

# Shusei Sato

## List of Publications by Year in descending order

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355  
papers

51,949  
citations

2311

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368  
docs citations

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times ranked

34746  
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#	ARTICLE	IF	CITATIONS
1	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336
2	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
3	Sequence Analysis of the Genome of the Unicellular Cyanobacterium <i>Synechocystis</i> sp. Strain PCC6803. II. Sequence Determination of the Entire Genome and Assignment of Potential Protein-coding Regions. <i>DNA Research</i> , 1996, 3, 109-136.	1.5	2,544
4	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
5	Plant recognition of symbiotic bacteria requires two LysM receptor-like kinases. <i>Nature</i> , 2003, 425, 585-592.	13.7	1,092
6	Sequence Analysis of the Genome of the Unicellular Cyanobacterium <i>Synechocystis</i> sp. Strain PCC6803. II. Sequence Determination of the Entire Genome and Assignment of Potential Protein-coding Regions (Supplement). <i>DNA Research</i> , 1996, 3, 185-209.	1.5	990
7	Activation Tagging in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2000, 122, 1003-1014.	2.3	896
8	A receptor kinase gene of the LysM type is involved in legume perception of rhizobial signals. <i>Nature</i> , 2003, 425, 637-640.	13.7	896
9	A plant receptor-like kinase required for both bacterial and fungal symbiosis. <i>Nature</i> , 2002, 417, 959-962.	13.7	874
10	Complete Genomic Sequence of Nitrogen-fixing Symbiotic Bacterium <i>Bradyrhizobium japonicum</i> USDA110. <i>DNA Research</i> , 2002, 9, 189-197.	1.5	768
11	Complete Genome Structure of the Nitrogen-fixing Symbiotic Bacterium <i>Mesorhizobium loti</i> . <i>DNA Research</i> , 2000, 7, 331-338.	1.5	739
12	Genome Structure of the Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2008, 15, 227-239.	1.5	691
13	Histidine Kinase Homologs That Act as Cytokinin Receptors Possess Overlapping Functions in the Regulation of Shoot and Root Growth in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2004, 16, 1365-1377.	3.1	545
14	Processing of ATG8s, Ubiquitin-Like Proteins, and Their Deconjugation by ATG4s Are Essential for Plant Autophagy. <i>Plant Cell</i> , 2004, 16, 2967-2983.	3.1	540
15	<i>Klebsormidium flaccidum</i> genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , 2014, 5, 3978.	5.8	532
16	Shoot control of root development and nodulation is mediated by a receptor-like kinase. <i>Nature</i> , 2002, 420, 422-426.	13.7	529
17	A Gain-of-Function Mutation in a Cytokinin Receptor Triggers Spontaneous Root Nodule Organogenesis. <i>Science</i> , 2007, 315, 104-107.	6.0	502
18	Roles of <i>Arabidopsis</i> ATP/ADP isopentenyltransferases and tRNA isopentenyltransferases in cytokinin biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16598-16603.	3.3	485

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19	Complete Structure of the Chloroplast Genome of <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 1999, 6, 283-290.	1.5	476
20	A Cytokinin Perception Mutant Colonized by <i>Rhizobium</i> in the Absence of Nodule Organogenesis. <i>Science</i> , 2007, 315, 101-104.	6.0	475
21	ARR1, a Transcription Factor for Genes Immediately Responsive to Cytokinins. <i>Science</i> , 2001, 294, 1519-1521.	6.0	461
22	Deregulation of a Ca <sup>2+</sup> /calmodulin-dependent kinase leads to spontaneous nodule development. <i>Nature</i> , 2006, 441, 1153-1156.	13.7	400
23	CYCLOPS, a mediator of symbiotic intracellular accommodation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20540-20545.	3.3	398
24	Positional cloning and characterization reveal the molecular basis for soybean maturity locus <i>E1</i> that regulates photoperiodic flowering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2155-64.	3.3	398
25	Plastid proteins crucial for symbiotic fungal and bacterial entry into plant roots. <i>Nature</i> , 2005, 433, 527-531.	13.7	391
26	A Map-Based Cloning Strategy Employing a Residual Heterozygous Line Reveals that the <i>GIGANTEA</i> Gene Is Involved in Soybean Maturity and Flowering. <i>Genetics</i> , 2011, 188, 395-407.	1.2	378
27	From The Cover: A nucleoporin is required for induction of Ca <sup>2+</sup> spiking in legume nodule development and essential for rhizobial and fungal symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 359-364.	3.3	361
28	<i>Arabidopsis</i> plasma membrane protein crucial for Ca <sup>2+</sup> influx and touch sensing in roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3639-3644.	3.3	352
29	Map-Based Cloning of the Gene Associated With the Soybean Maturity Locus <i>E3</i> . <i>Genetics</i> , 2009, 182, 1251-1262.	1.2	350
30	Nod Factor/Nitrate-Induced CLE Genes that Drive HAR1-Mediated Systemic Regulation of Nodulation. <i>Plant and Cell Physiology</i> , 2009, 50, 67-77.	1.5	342
31	Complete Genome Structure of the Thermophilic Cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1. <i>DNA Research</i> , 2002, 9, 123-130.	1.5	312
32	NUCLEOPORIN85 Is Required for Calcium Spiking, Fungal and Bacterial Symbioses, and Seed Production in <i>Lotus japonicus</i> . <i>Plant Cell</i> , 2007, 19, 610-624.	3.1	309
33	Two Coordinately Regulated Homologs of <i>FLOWERING LOCUS T</i> Are Involved in the Control of Photoperiodic Flowering in Soybean. <i>Plant Physiology</i> , 2010, 154, 1220-1231.	2.3	298
34	Sequence Analysis of the Genome of an Oil-Bearing Tree, <i>Jatropha curcas</i> L.. <i>DNA Research</i> , 2011, 18, 65-76.	1.5	294
35	Seven <i>Lotus japonicus</i> Genes Required for Transcriptional Reprogramming of the Root during Fungal and Bacterial Symbiosis. <i>Plant Cell</i> , 2005, 17, 2217-2229.	3.1	293
36	Sequence Analysis of the Genome of the Unicellular Cyanobacterium <i>Synechocystis</i> sp. strain PCC6803. I. Sequence Features in the 1 Mb Region from Map Positions 64% to 92% of the Genome. <i>DNA Research</i> , 1995, 2, 153-166.	1.5	292

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37	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14959-14964.	3.3	286
38	Complete Genome Structure of <i>Gloeobacter violaceus</i> PCC 7421, a Cyanobacterium that Lacks Thylakoids. DNA Research, 2003, 10, 137-145.	1.5	269
39	Control of petal shape and floral zygomorphy in <i>Lotus japonicus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4970-4975.	3.3	269
40	Prediction of the Coding Sequences of Unidentified Human Genes. II. The Coding Sequences of 40 New Genes (KIAA0041-KIAA0080) Deduced by Analysis of cDNA Clones from Human Cell Line KG-1. DNA Research, 1994, 1, 223-229.	1.5	261
41	Draft Genome Sequence of Eggplant ( <i>Solanum melongena</i> L.): the Representative <i>Solanum</i> Species Indigenous to the Old World. DNA Research, 2014, 21, 649-660.	1.5	254
42	Hijacking of leguminous nodulation signaling by the rhizobial type III secretion system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17131-17136.	3.3	245
43	Sequencing the Genespaces of <i>Medicago truncatula</i> and <i>Lotus japonicus</i> : Figure 1.. Plant Physiology, 2005, 137, 1174-1181.	2.3	243
44	Cell-to-cell movement of the CAPRICE protein in <i>Arabidopsis</i> root epidermal cell differentiation. Development (Cambridge), 2005, 132, 5387-5398.	1.2	231
45	The Sulfate Transporter SST1 Is Crucial for Symbiotic Nitrogen Fixation in <i>Lotus japonicus</i> Root Nodules. Plant Cell, 2005, 17, 1625-1636.	3.1	227
46	Disruption of the novel plant protein NEF1 affects lipid accumulation in the plastids of the tapetum and exine formation of pollen, resulting in male sterility in <i>Arabidopsis thaliana</i> . Plant Journal, 2004, 39, 170-181.	2.8	224
47	Prediction of the Coding Sequences of Unidentified Human Genes. I. The Coding Sequences of 40 New Genes (KIAA0001-KIAA0040) Deduced by Analysis of Randomly Sampled cDNA Clones from Human Immature Myeloid Cell Line KG-1. DNA Research, 1994, 1, 27-35.	1.5	219
48	<i>NENA</i> , a <i>Lotus japonicus</i> Homolog of <i>Sec13</i> , Is Required for Rhizodermal Infection by Arbuscular Mycorrhiza Fungi and Rhizobia but Dispensable for Cortical Endosymbiotic Development. Plant Cell, 2010, 22, 2509-2526.	3.1	215
49	<i>Arabidopsis</i> TRANSPARENT TESTA GLABRA2 Is Directly Regulated by R2R3 MYB Transcription Factors and Is Involved in Regulation of <i>GLABRA2</i> Transcription in Epidermal Differentiation. Plant Cell, 2007, 19, 2531-2543.	3.1	202
50	Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of <i>Fragaria</i> Species. DNA Research, 2014, 21, 169-181.	1.5	201
51	The AHK4 Gene Involved in the Cytokinin-Signaling Pathway as a Direct Receptor Molecule in <i>Arabidopsis thaliana</i> . Plant and Cell Physiology, 2001, 42, 751-755.	1.5	198
52	Genetic control of floral zygomorphy in pea ( <i>Pisum sativum</i> L.). Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10414-10419.	3.3	195
53	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . Nature, 2000, 408, 820-823.	13.7	188
54	Role of the Putative Membrane-Bound Endo-1,4-β-Glucanase KORRIGAN in Cell Elongation and Cellulose Synthesis in <i>Arabidopsis thaliana</i> . Plant and Cell Physiology, 2001, 42, 251-263.	1.5	185

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55	Loss of function of 3-hydroxy-3-methylglutaryl coenzyme A reductase 1 (HMG1) in <i>Arabidopsis</i> leads to dwarfing, early senescence and male sterility, and reduced sterol levels. <i>Plant Journal</i> , 2004, 37, 750-761.	2.8	184
56	A Cluster of Genes Encodes the Two Types of Chalcone Isomerase Involved in the Biosynthesis of General Flavonoids and Legume-Specific 5-Deoxy(iso)flavonoids in <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2003, 131, 941-951.	2.3	181
57	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	13.7	175
58	NODULE INCEPTION creates a long-distance negative feedback loop involved in homeostatic regulation of nodule organ production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14607-14612.	3.3	175
59	A Large-scale Protein-protein Interaction Analysis in <i>Synechocystis</i> sp. PCC6803. <i>DNA Research</i> , 2007, 14, 207-216.	1.5	170
60	Genomic clustering of cyanogenic glucoside biosynthetic genes aids their identification in <i>Lotus japonicus</i> and suggests the repeated evolution of this chemical defence pathway. <i>Plant Journal</i> , 2011, 68, 273-286.	2.8	162
61	Phosphatidylglycerol is Essential for the Development of Thylakoid Membranes in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2002, 43, 1456-1464.	1.5	156
62	A Large Scale Structural Analysis of cDNAs in a Unicellular Green Alga, <i>Chlamydomonas reinhardtii</i> . I. Generation of 3433 Non-redundant Expressed Sequence Tags. <i>DNA Research</i> , 1999, 6, 369-373.	1.5	152
63	Rearrangement of Actin Cytoskeleton Mediates Invasion of <i>Lotus japonicus</i> Roots by <i>Mesorhizobium loti</i> . <i>Plant Cell</i> , 2009, 21, 267-284.	3.1	149
64	Complete Genomic Structure of the Cultivated Rice Endophyte <i>Azospirillum</i> sp. B510. <i>DNA Research</i> , 2010, 17, 37-50.	1.5	148
65	A Link between Circadian-Controlled bHLH Factors and the APRR1/TOC1 Quintet in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2003, 44, 619-629.	1.5	147
66	Comprehensive Structural Analysis of the Genome of Red Clover ( <i>Trifolium pratense</i> L.). <i>DNA Research</i> , 2005, 12, 301-364.	1.5	145
67	The Type-A Response Regulator, ARR15, Acts as a Negative Regulator in the Cytokinin-Mediated Signal Transduction in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2003, 44, 868-874.	1.5	144
68	CyanoBase: the cyanobacteria genome database update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D379-D381.	6.5	142
69	Construction of a Genetic Linkage Map of the Model Legume <i>Lotus japonicus</i> Using an Intraspecific F2 Population. <i>DNA Research</i> , 2001, 8, 301-310.	1.5	141
70	Complete Structure of the Chloroplast Genome of a Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2000, 7, 323-330.	1.5	139
71	A novel male-sterile mutant of <i>Arabidopsis thaliana</i> , <i>faceless pollen-1</i> , produces pollen with a smooth surface and an acetolysis-sensitive exine. <i>Plant Molecular Biology</i> , 2003, 53, 107-116.	2.0	138
72	Prediction of the Coding Sequences of Unidentified Human Genes. I. The Coding Sequences of 40 New Genes (KIAA0001-KIAA0040) Deduced by Analysis of Randomly Sampled cDNA Clones from Human Immature Myeloid Cell Line KG-1 (Supplement). <i>DNA Research</i> , 1994, 1, 47-56.	1.5	137

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73	High-density Integrated Linkage Map Based on SSR Markers in Soybean. <i>DNA Research</i> , 2009, 16, 213-225.	1.5	137
74	Comparative Genetic Studies on the APRR5 and APRR7 Genes Belonging to the APRR1/TOC1 Quintet Implicated in Circadian Rhythm, Control of Flowering Time, and Early Photomorphogenesis. <i>Plant and Cell Physiology</i> , 2003, 44, 1119-1130.	1.5	136
75	The <i>NGATHA</i> Genes Direct Style Development in the <i>Arabidopsis</i> Gynoecium. <i>Plant Cell</i> , 2009, 21, 1394-1409.	3.1	135
76	Dissection of Symbiosis and Organ Development by Integrated Transcriptome Analysis of <i>Lotus japonicus</i> Mutant and Wild-Type Plants. <i>PLoS ONE</i> , 2009, 4, e6556.	1.1	134
77	Characterization of the Soybean Genome Using EST-derived Microsatellite Markers. <i>DNA Research</i> , 2007, 14, 271-281.	1.5	133
78	Sequence Analysis of the Genome of Carnation ( <i>Dianthus caryophyllus</i> L.). <i>DNA Research</i> , 2014, 21, 231-241.	1.5	132
79	A Large Scale Analysis of cDNA in <i>Arabidopsis thaliana</i> : Generation of 12,028 Non-redundant Expressed Sequence Tags from Normalized and Size-selected cDNA Libraries. <i>DNA Research</i> , 2000, 7, 175-180.	1.5	128
80	Biochemical and Functional Characterization of BLUF-Type Flavin-Binding Proteins of Two Species of Cyanobacteria. <i>Journal of Biochemistry</i> , 2005, 137, 741-750.	0.9	128
81	Spermine is not essential for survival of <i>Arabidopsis</i> . <i>FEBS Letters</i> , 2004, 556, 148-152.	1.3	127
82	Apoplastic plant subtilases support arbuscular mycorrhiza development in <i>Lotus japonicus</i> . <i>Plant Journal</i> , 2009, 58, 766-777.	2.8	127
83	Symbiotic <i>Rhizobium</i> and Nitric Oxide Induce Gene Expression of Non-symbiotic Hemoglobin in <i>Lotus japonicus</i> . <i>Plant and Cell Physiology</i> , 2005, 46, 99-107.	1.5	125
84	An analysis of synteny of <i>Arachis</i> with <i>Lotus</i> and <i>Medicago</i> sheds new light on the structure, stability and evolution of legume genomes.. <i>BMC Genomics</i> , 2009, 10, 45.	1.2	125
85	The <i>LORE1</i> insertion mutant resource. <i>Plant Journal</i> , 2016, 88, 306-317.	2.8	123
86	Community- and Genome-Based Views of Plant-Associated Bacteria: Plant-Bacterial Interactions in Soybean and Rice. <i>Plant and Cell Physiology</i> , 2010, 51, 1398-1410.	1.5	118
87	Evolution and Regulation of the <i>Lotus japonicus</i> LysM Receptor Gene Family. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 510-521.	1.4	117
88	klavier (klv), A novel hypernodulation mutant of <i>Lotus japonicus</i> affected in vascular tissue organization and floral induction. <i>Plant Journal</i> , 2005, 44, 505-515.	2.8	114
89	CERBERUS, a novel $\alpha$ box protein containing WD40 repeats, is required for formation of the infection thread and nodule development in the legume-Rhizobium symbiosis. <i>Plant Journal</i> , 2009, 60, 168-180.	2.8	114
90	<i>TOO MUCH LOVE</i> , a Root Regulator Associated with the Long-Distance Control of Nodulation in <i>Lotus japonicus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 259-268.	1.4	114

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91	Conservation of <i>Lotus</i> and Arabidopsis Basic Helix-Loop-Helix Proteins Reveals New Players in Root Hair Development. <i>Plant Physiology</i> , 2009, 151, 1175-1185.	2.3	113
92	Characterization of cDNAs Induced in Meiotic Prophase in Lily Microsporocytes. <i>DNA Research</i> , 1994, 1, 15-26.	1.5	110
93	The <i>Clavata2</i> genes of pea and <i>Lotus japonicus</i> affect autoregulation of nodulation. <i>Plant Journal</i> , 2011, 65, 861-871.	2.8	110
94	TOO MUCH LOVE, a Novel Kelch Repeat-Containing F-box Protein, Functions in the Long-Distance Regulation of the Legume-Rhizobium Symbiosis. <i>Plant and Cell Physiology</i> , 2013, 54, 433-447.	1.5	110
95	Polyubiquitin Promoter-Based Binary Vectors for Overexpression and Gene Silencing in <i>Lotus japonicus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 375-382.	1.4	109
96	The receptor-like kinase KLAVIER mediates systemic regulation of nodulation and non-symbiotic shoot development in <i>Lotus japonicus</i> . <i>Development (Cambridge)</i> , 2010, 137, 4317-4325.	1.2	109
97	Establishment of a <i>Lotus japonicus</i> gene tagging population using the exon-targeting endogenous retrotransposon <i>LORE1</i> . <i>Plant Journal</i> , 2012, 69, 720-730.	2.8	109
98	Development of a Bacterial Cell Enrichment Method and its Application to the Community Analysis in Soybean Stems. <i>Microbial Ecology</i> , 2009, 58, 703-714.	1.4	108
99	Complete Genome Sequence of the Soybean Symbiont Bradyrhizobium japonicum Strain USDA6T. <i>Genes</i> , 2011, 2, 763-787.	1.0	108
100	<i>Lotus japonicus</i> Cytokinin Receptors Work Partially Redundantly to Mediate Nodule Formation. <i>Plant Cell</i> , 2014, 26, 678-694.	3.1	107
101	Biosynthesis of the Nitrile Glucosides Rhodiocyanoside A and D and the Cyanogenic Glucosides Lotaustralin and Linamarin in <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2004, 135, 71-84.	2.3	105
102	A comprehensive analysis of six dihydroflavonol 4-reductases encoded by a gene cluster of the <i>Lotus japonicus</i> genome. <i>Journal of Experimental Botany</i> , 2005, 56, 2573-2585.	2.4	104
103	Host plant genome overcomes the lack of a bacterial gene for symbiotic nitrogen fixation. <i>Nature</i> , 2009, 462, 514-517.	13.7	103
104	<i>Lotus japonicus</i> nodulation is photomorphogenetically controlled by sensing the red/far red (R/FR) ratio through jasmonic acid (JA) signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16837-16842.	3.3	103
105	Identifying and Characterizing Plastidic 2-Oxoglutarate/Malate and Dicarboxylate Transporters in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2002, 43, 706-717.	1.5	98
106	Sequencing and Analysis of Approximately 40 000 Soybean cDNA Clones from a Full-Length-Enriched cDNA Library. <i>DNA Research</i> , 2008, 15, 333-346.	1.5	98
107	Genetic control of meristem arrest and life span in Arabidopsis by a FRUITFULL-APETALA2 pathway. <i>Nature Communications</i> , 2018, 9, 565.	5.8	98
108	Prediction of the Coding Sequences of Unidentified Human Genes. III. The Coding Sequences of 40 New Genes (KIAA0081-KIAA0120) Deduced by Analysis of cDNA Clones from Human Cell Line KG-1. <i>DNA Research</i> , 1995, 2, 37-43.	1.5	97

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109	High-temperature induction of male sterility during barley ( <i>Hordeum vulgare</i> L.) anther development is mediated by transcriptional inhibition. <i>Sexual Plant Reproduction</i> , 2005, 18, 91-100.	2.2	95
110	The Integral Membrane Protein SEN1 is Required for Symbiotic Nitrogen Fixation in <i>Lotus japonicus</i> Nodules. <i>Plant and Cell Physiology</i> , 2012, 53, 225-236.	1.5	95
111	Genetics of Symbiosis in <i>Lotus japonicus</i> : Recombinant Inbred Lines, Comparative Genetic Maps, and Map Position of 35 Symbiotic Loci. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 80-91.	1.4	94
112	RNA Interference of the Arabidopsis Putative Transcription Factor TCP16 Gene Results in Abortion of Early Pollen Development. <i>Plant Molecular Biology</i> , 2006, 61, 165-177.	2.0	94
113	Sugar-inducible expression of the nucleolin-1 gene of <i>Arabidopsis thaliana</i> and its role in ribosome synthesis, growth and development. <i>Plant Journal</i> , 2007, 49, 1053-1063.	2.8	94
114	A cytosolic invertase is required for normal growth and cell development in the model legume, <i>Lotus japonicus</i> . <i>Journal of Experimental Botany</i> , 2009, 60, 3353-3365.	2.4	93
115	An interspecific linkage map of SSR and intronic polymorphism markers in tomato. <i>Theoretical and Applied Genetics</i> , 2010, 121, 731-739.	1.8	92
116	Phytochelatin Synthases of the Model Legume <i>Lotus japonicus</i> . A Small Multigene Family with Differential Response to Cadmium and Alternatively Spliced Variants. <i>Plant Physiology</i> , 2007, 143, 1110-1118.	2.3	91
117	Structural Analysis of a <i>Lotus japonicus</i> Genome. I. Sequence Features and Mapping of Fifty-six TAC Clones Which Cover the 5.4 Mb Regions of the Genome. <i>DNA Research</i> , 2001, 8, 311-318.	1.5	90
118	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	4.7	90
119	TILLING Mutants of <i>Lotus japonicus</i> Reveal That Nitrogen Assimilation and Fixation Can Occur in the Absence of Nodule-Enhanced Sucrose Synthase. <i>Plant Physiology</i> , 2007, 144, 806-820.	2.3	89
120	Variation in bradyrhizobial NopP effector determines symbiotic incompatibility with Rj2-soybeans via effector-triggered immunity. <i>Nature Communications</i> , 2018, 9, 3139.	5.8	88
121	SNP Discovery and Linkage Map Construction in Cultivated Tomato. <i>DNA Research</i> , 2010, 17, 381-391.	1.5	87
122	Legume Anchor Markers Link Syntenic Regions Between <i>Phaseolus vulgaris</i> , <i>Lotus japonicus</i> , <i>Medicago truncatula</i> and <i>Arachis</i> . <i>Genetics</i> , 2008, 179, 2299-2312.	1.2	85
123	Generation of 7137 Non-redundant Expressed Sequence Tags from a Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2000, 7, 127-130.	1.5	80
124	AHK5 Histidine Kinase Regulates Root Elongation Through an ETR1-Dependent Abscisic Acid and Ethylene Signaling Pathway in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2006, 48, 375-380.	1.5	79
125	<i>Lotus japonicus</i> ARPC1 Is Required for Rhizobial Infection. <i>Plant Physiology</i> , 2012, 160, 917-928.	2.3	78
126	SCARN a Novel Class of SCAR Protein That Is Required for Root-Hair Infection during Legume Nodulation. <i>PLoS Genetics</i> , 2015, 11, e1005623.	1.5	78



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127	Functional Differentiation of Lotus japonicus TT2s, R2R3-MYB Transcription Factors Comprising a Multigene Family. <i>Plant and Cell Physiology</i> , 2008, 49, 157-169.	1.5	77
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135	Identification and Functional Analysis of Type III Effector Proteins in Mesorhizobium loti. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 223-234.	1.4	74
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157	Structural Analysis of a <i>Lotus japonicus</i> Genome. IV. Sequence Features and Mapping of Seventy-three TAC Clones Which Cover the 7.5 Mb Regions of the Genome. <i>DNA Research</i> , 2003, 10, 115-122.	1.5	62
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