Geert De Jaeger

List of Publications by Year in descending order

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93 papers 8,371 citations

43 h-index 51608 86 g-index

106 all docs

106 docs citations

106 times ranked 9323 citing authors

#	Article	IF	CITATIONS
1	SAMBA controls cell division rate during maize development. Plant Physiology, 2022, 188, 411-424.	4.8	9
2	NuA4 and H2A.Z control environmental responses and autotrophic growth in Arabidopsis. Nature Communications, 2022, 13, 277.	12.8	32
3	ROPGAP-dependent interaction between brassinosteroid and ROP2-GTPase signaling controls pavement cell shape in Arabidopsis. Current Biology, 2022, 32, 518-531.e6.	3.9	24
4	Proteomic characterization of isolated Arabidopsis clathrin-coated vesicles reveals evolutionarily conserved and plant-specific components. Plant Cell, 2022, 34, 2150-2173.	6.6	31
5	TOR promotes guard cell starch degradation by regulating the activity of \hat{l}^2 -AMYLASE1 in Arabidopsis. Plant Cell, 2022, 34, 1038-1053.	6.6	16
6	Arabidopsis casein kinase 2 triggers stem cell exhaustion under Al toxicity and phosphate deficiency through activating the DNA damage response pathway. Plant Cell, 2021, 33, 1361-1380.	6.6	26
7	Molecular architecture of the endocytic TPLATE complex. Science Advances, 2021, 7, .	10.3	31
8	Conditional destabilization of the TPLATE complex impairs endocytic internalization. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118 , .	7.1	17
9	The membrane-localized protein kinase MAP4K4/TOT3 regulates thermomorphogenesis. Nature Communications, 2021, 12, 2842.	12.8	30
10	Distinct EH domains of the endocytic TPLATE complex confer lipid and protein binding. Nature Communications, 2021, 12, 3050.	12.8	23
11	A Mutation in DNA Polymerase α Rescues WEE1KO Sensitivity to HU. International Journal of Molecular Sciences, 2021, 22, 9409.	4.1	3
12	The DREAM complex represses growth in response to DNA damage in <i>Arabidopsis</i> Life Science Alliance, 2021, 4, e202101141.	2.8	27
13	Unraveling the MAX2 Protein Network in Arabidopsis thaliana: Identification of the Protein Phosphatase PAPP5 as a Novel MAX2 Interactor. Molecular and Cellular Proteomics, 2021, 20, 100040.	3.8	11
14	SnRK2 Protein Kinases and mRNA Decapping Machinery Control Root Development and Response to Salt. Plant Physiology, 2020, 182, 361-377.	4.8	62
15	KIN10 promotes stomatal development through stabilization of the SPEECHLESS transcription factor. Nature Communications, 2020, 11, 4214.	12.8	48
16	Establishment of Proximity-Dependent Biotinylation Approaches in Different Plant Model Systems. Plant Cell, 2020, 32, 3388-3407.	6.6	91
17	High Temporal Resolution Reveals Simultaneous Plasma Membrane Recruitment of TPLATE Complex Subunits. Plant Physiology, 2020, 183, 986-997.	4.8	26
18	The CEP5 Peptide Promotes Abiotic Stress Tolerance, As Revealed by Quantitative Proteomics, and Attenuates the AUX/IAA Equilibrium in Arabidopsis. Molecular and Cellular Proteomics, 2020, 19, 1248-1262.	3.8	35

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19	The domesticated transposase ALP2 mediates formation of a novel Polycomb protein complex by direct interaction with MSI1, a core subunit of Polycomb Repressive Complex 2 (PRC2). PLoS Genetics, 2020, 16, e1008681.	3.5	22
20	SYNERGISTIC ON AUXIN AND CYTOKININ 1 positively regulates growth and attenuates soil pathogen resistance. Nature Communications, 2020, $11,2170$.	12.8	34
21	FRS7 and FRS12 recruit NINJA to regulate expression of glucosinolate biosynthesis genes. New Phytologist, 2020, 227, 1124-1137.	7.3	17
22	UBP12 and UBP13 negatively regulate the activity of the ubiquitin-dependent peptidases DA1, DAR1 and DAR2. ELife, 2020, 9, .	6.0	30
23	Title is missing!. , 2020, 16, e1008681.		0
24	Title is missing!. , 2020, 16, e1008681.		0
25	Title is missing!. , 2020, 16, e1008681.		0
26	Title is missing!. , 2020, 16, e1008681.		0
27	Mutations of the AtYAK1 Kinase Suppress TOR Deficiency in Arabidopsis. Cell Reports, 2019, 27, 3696-3708.e5.	6.4	54
28	TPX2-LIKE PROTEIN3 Is the Primary Activator of \hat{l}_{\pm} -Aurora Kinases and Is Essential for Embryogenesis. Plant Physiology, 2019, 180, 1389-1405.	4.8	16
29	Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. Nature Plants, 2019, 5, 316-327.	9.3	205
30	Histone 2B monoubiquitination complex integrates transcript elongation with RNA processing at circadian clock and flowering regulators. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8060-8069.	7.1	18
31	Patronus is the elusive plant securin, preventing chromosome separation by antagonizing separase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16018-16027.	7.1	22
32	Characterization of the \hat{I}^3 -secretase subunit interactome in Arabidopsis thaliana. Acta Physiologiae Plantarum, 2019, 41, 1.	2.1	1
33	The role of HEXOKINASE1 in Arabidopsis leaf growth. Plant Molecular Biology, 2019, 99, 79-93.	3.9	20
34	A Functional Study of AUXILIN-LIKE1 and 2, Two Putative Clathrin Uncoating Factors in Arabidopsis. Plant Cell, 2018, 30, 700-716.	6.6	75
35	GS ^{yellow} , a Multifaceted Tag for Functional Protein Analysis in Monocot and Dicot Plants. Plant Physiology, 2018, 177, 447-464.	4.8	19
36	POLAR-guided signalling complex assembly and localization drive asymmetric cell division. Nature, 2018, 563, 574-578.	27.8	167

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37	FIGL1 and its novel partner FLIP form a conserved complex that regulates homologous recombination. PLoS Genetics, 2018, 14, e1007317.	3.5	81
38	Quantitative Tandem Affinity Purification, an Effective Tool to Investigate Protein Complex Composition in Plant Hormone Signaling: Strigolactones in the Spotlight. Frontiers in Plant Science, 2018, 9, 528.	3.6	13
39	Recent Trends in Plant Protein Complex Analysis in a Developmental Context. Frontiers in Plant Science, 2018, 9, 640.	3.6	32
40	DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. ELife, 2018, 7 , .	6.0	63
41	De-Problematizing â€~GMOs': Suggestions for Communicating about Genetic Engineering. Trends in Biotechnology, 2017, 35, 185-186.	9.3	20
42	The Mitochondrial DNA (mtDNA)-Associated Protein SWIB5 Influences mtDNA Architecture and Homologous Recombination. Plant Cell, 2017, 29, tpc.00899.2016.	6.6	11
43	Identification of factors required for m ⁶ A mRNA methylation in <i>Arabidopsis</i> reveals a role for the conserved E3 ubiquitin ligase HAKAI. New Phytologist, 2017, 215, 157-172.	7.3	301
44	The transcriptional repressor complex FRS7-FRS12 regulates flowering time and growth in Arabidopsis. Nature Communications, 2017, 8, 15235.	12.8	54
45	Strigolactones, karrikins and beyond. Plant, Cell and Environment, 2017, 40, 1691-1703.	5.7	61
46	Ectopic application of the repressive histone modification H3K9me2 establishes post-zygotic reproductive isolation in <i>Arabidopsis thaliana</i> . Genes and Development, 2017, 31, 1272-1287.	5.9	61
47	Two interacting PPR proteins are major Arabidopsis editing factors in plastid and mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8877-8882.	7.1	111
48	The mutation <i>nrpb1â€A325V</i> in the largest subunit of <scp>RNA</scp> polymerase <scp>II</scp> suppresses compromised growth of <i>Arabidopsis</i> plants deficient in a function of the general transcription factor <scp>IIF</scp> . Plant Journal, 2017, 89, 730-745.	5.7	2
49	Functional characterization of the Arabidopsis transcription factor bZIP29 reveals its role in leaf and root development. Journal of Experimental Botany, 2016, 67, 5825-5840.	4.8	78
50	FYVE1/FREE1 Interacts with the PYL4 ABA Receptor and Mediates Its Delivery to the Vacuolar Degradation Pathway. Plant Cell, 2016, 28, 2291-2311.	6.6	129
51	The Arabidopsis Iron–Sulfur Protein GRXS17 is a Target of the Ubiquitin E3 Ligases RGLG3 and RGLG4. Plant and Cell Physiology, 2016, 57, 1801-1813.	3.1	16
52	Glutaredoxin GRXS17 Associates with the Cytosolic Iron-Sulfur Cluster Assembly Pathway. Plant Physiology, 2016, 172, pp.00261.2016.	4.8	35
53	Isolation of protein complexes from the model legume <i>Medicago truncatula</i> by tandem affinity purification in hairy root cultures. Plant Journal, 2016, 88, 476-489.	5.7	20
54	The heterodimeric transcription factor complex ERF115–PAT1 grants regeneration competence. Nature Plants, 2016, 2, 16165.	9.3	111

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55	The SBT6.1 subtilase processes the GOLVEN1 peptide controlling cell elongation. Journal of Experimental Botany, 2016, 67, 4877-4887.	4.8	51
56	PP2A-3 interacts with ACR4 and regulates formative cell division in the <i>Arabidopsis</i> root. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1447-1452.	7.1	43
57	Transferring an optimized TAP-toolbox for the isolation of protein complexes to a portfolio of rice tissues. Plant Molecular Biology, 2016, 91, 341-354.	3.9	7
58	ROTUNDA3 function in plant development by phosphatase 2A-mediated regulation of auxin transporter recycling. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2768-2773.	7.1	37
59	The Need to Understand GMO Opposition: Reply to Couée. Trends in Plant Science, 2016, 21, 92.	8.8	4
60	Unravelling plant molecular machineries through affinity purification coupled to mass spectrometry. Current Opinion in Plant Biology, 2015, 24, 1-9.	7.1	39
61	Dynamic Changes in ANGUSTIFOLIA3 Complex Composition Reveal a Growth Regulatory Mechanism in the Maize Leaf. Plant Cell, 2015, 27, 1605-1619.	6.6	154
62	Fatal attraction: the intuitive appeal of GMO opposition. Trends in Plant Science, 2015, 20, 414-418.	8.8	156
63	The Arabidopsis lectin EULS3 is involved in stomatal closure. Plant Science, 2015, 238, 312-322.	3.6	48
64	A Repressor Protein Complex Regulates Leaf Growth in Arabidopsis. Plant Cell, 2015, 27, 2273-2287.	6.6	118
65	The RING E3 Ligase KEEP ON GOING Modulates JASMONATE ZIM-DOMAIN12 Stability. Plant Physiology, 2015, 169, 1405-1417.	4.8	76
66	Multiple mechanisms limit meiotic crossovers: $TOP3\hat{l}\pm$ and two BLM homologs antagonize crossovers in parallel to FANCM. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4713-4718.	7.1	138
67	An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of Arabidopsis protein complexes. Nature Protocols, 2015, 10, 169-187.	12.0	160
68	The Non-JAZ TIFY Protein TIFY8 from Arabidopsis thaliana Is a Transcriptional Repressor. PLoS ONE, 2014, 9, e84891.	2.5	55
69	The Phragmoplast-Orienting Kinesin-12 Class Proteins Translate the Positional Information of the Preprophase Band to Establish the Cortical Division Zone in <i>Arabidopsis thaliana</i> ÂÂ. Plant Cell, 2014, 26, 2617-2632.	6.6	107
70	The TPLATE Adaptor Complex Drives Clathrin-Mediated Endocytosis in Plants. Cell, 2014, 156, 691-704.	28.9	238
71	<i>Arabidopsis thaliana</i> RNase H2 Deficiency Counteracts the Needs for the WEE1 Checkpoint Kinase but Triggers Genome Instability Â. Plant Cell, 2014, 26, 3680-3692.	6.6	33
72	A Generic Tool for Transcription Factor Target Gene Discovery in Arabidopsis Cell Suspension Cultures Based on Tandem Chromatin Affinity Purification. Plant Physiology, 2014, 164, 1122-1133.	4.8	43

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73	The Cyclin-Dependent Kinase Inhibitor KRP6 Induces Mitosis and Impairs Cytokinesis in Giant Cells Induced by Plant-Parasitic Nematodes in <i>Arabidopsis</i> Plant Cell, 2014, 26, 2633-2647.	6.6	30
74	Sulfenome mining in <i>Arabidopsis thaliana</i> li>. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11545-11550.	7.1	163
75	Targeted Degradation of Abscisic Acid Receptors Is Mediated by the Ubiquitin Ligase Substrate Adaptor DDA1 in <i>Arabidopsis</i>	6.6	186
76	ANGUSTIFOLIA3 Binds to SWI/SNF Chromatin Remodeling Complexes to Regulate Transcription during <i>Arabidopsis</i> Leaf Development. Plant Cell, 2014, 26, 210-229.	6.6	219
77	bHLH003, bHLH013 and bHLH017 Are New Targets of JAZ Repressors Negatively Regulating JA Responses. PLoS ONE, 2014, 9, e86182.	2.5	104
78	The Clathrin Adaptor Complex AP-2 Mediates Endocytosis of BRASSINOSTEROID INSENSITIVE1 in <i>Arabidopsis</i> A. Plant Cell, 2013, 25, 2986-2997.	6.6	171
79	ERF115 Controls Root Quiescent Center Cell Division and Stem Cell Replenishment. Science, 2013, 342, 860-863.	12.6	263
80	PYRABACTIN RESISTANCE1-LIKE8 Plays an Important Role for the Regulation of Abscisic Acid Signaling in Root \hat{A} \hat{A} \hat{A} . Plant Physiology, 2013, 161, 931-941.	4.8	244
81	Retromer Subunits VPS35A and VPS29 Mediate Prevacuolar Compartment (PVC) Function in Arabidopsis. Molecular Plant, 2013, 6, 1849-1862.	8.3	47
82	SAMBA, a plant-specific anaphase-promoting complex/cyclosome regulator is involved in early development and A-type cyclin stabilization. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13853-13858.	7.1	80
83	Adaptin-like protein TPLATE and clathrin recruitment during plant somatic cytokinesis occurs via two distinct pathways. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 615-620.	7.1	119
84	Isolation of Transcription Factor Complexes from Arabidopsis Cell Suspension Cultures by Tandem Affinity Purification. Methods in Molecular Biology, 2011, 754, 195-218.	0.9	64
85	The <i>Arabidopsis </i> bhlh Transcription Factors MYC3 and MYC4 Are Targets of JAZ Repressors and Act Additively with MYC2 in the Activation of Jasmonate Responses Â. Plant Cell, 2011, 23, 701-715.	6.6	906
86	NINJA connects the co-repressor TOPLESS to jasmonate signalling. Nature, 2010, 464, 788-791.	27.8	832
87	Plant Elongator regulates auxin-related genes during RNA polymerase II transcription elongation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1678-1683.	7.1	112
88	Targeted interactomics reveals a complex core cell cycle machinery in <i>Arabidopsis thaliana</i> Molecular Systems Biology, 2010, 6, 397.	7.2	315
89	Boosting tandem affinity purification of plant protein complexes. Trends in Plant Science, 2008, 13, 517-520.	8.8	108
90	A Tandem Affinity Purification-based Technology Platform to Study the Cell Cycle Interactome in Arabidopsis thaliana. Molecular and Cellular Proteomics, 2007, 6, 1226-1238.	3.8	196

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91	Boosting heterologous protein production in transgenic dicotyledonous seeds using Phaseolus vulgaris regulatory sequences. Nature Biotechnology, 2002, 20, 1265-1268.	17.5	162
92	Analysis of the interaction between single-chain variable fragments and their antigen in a reducing intracellular environment using the two-hybrid system. FEBS Letters, 2000, 467, 316-320.	2.8	20
93	Bacterial and plant-produced scFv proteins have similar antigen-binding properties. FEBS Letters, 1996, 386, 5-10.	2.8	60