Reidunn B Aalen

List of Publications by Year
in descending order

69 papers	4,503 citations	87723 38 h-index	106150 65 g-index
72 all docs	72 docs citations	72 times ranked	4338 citing authors

#	Article	IF	Citations
1	Editorial: Peptide Signaling in Plants. Frontiers in Plant Science, 2022, 13, 843918.	1.7	1
2	The sequenced genomes of nonflowering land plants reveal the innovative evolutionary history of peptide signaling. Plant Cell, 2021, 33, 2915-2934.	3.1	30
3	The Arabidopsis (ASHH2) CW domain binds monomethylated K4 of the histone H3 tail through conformational selection. FEBS Journal, 2020, 287, 4458-4480.	2.2	4
4	Control of Organ Abscission and Other Cell Separation Processes by Evolutionary Conserved Peptide Signaling. Plants, 2019, 8, 225.	1.6	31
5	The dynamics of root cap sloughing in Arabidopsis is regulated by peptide signalling. Nature Plants, 2018, 4, 596-604.	4.7	62
6	In Silico Prediction of Ligand-Binding Sites of Plant Receptor Kinases Using Conservation Mapping. Methods in Molecular Biology, 2017, 1621, 93-105.	0.4	2
7	Conservation of the abscission signaling peptide IDA during Angiosperm evolution: withstanding genome duplications and gain and loss of the receptors HAE/HSL2. Frontiers in Plant Science, 2015, 6, 931.	1.7	50
8	Antagonistic peptide technology for functional dissection of CLE peptides revisited. Journal of Experimental Botany, 2015, 66, 5367-5374.	2.4	27
9	The<i>IDA/IDA-LIKE</i>and<i>PIP/PIP-LIKE</i>gene families in<i>Arabidopsis</i>: phylogenetic relationship, expression patterns, and transcriptional effect of the PIPL3 peptide. Journal of Experimental Botany, 2015, 66, 5351-5365.	2.4	72
10	The ASH1-RELATED3 SET-Domain Protein Controls Cell Division Competence of the Meristem and the Quiescent Center of the Arabidopsis Primary Root Â Â. Plant Physiology, 2014, 166, 632-643.	2.3	35
11	The <i>Arabidopsis</i> Histone Methyltransferase SUVR4 Binds Ubiquitin via a Domain with a Four-Helix Bundle Structure. Biochemistry, 2014, 53, 2091-2100.	1.2	7
12	Tools and Strategies to Match Peptide-Ligand Receptor Pairs. Plant Cell, 2014, 26, 1838-1847.	3.1	98
13	NEVERSHED and INFLORESCENCE DEFICIENT IN ABSCISSION are differentially required for cell expansion and cell separation during floral organ abscission in Arabidopsis thaliana. Journal of Experimental Botany, 2013, 64, 5345-5357.	2.4	39
14	IDA/IDL. , 2013, , 24-30.		1
15	IDA: a peptide ligand regulating cell separation processes in Arabidopsis. Journal of Experimental Botany, 2013, 64, 5253-5261.	2.4	47
16	Maturing peptides open for communication. Journal of Experimental Botany, 2013, 64, 5231-5235.	2.4	6
17	Floral organ abscission peptide IDA and its HAE/HSL2 receptors control cell separation during lateral root emergence. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5235-5240.	3.3	213
18	KNAT1, KNAT2 and KNAT6 act downstream in the IDA-HAE/HSL2 signaling pathway to regulate floral organ abscission. Plant Signaling and Behavior, 2012, 7, 135-138.	1.2	16

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19	Tackling Drought Stress: RECEPTOR-LIKE KINASES Present New Approaches. Plant Cell, 2012, 24, 2262-2278.	3.1	155
20	Receptor Ligands in Development. Signaling and Communication in Plants, 2012, , 195-226.	0.5	8
21	Methods to Identify New Partners of Plant Signaling Peptides. Signaling and Communication in Plants, 2012, , 241-256.	0.5	1
22	SET domain proteins in plant development. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2011, 1809, 407-420.	0.9	99
23	The SUVR4 Histone Lysine Methyltransferase Binds Ubiquitin and Converts H3K9me1 to H3K9me3 on Transposon Chromatin in Arabidopsis. PLoS Genetics, 2011, 7, e1001325.	1.5	49
24	The CW domain, a new histone recognition module in chromatin proteins. EMBO Journal, 2011, 30, 1939-1952.	3.5	105
25	Genome-Wide Transcript Profiling of Endosperm without Paternal Contribution Identifies Parent-of-Originâ€"Dependent Regulation of AGAMOUS-LIKE36. PLoS Genetics, 2011, 7, e1001303.	1.5	65
26	<i>Arabidopsis</i> Class I KNOTTED-Like Homeobox Proteins Act Downstream in the IDA-HAE/HSL2 Floral Abscission Signaling Pathway. Plant Cell, 2011, 23, 2553-2567.	3.1	123
27	The ASH1 HOMOLOG 2 (ASHH2) Histone H3 Methyltransferase Is Required for Ovule and Anther Development in Arabidopsis. PLoS ONE, 2009, 4, e7817.	1.1	110
28	<i>AtMBD8</i> is involved in control of flowering time in the C24 ecotype of <i>Arabidopsis thaliana</i>. Physiologia Plantarum, 2009, 136, 110-126.	2.6	20
29	Plant peptides in signalling: looking for new partners. Trends in Plant Science, 2009, 14, 255-263.	4.3	121
30	The Arabidopsis SET-domain protein ASHR3 is involved in stamen development and interacts with the bHLH transcription factor ABORTED MICROSPORES (AMS). Plant Molecular Biology, 2008, 66, 47-59.	2.0	69
31	The<i>BLADE-ON-PETIOLE</i>genes are essential for abscission zone formation in<i>Arabidopsis</i>. Development (Cambridge), 2008, 135, 1537-1546.	1.2	186
32	Identification of a putative receptor-ligand pair controlling cell separation in plants. Plant Signaling and Behavior, 2008, 3, 1109-1110.	1.2	13
33	The EPIP Peptide of INFLORESCENCE DEFICIENT IN ABSCISSION Is Sufficient to Induce Abscission in<i>Arabidopsis</i>through the Receptor-Like Kinases HAESA and HAESA-LIKE2 Â. Plant Cell, 2008, 20, 1805-1817.	3.1	275
34	Drosophila dSet2 functions in H3-K36 methylation and is required for development. Biochemical and Biophysical Research Communications, 2007, 359, 784-789.	1.0	43
35	Overexpression of INFLORESCENCE DEFICIENT IN ABSCISSION Activates Cell Separation in Vestigial Abscission Zones in Arabidopsis. Plant Cell, 2006, 18, 1467-1476.	3.1	148
36	An inverted repeat transgene with a structure that cannot generate double-stranded RNA, suffers silencing independent of DNA methylation. Transgenic Research, 2006, 15, 489-500.	1.3	8

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37	The Drosophila SET domain encoding gene dEset is essential for proper development. Hereditas, 2006, 143, 177-188.	0.5	25
38	The Drosophila G9a gene encodes a multi-catalytic histone methyltransferase required for normal development. Nucleic Acids Research, 2006, 34, 4609-4621.	6.5	54
39	The Arabidopsis SUVR4 protein is a nucleolar histone methyltransferase with preference for monomethylated H3K9. Nucleic Acids Research, 2006, 34, 5461-5470.	6.5	55
40	Ethylene-dependent and -independent pathways controlling floral abscission are revealed to converge using promoter::reporter gene constructs in the ida abscission mutant. Journal of Experimental Botany, 2006, 57, 3627-3637.	2.4	62
41	Transgene silencing may be mediated by aberrant sense promoter sequence transcripts generated from cryptic promoters. Cellular and Molecular Life Sciences, 2005, 62, 3080-3091.	2.4	13
42	Molecular analysis of Arabidopsis endosperm and embryo promoter trap lines: reporter-gene expression can result from T-DNA insertions in antisense orientation, in introns and in intergenic regions, in addition to sense insertion at the 5â€² end of genes. Journal of Experimental Botany, 2005, 56, 2495-2505.	2.4	20
43	ABI3 mediates expression of the peroxiredoxin antioxidant AtPER1 gene and induction by oxidative stress. Plant Molecular Biology, 2003, 53, 313-326.	2.0	45
44	Ten members of the Arabidopsis gene family encoding methyl-CpG-binding domain proteins are transcriptionally active and at least one, AtMBD11, is crucial for normal development. Nucleic Acids Research, 2003, 31, 5291-5304.	6.5	56
45	Isolation of GUS marker lines for genes expressed in Arabidopsis endosperm, embryo and maternal tissues. Journal of Experimental Botany, 2003, 54, 279-290.	2.4	17
46	Seed 1-Cysteine Peroxiredoxin Antioxidants Are Not Involved in Dormancy, But Contribute to Inhibition of Germination during Stress. Plant Physiology, 2003, 133, 1148-1157.	2.3	116
47	INFLORESCENCE DEFICIENT IN ABSCISSION Controls Floral Organ Abscission in Arabidopsis and Identifies a Novel Family of Putative Ligands in Plants. Plant Cell, 2003, 15, 2296-2307.	3.1	340
48	Analyses of single-copy Arabidopsis T-DNA-transformed lines show that the presence of vector backbone sequences, short inverted repeats and DNA methylation is not sufficient or necessary for the induction of transgene silencing. Nucleic Acids Research, 2002, 30, 4556-4566.	6.5	59
49	A human CpG island randomly inserted into a plant genome is protected from methylation. Transgenic Research, 2002, 11, 133-142.	1.3	9
50	Stability of barley aleurone transcripts: Dependence on protein synthesis, influence of the starchy endosperm and destabilization by GA3. Physiologia Plantarum, 2001, 112, 403-413.	2.6	11
51	The frequency of silencing in Arabidopsis thaliana varies highly between progeny of siblings and can be influenced by environmental factors. Transgenic Research, 2001, 10, 53-67.	1.3	48
52	The Arabidopsis thaliana genome contains at least 29 active genes encoding SET domain proteins that can be assigned to four evolutionarily conserved classes. Nucleic Acids Research, 2001, 29, 4319-4333.	6.5	299
53	Peroxiredoxin antioxidants in seed physiology. Seed Science Research, 1999, 9, 285-295.	0.8	56
54	The dormancy-related peroxiredoxin anti-oxidant, PER1, is localized to the nucleus of barley embryo and aleurone cells. Plant Journal, 1999, 19, 1-8.	2.8	163

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55	The expression of a peroxiredoxin antioxidant gene, AtPer1, in Arabidopsis thaliana is seed-specific and related to dormancy. Plant Molecular Biology, 1998, 36, 833-845.	2.0	101
56	EcoR II is an Unreliable Enzyme for Studies of CpNpG Methylation in shape Arabidopsis thaliana. Plant Molecular Biology Reporter, 1998, 16, 19-32.	1.0	1
57	Identification of sequence homology between the internal hydrophilic repeated motifs of Group 1 late-embryogenesis-abundant proteinsin plants and hydrophilic repeats of the general stress protein GsiB of Bacillus subtilis. Planta, 1998, 206, 476-478.	1.6	69
58	Differential regulation of the barley (Hordeum vulgare) transcripts B22E and B12D in mature aleurone layers. Physiologia Plantarum, 1998, 102, 337-345.	2.6	18
59	A peroxiredoxin antioxidant is encoded by a dormancy-related gene,Per1, expressed during late development in the aleurone and embryo of barley grains. Plant Molecular Biology, 1996, 31, 1205-1216.	2.0	135
60	The transcripts encoding two oleosin isoforms are both present in the aleurone and in the embryo of barley (Hordeum vulgare L.) seeds. Plant Molecular Biology, 1995, 28, 583-588.	2.0	32
61	Transcripts encoding an oleosin and a dormancy-related protein are present in both the aleurone layer and the embryo of developing barley (Hordeum vulgare L.) seeds. Plant Journal, 1994, 5, 385-396.	2.8	114
62	Homology between cryptic plasmid from <i>Neisseria gonorrhoeae</i> and genomic DNA from <i>Neisseria meningitidis</i>. Apmis, 1993, 101, 201-206.	0.9	1
63	PCR amplification and sequences of cDNA clones for the small and large subunits of ADP-glucose pyrophosphorylase from barley tissues. Plant Molecular Biology, 1992, 19, 381-389.	2.0	72
64	Primary structure of a novel barley gene differentially expressed in immature aleurone layers. Molecular Genetics and Genomics, 1991, 228, 9-16.	2.4	40
65	Cell-autonomous behavior of the rolC gene of Agrobacterium rhizogenes during leaf development: a visual assay for transposon excision in transgenic plants.. Plant Cell, 1989, 1, 1157-1164.	3.1	68
66	Barley aleurone cell development: molecular cloning of aleurone-specific cDNAs from immature grains. Plant Molecular Biology, 1989, 12, 285-293.	2.0	45
67	Subcellular localization of proteins encoded by the phenotypically cryptic plasmid of Neisseria gonorrhoeae: biological evidence for outer membrane association of the cppB gene product. Molecular Microbiology, 1989, 3, 1433-1439.	1.2	1
68	MOLECULAR CHARACTERIZATION AND COMPARISON OF PLASMID CONTENT IN SEVEN DIFFERENT STRAINS OF <i>NEISSERIA GONORRHOEAE</i>. Acta Pathologica, Microbiologica, Et Immunologica Scandinavica Section B, Microbiology, 1987, 95B, 13-21.	0.1	8
69	Polypeptides encoded by cryptic plasmids from Neisseria gonorrhoeae. Plasmid, 1985, 14, 209-216.	0.4	8