

# Reinhard Hehl

## List of Publications by Year in descending order

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57  
papers

4,433  
citations

331670

21  
h-index

155660

55  
g-index

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.	7.1	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.	5.6	5
3	A strong NF- $\kappa$ B p65 responsive cis-regulatory sequence from <i>Arabidopsis thaliana</i> interacts with WRKY40. <i>Plant Cell Reports</i> , 2019, 38, 1139-1150.	5.6	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.	3.9	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.	5.6	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.	3.6	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.	2.1	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.	0.9	17
9	Plant Synthetic Promoters. <i>Methods in Molecular Biology</i> , 2016, , .	0.9	3
10	Bioinformatic Identification of Conserved Cis-Sequences in Coregulated Genes. <i>Methods in Molecular Biology</i> , 2016, 1482, 233-245.	0.9	7
11	In Silico Expression Analysis. <i>Methods in Molecular Biology</i> , 2016, 1482, 247-257.	0.9	0
12	Boosting AthaMap Database Content with Data from Protein Binding Microarrays. <i>Plant and Cell Physiology</i> , 2016, 57, e4-e4.	3.1	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.	8.3	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.	3.0	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.	3.9	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.	3.9	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.	2.8	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.	0.9	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.	3.2	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.	4.8	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.	4.0	23
22	Factors required for the high CO <sub>2</sub> specificity of the anaerobically induced maize GapC4 promoter in transgenic tobacco. <i>Plant, Cell and Environment</i> , 2011, 34, 220-229.	5.7	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.	3.9	8
24	AthaMap-assisted transcription factor target gene identification in Arabidopsis thaliana. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq034-baq034.	3.0	25
25	AthaMap, integrating transcriptional and post-transcriptional data. <i>Nucleic Acids Research</i> , 2009, 37, D983-D986.	14.5	51
26	Post-harvest regulated gene expression and splicing efficiency in storage roots of sugar beet ( <i>Beta</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.2	7
27	Internet Resources for Gene Expression Analysis in Arabidopsis thaliana. <i>Current Genomics</i> , 2008, 9, 375-380.	1.6	12
28	AthaMap web tools for the analysis and identification of co-regulated genes. <i>Nucleic Acids Research</i> , 2007, 35, D857-D862.	14.5	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.	14.5	38
30	Taproot promoters cause tissue specific gene expression within the storage root of sugar beet. <i>Planta</i> , 2006, 224, 485-495.	3.2	18
31	AthaMap: from in silico data to real transcription factor binding sites. <i>In Silico Biology</i> , 2006, 6, 243-52.	0.9	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.	14.5	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.	14.5	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.	3.3	21

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37	PathoPlant: a database on plant-pathogen interactions. In Silico Biology, 2004, 4, 529-36.	0.9	21
38	Anaerobic induction of the maize GapC4 promoter in poplar leaves requires light and high CO <sub>2</sub> . Planta, 2003, 218, 79-86.	3.2	7
39	TRANSFAC(R): transcriptional regulation, from patterns to profiles. Nucleic Acids Research, 2003, 31, 374-378.	14.5	1,825
40	Light-dependent Anaerobic Induction of the Maize Glyceraldehyde-3-Phosphate Dehydrogenase 4 (GapC4) Promoter in Arabidopsis thaliana and Nicotiana tabacum. Annals of Botany, 2003, 91, 149-154.	2.9	12
41	Isolation and molecular analysis of six taproot expressed genes from sugar beet. Journal of Experimental Botany, 2002, 53, 1533-1534.	4.8	13
42	Isolation and molecular analysis of six taproot expressed genes from sugar beet. Journal of Experimental Botany, 2002, 53, 1533-4.	4.8	6
43	Database-assisted promoter analysis. Trends in Plant Science, 2001, 6, 251-255.	8.8	44
44	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
45	Anaerobiosis-specific interaction of tobacco nuclear factors with cis-regulatory sequences in the maize GapC4 promoter. Plant Molecular Biology, 2000, 43, 11-21.	3.9	13
46	TMV resistance gene N homologues are linked to Synchytrium endobioticum resistance in potato. Theoretical and Applied Genetics, 1999, 98, 379-386.	3.6	90
47	Induction of the Maize GapC4 Promoter in Transgenic Potato under Anaerobiosis and in Erwinia carotovora-Inoculated Tuber Tissue. Molecular Plant-Microbe Interactions, 1999, 12, 182-188.	2.6	6
48	A promoter for strong and ubiquitous anaerobic gene expression in tobacco. Plant Journal, 1996, 10, 175-183.	5.7	16
49	Inhibition of CAT enzyme activity in Arabidopsis thaliana. Plant Cell, Tissue and Organ Culture, 1996, 45, 31-36.	2.3	1
50	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.	3.9	16
51	Transposon tagging in heterologous host plants. Trends in Genetics, 1994, 10, 385-386.	6.7	16
52	The product of the tobacco mosaic virus resistance gene N: Similarity to toll and the interleukin-1 receptor. Cell, 1994, 78, 1101-1115.	28.9	1,272
53	Structural analysis of Tam3, a transposable element from Antirrhinum majus, reveals homologies to the Ac element from maize. Plant Molecular Biology, 1991, 16, 369-371.	3.9	85
54	Induced transposition of Ds by a stable Ac in crosses of transgenic tobacco plants. Molecular Genetics and Genomics, 1989, 217, 53-59.	2.4	73

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