

# Marie-Anne Van Sluys

## List of Publications by Year in descending order

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107  
papers

9,582  
citations

57719

44  
h-index

40954

93  
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111  
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.	13.7	1,074
2	The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> . <i>Nature</i> , 2000, 406, 151-157.	13.7	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.	3.3	652
4	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
5	Pathogenomics of <i>Xanthomonas</i> : understanding bacterium-plant interactions. <i>Nature Reviews Microbiology</i> , 2011, 9, 344-355.	13.6	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.	1.0	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.	1.2	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.	1.0	307
9	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	5.8	299
10	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. <i>Genome Research</i> , 2003, 13, 2725-2735.	2.4	254
11	Stress activation and genomic impact of Tnt1 retrotransposons in Solanaceae. <i>Cytogenetic and Genome Research</i> , 2005, 110, 229-241.	0.6	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.	1.0	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.	3.5	180
14	Genome features of <i>Leptospira interrogans</i> serovar Copenhageni. <i>Brazilian Journal of Medical and Biological Research</i> , 2004, 37, 459-477.	0.7	175
15	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. <i>BMC Genomics</i> , 2010, 11, 261.	1.2	175
16	COMPARATIVE GENOMIC ANALYSIS OF PLANT-ASSOCIATED BACTERIA. <i>Annual Review of Phytopathology</i> , 2002, 40, 169-189.	3.5	171
17	Building the sugarcane genome for biotechnology and identifying evolutionary trends. <i>BMC Genomics</i> , 2014, 15, 540.	1.2	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.	1.6	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.	1.0	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.	1.4	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.	1.4	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.	0.7	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, .	3.3	106
25	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. <i>Tropical Plant Biology</i> , 2011, 4, 145-156.	1.0	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.	1.1	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.	2.3	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.	1.2	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.	2.0	76
30	The Role of Prophage in Plant-Pathogenic Bacteria. <i>Annual Review of Phytopathology</i> , 2013, 51, 429-451.	3.5	76
31	Structure of the Thiazole Biosynthetic Enzyme THI1 from <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 30957-30966.	1.6	72
32	High homologous gene conservation despite extreme autopolyploid redundancy in sugarcane. <i>New Phytologist</i> , 2011, 189, 629-642.	3.5	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.	1.6	67
34	Functional characterization of the thi1 promoter region from <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2005, 56, 1797-1804.	2.4	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.	1.0	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.	2.3	57
38	Analysis of plant LTR-retrotransposons at the fine-scale family level reveals individual molecular patterns. <i>BMC Genomics</i> , 2012, 13, 137.	1.2	57
39	Transcriptionally active transposable elements in recent hybrid sugarcane. <i>Plant Journal</i> , 2005, 44, 707-717.	2.8	56
40	RNAseq Transcriptional Profiling following Whip Development in Sugarcane Smut Disease. <i>PLoS ONE</i> , 2016, 11, e0162237.	1.1	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.	1.2	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.	0.8	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.	2.4	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.	2.8	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.	1.1	50
46	Title is missing!. <i>Plant Cell, Tissue and Organ Culture</i> , 2001, 65, 37-44.	1.2	48
47	<i>Xylella</i> and <i>Xanthomonas</i> Mobil'omics. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 146-159.	1.0	46
48	Laterally transferred genomic islands in Xanthomonadales related to pathogenicity and primary metabolism. <i>FEMS Microbiology Letters</i> , 2008, 281, 87-97.	0.7	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, evw293.	1.1	42
50	Survey of transposable elements in sugarcane expressed sequence tags (ESTs). <i>Genetics and Molecular Biology</i> , 2001, 24, 147-154.	0.6	41
51	Evaluation of Monocot and Eudicot Divergence Using the Sugarcane Transcriptome. <i>Plant Physiology</i> , 2004, 134, 951-959.	2.3	38
52	Cloning of a cDNA from <i>Arabidopsis thaliana</i> homologous to the human XPB gene. <i>Gene</i> , 1998, 208, 207-213.	1.0	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.	1.0	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. <i>BMC Genomics</i> , 2008, 9, 534.	1.2	33
56	Point Mutation is Responsible for Arabidopsis tz-201 Mutant Phenotype Affecting Thiamin Biosynthesis. <i>Plant and Cell Physiology</i> , 2003, 44, 856-860.	1.5	32
57	Comparative analysis of Mutator -like transposases in sugarcane. <i>Molecular Genetics and Genomics</i> , 2004, 272, 194-203.	1.0	31
58	Functional XPB/RAD25 redundancy in Arabidopsis genome: characterization of AtXPB2 and expression analysis. <i>Gene</i> , 2005, 344, 93-103.	1.0	29
59	Sucrose-phosphate phosphatase from sugarcane reveals an ancestral tandem duplication. <i>BMC Plant Biology</i> , 2021, 21, 23.	1.6	28
60	Gene Content Analysis of Sugarcane Public ESTs Reveals Thousands of Missing Coding-Genes and an Unexpected Pool of Grasses Conserved ncRNAs. <i>Tropical Plant Biology</i> , 2012, 5, 199-205.	1.0	27
61	Non-Gamma-Proteobacteria Gene Islands Contribute to the <i>Xanthomonas</i> Genome. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 160-172.	1.0	26
62	ESTs from Seeds to Assist the Selective Breeding of <i>Jatropha curcas</i> L. for Oil and Active Compounds. <i>Genomics Insights</i> , 2010, 3, GEI.S4340.	3.0	26
63	An operon for production of bioactive gibberellin A <sub>4</sub> phytohormone with wide distribution in the bacterial rice leaf streak pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>New Phytologist</i> , 2017, 214, 1260-1266.	3.5	26
64	The control of endopolygalacturonase expression by the sugarcane RAV transcription factor during aerenchyma formation. <i>Journal of Experimental Botany</i> , 2019, 70, 497-506.	2.4	24
65	Retrolyc1-1, a member of the Tnt1 retrotransposon super-family in the <i>Lycopersicon peruvianum</i> genome. <i>Genetica</i> , 1999, 107, 65-72.	0.5	23
66	Thermoperiod affects the diurnal cycle of nitrate reductase expression and activity in pineapple plants by modulating the endogenous levels of cytokinins. <i>Physiologia Plantarum</i> , 2009, 137, 201-212.	2.6	23
67	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. <i>Frontiers in Plant Science</i> , 2019, 10, 553.	1.7	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. <i>BMC Genomics</i> , 2019, 20, 809.	1.2	22
69	Radiation of the Tnt1 retrotransposon superfamily in three Solanaceae genera. <i>BMC Evolutionary Biology</i> , 2007, 7, 34.	3.2	19
70	Multiple invasions of Gypsy and Microplia retroelements in genus <i>Zaprionus</i> and melanogaster subgroup of the genus <i>Drosophila</i> . <i>BMC Evolutionary Biology</i> , 2009, 9, 279.	3.2	18
71	Molecular evidence of symbiotic activity between <i>Symbiodinium</i> and <i>Tridacna maxima</i> larvae. <i>Symbiosis</i> , 2017, 72, 13-22.	1.2	18
72	Somatic Excision of the Ac Transposable Element in Transgenic Arabidopsis thaliana after 5-Azacytidine Treatment. <i>Plant and Cell Physiology</i> , 1997, 38, 336-343.	1.5	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.	1.0	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.	1.2	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.	0.6	15
76	Negative effect of the 5'-untranslated leader sequence on Ac transposon promoter expression. <i>Plant Molecular Biology</i> , 1999, 40, 935-944.	2.0	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.	1.0	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.	1.3	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.	2.4	12
80	Reaching the top through a tortuous path: helical growth in climbing plants. <i>Current Opinion in Plant Biology</i> , 2021, 59, 101982.	3.5	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.	1.0	10
82	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. <i>Journal of Experimental Botany</i> , 2015, 66, 4239-4250.	2.4	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.	0.8	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.	0.6	9
85	Diversification of hAT transposase paralogues in the sugarcane genome. <i>Molecular Genetics and Genomics</i> , 2012, 287, 205-219.	1.0	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.	0.3	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.	0.8	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.	1.0	8
90	Ascorbate-copper induced DNA lesions and repair in <i>Escherichia coli</i> K12 cells. <i>Carcinogenesis</i> , 1986, 7, 197-200.	1.3	7

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91	Mutator System Derivatives Isolated from Sugarcane Genome Sequence. <i>Tropical Plant Biology</i> , 2012, 5, 233-243.	1.0	7
92	Molecular Genetic Dissection of Sugarcane Flowering under Equatorial Field Conditions. <i>Tropical Plant Biology</i> , 2016, 9, 252-266.	1.0	7
93	<i>Escherichia coli</i> xthA mutant is not hypersensitive to ascorbic acid/copper treatment an H2O2 generating reaction. <i>Mutation Research-Fundamental and Molecular Mechanisms of Mutagenesis</i> , 1986, 174, 265-269.	1.2	5
94	Brazilian-adapted soybean Bradyrhizobium strains uncover IS elements with potential impact on biological nitrogen fixation. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	5
95	Negative selection driven by cytosine deaminase gene in <i>Lycopersicon esculentum</i> hairy roots. <i>Plant Science</i> , 1999, 141, 175-181.	1.7	4
96	Transposon display supports transpositional activity of P elements in species of the saltans group of <i>Drosophila</i> . <i>Journal of Genetics</i> , 2007, 86, 37-43.	0.4	4
97	Axillary bud development in pineapple nodal segments correlates with changes on cell cycle gene expression, hormone level, and sucrose and glutamate contents. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2010, 46, 281-288.	0.9	4
98	Noise or Symphony: Comparative Evolutionary Analysis of Sugarcane Transposable Elements with Other Grasses. <i>Topics in Current Genetics</i> , 2012, , 169-192.	0.7	4
99	Virus-Like Attachment Sites and Plastic CpG Islands: Landmarks of Diversity in Plant Del Retrotransposons. <i>PLoS ONE</i> , 2014, 9, e97099.	1.1	4
100	Virus-like attachment sites as structural landmarks of plants retrotransposons. <i>Mobile DNA</i> , 2016, 7, 14.	1.3	3
101	Biotechnology approaches for production of antiulcerogenic dihydro-epideoxyarteannuin B isolated from <i>Artemisia annua</i> L.. <i>Revista Brasileira De Farmacognosia</i> , 2006, 16, 291-299.	0.6	3
102	Evidence for sub-functionalization of tandemly duplicated XPB nucleotide excision repair genes in <i>Arabidopsis thaliana</i> . <i>Gene</i> , 2020, 754, 144818.	1.0	2
103	An Efficient Approach to Explore and Discriminate Anomalous Regions in Bacterial Genomes Based on Maximum Entropy. <i>Journal of Computational Biology</i> , 2017, 24, 1125-1133.	0.8	1
104	<i>Arabidopsis</i> -Based Dual-Layered Biological Network Analysis Elucidates Fully Modulated Pathways Related to Sugarcane Resistance on Biotrophic Pathogen Infection. <i>Frontiers in Plant Science</i> , 2021, 12, 707904.	1.7	0
105	Characterization of <i>Agrobacterium tumefaciens</i> Strains Isolated from Brazilian Plant Species. <i>American Journal of Plant Physiology</i> , 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. <i>Biota Neotropica</i> , 2012, 12, 19-21.	1.0	0
107	Shaping a Plant Genetics and Molecular Biology research community in Brazil. <i>Genetics and Molecular Biology</i> , 2017, 40, I-I.	0.6	0