Abdelhafid Bendahmane

List of Publications by Year
in descending order

93 papers	10,260 citations	44069 48 h-index	39675 94 g-index
127 all docs	127 docs citations	127 times ranked	9752 citing authors

#	Article	IF	Citations
1	Cantaloupe melon genome reveals 3D chromatin features and structural relationship with the ancestral cucurbitaceae karyotype. IScience, 2022, 25, 103696.	4.1	12
2	A single substitution inVacuolar protein sorting 4is responsible for resistance toWatermelon mosaic virusin melon. Journal of Experimental Botany, 2022, 73, 4008-4021.	4.8	7
3	CmLHP1 proteins play a key role in plant development and sex determination in melon (Cucumis) Tj ETQq1 1 0.784314 rgBT /Over	5.7	6
4	Ethylene plays a dual role in sex determination and fruit shape in cucurbits. Current Biology, 2022, 32, 2390-2401.e4.	3.9	7
5	Spatially expressed WIP genes control Arabidopsis embryonic root development. Nature Plants, 2022, 8, 635-645.	9.3	5
6	The Genetic Control of Nectary Development. Trends in Plant Science, 2021, 26, 260-271.	8.8	10
7	Overexpression of a Cytochrome P450 Monooxygenase Involved in Orobanchol Biosynthesis Increases Susceptibility to Fusarium Head Blight. Frontiers in Plant Science, 2021, 12, 662025.	3.6	6
8	Induced mutations in SlE8 and SlACO1 control tomato fruit maturation and shelf-life. Journal of Experimental Botany, 2021, 72, 6920-6932.	4.8	7
9	Study of the genetic and phenotypic variation among wild and cultivated clary sages provides interesting avenues for breeding programs of a perfume, medicinal and aromatic plant. PLoS ONE, 2021, 16, e0248954.	2.5	4
10	The miR166â€“SlHB15A regulatory module controls ovule development and parthenocarpic fruit set under adverse temperatures in tomato. Molecular Plant, 2021, 14, 1185-1198.	8.3	39
11	Membrane Trafficking Proteins: A New Target to Identify Resistance to Viruses in Plants. Plants, 2021, 10, 2139.	3.5	10
12	The Melon Zym Locus Conferring Resistance to ZYMV: High Resolution Mapping and Candidate Gene Identification. Agronomy, 2021, 11, 2427.	3.0	5
13	Hybridizationâ€chainâ€reaction is a relevant method for in situ detection of M2dâ€like macrophages in a miniâ€pig model. FASEB Journal, 2020, 34, 15675-15686.	0.5	11
14	Integrative genome-wide analysis reveals the role of WIP proteins in inhibition of growth and development. Communications Biology, 2020, 3, 239.	4.4	16
15	GCN5 modulates salicylic acid homeostasis by regulating H3K14ac levels at the 5â€² and 3â€² ends of its target genes. Nucleic Acids Research, 2020, 48, 5953-5966.	14.5	44
16	Genetic Control of Glandular Trichome Development. Trends in Plant Science, 2020, 25, 477-487.	8.8	83
17	A pathogenesisâ€related protein GmPR08â€Bet VI promotes a molecular interaction between the GmSHMT08 and GmSNAP18 in resistance to Heterodera glycines. Plant Biotechnology Journal, 2020, 18, 1810-1829.	8.3	29
18	Roles of BdUNICULME4 and BdLAXATUMâ€A in the nonâ€domesticated grass Brachypodium distachyon. Plant Journal, 2020, 103, 645-659.	5.7	11

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19	Wheat chromatin architecture is organized in genome territories and transcription factories. Genome Biology, 2020, 21, 104.	8.8	99
20	The gynoecious CmWIP1 transcription factor interacts with CmbZIP48 to inhibit carpel development. Scientific Reports, 2019, 9, 15443.	3.3	14
21	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. Nature Genetics, 2019, 51, 1607-1615.	21.4	153
22	The Polycomb protein <scp>LHP</scp>1 regulates Arabidopsis thaliana stress responses through the repression of the <scp>MYC</scp>2â€dependent branch of immunity. Plant Journal, 2019, 100, 1118-1131.	5.7	52
23	A reference genome for pea provides insight into legume genome evolution. Nature Genetics, 2019, 51, 1411-1422.	21.4	363
24	Structural Variations in LysM Domains of LysM-RLK PsK1 May Result in a Different Effect on Peaâ€“Rhizobial Symbiosis Development. International Journal of Molecular Sciences, 2019, 20, 1624.	4.1	12
25	Gibberellins negatively regulate the development of Medicago truncatula root system. Scientific Reports, 2019, 9, 2335.	3.3	23
26	Development of a Sequence-Based Reference Physical Map of Pea (Pisum sativum L.). Frontiers in Plant Science, 2019, 10, 323.	3.6	13
27	Pivotal Roles of Cryptochromes 1a and 2 in Tomato Development and Physiology. Plant Physiology, 2019, 179, 732-748.	4.8	40
28	The Rosa genome provides new insights into the domestication of modern roses. Nature Genetics, 2018, 50, 772-777.	21.4	344
29	Translational Research: Exploring and Creating Genetic Diversity. Trends in Plant Science, 2018, 23, 42-52.	8.8	36
30	Whole-genome landscape of Medicago truncatula symbiotic genes. Nature Plants, 2018, 4, 1017-1025.	9.3	192
31	An improved assembly and annotation of the melon (Cucumis melo L.) reference genome. Scientific Reports, 2018, 8, 8088.	3.3	81
32	Modify the Histone to Win the Battle: Chromatin Dynamics in Plantâ€“Pathogen Interactions. Frontiers in Plant Science, 2018, 9, 355.	3.6	106
33	Role of a receptor-like kinase K1 in pea Rhizobium symbiosis development. Planta, 2018, 248, 1101-1120.	3.2	25
34	<scp>ETHQV</scp>6.3 is involved in melon climacteric fruit ripening and is encoded by a <scp>NAC</scp> domain transcription factor. Plant Journal, 2017, 91, 671-683.	5.7	71
35	The quest for epigenetic regulation underlying unisexual flower development in Cucumis melo. Epigenetics and Chromatin, 2017, 10, 22.	3.9	27
36	Natural and induced loss of function mutations in SlMBP21 MADS-box gene led to jointless-2 phenotype in tomato. Scientific Reports, 2017, 7, 4402.	3.3	70

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37	The heatâ€shock protein/chaperone network and multiple stress resistance. Plant Biotechnology Journal, 2017, 15, 405-414.	8.3	513
38	IpiRId: Integrative approach for piRNA prediction using genomic and epigenomic data. PLoS ONE, 2017, 12, e0179787.	2.5	17
39	The pea branching RMS2 gene encodes the PsAFB4/5 auxin receptor and is involved in an auxin-strigolactone regulation loop. PLoS Genetics, 2017, 13, e1007089.	3.5	45
40	A Brachypodium UDP-Glycosyltransferase Confers Root Tolerance to Deoxynivalenol and Resistance to Fusarium Infection. Plant Physiology, 2016, 172, 559-574.	4.8	81
41	ABI5 Is a Regulator of Seed Maturation and Longevity in Legumes. Plant Cell, 2016, 28, 2735-2754.	6.6	110
42	The battle for survival between viruses and their host plants. Current Opinion in Virology, 2016, 17, 32-38.	5.4	102
43	Induced mutations in tomato SlExp1 alter cell wall metabolism and delay fruit softening. Plant Science, 2016, 242, 195-202.	3.6	51
44	The Andromonoecious Sex Determination Gene Predates the Separation of Cucumis and Citrullus Genera. PLoS ONE, 2016, 11, e0155444.	2.5	43
45	A cucurbit androecy gene reveals how unisexual flowers develop and dioecy emerges. Science, 2015, 350, 688-691.	12.6	218
46	Eliminating Anti-Nutritional Plant Food Proteins: The Case of Seed Protease Inhibitors in Pea. PLoS ONE, 2015, 10, e0134634.	2.5	37
47	Genomics of sex determination. Current Opinion in Plant Biology, 2014, 18, 110-116.	7.1	41
48	Molecular and functional characterization of CpACS27A gene reveals its involvement in monoecy instability and other associated traits in squash (Cucurbita pepo L.). Planta, 2014, 239, 1201-1215.	3.2	45
49	The <scp>V</scp>at locus encodes for a <scp>CC</scp>â€<scp>NBS</scp>â€<scp>LRR</scp> protein that confers resistance to <scp>A</scp>phis gossypii infestation and <scp>A</scp>.Âgossypiiâ€mediated virus resistance. Plant Journal, 2014, 80, 993-1004.	5.7	90
50	Development of a Cucumis sativus TILLinG Platform for Forward and Reverse Genetics. PLoS ONE, 2014, 9, e97963.	2.5	43
51	First TILLING Platform in Cucurbita pepo: A New Mutant Resource for Gene Function and Crop Improvement. PLoS ONE, 2014, 9, e112743.	2.5	40
52	SMART â€“ Sunflower Mutant population And Reverse genetic Tool for crop improvement. BMC Plant Biology, 2013, 13, 38.	3.6	62
53	PT-Flax (phenotyping and TILLinG of flax): development of a flax (Linum usitatissimumL.) mutant population and TILLinG platform for forward and reverse genetics. BMC Plant Biology, 2013, 13, 159.	3.6	44
54	Dual Resistance of Melon to Fusarium oxysporum Races 0 and 2 and to Papaya ring-spot virus is Controlled by a Pair of Head-to-Head-Oriented NB-LRR Genes of Unusual Architecture. Molecular Plant, 2013, 6, 235-238.	8.3	82

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55	The Pea TCP Transcription Factor PsBRC1 Acts Downstream of Strigolactones to Control Shoot Branching Â. Plant Physiology, 2012, 158, 225-238.	4.8	348
56	A conserved molecular basis for photoperiod adaptation in two temperate legumes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21158-21163.	7.1	159
57	Isoprenoid biosynthesis is required for miRNA function and affects membrane association of ARGONAUTE 1 in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1778-1783.	7.1	101
58	Identification and Characterization of Tomato Mutants Affected in theRx-Mediated Resistance to PVX Isolates. Molecular Plant-Microbe Interactions, 2012, 25, 341-354.	2.6	5
59	Synchronization of the flowering transition by the tomato TERMINATING FLOWER gene. Nature Genetics, 2012, 44, 1393-1398.	21.4	122
60	Characterisation of alleles of tomato light signalling genes generated by TILLING. Phytochemistry, 2012, 79, 78-86.	2.9	23
61	Role of tomato BRANCHED1â€like genes in the control of shoot branching. Plant Journal, 2011, 67, 701-714.	5.7	179
62	Soybean cyst nematode resistance in soybean is independent of the Rhg4 locus LRR-RLK gene. Functional and Integrative Genomics, 2011, 11, 539-549.	3.5	40
63	Towards a TILLING platform for functional genomics in Piel de Sapo melons. BMC Research Notes, 2011, 4, 289.	1.4	59
64	Shoot Branching and Leaf Dissection in Tomato Are Regulated by Homologous Gene Modules. Plant Cell, 2011, 23, 3595-3609.	6.6	93
65	Multiple Coat Protein Mutations Abolish Recognition of Pepino mosaic potexvirus (PepMV) by the Potato Rx Resistance Gene in Transgenic Tomatoes. Molecular Plant-Microbe Interactions, 2010, 23, 376-383.	2.6	26
66	A new mutant genetic resource for tomato crop improvement by TILLING technology. BMC Research Notes, 2010, 3, 69.	1.4	200
67	An Induced Mutation in Tomato eIF4E Leads to Immunity to Two Potyviruses. PLoS ONE, 2010, 5, e11313.	2.5	208
68	Identification of Mendel's White Flower Character. PLoS ONE, 2010, 5, e13230.	2.5	135
69	Engineering Melon Plants with Improved Fruit Shelf Life Using the TILLING Approach. PLoS ONE, 2010, 5, e15776.	2.5	110
70	A blessing in disguise: Transposable elements are more than parasites. Epigenetics, 2010, 5, 378-380.	2.7	5
71	Host plant resistance to aphids in cultivated crops: Genetic and molecular bases, and interactions with aphid populations. Comptes Rendus - Biologies, 2010, 333, 566-573.	0.2	146
72	Tendril-lessRegulates Tendril Formation in Pea Leaves Â. Plant Cell, 2009, 21, 420-428.	6.6	129

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73	Non-synonymous single nucleotide polymorphisms in the watermelon eIF4E gene are closely associated with resistance to Zucchini yellow mosaic virus. Theoretical and Applied Genetics, 2009, 120, 191-200.	3.6	66
74	A transposon-induced epigenetic change leads to sex determination in melon. Nature, 2009, 461, 1135-1138.	27.8	555
75	A Conserved Ethylene Biosynthesis Enzyme Leads to Andromonoecy in Two Cucumis Species. PLoS ONE, 2009, 4, e6144.	2.5	134
76	UTILLdb, a Pisum sativum in silico forward and reverse genetics tool. Genome Biology, 2008, 9, R43.	9.6	157
77	A Conserved Mutation in an Ethylene Biosynthesis Enzyme Leads to Andromonoecy in Melons. Science, 2008, 321, 836-838.	12.6	330
78	The Rx Gene Confers Resistance to a Range of Potexviruses in Transgenic Nicotiana Plants. Molecular Plant-Microbe Interactions, 2008, 21, 1154-1164.	2.6	35
79	Characterization of Arabidopsis thaliana mismatch specific endonucleases: application to mutation discovery by TILLING in pea. Plant Journal, 2007, 51, 1116-1125.	5.7	143
80	AneIF4Eallele confers resistance to an uncapped and non-polyadenylated RNA virus in melon. Plant Journal, 2006, 48, 452-462.	5.7	203
81	A physical map covering the nsv locus that confers resistance to Melon necrotic spot virus in melon (Cucumis melo L.). Theoretical and Applied Genetics, 2005, 111, 914-922.	3.6	27
82	Advances in understanding recessive resistance to plant viruses. Molecular Plant Pathology, 2004, 5, 223-233.	4.2	157
83	Structural analysis of the eukaryotic initiation factor 4E gene controlling potyvirus resistance in pepper: exploitation of a BAC library. Gene, 2004, 338, 209-216.	2.2	30
84	High throughput virus-induced gene silencing implicates heat shock protein 90 in plant disease resistance. EMBO Journal, 2003, 22, 5690-5699.	7.8	493
85	Characterization of a radish introgression carrying the Ogura fertility restorer gene Rfo in rapeseed, using the Arabidopsis genome sequence and radish genetic mapping. Theoretical and Applied Genetics, 2003, 107, 1442-1451.	3.6	30
86	Identification of the fertility restoration locus, Rfo , in radish, as a member of the pentatricopeptideâ€repeat protein family. EMBO Reports, 2003, 4, 588-594.	4.5	291
87	Constitutive gain-of-function mutants in a nucleotide binding site-leucine rich repeat protein encoded at theRxlocus of potato. Plant Journal, 2002, 32, 195-204.	5.7	309
88	A natural recessive resistance gene against potato virus Y in pepper corresponds to the eukaryotic initiation factor 4E (eIF4E). Plant Journal, 2002, 32, 1067-1075.	5.7	310
89	Agrobacterium transient expression system as a tool for the isolation of disease resistance genes: application to the Rx2 locus in potato. Plant Journal, 2000, 21, 73-81.	5.7	288
90	Zero-Background Plasmid Vector for BAC Library Construction. BioTechniques, 1999, 26, 228-232.	1.8	7

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91	The Rx Gene from Potato Controls Separate Virus Resistance and Cell Death Responses. Plant Cell, 1999, 11, 781-791.	6.6	650
92	Tight Physical Linkage of the Nematode Resistance Gene Gpa2 and the Virus Resistance Gene Rx on a Single Segment Introgressed from the Wild Species Solanum tuberosum subsp. andigena CPC 1673 into Cultivated Potato. Molecular Plant-Microbe Interactions, 1999, 12, 197-206.	2.6	82
93	The coat protein of potato virus X is a strainâ€specific elicitor of Rx1â€mediated virus resistance in potato. Plant Journal, 1995, 8, 933-941.	5.7	172