

# Shusei Sato

## List of Publications by Year in descending order

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355  
papers

51,949  
citations

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368  
docs citations

368  
times ranked

34746  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of rhizobial symbiosis islands through insertion sequence-mediated deletion and duplication. ISME Journal, 2022, 16, 112-121.	9.8	12
2	Phenolic Acids Induce Nod Factor Production in <i>Lotus japonicus</i> and <i>Mesorhizobium</i> ; Symbiosis. Microbes and Environments, 2022, 37, n/a.	1.6	9
3	<i>In Vivo</i> Evidence of Single <sup>13</sup> C and <sup>15</sup> N Isotope-Labelled Methanotrophic Nitrogen-Fixing Bacterial Cells in Rice Roots. MBio, 2022, 13, .	4.1	4
4	<i>Lotus japonicus</i> Nuclear Factor YA1, a nodule emergence stage-specific regulator of auxin signalling. New Phytologist, 2021, 229, 1535-1552.	7.3	39
5	Identification of a Flavin Monooxygenase-Like Flavonoid 8-Hydroxylase with Gossypetin Synthase Activity from <i>Lotus japonicus</i> . Plant and Cell Physiology, 2021, 62, 411-423.	3.1	4
6	<i>Mesorhizobium</i> sp. J8 can establish symbiosis with <i>Glycyrrhiza uralensis</i> , increasing glycyrrhizin production. Plant Biotechnology, 2021, 38, 57-66.	1.0	3
7	Intragenic complementation at the <i>Lotus japonicus</i> CELLULOSE SYNTHASE-LIKE D1 locus rescues root hair defects. Plant Physiology, 2021, 186, 2037-2050.	4.8	13
8	A Dual-Color Tyr-FISH Method for Visualizing Genes/Markers on Plant Chromosomes to Create Integrated Genetic and Cytogenetic Maps. International Journal of Molecular Sciences, 2021, 22, 5860.	4.1	5
9	Construction of a high-density linkage map and graphical representation of the arrangement of transcriptome-based unigene markers on the chromosomes of onion, <i>Allium cepa</i> L. BMC Genomics, 2021, 22, 481.	2.8	13
10	Insights from the first genome assembly of Onion ( <i>Allium cepa</i> ). G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	32
11	Rhizobia use a pathogenic-like effector to hijack leguminous nodulation signalling. Scientific Reports, 2021, 11, 2034.	3.3	37
12	The <i>Lotus japonicus</i> nucleoporin GLE1 is involved in symbiotic association with rhizobia. Physiologia Plantarum, 2020, 168, 590-600.	5.2	3
13	LAZY3 plays a pivotal role in positive root gravitropism in <i>Lotus japonicus</i> . Journal of Experimental Botany, 2020, 71, 168-177.	4.8	16
14	The rhizobial autotransporter determines the symbiotic nitrogen fixation activity of <i>Lotus japonicus</i> in a host-specific manner. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1806-1815.	7.1	19
15	SEN1 gene from <i>Lotus japonicus</i> MC20 improves nitrogen fixation and plant growth. Soil Science and Plant Nutrition, 2020, 66, 864-869.	1.9	2
16	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
17	Efficient mutation induction using heavy-ion beam irradiation and simple genomic screening with random primers in taro ( <i>Colocasia esculenta</i> L. Schott). Scientia Horticulturae, 2020, 272, 109568.	3.6	6
18	Extreme genetic signatures of local adaptation during <i>Lotus japonicus</i> colonization of Japan. Nature Communications, 2020, 11, 253.	12.8	30

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19	<i>Lotus</i> Accessions Possess Multiple Checkpoints Triggered by Different Type III Secretion System Effectors of the Wide-Host-Range Symbiont <i>Bradyrhizobium elkanii</i>; USDA61. Microbes and Environments, 2020, 35, n/a.	1.6	20
20	Deploying root microbiome of halophytes to improve salinity tolerance of crops. Plant Biotechnology Reports, 2020, 14, 143-150.	1.5	9
21	Hemoglobins in the legume–<i>Rhizobium</i> symbiosis. New Phytologist, 2020, 228, 472-484.	7.3	33
22	Massive rhizobial genomic variation associated with partner quality in <i>Lotus</i>–<i>Mesorhizobium</i> symbiosis. FEMS Microbiology Ecology, 2020, 96, .	2.7	2
23	Development of molecular markers associated with resistance to Meloidogyne incognita by performing quantitative trait locus analysis and genome-wide association study in sweetpotato. DNA Research, 2019, 26, 399-409.	3.4	17
24	Expression and Functional Analyses of Five B-class Genes in the Grape Hyacinth (<i>Muscari</i>). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	3
25	Symbiotic incompatibility between soybean and Bradyrhizobium arises from one amino acid determinant in soybean Rj2 protein. PLoS ONE, 2019, 14, e0222469.	2.5	10
26	Isolation of Native Arbuscular Mycorrhizal Fungi within Young Thalli of the Liverwort Marchantia paleacea. Plants, 2019, 8, 142.	3.5	6
27	Exploring Genetic Diversity and Signatures of Horizontal Gene Transfer in Nodule Bacteria Associated with Lotus japonicus in Natural Environments. Molecular Plant-Microbe Interactions, 2019, 32, 1110-1120.	2.6	18
28	Widely targeted metabolome and transcriptome landscapes of Allium fistulosum–A. cepa chromosome addition lines revealed a flavonoid hot spot on chromosome 5A. Scientific Reports, 2019, 9, 3541.	3.3	31
29	Toward repositioning <i>Allium</i> vegetable crops as global commodities: opportunities and challenges for future application of omics and phytomedomics platforms to crop improvement. Acta Horticulturae, 2019, , 1-8.	0.2	1
30	Inflorescence Meristem Fate Is Dependent on Seed Development and FRUITFULL in Arabidopsis thaliana. Frontiers in Plant Science, 2019, 10, 1622.	3.6	19
31	Impact of Introduction of Arbuscular Mycorrhizal Fungi on the Root Microbial Community in Agricultural Fields. Microbes and Environments, 2019, 34, 23-32.	1.6	35
32	Complete Genome Sequence of the Nonheterocystous Cyanobacterium <i>Pseudanabaena</i> sp. ABRG5-3. Genome Announcements, 2018, 6, .	0.8	4
33	Genetic control of meristem arrest and life span in Arabidopsis by a FRUITFULL-APETALA2 pathway. Nature Communications, 2018, 9, 565.	12.8	98
34	Genome structure of Rosa multiflora, a wild ancestor of cultivated roses. DNA Research, 2018, 25, 113-121.	3.4	70
35	Loss of function of <sc>ASPARTIC PEPTIDASE NODULE</sc>–<sc>INDUCED</sc> 1 (<sc>APN</sc>1) in <i>Lotus japonicus</i> restricts efficient nitrogen-fixing symbiosis with specific <i>Mesorhizobium loti</i> strains. Plant Journal, 2018, 93, 5-16.	5.7	46
36	Divergent evolution of rice blast resistance Pi54 locus in the genus Oryza. Rice, 2018, 11, 63.	4.0	8

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37	Development of SSR markers linked to QTL reducing leaf hair density and grapevine downy mildew resistance in <i>Vitis vinifera</i> . <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	19
38	Structural and Functional Genomic Resources Developed. <i>Compendium of Plant Genomes</i> , 2018, , 161-172.	0.5	0
39	<i>Lotus japonicus</i> Genetic, Mutant, and Germplasm Resources. <i>Current Protocols in Plant Biology</i> , 2018, 3, e20070.	2.8	5
40	Dissection of niche competition between introduced and indigenous arbuscular mycorrhizal fungi with respect to soybean yield responses. <i>Scientific Reports</i> , 2018, 8, 7419.	3.3	36
41	Variation in bradyrhizobial NopP effector determines symbiotic incompatibility with Rj2-soybeans via effector-triggered immunity. <i>Nature Communications</i> , 2018, 9, 3139.	12.8	88
42	Inoculum effect of arbuscular mycorrhizal fungi on soybeans grown in long-term bare-fallowed field with low phosphate availability. <i>Soil Science and Plant Nutrition</i> , 2018, 64, 306-311.	1.9	4
43	A plant chitinase controls cortical infection thread progression and nitrogen-fixing symbiosis. <i>ELife</i> , 2018, 7, .	6.0	32
44	LjMOT1, a high-affinity molybdate transporter from <i>Lotus japonicus</i> , is essential for molybdate uptake, but not for the delivery to nodules. <i>Plant Journal</i> , 2017, 90, 1108-1119.	5.7	32
45	Large-scale collection of full-length cDNA and transcriptome analysis in <i>Hevea brasiliensis</i> . <i>DNA Research</i> , 2017, 24, dsw056.	3.4	18
46	Yotsuboshi™, a new F <sub>1</sub> hybrid strawberry of seed propagation type for year-round production. <i>Acta Horticulturae</i> , 2017, , 53-60.	0.2	4
47	Complete Genome Sequence of <i>Bradyrhizobium diazoefficiens</i> USDA 122, a Nitrogen-Fixing Soybean Symbiont. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
48	Genome Analysis. <i>Compendium of Plant Genomes</i> , 2017, , 3-19.	0.5	0
49	Establishment of a genome-wide and quantitative protocol for assessment of transcriptional activity at human retrotransposon L1 antisense promoters. <i>Genes and Genetic Systems</i> , 2017, 92, 243-249.	0.7	1
50	Genetic Tracing of <i>Jatropha curcas</i> L. from Its Mesoamerican Origin to the World. <i>Frontiers in Plant Science</i> , 2017, 8, 1539.	3.6	19
51	Identification of <i>Bradyrhizobium elkanii</i> Genes Involved in Incompatibility with <i>Vigna radiata</i> . <i>Genes</i> , 2017, 8, 374.	2.4	18
52	RNA-sequencing-based transcriptome and biochemical analyses of steroidal saponin pathway in a complete set of <i>Allium fistulosum</i> A. cepa monosomic addition lines. <i>PLoS ONE</i> , 2017, 12, e0181784.	2.5	67
53	Whole-Genome Sequence of the Nitrogen-Fixing Symbiotic Rhizobium <i>Mesorhizobium loti</i> Strain TONO. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
54	Genetic Structure and Speciation of Zoysiagrass Ecotypes Collected in Japan. <i>Crop Science</i> , 2016, 56, 818-826.	1.8	15

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55	The Complete Chloroplast Genome Sequence of <i>Zoysia matrella</i> (L.) Merr.. Crop Science, 2016, 56, 1206-1212.	1.8	9
56	The <i>LORE1</i> insertion mutant resource. Plant Journal, 2016, 88, 306-317.	5.7	123
57	High-resolution genetic maps of <i>Lotus japonicus</i> and <i>L. burttii</i> based on re-sequencing of recombinant inbred lines. DNA Research, 2016, 23, 487-494.	3.4	8
58	A high-density genetic linkage map of bronze loquat based on SSR and RAPD markers. Tree Genetics and Genomes, 2016, 12, 1.	1.6	6
59	Function and evolution of a <i>Lotus japonicus</i> AP2/ERF family transcription factor that is required for development of infection threads. DNA Research, 2016, 24, dsw052.	3.4	36
60	<i>Lotus japonicus</i> NF-YA1 Plays an Essential Role During Nodule Differentiation and Targets Members of the <i>SHI/STY</i> Gene Family. Molecular Plant-Microbe Interactions, 2016, 29, 950-964.	2.6	44
61	Sequencing and analysis of the complete organellar genomes of <i>Parmales</i> , a closely related group to <i>Bacillariophyta</i> (diatoms). Current Genetics, 2016, 62, 887-896.	1.7	31
62	Sequencing and comparative analyses of the genomes of <i>zoysiagrasses</i> . DNA Research, 2016, 23, 171-180.	3.4	68
63	Metagenomic Analysis Revealed Methylamine and Ureide Utilization of Soybean-Associated <i>Methylobacterium</i> . Microbes and Environments, 2016, 31, 268-278.	1.6	21
64	Blue Light Perception by Both Roots and Rhizobia Inhibits Nodule Formation in <i>Lotus japonicus</i> . Molecular Plant-Microbe Interactions, 2016, 29, 786-796.	2.6	25
65	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. Nature Plants, 2016, 2, 16167.	9.3	90
66	Tomato Genome Sequence. Biotechnology in Agriculture and Forestry, 2016, , 1-13.	0.2	2
67	Functional and expression analyses of transcripts based on full-length cDNAs of <i>Sorghum bicolor</i> . DNA Research, 2015, 22, 485-493.	3.4	3
68	The Arabidopsis TAC Position Viewer: a high-resolution map of transformation-competent artificial chromosome ( <i>TAC</i> ) clones aligned with the <i>Arabidopsis thaliana</i> genome. Plant Journal, 2015, 83, 1114-1122.	5.7	4
69	Genome Analysis of a Novel <i>Bradyrhizobium</i> sp. DOA9 Carrying a Symbiotic Plasmid. PLoS ONE, 2015, 10, e0117392.	2.5	52
70	SCARN a Novel Class of SCAR Protein That Is Required for Root-Hair Infection during Legume Nodulation. PLoS Genetics, 2015, 11, e1005623.	3.5	78
71	Development of transcriptome shotgun assembly-derived markers in bunching onion ( <i>Allium</i> ) Tj ETQq1 1 0.784314, rgBT / Overlock 10	2.1	27
72	Identification of <i>Bradyrhizobium elkanii</i> Genes Involved in Incompatibility with Soybean Plants Carrying the <i>Rj4</i> Allele. Applied and Environmental Microbiology, 2015, 81, 6710-6717.	3.1	62

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73	Symbiosis Island Shuffling with Abundant Insertion Sequences in the Genomes of Extra-Slow-Growing Strains of Soybean Bradyrhizobia. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4143-4154.	3.1	16
74	Integrating transcriptome and target metabolome variability in doubled haploids of <i>Allium cepa</i> for abiotic stress protection. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	49
75	Gene Expression Profiles in <i>Jatropha</i> Under Drought Stress and During Recovery. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1075-1087.	1.8	9
76	Molecular Characterization of LjABCG1, an ATP-Binding Cassette Protein in <i>Lotus japonicus</i> . <i>PLoS ONE</i> , 2015, 10, e0139127.	2.5	7
77	Development of F&lt;sub>1&lt;/sub>-hybrid Strawberry of Seed Propagation Type Named "Yotsuboshi"™ by Collaborative Breeding among Institutes. <i>Horticultural Research (Japan)</i> , 2015, 14, 409-418.	0.1	8
78	Transcriptomic profiles of nodule senescence in &lt;i>Lotus japonicus&lt;/i> and &lt;i>Mesorhizobium loti&lt;/i> symbiosis. <i>Plant Biotechnology</i> , 2014, 31, 345-349.	1.0	17
79	Polymorphisms of E1 and GIGANTEA in wild populations of <i>Lotus japonicus</i> . <i>Journal of Plant Research</i> , 2014, 127, 651-660.	2.4	5
80	Development of EST-SSR markers and construction of a linkage map in faba bean (&lt;i>Vicia</i>). <i>Journal of Plant Research</i> , 2014, 127, 651-660.	1.9	30
81	Draft Genome Sequence of Eggplant ( <i>Solanum melongena</i> L.): the Representative <i>Solanum</i> Species Indigenous to the Old World. <i>DNA Research</i> , 2014, 21, 649-660.	3.4	254
82	Rhizobial infection does not require cortical expression of upstream common symbiosis genes responsible for the induction of <sup>2+</sup> spiking. <i>Plant Journal</i> , 2014, 77, 146-159.	5.7	50
83	<i>Lotus japonicus</i> SUNERGOS 1 encodes a predicted subunit A of a DNA topoisomerase VI that is required for nodule differentiation and accommodation of rhizobial infection. <i>Plant Journal</i> , 2014, 78, 811-821.	5.7	28
84	Analysis of the complete plastid genome of the unicellular red alga <i>Porphyridium purpureum</i> . <i>Journal of Plant Research</i> , 2014, 127, 389-397.	2.4	45
85	Sll0939 is induced by Slr0967 in the cyanobacterium <i>Synechocystis</i> sp. PCC6803 and is essential for growth under various stress conditions. <i>Plant Physiology and Biochemistry</i> , 2014, 81, 36-43.	5.8	9
86	<i>Klebsormidium flaccidum</i> genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , 2014, 5, 3978.	12.8	532
87	<i>Lotus japonicus</i> Cytokinin Receptors Work Partially Redundantly to Mediate Nodule Formation. <i>Plant Cell</i> , 2014, 26, 678-694.	6.6	107
88	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.	7.1	175
89	Transcriptome-based single nucleotide polymorphism markers for genome mapping in Japanese pear ( <i>Pyrus pyrifolia</i> Nakai). <i>Tree Genetics and Genomes</i> , 2014, 10, 853-863.	1.6	24
90	Genetic mapping of the loquat canker resistance locus in bronze loquat ( <i>Eriobotrya deflexa</i> ). <i>Tree Genetics and Genomes</i> , 2014, 10, 875-883.	1.6	12

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91	Endoreduplication-mediated initiation of symbiotic organ development in <i>Lotus japonicus</i> . Development (Cambridge), 2014, 141, 2441-2445.	2.5	52
92	Sequence Analysis of the Genome of Carnation ( <i>Dianthus caryophyllus</i> L.). DNA Research, 2014, 21, 231-241.	3.4	132
93	Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of <i>Fragaria</i> Species. DNA Research, 2014, 21, 169-181.	3.4	201
94	Genetic Linkage Maps, Synteny and Map-based Cloning. Compendium of Plant Genomes, 2014, , 21-31.	0.5	1
95	Genome Sequencing. Compendium of Plant Genomes, 2014, , 35-40.	0.5	1
96	Legume and <i>Lotus japonicus</i> Databases. Compendium of Plant Genomes, 2014, , 259-267.	0.5	0
97	Genome Structure of <i>Jatropha curcas</i> L., 2013, , 563-576.		4
98	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.	7.1	245
99	The <i>cis</i> -acting <i>CTTC</i> "P1 <sub>BS</sub> " module is indicative for gene function of <i>LjVIT12</i> , a <i>Q</i> -SNARE protein gene that is required for arbuscule formation in <i>Lotus japonicus</i> . Plant Journal, 2013, 74, 280-293.	5.7	67
100	Control of Plant Trichome and Root-Hair Development by a Tomato ( <i>Solanum lycopersicum</i> ) R3 MYB Transcription Factor. PLoS ONE, 2013, 8, e54019.	2.5	61
101	Whole-Genome Sequence of the Purple Photosynthetic Bacterium <i>Rhodovulum sulfidophilum</i> Strain W4. Genome Announcements, 2013, 1, .	0.8	16
102	<i>LjMATE1</i> : A Citrate Transporter Responsible for Iron Supply to the Nodule Infection Zone of <i>Lotus japonicus</i> . Plant and Cell Physiology, 2013, 54, 1749-1749.	3.1	5
103	Structural analyses of the tomato genome. Plant Biotechnology, 2013, 30, 257-263.	1.0	2
104	<i>LjMATE1</i> : A Citrate Transporter Responsible for Iron Supply to the Nodule Infection Zone of <i>Lotus japonicus</i> . Plant and Cell Physiology, 2013, 54, 585-594.	3.1	70
105	TOO MUCH LOVE, a Novel Kelch Repeat-Containing F-box Protein, Functions in the Long-Distance Regulation of the Legume "Rhizobium Symbiosis. Plant and Cell Physiology, 2013, 54, 433-447.	3.1	110
106	The Type III Secretion System of <i>Bradyrhizobium japonicum</i> USDA122 Mediates Symbiotic Incompatibility with <i>Rj2</i> Soybean Plants. Applied and Environmental Microbiology, 2013, 79, 1048-1051.	3.1	71
107	Genome-Wide SNP Genotyping to Infer the Effects on Gene Functions in Tomato. DNA Research, 2013, 20, 221-233.	3.4	58
108	Construction of an Integrated High Density Simple Sequence Repeat Linkage Map in Cultivated Strawberry ( <i>Fragaria x ananassa</i> ) and its Applicability. DNA Research, 2013, 20, 79-92.	3.4	59



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109	Two <i>Lotus japonicus</i> symbiosis mutants impaired at distinct steps of arbuscule development. <i>Plant Journal</i> , 2013, 75, 117-129.	5.7	15
110	Commonalities and Differences among Symbiosis Islands of Three <i>Mesorhizobium loti</i> Strains. <i>Microbes and Environments</i> , 2013, 28, 275-278.	1.6	17
111	Mapping of Micro-Tom BAC-End Sequences to the Reference Tomato Genome Reveals Possible Genome Rearrangements and Polymorphisms. <i>International Journal of Plant Genomics</i> , 2012, 2012, 1-8.	2.2	13
112	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.	7.1	398
113	Comparative Genetic Mapping and Discovery of Linkage Disequilibrium Across Linkage Groups in White Clover ( <i>Trifolium repens</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 607-617.	1.8	28
114	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.	3.1	95
115	Transcription Factors of Lotus: Regulation of Isoflavonoid Biosynthesis Requires Coordinated Changes in Transcription Factor Activity. <i>Plant Physiology</i> , 2012, 159, 531-547.	4.8	64
116	A Set of <i>Lotus japonicus</i> Gifu x <i>Lotus burttii</i> Recombinant Inbred Lines Facilitates Map-based Cloning and QTL Mapping. <i>DNA Research</i> , 2012, 19, 317-323.	3.4	40
117	Upgraded genomic information of <i>Jatropha curcas</i> L.. <i>Plant Biotechnology</i> , 2012, 29, 123-130.	1.0	74
118	The SNARE Protein SYP71 Expressed in Vascular Tissues Is Involved in Symbiotic Nitrogen Fixation in <i>Lotus japonicus</i> Nodules. <i>Plant Physiology</i> , 2012, 160, 897-905.	4.8	36
119	Complete Genome Sequence of <i>Bradyrhizobium</i> sp. S23321: Insights into Symbiosis Evolution in Soil Oligotrophs. <i>Microbes and Environments</i> , 2012, 27, 306-315.	1.6	76
120	Negative regulation of CCaMK is essential for symbiotic infection. <i>Plant Journal</i> , 2012, 72, 572-584.	5.7	43
121	<i>Lotus japonicus</i> ARPC1 Is Required for Rhizobial Infection. <i>Plant Physiology</i> , 2012, 160, 917-928.	4.8	78
122	Functional Divergence of MYB-Related Genes, <i>WEREWOLF</i> and <i>AtMYB23</i> in <i>Arabidopsis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 883-887.	1.3	27
123	LjABCB1, an ATP-binding cassette protein specifically induced in uninfected cells of <i>Lotus japonicus</i> nodules. <i>Journal of Plant Physiology</i> , 2012, 169, 322-326.	3.5	32
124	Integration of Linkage and Chromosome Maps of Red Clover ( <i>Trifolium</i> ) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 142 Td (	1.1	20
125	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
126	Comparative Analyses in Lotus: The Cytogenetic Map of <i>Lotus uliginosus</i> Schkuhr. <i>Cytogenetic and Genome Research</i> , 2012, 137, 42-49.	1.1	5



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127	Large-scale development of expressed sequence tag-derived simple sequence repeat markers and diversity analysis in <i>Arachis</i> spp.. <i>Molecular Breeding</i> , 2012, 30, 125-138.	2.1	75
128	The first genetic maps for subterranean clover ( <i>Trifolium subterraneum</i> L.) and comparative genomics with <i>T. pratense</i> L. and <i>Medicago truncatula</i> Gaertn. to identify new molecular markers for breeding. <i>Molecular Breeding</i> , 2012, 30, 213-226.	2.1	28
129	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.	5.7	109
130	Sequence Analysis of the Genome of an Oil-Bearing Tree, <i>Jatropha curcas</i> L.. <i>DNA Research</i> , 2011, 18, 65-76.	3.4	294
131	<i>Lotus</i> ., 2011, , 141-151.		0
132	Survey of the genetic information carried in the genome of <i>Eucalyptus camaldulensis</i> . <i>Plant Biotechnology</i> , 2011, 28, 471-480.	1.0	33
133	Complete Genome Sequence of the Soybean Symbiont <i>Bradyrhizobium japonicum</i> Strain USDA6T. <i>Genes</i> , 2011, 2, 763-787.	2.4	108
134	Activation of a <i>Lotus japonicus</i> Subtilase Gene During Arbuscular Mycorrhiza Is Dependent on the Common Symbiosis Genes and Two <i>cis</i> -Active Promoter Regions. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 662-670.	2.6	26
135	Isolation and Genetic Characterization of <i>Aurantimonas</i> and <i>Methylobacterium</i> Strains from Stems of Hypernodulated Soybeans. <i>Microbes and Environments</i> , 2011, 26, 172-180.	1.6	19
136	Identification of <i>Mesorhizobium loti</i> Genes Relevant to Symbiosis by Using Signature-Tagged Mutants. <i>Microbes and Environments</i> , 2011, 26, 165-171.	1.6	6
137	The <i>Clavata2</i> genes of pea and <i>Lotus japonicus</i> affect autoregulation of nodulation. <i>Plant Journal</i> , 2011, 65, 861-871.	5.7	110
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