

# Dominique Eeckhout

## List of Publications by Year in descending order

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36  
papers

3,817  
citations

304743

22  
h-index

345221

36  
g-index

46  
all docs

46  
docs citations

46  
times ranked

5370  
citing authors

#	ARTICLE	IF	CITATIONS
1	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. <i>Plant Cell</i> , 2011, 23, 701-715.	6.6	906
2	Identification of factors required for mRNA methylation in <i>Arabidopsis</i> reveals a role for the conserved E3 ubiquitin ligase HAKAI. <i>New Phytologist</i> , 2017, 215, 157-172.	7.3	301
3	The TPLATE Adaptor Complex Drives Clathrin-Mediated Endocytosis in Plants. <i>Cell</i> , 2014, 156, 691-704.	28.9	238
4	ANGUSTIFOLIA3 Binds to SWI/SNF Chromatin Remodeling Complexes to Regulate Transcription during <i>Arabidopsis</i> Leaf Development. <i>Plant Cell</i> , 2014, 26, 210-229.	6.6	219
5	Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. <i>Nature Plants</i> , 2019, 5, 316-327.	9.3	205
6	A Tandem Affinity Purification-based Technology Platform to Study the Cell Cycle Interactome in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1226-1238.	3.8	196
7	The Clathrin Adaptor Complex AP-2 Mediates Endocytosis of BRASSINOSTEROID INSENSITIVE1 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 2986-2997.	6.6	171
8	POLAR-guided signalling complex assembly and localization drive asymmetric cell division. <i>Nature</i> , 2018, 563, 574-578.	27.8	167
9	Sulfenome mining in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11545-11550.	7.1	163
10	An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of <i>Arabidopsis</i> protein complexes. <i>Nature Protocols</i> , 2015, 10, 169-187.	12.0	160
11	Dynamic Changes in ANGUSTIFOLIA3 Complex Composition Reveal a Growth Regulatory Mechanism in the Maize Leaf. <i>Plant Cell</i> , 2015, 27, 1605-1619.	6.6	154
12	A Repressor Protein Complex Regulates Leaf Growth in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 2273-2287.	6.6	118
13	Establishment of Proximity-Dependent Biotinylation Approaches in Different Plant Model Systems. <i>Plant Cell</i> , 2020, 32, 3388-3407.	6.6	91
14	Functional characterization of the <i>Arabidopsis</i> transcription factor bZIP29 reveals its role in leaf and root development. <i>Journal of Experimental Botany</i> , 2016, 67, 5825-5840.	4.8	78
15	Isolation of Transcription Factor Complexes from <i>Arabidopsis</i> Cell Suspension Cultures by Tandem Affinity Purification. <i>Methods in Molecular Biology</i> , 2011, 754, 195-218.	0.9	64
16	DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. <i>ELife</i> , 2018, 7, .	6.0	63
17	The transcriptional repressor complex FRS7-FRS12 regulates flowering time and growth in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2017, 8, 15235.	12.8	54
18	The SBT6.1 subtilase processes the GOLVEN1 peptide controlling cell elongation. <i>Journal of Experimental Botany</i> , 2016, 67, 4877-4887.	4.8	51

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19	A Generic Tool for Transcription Factor Target Gene Discovery in Arabidopsis Cell Suspension Cultures Based on Tandem Chromatin Affinity Purification. <i>Plant Physiology</i> , 2014, 164, 1122-1133.	4.8	43
20	Recent Trends in Plant Protein Complex Analysis in a Developmental Context. <i>Frontiers in Plant Science</i> , 2018, 9, 640.	3.6	32
21	Molecular architecture of the endocytic TPLATE complex. <i>Science Advances</i> , 2021, 7, .	10.3	31
22	Proteomic characterization of isolated Arabidopsis clathrin-coated vesicles reveals evolutionarily conserved and plant-specific components. <i>Plant Cell</i> , 2022, 34, 2150-2173.	6.6	31
23	The Cyclin-Dependent Kinase Inhibitor KRP6 Induces Mitosis and Impairs Cytokinesis in Giant Cells Induced by Plant-Parasitic Nematodes in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 2633-2647.	6.6	30
24	The DREAM complex represses growth in response to DNA damage in <i>Arabidopsis</i> . <i>Life Science Alliance</i> , 2021, 4, e202101141.	2.8	27
25	Arabidopsis casein kinase 2 triggers stem cell exhaustion under Al toxicity and phosphate deficiency through activating the DNA damage response pathway. <i>Plant Cell</i> , 2021, 33, 1361-1380.	6.6	26
26	ROPGAP-dependent interaction between brassinosteroid and ROP2-GTPase signaling controls pavement cell shape in Arabidopsis. <i>Current Biology</i> , 2022, 32, 518-531.e6.	3.9	24
27	Distinct EH domains of the endocytic TPLATE complex confer lipid and protein binding. <i>Nature Communications</i> , 2021, 12, 3050.	12.8	23
28	Isolation of protein complexes from the model legume <i>Medicago truncatula</i> by tandem affinity purification in hairy root cultures. <i>Plant Journal</i> , 2016, 88, 476-489.	5.7	20
29	GS <sup>yellow</sup> , a Multifaceted Tag for Functional Protein Analysis in Monocot and Dicot Plants. <i>Plant Physiology</i> , 2018, 177, 447-464.	4.8	19
30	FRS7 and FRS12 recruit NINJA to regulate expression of glucosinolate biosynthesis genes. <i>New Phytologist</i> , 2020, 227, 1124-1137.	7.3	17
31	Conditional destabilization of the TPLATE complex impairs endocytic internalization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	17
32	TPX2-LIKE PROTEIN3 Is the Primary Activator of $\hat{\pm}$ -Aurora Kinases and Is Essential for Embryogenesis. <i>Plant Physiology</i> , 2019, 180, 1389-1405.	4.8	16
33	A technology platform for the fast production of monoclonal recombinant antibodies against plant proteins and peptides. <i>Journal of Immunological Methods</i> , 2004, 294, 181-187.	1.4	14
34	Unraveling the MAX2 Protein Network in Arabidopsis thaliana: Identification of the Protein Phosphatase PAPP5 as a Novel MAX2 Interactor. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100040.	3.8	11
35	SAMBA controls cell division rate during maize development. <i>Plant Physiology</i> , 2022, 188, 411-424.	4.8	9
36	Transferring an optimized TAP-toolbox for the isolation of protein complexes to a portfolio of rice tissues. <i>Plant Molecular Biology</i> , 2016, 91, 341-354.	3.9	7