

Shusei Sato

List of Publications by Year in descending order

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355
papers

51,949
citations

2311

98
h-index

1527

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g-index

368
all docs

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. <i>ISME Journal</i> , 2022, 16, 112-121.	4.4	12
2	Phenolic Acids Induce Nod Factor Production in <i>Lotus japonicus</i> and <i>Mesorhizobium lotii</i> . <i>Symbiosis. Microbes and Environments</i> , 2022, 37, n/a.	0.7	9
3	In Vivo Evidence of Single ¹³ C and ¹⁵ N Isotope-Labeled Methanotrophic Nitrogen-Fixing Bacterial Cells in Rice Roots. <i>MBio</i> , 2022, 13, .	1.8	4
4	<i>Lotus japonicus</i> Nuclear Factor YA1, a nodule emergence stage-specific regulator of auxin signalling. <i>New Phytologist</i> , 2021, 229, 1535-1552.	3.5	39
5	Identification of a Flavin Monooxygenase-Like Flavonoid 8-Hydroxylase with Gossypetin Synthase Activity from <i>Lotus japonicus</i> . <i>Plant and Cell Physiology</i> , 2021, 62, 411-423.	1.5	4
6	<i>Mesorhizobium lotii</i> sp. J8 can establish symbiosis with <i>Glycyrrhiza uralensis</i> , increasing glycyrrhizin production. <i>Plant Biotechnology</i> , 2021, 38, 57-66.	0.5	3
7	Intragenic complementation at the <i>Lotus japonicus</i> CELLULOSE SYNTHASE-LIKE D1 locus rescues root hair defects. <i>Plant Physiology</i> , 2021, 186, 2037-2050.	2.3	13
8	A Dual-Color Tyr-FISH Method for Visualizing Genes/Markers on Plant Chromosomes to Create Integrated Genetic and Cytogenetic Maps. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5860.	1.8	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. <i>BMC Genomics</i> , 2021, 22, 481.	1.2	13
10	Insights from the first genome assembly of Onion (<i>Allium cepa</i>). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	32
11	Rhizobia use a pathogenic-like effector to hijack leguminous nodulation signalling. <i>Scientific Reports</i> , 2021, 11, 2034.	1.6	37
12	The <i>Lotus japonicus</i> nucleoporin GLE1 is involved in symbiotic association with rhizobia. <i>Physiologia Plantarum</i> , 2020, 168, 590-600.	2.6	3
13	LAZY3 plays a pivotal role in positive root gravitropism in <i>Lotus japonicus</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 168-177.	2.4	16
14	The rhizobial autotransporter determines the symbiotic nitrogen fixation activity of <i>Lotus japonicus</i> in a host-specific manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1806-1815.	3.3	19
15	SEN1 gene from <i>Lotus japonicus</i> MG20 improves nitrogen fixation and plant growth. <i>Soil Science and Plant Nutrition</i> , 2020, 66, 864-869.	0.8	2
16	Insights into the evolution of symbiosis gene copy number and distribution from a chromosome-scale <i>Lotus japonicus</i> Gifu genome sequence. <i>DNA Research</i> , 2020, 27, .	1.5	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). <i>Scientia Horticulturae</i> , 2020, 272, 109568.	1.7	6
18	Extreme genetic signatures of local adaptation during <i>Lotus japonicus</i> colonization of Japan. <i>Nature Communications</i> , 2020, 11, 253.	5.8	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.	0.7	20
20	Deploying root microbiome of halophytes to improve salinity tolerance of crops. Plant Biotechnology Reports, 2020, 14, 143-150.	0.9	9
21	Hemoglobins in the legume<i> Rhizobium </i>symbiosis. New Phytologist, 2020, 228, 472-484.	3.5	33
22	Massive rhizobial genomic variation associated with partner quality in <i>Lotus</i>–<i>Mesorhizobium</i> symbiosis. FEMS Microbiology Ecology, 2020, 96, .	1.3	2
23	Development of molecular markers associated with resistance to <i>Meloidogyne incognita</i> by performing quantitative trait locus analysis and genome-wide association study in sweetpotato. DNA Research, 2019, 26, 399-409.	1.5	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	0.3	3
25	Symbiotic incompatibility between soybean and <i>Bradyrhizobium</i> arises from one amino acid determinant in soybean Rj2 protein. PLoS ONE, 2019, 14, e0222469.	1.1	10
26	Isolation of Native Arbuscular Mycorrhizal Fungi within Young Thalli of the Liverwort <i>Marchantia paleacea</i> . Plants, 2019, 8, 142.	1.6	6
27	Exploring Genetic Diversity and Signatures of Horizontal Gene Transfer in Nodule Bacteria Associated with <i>Lotus japonicus</i> in Natural Environments. Molecular Plant-Microbe Interactions, 2019, 32, 1110-1120.	1.4	18
28	Widely targeted metabolome and transcriptome landscapes of <i>Allium fistulosum</i> – <i>A. cepa</i> chromosome addition lines revealed a flavonoid hot spot on chromosome 5A. Scientific Reports, 2019, 9, 3541.	1.6	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.	0.1	1
30	Inflorescence Meristem Fate Is Dependent on Seed Development and FRUITFULL in <i>Arabidopsis thaliana</i> . Frontiers in Plant Science, 2019, 10, 1622.	1.7	19
31	Impact of Introduction of Arbuscular Mycorrhizal Fungi on the Root Microbial Community in Agricultural Fields. Microbes and Environments, 2019, 34, 23-32.	0.7	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 <i>Arabidopsis</i> by a FRUITFULL-APETALA2 pathway. Nature Communications, 2018, 9, 565.	5.8	98
34	Genome structure of <i>Rosa multiflora</i> , a wild ancestor of cultivated roses. DNA Research, 2018, 25, 113-121.	1.5	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.	2.8	46
36	Divergent evolution of rice blast resistance Pi54 locus in the genus <i>Oryza</i> . Rice, 2018, 11, 63.	1.7	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.	1.0	19
38	Structural and Functional Genomic Resources Developed. <i>Compendium of Plant Genomes</i> , 2018, , 161-172.	0.3	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.	1.6	36
41	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
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.	0.8	4
43	A plant chitinase controls cortical infection thread progression and nitrogen-fixing symbiosis. <i>ELife</i> , 2018, 7, .	2.8	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.	2.8	32
45	Large-scale collection of full-length cDNA and transcriptome analysis in <i>Hevea brasiliensis</i> . <i>DNA Research</i> , 2017, 24, dsw056.	1.5	18
46	Yotsuboshi™, a new F ₁ hybrid strawberry of seed propagation type for year-round production. <i>Acta Horticulturae</i> , 2017, , 53-60.	0.1	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.	0.3	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.	0.2	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.	1.7	19
51	Identification of <i>Bradyrhizobium elkanii</i> Genes Involved in Incompatibility with <i>Vigna radiata</i> . <i>Genes</i> , 2017, 8, 374.	1.0	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.	1.1	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.	0.8	15

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55	The Complete Chloroplast Genome Sequence of <i>Zoysia matrella</i> (L.) Merr.. Crop Science, 2016, 56, 1206-1212.	0.8	9
56	The <i>LORE1</i> insertion mutant resource. Plant Journal, 2016, 88, 306-317.	2.8	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.	1.5	8
58	A high-density genetic linkage map of bronze loquat based on SSR and RAPD markers. Tree Genetics and Genomes, 2016, 12, 1.	0.6	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.	1.5	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.	1.4	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.	0.8	31
62	Sequencing and comparative analyses of the genomes of <i>zoysiagrasses</i> . DNA Research, 2016, 23, 171-180.	1.5	68
63	Metagenomic Analysis Revealed Methylamine and Ureide Utilization of Soybean-Associated <i>Methylobacterium</i> . Microbes and Environments, 2016, 31, 268-278.	0.7	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.	1.4	25
65	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. Nature Plants, 2016, 2, 16167.	4.7	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.	1.5	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> Columbia genome. Plant Journal, 2015, 83, 1114-1122.	2.8	4
69	Genome Analysis of a Novel Bradyrhizobium sp. DOA9 Carrying a Symbiotic Plasmid. PLoS ONE, 2015, 10, e0117392.	1.1	52
70	SCARN a Novel Class of SCAR Protein That Is Required for Root-Hair Infection during Legume Nodulation. PLoS Genetics, 2015, 11, e1005623.	1.5	78
71	Development of transcriptome shotgun assembly-derived markers in bunching onion (<i>Allium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.8	27
72	Identification of Bradyrhizobium elkanii Genes Involved in Incompatibility with Soybean Plants Carrying the <i>Rj4</i> Allele. Applied and Environmental Microbiology, 2015, 81, 6710-6717.	1.4	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.	1.4	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.	1.0	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.	1.0	9
76	Molecular Characterization of LjABCG1, an ATP-Binding Cassette Protein in <i>Lotus japonicus</i> . <i>PLoS ONE</i> , 2015, 10, e0139127.	1.1	7
77	Development of F<sub>1</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 <i>Lotus japonicus</i> and <i>Mesorhizobium loti</i> symbiosis. <i>Plant Biotechnology</i> , 2014, 31, 345-349.	0.5	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.	1.2	5
80	Development of EST-SSR markers and construction of a linkage map in faba bean (<i>Vicia faba</i>). <i>Overlook</i> , 2010, 10, 50-54.	0.9	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.	1.5	254
82	Rhizobial infection does not require cortical expression of upstream common symbiosis genes responsible for the induction of C ²⁺ spiking. <i>Plant Journal</i> , 2014, 77, 146-159.	2.8	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.	2.8	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.	1.2	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.	2.8	9
86	<i>Klebsormidium flaccidum</i> genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , 2014, 5, 3978.	5.8	532
87	<i>Lotus japonicus</i> Cytokinin Receptors Work Partially Redundantly to Mediate Nodule Formation. <i>Plant Cell</i> , 2014, 26, 678-694.	3.1	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.	3.3	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.	0.6	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.	0.6	12

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91	Endoreduplication-mediated initiation of symbiotic organ development in <i>Lotus japonicus</i> . Development (Cambridge), 2014, 141, 2441-2445.	1.2	52
92	Sequence Analysis of the Genome of Carnation (<i>Dianthus caryophyllus</i> L.). DNA Research, 2014, 21, 231-241.	1.5	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.	1.5	201
94	Genetic Linkage Maps, Synteny and Map-based Cloning. Compendium of Plant Genomes, 2014, , 21-31.	0.3	1
95	Genome Sequencing. Compendium of Plant Genomes, 2014, , 35-40.	0.3	1
96	Legume and <i>Lotus japonicus</i> Databases. Compendium of Plant Genomes, 2014, , 259-267.	0.3	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.	3.3	245
99	The <i>cis</i> -acting CTTC-P1BS module is indicative for gene function of <i>LjVTI12</i> , a SNARE protein gene that is required for arbuscule formation in <i>Lotus japonicus</i> . Plant Journal, 2013, 74, 280-293.	2.8	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.	1.1	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.	1.5	5
103	Structural analyses of the tomato genome. Plant Biotechnology, 2013, 30, 257-263.	0.5	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.	1.5	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.	1.5	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.	1.4	71
107	Genome-Wide SNP Genotyping to Infer the Effects on Gene Functions in Tomato. DNA Research, 2013, 20, 221-233.	1.5	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.	1.5	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.	2.8	15
110	Commonalities and Differences among Symbiosis Islands of Three <i>Mesorhizobium loti</i> Strains. <i>Microbes and Environments</i> , 2013, 28, 275-278.	0.7	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.	3.3	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.	0.8	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.	1.5	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.	2.3	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.	1.5	40
117	Upgraded genomic information of <i>Jatropha curcas</i> L.. <i>Plant Biotechnology</i> , 2012, 29, 123-130.	0.5	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.	2.3	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.	0.7	76
120	Negative regulation of CCaMK is essential for symbiotic infection. <i>Plant Journal</i> , 2012, 72, 572-584.	2.8	43
121	<i>Lotus japonicus</i> ARPC1 Is Required for Rhizobial Infection. <i>Plant Physiology</i> , 2012, 160, 917-928.	2.3	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.	0.6	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.	1.6	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 (0.6	20
125	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	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.	0.6	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.	1.0	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.	1.0	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.	2.8	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.	1.5	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.	0.5	33
133	Complete Genome Sequence of the Soybean Symbiont <i>Bradyrhizobium japonicum</i> Strain USDA6T. <i>Genes</i> , 2011, 2, 763-787.	1.0	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.	1.4	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.	0.7	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.	0.7	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.	2.8	110
138	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
139	Regulation of nonsymbiotic and truncated hemoglobin genes of <i>Lotus japonicus</i> in plant organs and in response to nitric oxide and hormones. <i>New Phytologist</i> , 2011, 189, 765-776.	3.5	71
140	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
141	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
142	Genomic Structure of the Cyanobacterium <i>Synechocystis</i> sp. PCC 6803 Strain GT-S. <i>DNA Research</i> , 2011, 18, 393-399.	1.5	42
143	<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
144	An EST-SSR Linkage Map of <i>Raphanus sativus</i> and Comparative Genomics of the Brassicaceae. <i>DNA Research</i> , 2011, 18, 221-232.	1.5	70

#	ARTICLE	IF	CITATIONS
145	Peroxiredoxins and NADPH-Dependent Thioredoxin Systems in the Model Legume <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2011, 156, 1535-1547.	2.3	37
146	Autoregulation of Nodulation Interferes with Impacts of Nitrogen Fertilization Levels on the Leaf-Associated Bacterial Community in Soybeans. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1973-1980.	1.4	50
147	Identification and Functional Analysis of Type III Effector Proteins in <i>Mesorhizobium loti</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 223-234.	1.4	74
148	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
149	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
150	Integration of cytogenetic and genetic linkage maps of <i>Lotus japonicus</i> , a model plant for legumes. <i>Chromosome Research</i> , 2010, 18, 287-299.	1.0	32
151	3-Phosphoglycerate dehydrogenase in <i>Mesorhizobium loti</i> is essential for maintaining symbiotic nitrogen fixation of <i>Lotus japonicus</i> root nodules. <i>Plant and Soil</i> , 2010, 336, 233-240.	1.8	4
152	Structural analyses of the genomes in legumes. <i>Current Opinion in Plant Biology</i> , 2010, 13, 146-152.	3.5	38
153	Differential protein profiles of <i>Bradyrhizobium japonicum</i> USDA110 bacteroid during soybean nodule development. <i>Soil Science and Plant Nutrition</i> , 2010, 56, 579-590.	0.8	17
154	Community shifts of soybean stem-associated bacteria responding to different nodulation phenotypes and N levels. <i>ISME Journal</i> , 2010, 4, 315-326.	4.4	63
155	NAD ⁺ -malic enzyme affects nitrogenase activity of <i>Mesorhizobium loti</i> bacteroids in <i>Lotus japonicus</i> nodules. <i>Plant Biotechnology</i> , 2010, 27, 311-316.	0.5	4
156	Genomewide Characterization of the Light-Responsive and Clock-Controlled Output Pathways in <i>Lotus japonicus</i> with Special Emphasis of its Uniqueness. <i>Plant and Cell Physiology</i> , 2010, 51, 1800-1814.	1.5	25
157	The REDUCED LEAFLET Genes Encode Key Components of the trans-Acting Small Interfering RNA Pathway and Regulate Compound Leaf and Flower Development in <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2010, 152, 797-807.	2.3	40
158	<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. <i>Plant Cell</i> , 2010, 22, 2509-2526.	3.1	215
159	The receptor-like kinase KLAVER 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
160	Derepression of the Plant Chromovirus LORE1 Induces Germline Transposition in Regenerated Plants. <i>PLoS Genetics</i> , 2010, 6, e1000868.	1.5	48
161	CyanoBase: the cyanobacteria genome database update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D379-D381.	6.5	142
162	A Suite of <i>Lotus japonicus</i> Starch Mutants Reveals Both Conserved and Novel Features of Starch Metabolism. <i>Plant Physiology</i> , 2010, 154, 643-655.	2.3	63

#	ARTICLE	IF	CITATIONS
163	Complete Genomic Structure of the Cultivated Rice Endophyte <i>Azospirillum</i> sp. B510. <i>DNA Research</i> , 2010, 17, 37-50.	1.5	148
164	Proteome Analysis of Pod and Seed Development in the Model Legume <i>Lotus japonicus</i> . <i>Journal of Proteome Research</i> , 2010, 9, 5715-5726.	1.8	34
165	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
166	SNP Discovery and Linkage Map Construction in Cultivated Tomato. <i>DNA Research</i> , 2010, 17, 381-391.	1.5	87
167	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
168	A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009, 2, .	1.6	73
169	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
170	Analyses of expression and phenotypes of knockout lines for <i>Arabidopsis</i> ABCF subfamily members. <i>Plant Biotechnology</i> , 2009, 26, 409-414.	0.5	11
171	ChlH, the H subunit of the Mg-chelatase, is an anti-sigma factor for SigE in <i>Synechocystis</i> sp. PCC 6803. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6860-6865.	3.3	71
172	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
173	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
174	The Proteome of Seed Development in the Model Legume <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2009, 149, 1325-1340.	2.3	76
175	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
176	Conservation of <i>Lotus</i> and <i>Arabidopsis</i> Basic Helix-Loop-Helix Proteins Reveals New Players in Root Hair Development. <i>Plant Physiology</i> , 2009, 151, 1175-1185.	2.3	113
177	The Temperature-Sensitive <i>brush</i> Mutant of the Legume <i>Lotus japonicus</i> Reveals a Link between Root Development and Nodule Infection by Rhizobia. <i>Plant Physiology</i> , 2009, 149, 1785-1796.	2.3	22
178	High-density Integrated Linkage Map Based on SSR Markers in Soybean. <i>DNA Research</i> , 2009, 16, 213-225.	1.5	137
179	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
180	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

#	ARTICLE	IF	CITATIONS
181	Nicotianamine synthase specifically expressed in root nodules of <i>Lotus japonicus</i> . <i>Planta</i> , 2009, 230, 309-317.	1.6	36
182	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
183	Apoplastic plant subtilases support arbuscular mycorrhiza development in <i>Lotus japonicus</i> . <i>Plant Journal</i> , 2009, 58, 766-777.	2.8	127
184	CERBERUS, a novel U-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
185	Host plant genome overcomes the lack of a bacterial gene for symbiotic nitrogen fixation. <i>Nature</i> , 2009, 462, 514-517.	13.7	103
186	Identification of <i>Arabidopsis</i> subtilisin-like serine protease specifically expressed in root stele by gene trapping. <i>Physiologia Plantarum</i> , 2009, 137, 281-288.	2.6	10
187	The glutathione peroxidase gene family of <i>Lotus japonicus</i> : characterization of genomic clones, expression analyses and immunolocalization in legumes. <i>New Phytologist</i> , 2009, 181, 103-114.	3.5	56
188	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
189	A novel manual pooling system for preparing three-dimensional pools of a deep coverage soybean bacterial artificial chromosome library. <i>Molecular Ecology Resources</i> , 2009, 9, 516-524.	2.2	2
190	Nodulation-Dependent Communities of Culturable Bacterial Endophytes from Stems of Field-Grown Soybeans. <i>Microbes and Environments</i> , 2009, 24, 253-258.	0.7	32
191	<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
192	Proanthocyanidin Biosynthesis in Forage Legumes with Especial Reference to the Regulatory Role of R2R3MYB Transcription Factors and Their Analysis in <i>Lotus japonicus</i> . , 2009, , 125-132.		0
193	Genetic control of floral zygomorphy in pea (<i>Pisum sativum</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10414-10419.	3.3	195
194	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
195	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
196	Ultrastructural Characterization of Exine Development of the transient defective exine 1 Mutant Suggests the Existence of a Factor Involved in Constructing Reticulate Exine Architecture from Sporopollenin Aggregates. <i>Plant and Cell Physiology</i> , 2008, 49, 58-67.	1.5	45
197	The <i>Arabidopsis</i> OBERON1 and OBERON2 genes encode plant homeodomain finger proteins and are required for apical meristem maintenance. <i>Development (Cambridge)</i> , 2008, 135, 1751-1759.	1.2	55
198	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

#	ARTICLE	IF	CITATIONS
199	A Large Scale Analysis of Protein-Protein Interactions in the Nitrogen-fixing Bacterium <i>Mesorhizobium loti</i> . <i>DNA Research</i> , 2008, 15, 13-23.	1.5	73
200	A High-density Linkage Map of <i>Lotus japonicus</i> Based on AFLP and SSR Markers. <i>DNA Research</i> , 2008, 15, 323-332.	1.5	15
201	Functional Differentiation of <i>Lotus japonicus</i> TT2s, R2R3-MYB Transcription Factors Comprising a Multigene Family. <i>Plant and Cell Physiology</i> , 2008, 49, 157-169.	1.5	77
202	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
203	Markov Chain-based Promoter Structure Modeling for Tissue-specific Expression Pattern Prediction. <i>DNA Research</i> , 2008, 15, 3-11.	1.5	7
204	Genome Structure of the Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2008, 15, 227-239.	1.5	691
205	A Positive Regulatory Role for <i>LjJERF1</i> in the Nodulation Process Is Revealed by Systematic Analysis of Nodule-Associated Transcription Factors of <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2008, 147, 2030-2040.	2.3	59
206	Construction of Signature-tagged Mutant Library in <i>Mesorhizobium loti</i> as a Powerful Tool for Functional Genomics. <i>DNA Research</i> , 2008, 15, 297-308.	1.5	41
207	Characterization of soybean genome based on synteny analysis with <i>Lotus japonicus</i> . <i>Breeding Science</i> , 2008, 58, 157-167.	0.9	8
208	<i>Arabidopsis</i> VIP6/ELF8, the homolog of CTR9 component of the transcriptional complex PAF1, is essential for plant development. <i>Plant Biotechnology</i> , 2008, 25, 447-455.	0.5	5
209	Gene trap strategy, an effective tool for identification of novel genes expressed in anther tissues in <i>Arabidopsis thaliana</i> . <i>Plant Biotechnology</i> , 2008, 25, 391-395.	0.5	1
210	A Novel Ankyrin-Repeat Membrane Protein, IG1, Is Required for Persistence of Nitrogen-Fixing Symbiosis in Root Nodules of <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2007, 143, 1293-1305.	2.3	76
211	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
212	A Large-scale Protein-protein Interaction Analysis in <i>Synechocystis</i> sp. PCC6803. <i>DNA Research</i> , 2007, 14, 207-216.	1.5	170
213	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
214	<i>Arabidopsis</i> plasma membrane protein crucial for Ca ²⁺ 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
215	<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. <i>Plant Cell</i> , 2007, 19, 2531-2543.	3.1	202
216	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

#	ARTICLE	IF	CITATIONS
217	Genome-wide Analyses of the Structural Gene Families Involved in the Legume-specific 5-Deoxyisoflavonoid Biosynthesis of <i>Lotus japonicus</i> . <i>DNA Research</i> , 2007, 14, 25-36.	1.5	41
218	Genome Sequencing and Genome Resources in Model Legumes. <i>Plant Physiology</i> , 2007, 144, 588-593.	2.3	53
219	Characterization of Genomic Clones and Expression Analysis of the Three Types of Superoxide Dismutases During Nodule Development in <i>Lotus japonicus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 262-275.	1.4	46
220	<i>C. elegans</i> RBX-2-CUL-5- and RBX-1-CUL-2-based complexes are redundant for oogenesis and activation of the MAP kinase MPK-1. <i>FEBS Letters</i> , 2007, 581, 145-150.	1.3	17
221	A Gain-of-Function Mutation in a Cytokinin Receptor Triggers Spontaneous Root Nodule Organogenesis. <i>Science</i> , 2007, 315, 104-107.	6.0	502
222	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
223	Characterization of the Soybean Genome Using EST-derived Microsatellite Markers. <i>DNA Research</i> , 2007, 14, 271-281.	1.5	133
224	Quantitative trait locus analysis of multiple agronomic traits in the model legume <i>Lotus japonicus</i> . <i>Genome</i> , 2007, 50, 627-637.	0.9	46
225	Proteases in plant root symbiosis. <i>Phytochemistry</i> , 2007, 68, 111-121.	1.4	50
226	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
227	Chromosome maps of legumes. <i>Chromosome Research</i> , 2007, 15, 97-103.	1.0	16
228	Expression analysis of gene trap lines and mapping of donor loci for Dissociation transposition in <i>Arabidopsis</i> . <i>Plant Biotechnology</i> , 2007, 24, 467-479.	0.5	6
229	Functional and structural analysis of genes encoding oxidosqualene cyclases of <i>Lotus japonicus</i> . <i>Plant Science</i> , 2006, 170, 247-257.	1.7	74
230	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
231	Deregulation of a Ca ²⁺ /calmodulin-dependent kinase leads to spontaneous nodule development. <i>Nature</i> , 2006, 441, 1153-1156.	13.7	400
232	RNA Interference of the <i>Arabidopsis</i> Putative Transcription Factor TCP16 Gene Results in Abortion of Early Pollen Development. <i>Plant Molecular Biology</i> , 2006, 61, 165-177.	2.0	94
233	Accumulation of chloroplast DNA sequences on the Y chromosome of <i>Silene latifolia</i> . <i>Genetica</i> , 2006, 128, 167-175.	0.5	55
234	A starvation-specific serine protease gene, <i>isp6 +</i> , is involved in both autophagy and sexual development in <i>Schizosaccharomyces pombe</i> . <i>Current Genetics</i> , 2006, 49, 403-413.	0.8	33

#	ARTICLE	IF	CITATIONS
235	Lotus japonicus as a platform for legume research. <i>Current Opinion in Plant Biology</i> , 2006, 9, 128-132.	3.5	67
236	Gene Trapping in Arabidopsis Reveals Genes Involved in Vascular Development. <i>Plant and Cell Physiology</i> , 2006, 47, 1394-1405.	1.5	30
237	From The Cover: A nucleoporin is required for induction of Ca ²⁺ 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
238	AHK5 Histidine Kinase Regulates Root Elongation Through an ETR1-Dependent Abscisic Acid and Ethylene Signaling Pathway in Arabidopsis thaliana. <i>Plant and Cell Physiology</i> , 2006, 48, 375-380.	1.5	79
239	Biosynthesis of Ascorbic Acid in Legume Root Nodules. <i>Plant Physiology</i> , 2006, 141, 1068-1077.	2.3	53
240	Genome-wide analysis of ATP-binding cassette (ABC) proteins in a model legume plant, Lotus japonicus: comparison with Arabidopsis ABC protein family. <i>DNA Research</i> , 2006, 13, 205-228.	1.5	71
241	Roles of Arabidopsis 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
242	Identification of a Sed5 -like SNARE Gene LjSYP32-1 that Contributes to Nodule Tissue Formation of Lotus japonicus. <i>Plant and Cell Physiology</i> , 2006, 47, 829-838.	1.5	15
243	Control of petal shape and floral zygomorphy in Lotus japonicus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4970-4975.	3.3	269
244	Legume genome evolution viewed through the Medicago truncatula and Lotus japonicus genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	3.3	286
245	Comparison of the Transcript Profiles from the Root and the Nodulating Root of the Model Legume Lotus japonicus by Serial Analysis of Gene Expression. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 487-498.	1.4	57
246	klavier (klv), A novel hypernodulation mutant of Lotus japonicus affected in vascular tissue organization and floral induction. <i>Plant Journal</i> , 2005, 44, 505-515.	2.8	114
247	Plastid proteins crucial for symbiotic fungal and bacterial entry into plant roots. <i>Nature</i> , 2005, 433, 527-531.	13.7	391
248	High-temperature induction of male sterility during barley (Hordeum vulgare L.) anther development is mediated by transcriptional inhibition. <i>Sexual Plant Reproduction</i> , 2005, 18, 91-100.	2.2	95
249	The HKM gene, which is identical to the MS1 gene of Arabidopsis thaliana, is essential for primexine formation and exine pattern formation. <i>Sexual Plant Reproduction</i> , 2005, 18, 1-7.	2.2	51
250	Activation tagging approach in a model legume, Lotus japonicus. <i>Journal of Plant Research</i> , 2005, 118, 391-399.	1.2	32
251	A comprehensive analysis of six dihydroflavonol 4-reductases encoded by a gene cluster of the Lotus japonicus genome. <i>Journal of Experimental Botany</i> , 2005, 56, 2573-2585.	2.4	104
252	Cell-to-cell movement of the CAPRICE protein in Arabidopsis root epidermal cell differentiation. <i>Development (Cambridge)</i> , 2005, 132, 5387-5398.	1.2	231

#	ARTICLE	IF	CITATIONS
253	Symbiotic Rhizobium 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
254	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
255	Invasion of <i>Lotus japonicus</i> root hairless 1 by <i>Mesorhizobium loti</i> Involves the Nodulation Factor-Dependent Induction of Root Hairs. <i>Plant Physiology</i> , 2005, 137, 1331-1344.	2.3	63
256	Roles of <i>Arabidopsis</i> AtREV1 and AtREV7 in Translesion Synthesis. <i>Plant Physiology</i> , 2005, 138, 870-881.	2.3	54
257	Characterization of the <i>Lotus japonicus</i> Symbiotic Mutant lot1 That Shows a Reduced Nodule Number and Distorted Trichomes. <i>Plant Physiology</i> , 2005, 137, 1261-1271.	2.3	31
258	Sequencing the Genespaces of <i>Medicago truncatula</i> and <i>Lotus japonicus</i> : Figure 1.. <i>Plant Physiology</i> , 2005, 137, 1174-1181.	2.3	243
259	Identification of PamA as a PII-binding Membrane Protein Important in Nitrogen-related and Sugar-catabolic Gene Expression in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Biological Chemistry</i> , 2005, 280, 34684-34690.	1.6	50
260	Promoter trapping in <i>Lotus japonicus</i> reveals novel root and nodule GUS expression domains. <i>Plant and Cell Physiology</i> , 2005, 46, 1202-1212.	1.5	19
261	<i>Lotus burtii</i> Takes a Position of the Third Corner in the <i>Lotus</i> Molecular Genetics Triangle. <i>DNA Research</i> , 2005, 12, 69-77.	1.5	38
262	The Sulfate Transporter SST1 Is Crucial for Symbiotic Nitrogen Fixation in <i>Lotus japonicus</i> Root Nodules. <i>Plant Cell</i> , 2005, 17, 1625-1636.	3.1	227
263	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
264	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
265	Poster Summaries. <i>Current Plant Science and Biotechnology in Agriculture</i> , 2005, , 313-335.	0.0	0
266	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
267	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
268	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
269	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> . <i>Plant Journal</i> , 2004, 39, 170-181.	2.8	224
270	Characteristics of the <i>Lotus japonicus</i> Gene Repertoire Deduced from Large-Scale Expressed Sequence Tag (EST) Analysis. <i>Plant Molecular Biology</i> , 2004, 54, 405-414.	2.0	63

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271	Exploitation of colinear relationships between the genomes of <i>Lotus japonicus</i> , <i>Pisum sativum</i> and <i>Arabidopsis thaliana</i> , for positional cloning of a legume symbiosis gene. <i>Theoretical and Applied Genetics</i> , 2004, 108, 442-449.	1.8	51
272	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
273	Spermine is not essential for survival of <i>Arabidopsis</i> . <i>FEBS Letters</i> , 2004, 556, 148-152.	1.3	127
274	A novel male-sterile mutant of <i>Arabidopsis thaliana</i> , faceless pollen-1, produces pollen with a smooth surface and an acetolysis-sensitive exine. <i>Plant Molecular Biology</i> , 2003, 53, 107-116.	2.0	138
275	Evolution and microsynteny of the apyrase gene family in three legume genomes. <i>Molecular Genetics and Genomics</i> , 2003, 270, 347-361.	1.0	50
276	Plant recognition of symbiotic bacteria requires two LysM receptor-like kinases. <i>Nature</i> , 2003, 425, 585-592.	13.7	1,092
277	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
278	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
279	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
280	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
281	Structural Analysis of a <i>Lotus japonicus</i> Genome. V. Sequence Features and Mapping of Sixty-four TAC Clones Which Cover the 6.4 Mb Regions of the Genome. <i>DNA Research</i> , 2003, 10, 277-285.	1.5	46
282	Complete Genome Structure of <i>Gloeobacter violaceus</i> PCC 7421, a Cyanobacterium that Lacks Thylakoids (Supplement). <i>DNA Research</i> , 2003, 10, 181-201.	1.5	42
283	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
284	Complete Genome Structure of <i>Gloeobacter violaceus</i> PCC 7421, a Cyanobacterium that Lacks Thylakoids. <i>DNA Research</i> , 2003, 10, 137-145.	1.5	269
285	A HEAT-Repeats Containing Protein, IaiH, Stabilizes the Iron-Sulfur Cluster Bound to the Cyanobacterial IscA Homologue, IscA2. <i>Journal of Biochemistry</i> , 2003, 134, 211-217.	0.9	25
286	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
287	Characterization of the APRR9 Pseudo-Response Regulator Belonging to the APRR1/TOC1 Quintet in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2003, 44, 1237-1245.	1.5	66
288	Structural Analysis of a <i>Lotus japonicus</i> Genome. III. Sequence Features and Mapping of Sixty-two TAC Clones Which Cover the 6.7 Mb Regions of the Genome. <i>DNA Research</i> , 2003, 10, 27-33.	1.5	25

#	ARTICLE	IF	CITATIONS
289	Molecular Analysis of the Pathway for the Synthesis of Thiol Tripeptides in the Model Legume <i>Lotus japonicus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 1039-1046.	1.4	41
290	Complete Genomic Sequence of Nitrogen-fixing Symbiotic Bacterium <i>Bradyrhizobium japonicum</i> USDA110. <i>DNA Research</i> , 2002, 9, 189-197.	1.5	768
291	Complete Genome Structure of the Thermophilic Cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1. <i>DNA Research</i> , 2002, 9, 123-130.	1.5	312
292	Structural Analysis of a <i>Lotus japonicus</i> Genome. II. Sequence Features and Mapping of Sixty-five TAC Clones Which Cover the 6.5-Mb Regions of the Genome. <i>DNA Research</i> , 2002, 9, 63-70.	1.5	50
293	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
294	Complete Genome Structure of the Thermophilic Cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1 (Supplement). <i>DNA Research</i> , 2002, 9, 135-148.	1.5	29
295	Expression of Symbiotic and Nonsymbiotic Globin Genes Responding to Microsymbionts on <i>Lotus japonicus</i> . <i>Plant and Cell Physiology</i> , 2002, 43, 1351-1358.	1.5	39
296	Complete Genomic Sequence of Nitrogen-fixing Symbiotic Bacterium <i>Bradyrhizobium japonicum</i> USDA110 (Supplement). <i>DNA Research</i> , 2002, 9, 225-256.	1.5	76
297	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
298	A plant receptor-like kinase required for both bacterial and fungal symbiosis. <i>Nature</i> , 2002, 417, 959-962.	13.7	874
299	Shoot control of root development and nodulation is mediated by a receptor-like kinase. <i>Nature</i> , 2002, 420, 422-426.	13.7	529
300	A Genetic Linkage Map of the Model Legume <i>Lotus japonicus</i> and Strategies for Fast Mapping of New Loci. <i>Genetics</i> , 2002, 161, 1673-1683.	1.2	74
301	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
302	The AHK4 Gene Involved in the Cytokinin-Signaling Pathway as a Direct Receptor Molecule in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2001, 42, 751-755.	1.5	198
303	ARR1, a Transcription Factor for Genes Immediately Responsive to Cytokinins. <i>Science</i> , 2001, 294, 1519-1521.	6.0	461
304	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
305	Role of the Putative Membrane-Bound Endo-1,4- β -Glucanase KORRIGAN in Cell Elongation and Cellulose Synthesis in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2001, 42, 251-263.	1.5	185
306	Structural Analysis of <i>Arabidopsis thaliana</i> Chromosome 3. I. Sequence Features of the Regions of 4,504,864 bp Covered by Sixty P1 and TAC Clones. <i>DNA Research</i> , 2000, 7, 131-135.	1.5	30

#	ARTICLE	IF	CITATIONS
307	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	13.7	175
308	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336
309	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 820-823.	13.7	188
310	Characterization of Ce-atl-1, an ATM-like gene from <i>Caenorhabditis elegans</i> . <i>Molecular Genetics and Genomics</i> , 2000, 264, 119-126.	2.4	19
311	Complete Genome Structure of the Nitrogen-fixing Symbiotic Bacterium <i>Mesorhizobium loti</i> . <i>DNA Research</i> , 2000, 7, 331-338.	1.5	739
312	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
313	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
314	Complete Genome Structure of the Nitrogen-fixing Symbiotic Bacterium <i>Mesorhizobium loti</i> (Supplement). <i>DNA Research</i> , 2000, 7, 381-406.	1.5	76
315	Complete Structure of the Chloroplast Genome of a Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2000, 7, 323-330.	1.5	139
316	Structural Analysis of <i>Arabidopsis thaliana</i> Chromosome 3. II. Sequence Features of the 4,251,695 bp Regions Covered by 90 P1, TAC and BAC Clones. <i>DNA Research</i> , 2000, 7, 217-221.	1.5	21
317	Activation Tagging in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2000, 122, 1003-1014.	2.3	896
318	hosoba toge toge , a Syndrome Caused by a Large Chromosomal Deletion Associated with a T-DNA Insertion in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2000, 41, 1055-1066.	1.5	37
319	Structural Analysis of <i>Arabidopsis thaliana</i> Chromosome 5. X. Sequence Features of the Regions of 3,076,755 bp Covered by Sixty P1 and TAC Clones. <i>DNA Research</i> , 2000, 7, 31-63.	1.5	30
320	Chloroplast development in <i>Arabidopsis thaliana</i> requires the nuclear-encoded transcription factor Sigma B. <i>FEBS Letters</i> , 2000, 485, 178-182.	1.3	55
321	A Sequence-ready Contig Map of the Top Arm of <i>Arabidopsis thaliana</i> Chromosome 3. <i>DNA Research</i> , 1999, 6, 117-121.	1.5	7
322	Structural Analysis of <i>Arabidopsis thaliana</i> chromosome 5. IX. Sequence Features of the Regions of 1,011,550 bp Covered by Seventeen P1 and TAC Clones. <i>DNA Research</i> , 1999, 6, 183-195.	1.5	13
323	Complete Structure of the Chloroplast Genome of <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 1999, 6, 283-290.	1.5	476
324	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

#	ARTICLE	IF	CITATIONS
325	Structural Analysis of Arabidopsis thaliana Chromosome 5. VII. Sequence Features of the Regions of 1,013,767 bp Covered by Sixteen Physically assigned P1 and TAC Clones. DNA Research, 1998, 5, 297-308.	1.5	9
326	Structural Analysis of Arabidopsis thaliana Chromosome 5. V. Sequence Features of the Regions of 1,381,565 bp Covered by twenty one Physically assigned P1 and TAC Clones. DNA Research, 1998, 5, 131-145.	1.5	42
327	Structural Analysis of Arabidopsis thaliana Chromosome 5. VI. Sequence Features of the Regions of 1,367,185 bp Covered by 19 Physically Assigned P1 and TAC Clones. DNA Research, 1998, 5, 203-216.	1.5	9
328	Structural Analysis of Arabidopsis thaliana Chromosome 5. IV. Sequence Features of the Regions of 1,456,315 bp Covered by Nineteen Physically Assigned P1 and TAC Clones. DNA Research, 1998, 5, 41-54.	1.5	17
329	Characterization of a Caenorhabditis elegans recA-like Gene Ce-rdh-1 Involved in Meiotic Recombination. DNA Research, 1998, 5, 373-377.	1.5	39
330	A Physical Map of Arabidopsis thaliana Chromosome 3 Represented by Two Contigs of CIC YAC, P1, TAC and BAC Clones. DNA Research, 1998, 5, 163-168.	1.5	28
331	Structural Analysis of Arabidopsis thaliana Chromosome 5. VIII. Sequence Features of the Regions of 1,081,958 bp Covered by Seventeen Physically assigned P1 and TAC Clones. DNA Research, 1998, 5, 379-391.	1.5	22
332	Structural Analysis of Arabidopsis thaliana Chromosome 5. III. Sequence Features of the Regions of 1,191,918 bp Covered by Seventeen Physically Assigned P1 Clones. DNA Research, 1997, 4, 401-404.	1.5	35
333	A Fine Physical Map of Arabidopsis thaliana Chromosome 5: Construction of a Sequence-ready Contig Map. DNA Research, 1997, 4, 371-378.	1.5	39
334	Sequence Analysis of the Genome of the Unicellular Cyanobacterium Synechocystis sp. Strain PCC6803. II. Sequence Determination of the Entire Genome and Assignment of Potential Protein-coding Regions. DNA Research, 1996, 3, 109-136.	1.5	2,544
335	Localization of mouse Rad51 and Lim15 proteins on meiotic chromosomes at late stages of prophase 1. Genes To Cells, 1996, 1, 379-389.	0.5	25
336	Sequence Analysis of the Genome of the Unicellular Cyanobacterium Synechocystis sp. Strain PCC6803. II. Sequence Determination of the Entire Genome and Assignment of Potential Protein-coding Regions (Supplement). DNA Research, 1996, 3, 185-209.	1.5	990
337	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 (Supplement). DNA Research, 1995, 2, 51-59.	1.5	22
338	Assignment of 82 Known Genes and Gene Clusters on the Genome of the Unicellular Cyanobacterium Synechocystis sp. Strain PCC6803. DNA Research, 1995, 2, 133-142.	1.5	29
339	Sequence Analysis of the Genome of the Unicellular Cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence Features in the 1 Mb Region from Map Positions 64% to 92% of the Genome. DNA Research, 1995, 2, 153-166.	1.5	292
340	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. DNA Research, 1995, 2, 37-43.	1.5	97
341	Characterization of a Mouse recA-like Gene Specifically Expressed in Testis. DNA Research, 1995, 2, 147-150.	1.5	23
342	Expression Profiles of a Human Gene Identified as a Structural Homologue of Meiosis-specific recA-like Genes. DNA Research, 1995, 2, 183-186.	1.5	24

#	ARTICLE	IF	CITATIONS
343	Structural Analysis of a recA-like Gene in the Genome of Arabidopsis thaliana. DNA Research, 1995, 2, 89-93.	1.5	46
344	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 (Supplement). DNA Research, 1994, 1, 251-262.	1.5	37
345	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
346	Characterization of cDNAs Induced in Meiotic Prophase in Lily Microsporocytes. DNA Research, 1994, 1, 15-26.	1.5	110
347	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
348	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). DNA Research, 1994, 1, 47-56.	1.5	137
349	A Physical Map of the Genome of a Unicellular Cyanobacterium Synechocystis sp. Strain PCC6803. DNA Research, 1994, 1, 303-307.	1.5	20
350	Identification and characterization of genes induced during sexual differentiation in Schizosaccharomyces pombe. Current Genetics, 1994, 26, 31-37.	0.8	56
351	APOPTOSIS OF MURINE LARGE INTESTINE IN ACUTE GRAFT-VERSUS-HOST DISEASE AFTER ALLOGENEIC BONE MARROW TRANSPLANTATION ACROSS MINOR HISTOCOMPATIBILITY BARRIERS. Transplantation, 1994, 57, 1284-1287.	0.5	17
352	Evidence of meiosis-specific regulation of gene expression in lily microsporocytes. Plant Science, 1993, 89, 31-41.	1.7	5
353	Changes in Intracellular cAMP Level and Activities of Adenylcyclase and Phosphodiesterase during Meiosis of Lily Microsporocytes.. Cell Structure and Function, 1992, 17, 335-339.	0.5	5
354	Tracking an Introduced Arbuscular Mycorrhizal Fungus in Allium fistulosum in a Field Condition With or Without Controlling Indigenous Fungi by Soil Fumigation As Well as Evaluation on Plant Phosphorus and Growth. Journal of Soil Science and Plant Nutrition, 0, , 1.	1.7	1
355	<i>KEEL LOSS1</i> Regulates Petal Number Along the Floral Dorsoventral Axis in <i>Lotus Japonicus</i> and <i>Pisum Sativum</i>. SSRN Electronic Journal, 0, , .	0.4	1