

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
g-index

59
all docs

59
docs citations

59
times ranked

6149
citing authors

#	ARTICLE	IF	CITATIONS
1	TRANSFAC(R): transcriptional regulation, from patterns to profiles. <i>Nucleic Acids Research</i> , 2003, 31, 374-378.	6.5	1,825
2	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
3	AthaMap: an online resource for in silico transcription factor binding sites in the <i>Arabidopsis thaliana</i> genome. <i>Nucleic Acids Research</i> , 2004, 32, 368D-372.	6.5	113
4	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
5	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
6	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
7	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
8	Integration of Bioinformatics and Synthetic Promoters Leads to the Discovery of Novel Elicitor-Responsive cis-Regulatory Sequences in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2012, 160, 178-191.	2.3	53
9	AthaMap, integrating transcriptional and post-transcriptional data. <i>Nucleic Acids Research</i> , 2009, 37, D983-D986.	6.5	51
10	AthaMap web tools for the analysis and identification of co-regulated genes. <i>Nucleic Acids Research</i> , 2007, 35, D857-D862.	6.5	48
11	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
12	Database-assisted promoter analysis. <i>Trends in Plant Science</i> , 2001, 6, 251-255.	4.3	44
13	AthaMap web tools for database-assisted identification of combinatorial cis-regulatory elements and the display of highly conserved transcription factor binding sites in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2005, 33, W397-W402.	6.5	40
14	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
15	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
16	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
17	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
18	Boosting AthaMap Database Content with Data from Protein Binding Microarrays. <i>Plant and Cell Physiology</i> , 2016, 57, e4-e4.	1.5	29

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19	AthaMap-assisted transcription factor target gene identification in <i>Arabidopsis thaliana</i> . Database: the Journal of Biological Databases and Curation, 2010, 2010, baq034-baq034.	1.4	25
20	â€œMicroRNA Targetsâ€™, a new AthaMap web-tool for genome-wide identification of miRNA targets in <i>Arabidopsis thaliana</i> . BioData Mining, 2012, 5, 7.	2.2	23
21	The TATA box and a Myb binding site are essential for anaerobic expression of a maize GapC4 minimal promoter in tobacco. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2001, 1521, 120-125.	2.4	22
22	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. BMC Biotechnology, 2004, 4, 31.	1.7	21
23	PathoPlant: a database on plant-pathogen interactions. In Silico Biology, 2004, 4, 529-36.	0.4	21
24	AthaMap: from in silico data to real transcription factor binding sites. In Silico Biology, 2006, 6, 243-52.	0.4	20
25	Integrating bioinformatic resources to predict transcription factors interacting with cis-sequences conserved in co-regulated genes. BMC Genomics, 2014, 15, 317.	1.2	19
26	Taproot promoters cause tissue specific gene expression within the storage root of sugar beet. Planta, 2006, 224, 485-495.	1.6	18
27	Functional dissection of a strong and specific microbe-associated molecular pattern-responsive synthetic promoter. Plant Biotechnology Journal, 2016, 14, 61-71.	4.1	18
28	Functional dissection of a small anaerobically induced bZIP transcription factor from tomato. FEBS Journal, 2004, 271, 4534-4544.	0.2	17
29	'In silico expression analysis', a novel PathoPlant web tool to identify abiotic and biotic stress conditions associated with specific cis-regulatory sequences. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau030-bau030.	1.4	17
30	Analysis of Microbe-Associated Molecular Pattern-Responsive Synthetic Promoters with the Parsley Protoplast System. Methods in Molecular Biology, 2016, 1482, 163-174.	0.4	17
31	Transposon tagging in heterologous host plants. Trends in Genetics, 1994, 10, 385-386.	2.9	16
32	The maize GapC4 promoter confers anaerobic reporter gene expression and shows homology to the maize anthocyanin regulatory locus C1. Plant Molecular Biology, 1995, 29, 1293-1298.	2.0	16
33	A promoter for strong and ubiquitous anaerobic gene expression in tobacco. Plant Journal, 1996, 10, 175-183.	2.8	16
34	Combinatorial requirement of W- and WT-boxes in microbe-associated molecular pattern-responsive synthetic promoters. Plant Cell Reports, 2017, 36, 971-986.	2.8	16
35	A dialogue-like cell communication mechanism is conserved in filamentous ascomycete fungi and mediates interspecies interactions. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2112518119.	3.3	15
36	Anaerobiosis-specific interaction of tobacco nuclear factors with cis-regulatory sequences in the maize GapC4 promoter. Plant Molecular Biology, 2000, 43, 11-21.	2.0	13

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37	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
38	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
39	Internet Resources for Gene Expression Analysis in <i>Arabidopsis thaliana</i> . <i>Current Genomics</i> , 2008, 9, 375-380.	0.7	12
40	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
41	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
42	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
43	Post-harvest regulated gene expression and splicing efficiency in storage roots of sugar beet (<i>Beta</i>) Tj ETQq1 1 0.784314 rgBJ /Overlo	1.6	7
44	Bioinformatic Identification of Conserved Cis-Sequences in Coregulated Genes. <i>Methods in Molecular Biology</i> , 2016, 1482, 233-245.	0.4	7
45	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
46	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
47	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
48	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
49	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
50	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
51	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
52	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
53	Plant Synthetic Promoters. <i>Methods in Molecular Biology</i> , 2016, , .	0.4	3
54	Isolation and Analysis of Gene Regulatory Sequences. , 0, , .		2

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55	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
56	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
57	In Silico Expression Analysis. <i>Methods in Molecular Biology</i> , 2016, 1482, 247-257.	0.4	0