Stig UggerhÃ¸j Andersen

List of Publications by Year
in descending order

63 papers	10,307 citations	159585 30 h-index	128289 60 g-index
81 all docs	81 docs citations	81 times ranked	20796 citing authors

#	Article	IF	Citations
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
2	Guidelines for the use and interpretation of assays for monitoring autophagy (4th) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td (edition	9.1	1,430
3	SHOREmap: simultaneous mapping and mutation identification by deep sequencing. Nature Methods, 2009, 6, 550-551.	19.0	558
4	Hormonal control of the shoot stem-cell niche. Nature, 2010, 465, 1089-1092.	27.8	421
5	Receptor-mediated exopolysaccharide perception controls bacterial infection. Nature, 2015, 523, 308-312.	27.8	410
6	Spider genomes provide insight into composition and evolution of venom and silk. Nature Communications, 2014, 5, 3765.	12.8	235
7	Requirement of B2-Type<i>Cyclin-Dependent Kinases</i>for Meristem Integrity in<i>Arabidopsis thaliana</i>. Plant Cell, 2008, 20, 88-100.	6.6	181
8	Genomeâ€wide <i>LORE1</i> retrotransposon mutagenesis and highâ€throughput insertion detection in <i>Lotus japonicus</i>. Plant Journal, 2012, 69, 731-741.	5.7	149
9	RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. GigaScience, 2015, 4, 5.	6.4	138
10	Genetic Diversity and Population Structure Analysis of European Hexaploid Bread Wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.5	133
11	Lotus Base: An integrated information portal for the model legume Lotus japonicus. Scientific Reports, 2016, 6, 39447.	3.3	124
12	The <i><scp>LORE</scp>1</i> insertion mutant resource. Plant Journal, 2016, 88, 306-317.	5.7	123
13	SKI2 mediates degradation of RISC 5â€²-cleavage fragments and prevents secondary siRNA production from miRNA targets in<i>Arabidopsis</i>. Nucleic Acids Research, 2015, 43, 10975-10988.	14.5	109
14	Role of A-type ARABIDOPSIS RESPONSE REGULATORS in meristem maintenance and regeneration. European Journal of Cell Biology, 2010, 89, 279-284.	3.6	103
15	Catalase and<i>NO CATALASE ACTIVITY1</i>Promote Autophagy-Dependent Cell Death in<i>Arabidopsis</i>Â Â Â. Plant Cell, 2013, 25, 4616-4626.	6.6	101
16	Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. Plant Cell, 2019, 31, 1466-1487.	6.6	89
17	Eliminating vicine and convicine, the main anti-nutritional factors restricting faba bean usage. Trends in Food Science and Technology, 2019, 91, 549-556.	15.1	84
18	DETORQUEO, QUIRKY, and ZERZAUST Represent Novel Components Involved in Organ Development Mediated by the Receptor-Like Kinase STRUBBELIG in Arabidopsis thaliana. PLoS Genetics, 2009, 5, e1000355.	3.5	78

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19	The conserved cysteine-rich domain of a tesmin/TSO1-like protein binds zinc in vitro and TSO1 is required for both male and female fertility in Arabidopsis thaliana. Journal of Experimental Botany, 2007, 58, 3657-3670.	4.8	59
20	The in Vivo Toxicity of Hydroxyurea Depends on Its Direct Target Catalase. Journal of Biological Chemistry, 2010, 285, 21411-21415.	3.4	49
21	Competition, Nodule Occupancy, and Persistence of Inoculant Strains: Key Factors in the Rhizobium-Legume Symbioses. Frontiers in Plant Science, 2021, 12, 690567.	3.6	49
22	Dynamics of Ethylene Production in Response to Compatible Nod Factor. Plant Physiology, 2018, 176, 1764-1772.	4.8	48
23	micro RNA 172 (miR172) signals epidermal infection and is expressed in cells primed for bacterial invasion in <i>Lotus japonicus</i> roots and nodules. New Phytologist, 2015, 208, 241-256.	7.3	45
24	The Glucocorticoid-Inducible GVG System Causes Severe Growth Defects in Both Root and Shoot of the Model Legume Lotus japonicus. Molecular Plant-Microbe Interactions, 2003, 16, 1069-1076.	2.6	43
25	Negative regulation of CCaMK is essential for symbiotic infection. Plant Journal, 2012, 72, 572-584.	5.7	43
26	Distinct Lotus japonicus Transcriptomic Responses to a Spectrum of Bacteria Ranging From Symbiotic to Pathogenic. Frontiers in Plant Science, 2018, 9, 1218.	3.6	43
27	Sinorhizobium fredii HH103 Invades Lotus burttii by Crack Entry in a Nod Factorâ€“and Surface Polysaccharideâ€“Dependent Manner. Molecular Plant-Microbe Interactions, 2016, 29, 925-937.	2.6	41
28	A Set of Lotus japonicus Gifu x Lotus burttii Recombinant Inbred Lines Facilitates Map-based Cloning and QTL Mapping. DNA Research, 2012, 19, 317-323.	3.4	40
29	<i>Lotus japonicus Nuclear Factor YA1</i>, a nodule emergence stageâ€specific regulator of auxin signalling. New Phytologist, 2021, 229, 1535-1552.	7.3	39
30	Recent advances in faba bean genetic and genomic tools for crop improvement. , 2021, 3, e75.		38
31	Naturally occurring diversity helps to reveal genes of adaptive importance in legumes. Frontiers in Plant Science, 2015, 6, 269.	3.6	37
32	The Brassicaceae Family Displays Divergent, Shoot-Skewed NLR Resistance Gene Expression. Plant Physiology, 2018, 176, 1598-1609.	4.8	36
33	Insights into the evolution of symbiosis gene copy number and distribution from a chromosome-scale<i>Lotus japonicus</i>Gifu genome sequence. DNA Research, 2020, 27, .	3.4	35
34	VC1 catalyses a key step in the biosynthesis of vicine in faba bean. Nature Plants, 2021, 7, 923-931.	9.3	34
35	<i>Lotus japonicus <scp>NOOT</scp>â€‹scp>BOP</scp>â€‹scp>COCH</scp>â€‹scp>LIKE</scp>1</i> is essential for nodule, nectary, leaf and flower development. Plant Journal, 2018, 94, 880-894.	5.7	32
36	A plant chitinase controls cortical infection thread progression and nitrogen-fixing symbiosis. ELife, 2018, 7, .	6.0	32

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37	Symbiosis genes show a unique pattern of introgression and selection within a Rhizobium leguminosarum species complex. Microbial Genomics, 2020, 6, .	2.0	31
38	Extreme genetic signatures of local adaptation during Lotus japonicus colonization of Japan. Nature Communications, 2020, 11, 253.	12.8	30
39	Lotus japonicus SUNERGOS 1 encodes a predicted subunit A of a DNA topoisomerase VI that is required for nodule differentiation and accommodation of rhizobial infection. Plant Journal, 2014, 78, 811-821.	5.7	28
40	Atypical Receptor Kinase RINRK1 Required for Rhizobial Infection But Not Nodule Development in <i>Lotus japonicus</i>. Plant Physiology, 2019, 181, 804-816.	4.8	28
41	<i>shortran</i>: a pipeline for small RNA-seq data analysis. Bioinformatics, 2012, 28, 2698-2700.	4.1	27
42	Signaling unmasked. Autophagy, 2014, 10, 520-521.	9.1	26
43	Greenotyper: Image-Based Plant Phenotyping Using Distributed Computing and Deep Learning. Frontiers in Plant Science, 2020, 11, 1181.	3.6	25
44	Evaluation of yield, yield stability, and yieldâ€"protein relationship in 17 commercial faba bean cultivars. , 2020, 2, e39.		22
45	Proteome reference maps of the <i>Lotus japonicus</i> nodule and root. Proteomics, 2014, 14, 230-240.	2.2	21
46	The deubiquitinating enzyme <scp>AMSH</scp>1 is required for rhizobial infection and nodule organogenesis in <i>Lotus japonicus</i>. Plant Journal, 2015, 83, 719-731.	5.7	19
47	Identification of novel genes involved in phosphate accumulation in Lotus japonicusÂthrough Genome Wide Association mapping of root system architecture and anion content. PLoS Genetics, 2019, 15, e1008126.	3.5	15
48	Chromosomal regions associated with the <i>in vitro</i> culture response of wheat (<i><scp>T</scp>riticum aestivum </i><scp>L</scp>.) microspores. Plant Breeding, 2015, 134, 255-263.	1.9	13
49	Editorial: Molecular and Cellular Mechanisms of the Legume-Rhizobia Symbiosis. Frontiers in Plant Science, 2018, 9, 1839.	3.6	12
50	High-Throughput and Targeted Genotyping of Lotus japonicus LORE1 Insertion Mutants. Methods in Molecular Biology, 2013, 1069, 119-146.	0.9	12
51	MAUIâ€seq: Metabarcoding using amplicons with unique molecular identifiers to improve error correction. Molecular Ecology Resources, 2021, 21, 703-720.	4.8	11
52	Genetic variation is associated with differences in facilitative and competitive interactions in the Rhizobium leguminosarum species complex. Environmental Microbiology, 2021, , .	3.8	9
53	High-resolution genetic maps ofLotus japonicusandL. burttiibased on re-sequencing of recombinant inbred lines. DNA Research, 2016, 23, 487-494.	3.4	8
54	Natural variation identifies a <i>Pxy</i> gene controlling vascular organisation and formation of nodules and lateral roots in <i>Lotus japonicus</i>. New Phytologist, 2021, 230, 2459-2473.	7.3	7

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55	Recombination Facilitates Adaptive Evolution in Rhizobial Soil Bacteria. Molecular Biology and Evolution, 2021, 38, 5480-5490.	8.9	7
56	<i>Lotus japonicus</i> Genetic, Mutant, and Germplasm Resources. Current Protocols in Plant Biology, 2018, 3, e20070.	2.8	5
57	Major effect loci for plant size before onset of nitrogen fixation allow accurate prediction of yield in white clover. Theoretical and Applied Genetics, 2022, 135, 125-143.	3.6	4
58	Widespread and transgenerational retrotransposon activation in interâ€•and intraspecies recombinant inbred populations of <i>Lotus japonicus</i>. Plant Journal, 2022, 111, 1397-1410.	5.7	3
59	User Guide for the LORE1 Insertion Mutant Resource. Methods in Molecular Biology, 2017, 1610, 13-23.	0.9	2
60	Genome Sequencing. Compendium of Plant Genomes, 2014, , 35-40.	0.5	1
61	Forward and Reverse Genetics: The LORE1 Retrotransposon Insertion Mutants. Compendium of Plant Genomes, 2014, , 221-227.	0.5	1
62	Lotus japonicus. Current Biology, 2022, 32, R149-R150.	3.9	1
63	Legume and Lotus japonicus Databases. Compendium of Plant Genomes, 2014, , 259-267.	0.5	0