

Frank Hochholdinger

List of Publications by Year in descending order

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108
papers

7,882
citations

41258

49
h-index

58464

82
g-index

114
all docs

114
docs citations

114
times ranked

6647
citing authors

#	ARTICLE	IF	CITATIONS
1	From weeds to crops: genetic analysis of root development in cereals. Trends in Plant Science, 2004, 9, 42-48.	4.3	313
2	Towards the molecular basis of heterosis. Trends in Plant Science, 2007, 12, 427-432.	4.3	291
3	An Exocyst Complex Functions in Plant Cell Growth in Arabidopsis and Tobacco. Plant Cell, 2008, 20, 1330-1345.	3.1	280
4	The maize (<i>Zea mays</i> L.) RTCS gene encodes a LOB domain protein that is a key regulator of embryonic seminal and post-embryonic shoot-borne root initiation. Plant Journal, 2007, 50, 649-659.	2.8	259
5	Plant flavones enrich rhizosphere Oxalobacteraceae to improve maize performance under nitrogen deprivation. Nature Plants, 2021, 7, 481-499.	4.7	247
6	Genetic and genomic dissection of maize root development and architecture. Current Opinion in Plant Biology, 2009, 12, 172-177.	3.5	230
7	Genetic Dissection of Root Formation in Maize (<i>Zea mays</i>) Reveals Root-type Specific Developmental Programmes. Annals of Botany, 2004, 93, 359-368.	1.4	226
8	Conserved and diverse mechanisms in root development. Current Opinion in Plant Biology, 2008, 11, 70-74.	3.5	188
9	The maize (<i>Zea mays</i> L.) <i>roothairless3</i> gene encodes a putative GPI-anchored, monocot-specific, COBRA-like protein that significantly affects grain yield. Plant Journal, 2008, 54, 888-898.	2.8	185
10	The <i>roothairless1</i> Gene of Maize Encodes a Homolog of <i>sec3</i> , Which Is Involved in Polar Exocytosis. Plant Physiology, 2005, 138, 1637-1643.	2.3	183
11	Isolation, Characterization, and Pericycle-Specific Transcriptome Analyses of the Novel Maize Lateral and Seminal Root Initiation Mutant <i>rum1</i> . Plant Physiology, 2005, 139, 1255-1267.	2.3	179
12	Defining the boundaries: structure and function of LOB domain proteins. Trends in Plant Science, 2011, 16, 47-52.	4.3	173
13	Isolation and characterization of <i>rtcs</i> , a maize mutant deficient in the formation of nodal roots. Plant Journal, 1996, 10, 845-857.	2.8	163
14	Complementation contributes to transcriptome complexity in maize (<i>Zea mays</i> L.) hybrids relative to their inbred parents. Genome Research, 2012, 22, 2445-2454.	2.4	154
15	Genetic Control of Root System Development in Maize. Trends in Plant Science, 2018, 23, 79-88.	4.3	148
16	Transcriptomic and Proteomic Analyses of Pericycle Cells of the Maize Primary Root. Plant Physiology, 2007, 145, 575-588.	2.3	144
17	Analyzing Lateral Root Development: How to Move Forward. Plant Cell, 2012, 24, 15-20.	3.1	125
18	LOB Domain Proteins: Beyond Lateral Organ Boundaries. Trends in Plant Science, 2016, 21, 159-167.	4.3	124

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19	<i>Rootless5</i> , which functions in maize (<i>Zea mays</i> L.) root hair initiation and elongation encodes a monocot-specific NADPH oxidase. <i>Plant Journal</i> , 2014, 79, 729-740.	2.8	118
20	Comparison of Maize (<i>Zea mays</i> L.) F1-Hybrid and Parental Inbred Line Primary Root Transcriptomes Suggests Organ-Specific Patterns of Nonadditive Gene Expression and Conserved Expression Trends. <i>Genetics</i> , 2008, 179, 1275-1283.	1.2	111
21	Grasses suppress shoot-borne roots to conserve water during drought. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8861-8866.	3.3	111
22	<i>Rootless with undetectable meristem 1</i> encodes a monocot-specific AUX/IAA protein that controls embryonic seminal and post-embryonic lateral root initiation in maize. <i>Plant Journal</i> , 2011, 66, 341-353.	2.8	110
23	Genetic Control of Lateral Root Formation in Cereals. <i>Trends in Plant Science</i> , 2016, 21, 951-961.	4.3	107
24	Manifestation of heterosis during early maize (<i>Zea mays</i> L.) root development. <i>Theoretical and Applied Genetics</i> , 2006, 112, 421-429.	1.8	104
25	Heterosis in plants. <i>Current Biology</i> , 2018, 28, R1089-R1092.	1.8	103
26	Phenotypic plasticity of the maize root system in response to heterogeneous nitrogen availability. <i>Planta</i> , 2014, 240, 667-678.	1.6	95
27	Auxin Immunolocalization Implicates Vesicular Neurotransmitter-Like Mode of Polar Auxin Transport in Root Apices. <i>Plant Signaling and Behavior</i> , 2006, 1, 122-133.	1.2	91
28	The Maize Root System: Morphology, Anatomy, and Genetics. , 2009, , 145-160.		89
29	Osmotic stress enhances suberization of apoplastic barriers in barley seminal roots: analysis of chemical, transcriptomic and physiological responses. <i>New Phytologist</i> , 2019, 221, 180-194.	3.5	89
30	The <i>Gibberellic Acid Stimulated-Like</i> Gene Family in Maize and Its Role in Lateral Root Development. <i>Plant Physiology</i> , 2009, 152, 356-365.	2.3	88
31	Early post-embryonic root formation is specifically affected in the maize mutant <i>lrt1</i> . <i>Plant Journal</i> , 1998, 16, 247-255.	2.8	85
32	Molecular dissection of heterosis manifestation during early maize root development. <i>Theoretical and Applied Genetics</i> , 2010, 120, 383-388.	1.8	84
33	European maize genomes highlight intraspecies variation in repeat and gene content. <i>Nature Genetics</i> , 2020, 52, 950-957.	9.4	84
34	Global expression profiling applied to plant development. <i>Current Opinion in Plant Biology</i> , 2004, 7, 50-56.	3.5	81
35	Nonsynthetic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948.	3.1	80
36	Root type and soil phosphate determine the taxonomic landscape of colonizing fungi and the transcriptome of field-grown maize roots. <i>New Phytologist</i> , 2018, 217, 1240-1253.	3.5	80

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37	Extensive tissue-specific transcriptomic plasticity in maize primary roots upon water deficit. <i>Journal of Experimental Botany</i> , 2016, 67, 1095-1107.	2.4	78
38	Transcriptomic and anatomical complexity of primary, seminal, and crown roots highlight root type-specific functional diversity in maize (<i>Zea mays</i> L.). <i>Journal of Experimental Botany</i> , 2016, 67, 1123-1135.	2.4	76
39	Cooperative action of the paralogous maize lateral organ boundaries (LOB) domain proteins RTCS and RTCL in shoot-borne root formation. <i>New Phytologist</i> , 2015, 207, 1123-1133.	3.5	75
40	LATERAL ROOT PRIMORDIA 1 of maize acts as a transcriptional activator in auxin signalling downstream of the Aux/IAA gene rootless with undetectable meristem 1. <i>Journal of Experimental Botany</i> , 2015, 66, 3855-3863.	2.4	71
41	Transcriptomic complexity in young maize primary roots in response to low water potentials. <i>BMC Genomics</i> , 2014, 15, 741.	1.2	69
42	The Aux/IAA gene rum1 involved in seminal and lateral root formation controls vascular patterning in maize (<i>Zea mays</i> L.) primary roots. <i>Journal of Experimental Botany</i> , 2014, 65, 4919-4930.	2.4	69
43	A High-Resolution Tissue-Specific Proteome and Phosphoproteome Atlas of Maize Primary Roots Reveals Functional Gradients along the Root Axes. <i>Plant Physiology</i> , 2015, 168, 233-246.	2.3	64
44	Comparative proteome analyses of maize (<i>Zea mays</i> L.) primary roots prior to lateral root initiation reveal differential protein expression in the lateral root initiation mutant rum1. <i>Proteomics</i> , 2006, 6, 4300-4308.	1.3	58
45	Analysis of nonadditive protein accumulation in young primary roots of a maize (<i>Zea mays</i> L.) mutant. <i>Journal of Experimental Botany</i> , 2015, 66, 3882-3894.	1.3	57
46	Shared Genetic Control of Root System Architecture between <i>Zea mays</i> and <i>Sorghum bicolor</i> . <i>Plant Physiology</i> , 2020, 182, 977-991.	2.3	57
47	Assembly Patterns of the Rhizosphere Microbiome Along the Longitudinal Root Axis of Maize (<i>Zea mays</i> L.). <i>Journal of Experimental Botany</i> , 2020, 71, 1000-1010.	1.5	57
48	Specification of Cortical Parenchyma and Stele of Maize Primary Roots by Asymmetric Levels of Auxin, Cytokinin, and Cytokinin-Regulated Proteins. <i>Plant Physiology</i> , 2009, 152, 4-18.	2.3	56
49	Proteomic analysis of shoot-borne root initiation in maize (<i>Zea mays</i> L.). <i>Proteomics</i> , 2006, 6, 2530-2541.	1.3	55
50	Cell Type-Specific Gene Expression Analyses by RNA Sequencing Reveal Local High Nitrate-Triggered Lateral Root Initiation in Shoot-Borne Roots of Maize by Modulating Auxin-Related Cell Cycle Regulation. <i>Plant Physiology</i> , 2015, 169, 690-704.	2.3	55
51	Cooperative Action of SLR1 and SLR2 Is Required for Lateral Root-Specific Cell Elongation in Maize. <i>Plant Physiology</i> , 2001, 125, 1529-1539.	2.3	54
52	Molecular interactions of ROOTLESS CONCERNING CROWN AND SEMINAL ROOTS, a LOB domain protein regulating shoot-borne root initiation in maize (<i>Zea mays</i> L.). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 1542-1551.	1.8	54
53	Genotypic variation for root architecture traits in seedlings of maize (<i>Zea mays</i> L.) inbred lines. <i>Plant Breeding</i> , 2012, 131, 465-478.	1.0	54
54	Root Type-Specific Reprogramming of Maize Pericycle Transcriptomes by Local High Nitrate Results in Disparate Lateral Root Branching Patterns. <i>Plant Physiology</i> , 2016, 170, 1783-1798.	2.3	53

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55	The Mucilage Proteome of Maize (<i>Zea mays</i> L.) Primary Roots. <i>Journal of Proteome Research</i> , 2010, 9, 2968-2976.	1.8	51
56	Lateral roots affect the proteome of the primary root of maize (<i>Zea mays</i> L.). <i>Plant Molecular Biology</i> , 2004, 56, 397-412.	2.0	50
57	Single-Parent Expression Is a General Mechanism Driving Extensive Complementation of Non-syntenic Genes in Maize Hybrids. <i>Current Biology</i> , 2018, 28, 431-437.e4.	1.8	50
58	Experimental platforms for the investigation of spatiotemporal patterns in the rhizosphere—Laboratory and field scale. <i>Journal of Plant Nutrition and Soil Science</i> , 2021, 184, 35-50.	1.1	49
59	Proteomic dissection of plant development. <i>Proteomics</i> , 2006, 6, 4076-4083.	1.3	48
60	Untapping root system architecture for crop improvement. <i>Journal of Experimental Botany</i> , 2016, 67, 4431-4433.	2.4	48
61	Cytoplasmic regulation of the accumulation of nuclear-encoded proteins in the mitochondrial proteome of maize. <i>Plant Journal</i> , 2004, 37, 199-208.	2.8	47
62	The Role of Host Genetic Signatures on Root-Microbe Interactions in the Rhizosphere and Endosphere. <i>Frontiers in Plant Science</i> , 2018, 9, 1896.	1.7	45
63	Release of the benzoxazinoids defense molecules during lateral- and crown root emergence in <i>Zea mays</i> . <i>Journal of Plant Physiology</i> , 2004, 161, 981-985.	1.6	44
64	The accumulation of abundant soluble proteins changes early in the development of the primary roots of maize (<i>Zea mays</i> L.). <i>Proteomics</i> , 2005, 5, 4885-4893.	1.3	42
65	Nonadditive Protein Accumulation Patterns in Maize (<i>Zea mays</i> L.) Hybrids during Embryo Development. <i>Journal of Proteome Research</i> , 2010, 9, 6511-6522.	1.8	42
66	Nonsyntenic genes drive tissue-specific dynamics of differential, nonadditive and allelic expression patterns in maize hybrids. <i>Plant Physiology</i> , 2016, 171, pp.00262.2016.	2.3	42
67	Transcriptomic reprogramming of barley seminal roots by combined water deficit and salt stress. <i>BMC Genomics</i> , 2019, 20, 325.	1.2	42
68	Conserved and Unique Features of the Maize (<i>Zea mays</i> L.) Root Hair Proteome. <i>Journal of Proteome Research</i> , 2011, 10, 2525-2537.	1.8	41
69	Seminal roots of wild and cultivated barley differentially respond to osmotic stress in gene expression, suberization, and hydraulic conductivity. <i>Plant, Cell and Environment</i> , 2020, 43, 344-357.	2.8	39
70	Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. <i>Plant Physiology</i> , 2017, 173, 1247-1257.	2.3	36
71	Ethylenediurea (EDU) mitigates the negative effects of ozone in rice: Insights into its mode of action. <i>Plant, Cell and Environment</i> , 2018, 41, 2882-2898.	2.8	36
72	The Maize (<i>Zea mays</i> L.) AUXIN/INDOLE-3-ACETIC ACID Gene Family: Phylogeny, Syteny, and Unique Root-Type and Tissue-Specific Expression Patterns during Development. <i>PLoS ONE</i> , 2013, 8, e78859.	1.1	35

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73	Association analysis of single nucleotide polymorphisms in candidate genes with root traits in maize (<i>Zea mays</i> L.) seedlings. <i>Plant Science</i> , 2014, 224, 9-19.	1.7	34
74	Estimating the importance of maize root hairs in low phosphorus conditions and under drought. <i>Annals of Botany</i> , 2019, 124, 961-968.	1.4	34
75	Root-type-specific plasticity in response to localized high nitrate supply in maize (<i>Zea mays</i>). <i>Annals of Botany</i> , 2015, 116, 751-762.	1.4	33
76	<i>ENHANCED GRAVITROPISM 2</i> encodes a STERILE ALPHA MOTIF-containing protein that controls root growth angle in barley and wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
77	Tissue-specific expression of AUX1 in maize roots. <i>Journal of Plant Physiology</i> , 2000, 157, 315-319.	1.6	31
78	Heterosis-associated proteome analyses of maize (<i>Zea mays</i> L.) seminal roots by quantitative label-free LC-MS. <i>Journal of Proteomics</i> , 2013, 93, 295-302.	1.2	31
79	Characterization of maize <i>roothairless6</i> which encodes a D-type cellulose synthase and controls the switch from bulge formation to tip growth. <i>Scientific Reports</i> , 2016, 6, 34395.	1.6	31
80	Plasticity of Lateral Root Branching in Maize. <i>Frontiers in Plant Science</i> , 2019, 10, 363.	1.7	30
81	Conserved and unique features of the homeologous maize Aux/IAA proteins ROOTLESS WITH UNDETECTABLE MERISTEM 1 and RUM1-like 1. <i>Journal of Experimental Botany</i> , 2016, 67, 1137-1147.	2.4	29
82	Regulation of the pericycle proteome in maize (<i>Zea mays</i> L.) primary roots by RUM1 which is required for lateral root initiation. <i>European Journal of Cell Biology</i> , 2010, 89, 236-241.	1.6	26
83	Comparative Transcriptome Profiling of Maize Coleoptilar Nodes during Shoot-Borne Root Initiation. <i>Plant Physiology</i> , 2013, 163, 419-430.	2.3	25
84	An improved procedure for isolation of high-quality RNA from nematode-infected <i>Arabidopsis</i> roots through laser capture microdissection. <i>Plant Methods</i> , 2016, 12, 25.	1.9	25
85	<i>BonnMu</i> : A Sequence-Indexed Resource of Transposon-Induced Maize Mutations for Functional Genomics Studies. <i>Plant Physiology</i> , 2020, 184, 620-631.	2.3	25
86	Proteomics of Maize Root Development. <i>Frontiers in Plant Science</i> , 2018, 9, 143.	1.7	24
87	Tissue Specific Control of the Maize (<i>Zea mays</i> L.) Embryo, Cortical Parenchyma, and Stele Proteomes by <i>RUM1</i> Which Regulates Seminal and Lateral Root Initiation. <i>Journal of Proteome Research</i> , 2009, 8, 2285-2297.	1.8	21
88	Spatiotemporal Dynamics of Maize (<i>Zea mays</i> L.) Root Growth and Its Potential Consequences for the Assembly of the Rhizosphere Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 619499.	1.5	21
89	Genetic Control of Root Organogenesis in Cereals. <i>Methods in Molecular Biology</i> , 2013, 959, 69-81.	0.4	20
90	Comparative analyses of three legume species reveals conserved and unique root extracellular proteins. <i>Proteomics</i> , 2012, 12, 3219-3228.	1.3	19

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91	Complexity and specificity of the maize (<i>Zea mays</i> L.) root hair transcriptome. <i>Journal of Experimental Botany</i> , 2017, 68, 2175-2185.	2.4	19
92	Lateral root development in the maize (<i>Zea mays</i>) lateral rootless1 mutant. <i>Annals of Botany</i> , 2013, 112, 417-428.	1.4	18
93	Regulation of the maize (<i>Zea mays</i> L.) embryo proteome by RTCS which controls seminal root initiation. <i>European Journal of Cell Biology</i> , 2010, 89, 242-249.	1.6	17
94	Diversity of Stability, Localization, Interaction and Control of Downstream Gene Activity in the Maize Aux/IAA Protein Family. <i>PLoS ONE</i> , 2014, 9, e107346.	1.1	14
95	Transcriptomic diversity in seedling roots of European flint maize in response to cold. <i>BMC Genomics</i> , 2020, 21, 300.	1.2	14
96	Laser Microdissection of Plant Cells. <i>Methods in Molecular Biology</i> , 2014, 1080, 249-258.	0.4	13
97	Non-syntenic genes drive RTCS-dependent regulation of the embryo transcriptome during formation of seminal root primordia in maize (<i>Zea mays</i> L.). <i>Journal of Experimental Botany</i> , 2017, 68, erw422.	2.4	11
98	Cyclin expression is completely suppressed at the site of crown root formation in the nodal region of the maize root mutant <i>rtcs</i> . <i>Journal of Plant Physiology</i> , 1998, 153, 425-429.	1.6	10
99	Designing a microarray experiment to estimate dominance in maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2005, 111, 57-64.	1.8	10
100	Cell Type-Specific Transcriptomics of Lateral Root Formation and Plasticity. <i>Frontiers in Plant Science</i> , 2019, 10, 21.	1.7	10
101	ZmGrp3: identification of a novel marker for root initiation in maize and development of a robust assay to quantify allele-specific contribution to gene expression in hybrids. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1305-1315.	1.8	8
102	Cold response and tolerance in cereal roots. <i>Journal of Experimental Botany</i> , 2021, , .	2.4	7
103	Single-parent expression complementation contributes to phenotypic heterosis in maize hybrids. <i>Plant Physiology</i> , 2022, , .	2.3	6
104	Molecular and Genetic Dissection of Cereal Root System Development. , 0, , 175-191.		4
105	Robust non-syntenic gene expression patterns in diverse maize hybrids during root development. <i>Journal of Experimental Botany</i> , 2020, 71, 865-876.	2.4	3
106	MuWU: Mutant-seq library analysis and annotation. <i>Bioinformatics</i> , 2022, 38, 837-838.	1.8	1
107	Maize Root System and Genetic Analysis of Its Formation. , 2002, , 239-248.		0
108	Transcriptomic Dissection of Maize Root System Development. <i>Compendium of Plant Genomes</i> , 2018, , 247-257.	0.3	0