

Reinhard Hehl

List of Publications by Year in descending order

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57
papers

4,433
citations

331259

21
h-index

155451

55
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59
all docs

59
docs citations

59
times ranked

6149
citing authors

#	ARTICLE	IF	CITATIONS
1	A dialogue-like cell communication mechanism is conserved in filamentous ascomycete fungi and mediates interspecies interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2112518119.	3.3	15
2	Unusual DNA-binding properties of the <i>Arabidopsis thaliana</i> WRKY50 transcription factor at target gene promoters. <i>Plant Cell Reports</i> , 2021, 40, 69-83.	2.8	5
3	A strong NF- κ B p65 responsive cis-regulatory sequence from <i>Arabidopsis thaliana</i> interacts with WRKY40. <i>Plant Cell Reports</i> , 2019, 38, 1139-1150.	2.8	6
4	Transcription factors involved in basal immunity in mammals and plants interact with the same MAMP-responsive cis-sequence from <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2018, 98, 565-578.	2.0	7
5	Combinatorial requirement of W- and WT-boxes in microbe-associated molecular pattern-responsive synthetic promoters. <i>Plant Cell Reports</i> , 2017, 36, 971-986.	2.8	16
6	From experiment-driven database analyses to database-driven experiments in <i>Arabidopsis thaliana</i> transcription factor research. <i>Plant Science</i> , 2017, 262, 141-147.	1.7	6
7	A cis-regulatory sequence from a short intergenic region gives rise to a strong microbe-associated molecular pattern-responsive synthetic promoter. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1155-1165.	1.0	1
8	Analysis of Microbe-Associated Molecular Pattern-Responsive Synthetic Promoters with the Parsley Protoplast System. <i>Methods in Molecular Biology</i> , 2016, 1482, 163-174.	0.4	17
9	Plant Synthetic Promoters. <i>Methods in Molecular Biology</i> , 2016, , .	0.4	3
10	Bioinformatic Identification of Conserved Cis-Sequences in Coregulated Genes. <i>Methods in Molecular Biology</i> , 2016, 1482, 233-245.	0.4	7
11	In Silico Expression Analysis. <i>Methods in Molecular Biology</i> , 2016, 1482, 247-257.	0.4	0
12	Boosting AthaMap Database Content with Data from Protein Binding Microarrays. <i>Plant and Cell Physiology</i> , 2016, 57, e4-e4.	1.5	29
13	Functional dissection of a strong and specific microbe-associated molecular pattern-responsive synthetic promoter. <i>Plant Biotechnology Journal</i> , 2016, 14, 61-71.	4.1	18
14	'In silico expression analysis', a novel PathoPlant web tool to identify abiotic and biotic stress conditions associated with specific cis-regulatory sequences. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau030-bau030.	1.4	17
15	Inducible expression of p50 from TMV for increased resistance to bacterial crown gall disease in tobacco. <i>Plant Molecular Biology</i> , 2014, 84, 111-123.	2.0	11
16	Identification of a novel type of WRKY transcription factor binding site in elicitor-responsive cis-sequences from <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2014, 84, 371-385.	2.0	55
17	Integrating bioinformatic resources to predict transcription factors interacting with cis-sequences conserved in co-regulated genes. <i>BMC Genomics</i> , 2014, 15, 317.	1.2	19
18	AthaMap Web Tools for the Analysis of Transcriptional and Posttranscriptional Regulation of Gene Expression in <i>Arabidopsis thaliana</i> . <i>Methods in Molecular Biology</i> , 2014, 1158, 139-156.	0.4	33

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19	Differential expression of the TMV resistance gene N prevents a hypersensitive response in seeds and during germination. <i>Planta</i> , 2013, 237, 909-915.	1.6	4
20	Integration of Bioinformatics and Synthetic Promoters Leads to the Discovery of Novel Elicitor-Responsive cis-Regulatory Sequences in Arabidopsis. <i>Plant Physiology</i> , 2012, 160, 178-191.	2.3	53
21	MicroRNA Targets, a new AthaMap web-tool for genome-wide identification of miRNA targets in Arabidopsis thaliana. <i>BioData Mining</i> , 2012, 5, 7.	2.2	23
22	Factors required for the high CO ₂ specificity of the anaerobically induced maize GapC4 promoter in transgenic tobacco. <i>Plant, Cell and Environment</i> , 2011, 34, 220-229.	2.8	3
23	Alternative splicing of the maize Ac transposase transcript in transgenic sugar beet (<i>Beta vulgaris</i> L.). <i>Plant Molecular Biology</i> , 2010, 74, 19-32.	2.0	8
24	AthaMap-assisted transcription factor target gene identification in Arabidopsis thaliana. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq034-baq034.	1.4	25
25	AthaMap, integrating transcriptional and post-transcriptional data. <i>Nucleic Acids Research</i> , 2009, 37, D983-D986.	6.5	51
26	Post-harvest regulated gene expression and splicing efficiency in storage roots of sugar beet (<i>Beta</i>). <i>Journal of Experimental Botany</i> , 2010, 61, 1077-1087.	1.6	7
27	Internet Resources for Gene Expression Analysis in Arabidopsis thaliana. <i>Current Genomics</i> , 2008, 9, 375-380.	0.7	12
28	AthaMap web tools for the analysis and identification of co-regulated genes. <i>Nucleic Acids Research</i> , 2007, 35, D857-D862.	6.5	48
29	PathoPlant(R): a platform for microarray expression data to analyze co-regulated genes involved in plant defense responses. <i>Nucleic Acids Research</i> , 2007, 35, D841-D845.	6.5	38
30	Taproot promoters cause tissue specific gene expression within the storage root of sugar beet. <i>Planta</i> , 2006, 224, 485-495.	1.6	18
31	AthaMap: from in silico data to real transcription factor binding sites. <i>In Silico Biology</i> , 2006, 6, 243-52.	0.4	20
32	AthaMap web tools for database-assisted identification of combinatorial cis-regulatory elements and the display of highly conserved transcription factor binding sites in Arabidopsis thaliana. <i>Nucleic Acids Research</i> , 2005, 33, W397-W402.	6.5	40
33	A fifth member of the tomato 1-aminocyclopropane-1-carboxylic acid (ACC) oxidase gene family harbours a leucine zipper and is anaerobically induced. <i>DNA Sequence</i> , 2005, 16, 80-82.	0.7	32
34	AthaMap: an online resource for in silico transcription factor binding sites in the Arabidopsis thaliana genome. <i>Nucleic Acids Research</i> , 2004, 32, 368D-372.	6.5	113
35	Functional dissection of a small anaerobically induced bZIP transcription factor from tomato. <i>FEBS Journal</i> , 2004, 271, 4534-4544.	0.2	17
36	A sugar beet chlorophyll a/b binding protein promoter void of G-box like elements confers strong and leaf specific reporter gene expression in transgenic sugar beet. <i>BMC Biotechnology</i> , 2004, 4, 31.	1.7	21

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37	PathoPlant: a database on plant-pathogen interactions. <i>In Silico Biology</i> , 2004, 4, 529-36.	0.4	21
38	Anaerobic induction of the maize GapC4 promoter in poplar leaves requires light and high CO ₂ . <i>Planta</i> , 2003, 218, 79-86.	1.6	7
39	TRANSFAC(R): transcriptional regulation, from patterns to profiles. <i>Nucleic Acids Research</i> , 2003, 31, 374-378.	6.5	1,825
40	Light-dependent Anaerobic Induction of the Maize Glyceraldehyde-3-Phosphate Dehydrogenase 4 (GapC4) Promoter in <i>Arabidopsis thaliana</i> and <i>Nicotiana tabacum</i> . <i>Annals of Botany</i> , 2003, 91, 149-154.	1.4	12
41	Isolation and molecular analysis of six taproot expressed genes from sugar beet. <i>Journal of Experimental Botany</i> , 2002, 53, 1533-1534.	2.4	13
42	Isolation and molecular analysis of six taproot expressed genes from sugar beet. <i>Journal of Experimental Botany</i> , 2002, 53, 1533-4.	2.4	6
43	Database-assisted promoter analysis. <i>Trends in Plant Science</i> , 2001, 6, 251-255.	4.3	44
44	The TATA box and a Myb binding site are essential for anaerobic expression of a maize GapC4 minimal promoter in tobacco. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2001, 1521, 120-125.	2.4	22
45	Anaerobiosis-specific interaction of tobacco nuclear factors with cis-regulatory sequences in the maize GapC4 promoter. <i>Plant Molecular Biology</i> , 2000, 43, 11-21.	2.0	13
46	TMV resistance gene N homologues are linked to <i>Synchytrium endobioticum</i> resistance in potato. <i>Theoretical and Applied Genetics</i> , 1999, 98, 379-386.	1.8	90
47	Induction of the Maize GapC4 Promoter in Transgenic Potato under Anaerobiosis and in <i>Erwinia carotovora</i> -Inoculated Tuber Tissue. <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 182-188.	1.4	6
48	A promoter for strong and ubiquitous anaerobic gene expression in tobacco. <i>Plant Journal</i> , 1996, 10, 175-183.	2.8	16
49	Inhibition of CAT enzyme activity in <i>Arabidopsis thaliana</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 1996, 45, 31-36.	1.2	1
50	The maize GapC4 promoter confers anaerobic reporter gene expression and shows homology to the maize anthocyanin regulatory locus C1. <i>Plant Molecular Biology</i> , 1995, 29, 1293-1298.	2.0	16
51	Transposon tagging in heterologous host plants. <i>Trends in Genetics</i> , 1994, 10, 385-386.	2.9	16
52	The product of the tobacco mosaic virus resistance gene N: Similarity to toll and the interleukin-1 receptor. <i>Cell</i> , 1994, 78, 1101-1115.	13.5	1,272
53	Structural analysis of Tam3, a transposable element from <i>Antirrhinum majus</i> , reveals homologies to the Ac element from maize. <i>Plant Molecular Biology</i> , 1991, 16, 369-371.	2.0	85
54	Induced transposition of Ds by a stable Ac in crosses of transgenic tobacco plants. <i>Molecular Genetics and Genomics</i> , 1989, 217, 53-59.	2.4	73

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55	Molecular analysis of paramutant plants of <i>Antirrhinum majus</i> and the involvement of transposable elements. <i>Molecular Genetics and Genomics</i> , 1987, 209, 499-507.	2.4	44
56	Interaction between the Tam1 and Tam2 transposable elements of <i>Antirrhinum majus</i> . <i>Molecular Genetics and Genomics</i> , 1987, 207, 47-53.	2.4	29
57	Isolation and Analysis of Gene Regulatory Sequences. , 0, , .		2