

# Maike Stam

## List of Publications by Year in descending order

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33  
papers

2,734  
citations

304743

22  
h-index

454955

30  
g-index

37  
all docs

37  
docs citations

37  
times ranked

2989  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cis-regulatory sequences in plants: Their importance, discovery, and future challenges. <i>Plant Cell</i> , 2022, 34, 718-741.	6.6	125
2	CHROMOMETHYLTRANSFERASE3/KRYPTONITE maintains the <i>Sulfurea</i> paramutation in <i>Solanum lycopersicum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2112240119.	7.1	4
3	Maize E2F transcription factors. Expression, association to promoters of S-phase genes and interaction with the RBR1 protein in chromatin during seed germination. <i>Plant Science</i> , 2020, 296, 110491.	3.6	5
4	Analysis of 4C-seq data: A comparison of methods. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050001.	0.8	0
5	Identification of Key Tissue-Specific, Biological Processes by Integrating Enhancer Information in Maize Gene Regulatory Networks. <i>Frontiers in Genetics</i> , 2020, 11, 606285.	2.3	11
6	3D genome organization: a role for phase separation and loop extrusion?. <i>Current Opinion in Plant Biology</i> , 2019, 48, 36-46.	7.1	43
7	3C in Maize and Arabidopsis. <i>Methods in Molecular Biology</i> , 2018, 1675, 247-270.	0.9	7
8	Parental DNA Methylation States Are Associated with Heterosis in Epigenetic Hybrids. <i>Plant Physiology</i> , 2018, 176, 1627-1645.	4.8	93
9	Protocol for Chromatin Immunoprecipitation of Meiotic Stage-Specific Tomato Anthers. <i>Current Protocols in Plant Biology</i> , 2018, 3, e20074.	2.8	0
10	Generating Transgenic Plants with Single-copy Insertions Using BIBAC-GW Binary Vector. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	2
11	BIBAC-GW-based vectors for generating reporter lines for site-specific genome editing in planta. <i>Plasmid</i> , 2017, 89, 27-36.	1.4	3
12	A cautionary note on the use of chromosome conformation capture in plants. <i>Plant Methods</i> , 2017, 13, 101.	4.3	1
13	Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. <i>Genome Biology</i> , 2017, 18, 137.	8.8	134
14	Plant Enhancers: A Call for Discovery. <i>Trends in Plant Science</i> , 2016, 21, 974-987.	8.8	115
15	Accessible DNA and Relative Depletion of H3K9me2 at Maize Loci Undergoing RNA-Directed DNA Methylation. <i>Plant Cell</i> , 2015, 26, 4903-4917.	6.6	106
16	Cis-acting determinants of paramutation. <i>Seminars in Cell and Developmental Biology</i> , 2015, 44, 22-32.	5.0	29
17	Specific Tandem Repeats Are Sufficient for Paramutation-Induced Trans-Generational Silencing. <i>PLoS Genetics</i> , 2013, 9, e1003773.	3.5	48
18	3C Technologies in plants. <i>Methods</i> , 2012, 58, 204-211.	3.8	13

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19	The role of DNA methylation, nucleosome occupancy and histone modifications in paramutation. <i>Plant Journal</i> , 2010, 63, 366-378.	5.7	54
20	Paramutation: A Heritable Change in Gene Expression by Allelic Interactions In Trans. <i>Molecular Plant</i> , 2009, 2, 578-588.	8.3	36
21	Tissue- and Expression Level-Specific Chromatin Looping at Maize <i>b1</i> Epialleles. <i>Plant Cell</i> , 2009, 21, 832-842.	6.6	126
22	Studying physical chromatin interactions in plants using Chromosome Conformation Capture (3C). <i>Nature Protocols</i> , 2009, 4, 1216-1229.	12.0	85
23	Chromatin immunoprecipitation: optimization, quantitative analysis and data normalization. <i>Plant Methods</i> , 2007, 3, 11.	4.3	438
24	Paramutation: an encounter leaving a lasting impression. <i>Trends in Plant Science</i> , 2005, 10, 283-290.	8.8	48
25	Chromatin conversions: mechanisms and implications of paramutation. <i>Nature Reviews Genetics</i> , 2004, 5, 532-544.	16.3	200
26	Differential chromatin structure within a tandem array 100 kb upstream of the maize <i>b1</i> locus is associated with paramutation. <i>Genes and Development</i> , 2002, 16, 1906-1918.	5.9	243
27	The Regulatory Regions Required for <i>B</i> Paramutation and Expression Are Located Far Upstream of the Maize <i>b1</i> Transcribed Sequences. <i>Genetics</i> , 2002, 162, 917-930.	2.9	116
28	Distinct features of post-transcriptional gene silencing by antisense transgenes in single copy and inverted T-DNA repeat loci. <i>Plant Journal</i> , 2000, 21, 27-42.	5.7	85
29	Position-Dependent Methylation and Transcriptional Silencing of Transgenes in Inverted T-DNA Repeats: Implications for Posttranscriptional Silencing of Homologous Host Genes in Plants. <i>Molecular and Cellular Biology</i> , 1998, 18, 6165-6177.	2.3	138
30	Post-transcriptional silencing of chalcone synthase in <i>Petunia</i> by inverted transgene repeats. <i>Plant Journal</i> , 1997, 12, 63-82.	5.7	177
31	Developmentally regulated silencing and reactivation of tobacco chitinase transgene expression. <i>Plant Journal</i> , 1996, 10, 437-450.	5.7	109
32	Detection of single-copy genes and chromosome rearrangements in <i>Petunia hybrida</i> by fluorescence <i>in situ</i> hybridization. <i>Plant Journal</i> , 1996, 9, 767-774.	5.7	88
33	<i>cry IA(b)</i> transcript formation in tobacco is inefficient. <i>Plant Molecular Biology</i> , 1995, 28, 513-524.	3.9	46