</i> Serovars Reveals Novel Insights into Physiology and Pathogenesis. <i>Journal of Bacteriology</i> , 2004, 186, 2164-2172.	2.2	406
7	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 204.	2.8	327
8	Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of <i>Xylella fastidiosa</i> . <i>Journal of Bacteriology</i> , 2003, 185, 1018-1026.	2.2	307
9	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	12.8	299
10	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. <i>Genome Research</i> , 2003, 13, 2725-2735.	5.5	254
11	Stress activation and genomic impact of Tnt1 retrotransposons in Solanaceae. <i>Cytogenetic and Genome Research</i> , 2005, 110, 229-241.	1.1	238
12	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , 2011, 193, 5450-5464.	2.2	189
13	Studies on the introduction and mobility of the maize Activator element in <i>Arabidopsis thaliana</i> and <i>Daucus carota</i> .. <i>EMBO Journal</i> , 1987, 6, 3881-3889.	7.8	180
14	Genome features of <i>Leptospira interrogans</i> serovar Copenhageni. <i>Brazilian Journal of Medical and Biological Research</i> , 2004, 37, 459-477.	1.5	175
15	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. <i>BMC Genomics</i> , 2010, 11, 261.	2.8	175
16	COMPARATIVE GENOMIC ANALYSIS OF PLANT-ASSOCIATED BACTERIA. <i>Annual Review of Phytopathology</i> , 2002, 40, 169-189.	7.8	171
17	Building the sugarcane genome for biotechnology and identifying evolutionary trends. <i>BMC Genomics</i> , 2014, 15, 540.	2.8	136
18	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. <i>Scientific Reports</i> , 2013, 3, 3399.	3.3	129

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19	Genomic distribution and characterization of EST-derived resistance gene analogs (RGAs) in sugarcane. <i>Molecular Genetics and Genomics</i> , 2003, 269, 406-419.	2.1	125
20	The Genome Sequence of the Gram-Positive Sugarcane Pathogen <i>Leifsonia xyli</i> subsp. <i>xyli</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 827-836.	2.6	119
21	The role of auxin in hairy root induction. <i>Molecular Genetics and Genomics</i> , 1987, 208, 457-463.	2.4	117
22	Plant immunity: unravelling the complexity of plant responses to biotic stresses. <i>Annals of Botany</i> , 2017, 119, 681-687.	2.9	116
23	Genomics-Based Diagnostic Marker Development for <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> and <i>X. oryzae</i> pv. <i>oryzicola</i> . <i>Plant Disease</i> , 2010, 94, 311-319.	1.4	114
24	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	6.4	106
25	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. <i>Tropical Plant Biology</i> , 2011, 4, 145-156.	1.9	91
26	Acquisition and Evolution of Plant Pathogenesis-Associated Gene Clusters and Candidate Determinants of Tissue-Specificity in <i>Xanthomonas</i> . <i>PLoS ONE</i> , 2008, 3, e3828.	2.5	89
27	Nitric Oxide Mediates the Hormonal Control of Crassulacean Acid Metabolism Expression in Young Pineapple Plants. <i>Plant Physiology</i> , 2010, 152, 1971-1985.	4.8	80
28	Differential usage of two in-frame translational start codons regulates subcellular localization of <i>Arabidopsis thaliana</i> THI1. <i>Journal of Cell Science</i> , 2003, 116, 285-291.	2.0	78
29	Dual targeting properties of the N-terminal signal sequence of <i>Arabidopsis thaliana</i> THI1 protein to mitochondria and chloroplasts. <i>Plant Molecular Biology</i> , 2001, 46, 639-650.	3.9	76
30	The Role of Prophage in Plant-Pathogenic Bacteria. <i>Annual Review of Phytopathology</i> , 2013, 51, 429-451.	7.8	76
31	Structure of the Thiazole Biosynthetic Enzyme THI1 from <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 30957-30966.	3.4	72
32	High homologous gene conservation despite extreme autopolyploid redundancy in sugarcane. <i>New Phytologist</i> , 2011, 189, 629-642.	7.3	69
33	An EST-based analysis identifies new genes and reveals distinctive gene expression features of <i>Coffea arabica</i> and <i>Coffea canephora</i> . <i>BMC Plant Biology</i> , 2011, 11, 30.	3.6	67
34	Functional characterization of the thi1 promoter region from <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2005, 56, 1797-1804.	4.8	66
35	Sugarcane Functional Genomics: Gene Discovery for Agronomic Trait Development. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-11.	2.2	64
36	The Biotechnology Roadmap for Sugarcane Improvement. <i>Tropical Plant Biology</i> , 2010, 3, 75-87.	1.9	62

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37	Genomic Analysis of Wild Tomato Introgressions Determining Metabolism- and Yield-Associated Traits. <i>Plant Physiology</i> , 2010, 152, 1772-1786.	4.8	57
38	Analysis of plant LTR-retrotransposons at the fine-scale family level reveals individual molecular patterns. <i>BMC Genomics</i> , 2012, 13, 137.	2.8	57
39	Transcriptionally active transposable elements in recent hybrid sugarcane. <i>Plant Journal</i> , 2005, 44, 707-717.	5.7	56
40	RNAseq Transcriptional Profiling following Whip Development in Sugarcane Smut Disease. <i>PLoS ONE</i> , 2016, 11, e0162237.	2.5	56
41	Genome sequence of <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> strain 4834-R reveals that flagellar motility is not a general feature of xanthomonads. <i>BMC Genomics</i> , 2013, 14, 761.	2.8	55
42	Complete chloroplast genome sequences contribute to plant species delimitation: A case study of the <i>Anemopaegma</i> species complex. <i>American Journal of Botany</i> , 2017, 104, 1493-1509.	1.7	54
43	A candidate gene survey of quantitative trait loci affecting chemical composition in tomato fruit. <i>Journal of Experimental Botany</i> , 2008, 59, 2875-2890.	4.8	52
44	The participation of AtXPB1, the XPB/RAD25 homologue gene from <i>Arabidopsis thaliana</i> , in DNA repair and plant development. <i>Plant Journal</i> , 2002, 28, 385-395.	5.7	51
45	Origins of the <i>Xylella fastidiosa</i> Prophage-Like Regions and Their Impact in Genome Differentiation. <i>PLoS ONE</i> , 2008, 3, e4059.	2.5	50
46	Title is missing!. <i>Plant Cell, Tissue and Organ Culture</i> , 2001, 65, 37-44.	2.3	48
47	<i>Xylella</i> and <i>Xanthomonas</i> Mobil'omics. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 146-159.	2.0	46
48	Laterally transferred genomic islands in Xanthomonadales related to pathogenicity and primary metabolism. <i>FEMS Microbiology Letters</i> , 2008, 281, 87-97.	1.8	43
49	Analysis of three sugarcane homo/homeologous regions suggests independent polyploidization events of <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> . <i>Genome Biology and Evolution</i> , 2017, 9, eww293.	2.5	42
50	Survey of transposable elements in sugarcane expressed sequence tags (ESTs). <i>Genetics and Molecular Biology</i> , 2001, 24, 147-154.	1.3	41
51	Evaluation of Monocot and Eudicot Divergence Using the Sugarcane Transcriptome. <i>Plant Physiology</i> , 2004, 134, 951-959.	4.8	38
52	Cloning of a cDNA from <i>Arabidopsis thaliana</i> homologous to the human XPB gene. <i>Gene</i> , 1998, 208, 207-213.	2.2	37
53	Retrolyc1 subfamilies defined by different U3 LTR regulatory regions in the <i>Lycopersicon</i> genus. <i>Molecular Genetics and Genomics</i> , 2001, 266, 35-41.	2.1	35
54	A novel linkage map of sugarcane with evidence for clustering of retrotransposon-based markers. <i>BMC Genetics</i> , 2012, 13, 51.	2.7	34

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55	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. BMC Genomics, 2008, 9, 534.	2.8	33
56	Point Mutation is Responsible for Arabidopsis tz-201 Mutant Phenotype Affecting Thiamin Biosynthesis. Plant and Cell Physiology, 2003, 44, 856-860.	3.1	32
57	Comparative analysis of Mutator -like transposases in sugarcane. Molecular Genetics and Genomics, 2004, 272, 194-203.	2.1	31
58	Functional XPB/RAD25 redundancy in Arabidopsis genome: characterization of AtXPB2 and expression analysis. Gene, 2005, 344, 93-103.	2.2	29
59	Sucrose-phosphate phosphatase from sugarcane reveals an ancestral tandem duplication. BMC Plant Biology, 2021, 21, 23.	3.6	28
60	Gene Content Analysis of Sugarcane Public ESTs Reveals Thousands of Missing Coding-Genes and an Unexpected Pool of Grasses Conserved ncRNAs. Tropical Plant Biology, 2012, 5, 199-205.	1.9	27
61	Non-Gamma-Proteobacteria Gene Islands Contribute to the <i>Xanthomonas</i> Genome. OMICS A Journal of Integrative Biology, 2005, 9, 160-172.	2.0	26
62	ESTs from Seeds to Assist the Selective Breeding of <i>Jatropha curcas</i> L. for Oil and Active Compounds. Genomics Insights, 2010, 3, GEI.S4340.	3.0	26
63	An operon for production of bioactive gibberellin A ₄ phytohormone with wide distribution in the bacterial rice leaf streak pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . New Phytologist, 2017, 214, 1260-1266.	7.3	26
64	The control of endopolygalacturonase expression by the sugarcane RAV transcription factor during aerenchyma formation. Journal of Experimental Botany, 2019, 70, 497-506.	4.8	24
65	Retrolyc1-1, a member of the Tnt1 retrotransposon super-family in the <i>Lycopersicon peruvianum</i> genome. Genetica, 1999, 107, 65-72.	1.1	23
66	Thermoperiod affects the diurnal cycle of nitrate reductase expression and activity in pineapple plants by modulating the endogenous levels of cytokinins. Physiologia Plantarum, 2009, 137, 201-212.	5.2	23
67	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. Frontiers in Plant Science, 2019, 10, 553.	3.6	23
68	Genome survey of resistance gene analogs in sugarcane: genomic features and differential expression of the innate immune system from a smut-resistant genotype. BMC Genomics, 2019, 20, 809.	2.8	22
69	Radiation of the Tnt1 retrotransposon superfamily in three Solanaceae genera. BMC Evolutionary Biology, 2007, 7, 34.	3.2	19
70	Multiple invasions of Gypsy and Microtia retroelements in genus <i>Zaprionus</i> and melanogaster subgroup of the genus <i>Drosophila</i> . BMC Evolutionary Biology, 2009, 9, 279.	3.2	18
71	Molecular evidence of symbiotic activity between <i>Symbiodinium</i> and <i>Tridacna maxima</i> larvae. Symbiosis, 2017, 72, 13-22.	2.3	18
72	Somatic Excision of the Ac Transposable Element in Transgenic <i>Arabidopsis thaliana</i> after 5-Azacytidine Treatment. Plant and Cell Physiology, 1997, 38, 336-343.	3.1	17

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73	MudrA-like sequences from rice and sugarcane cluster as two bona fide transposon clades and two domesticated transposases. <i>Gene</i> , 2007, 392, 117-125.	2.2	17
74	Combined genotypicâ€“phenotypic phylogeny of the tribe Spathicarpeae (Araceae) with reference to independent events of invasion to Andean regions. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 1023-1039.	2.7	17
75	<i>Xylella fastidiosa</i> comparative genomic database is an information resource to explore the annotation, genomic features, and biology of different strains. <i>Genetics and Molecular Biology</i> , 2012, 35, 149-152.	1.3	15
76	Negative effect of the 5'-untranslated leader sequence on Ac transposon promoter expression. <i>Plant Molecular Biology</i> , 1999, 40, 935-944.	3.9	13
77	Genetic Discovery in <i>Xylella fastidiosa</i> Through Sequence Analysis of Selected Randomly Amplified Polymorphic DNAs. <i>Current Microbiology</i> , 2005, 50, 78-83.	2.2	12
78	Characterization of new IS elements and studies of their dispersion in two subspecies of <i>Leifsonia xyli</i> . <i>BMC Microbiology</i> , 2008, 8, 127.	3.3	12
79	How macroalgae can deal with radiation variability and photoacclimation capacity: The example of <i>Gracilaria tenuistipitata</i> (Rhodophyta) in laboratory. <i>Algal Research</i> , 2020, 50, 102007.	4.6	12
80	Reaching the top through a tortuous path: helical growth in climbing plants. <i>Current Opinion in Plant Biology</i> , 2021, 59, 101982.	7.1	11
81	The Tnt1 family member Retrosol copy number and structure disclose retrotransposon diversification in different <i>Solanum</i> species. <i>Molecular Genetics and Genomics</i> , 2009, 281, 261-271.	2.1	10
82	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. <i>Journal of Experimental Botany</i> , 2015, 66, 4239-4250.	4.8	10
83	Copia Retrotransposon in the <i>Zaprionus</i> Genus: Another Case of Transposable Element Sharing with the <i>Drosophila melanogaster</i> Subgroup. <i>Journal of Molecular Evolution</i> , 2011, 72, 326-338.	1.8	9
84	Functional characterization of sugarcane mustang domesticated transposases and comparative diversity in sugarcane, rice, maize and sorghum. <i>Genetics and Molecular Biology</i> , 2012, 35, 632-639.	1.3	9
85	Diversification of hAT transposase paralogues in the sugarcane genome. <i>Molecular Genetics and Genomics</i> , 2012, 287, 205-219.	2.1	9
86	Complete Genome Sequence of <i>Leifsonia xyli</i> subsp. <i>cynodontis</i> Strain DSM46306, a Gram-Positive Bacterial Pathogen of Grasses. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
87	GMOs: building the future on the basis of past experience. <i>Anais Da Academia Brasileira De Ciencias</i> , 2006, 78, 667-686.	0.8	8
88	Toward understanding inflorescence development and architecture in <i>Passiflora</i> : insights from comparative anatomy and expression of <i>APETALA1</i> . <i>American Journal of Botany</i> , 2019, 106, 1173-1189.	1.7	8
89	Transposable element discovery and characterization of LTR-retrotransposon evolutionary lineages in the tropical fruit species <i>Passiflora edulis</i> . <i>Molecular Biology Reports</i> , 2019, 46, 6117-6133.	2.3	8
90	Ascorbate-copper induced DNA lesions and repair in <i>Escherichia coli</i> K12 cells. <i>Carcinogenesis</i> , 1986, 7, 197-200.	2.8	7

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91	Mutator System Derivatives Isolated from Sugarcane Genome Sequence. Tropical Plant Biology, 2012, 5, 233-243.	1.9	7
92	Molecular Genetic Dissection of Sugarcane Flowering under Equatorial Field Conditions. Tropical Plant Biology, 2016, 9, 252-266.	1.9	7
93	Escherichia coli xthA mutant is not hypersensitive to ascorbic acid/copper treatment an H2O2 generating reaction. Mutation Research-Fundamental and Molecular Mechanisms of Mutagenesis, 1986, 174, 265-269.	1.1	5
94	Brazilian-adapted soybean Bradyrhizobium strains uncover IS elements with potential impact on biological nitrogen fixation. FEMS Microbiology Letters, 2019, 366, .	1.8	5
95	Negative selection driven by cytosine deaminase gene in Lycopersicon esculentum hairy roots. Plant Science, 1999, 141, 175-181.	3.6	4
96	Transposon display supports transpositional activity of P elements in species of the saltans group of Drosophila. Journal of Genetics, 2007, 86, 37-43.	0.7	4
97	Axillary bud development in pineapple nodal segments correlates with changes on cell cycle gene expression, hormone level, and sucrose and glutamate contents. In Vitro Cellular and Developmental Biology - Plant, 2010, 46, 281-288.	2.1	4
98	Noise or Symphony: Comparative Evolutionary Analysis of Sugarcane Transposable Elements with Other Grasses. Topics in Current Genetics, 2012, , 169-192.	0.7	4
99	Virus-Like Attachment Sites and Plastic CpG Islands: Landmarks of Diversity in Plant Del Retrotransposons. PLoS ONE, 2014, 9, e97099.	2.5	4
100	Virus-like attachment sites as structural landmarks of plants retrotransposons. Mobile DNA, 2016, 7, 14.	3.6	3
101	Biotechnology approaches for production of antiulcerogenic dihydro-epideoxyarteannuin B isolated from Artemisia annua L.. Revista Brasileira De Farmacognosia, 2006, 16, 291-299.	1.4	3
102	Evidence for sub-functionalization of tandemly duplicated XPB nucleotide excision repair genes in Arabidopsis thaliana. Gene, 2020, 754, 144818.	2.2	2
103	An Efficient Approach to Explore and Discriminate Anomalous Regions in Bacterial Genomes Based on Maximum Entropy. Journal of Computational Biology, 2017, 24, 1125-1133.	1.6	1
104	Arabidopsis-Based Dual-Layered Biological Network Analysis Elucidates Fully Modulated Pathways Related to Sugarcane Resistance on Biotrophic Pathogen Infection. Frontiers in Plant Science, 2021, 12, 707904.	3.6	0
105	Characterization of Agrobacterium tumefaciens Strains Isolated from Brazilian Plant Species. American Journal of Plant Physiology, 2006, 1, 142-150.	0.2	0
106	Principais conclusões do workshop conjunto dos programas FAPESP BIOTA-BIOEN-mudanças climáticas: ciência e políticas públicas para uma economia mais verde, no contexto da RIO+20. Biota Neotropica, 2012, 12, 19-21.	1.0	0
107	Shaping a Plant Genetics and Molecular Biology research community in Brazil. Genetics and Molecular Biology, 2017, 40, 1-1.	1.3	0