

A rice gene activation/knockout mutant resource for hi genomics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	14.5	295
2	The SnRK1A Protein Kinase Plays a Key Role in Sugar Signaling during Germination and Seedling Growth of Rice. <i>Plant Cell</i> , 2007, 19, 2484-2499.	6.6	207
3	T-DNA Insertion Mutants as a Resource for Rice Functional Genomics. , 2007, , 181-221.		10
4	Activation Tagging Systems in Rice. , 2007, , 333-353.		3
6	Activation tagging in plantsâ€™ generation of novel, gain-of-function mutations. <i>Australian Journal of Agricultural Research</i> , 2007, 58, 490.	1.5	15
7	Characterization of left-border flanking sequences of T-DNA integration in transgenic rice (<i>Oryza Tj ETQq1 1 0.784314 rgBT /Over	1.6	4
8	A barley activation tagging system. <i>Plant Molecular Biology</i> , 2007, 64, 329-347.	3.9	72
9	Analysis of gene-trap Ds rice populations in Korea. <i>Plant Molecular Biology</i> , 2007, 65, 373-384.	3.9	35
10	A rice phenomics studyâ€™ phenotype scoring and seed propagation of a T-DNA insertion-induced rice mutant population. <i>Plant Molecular Biology</i> , 2007, 65, 427-438.	3.9	52
11	Large-scale characterization of Tos17 insertion sites in a rice T-DNA mutant library. <i>Plant Molecular Biology</i> , 2007, 65, 587-601.	3.9	66
12	Global functional analyses of rice promoters by genomics approaches. <i>Plant Molecular Biology</i> , 2007, 65, 417-425.	3.9	14
13	Ds insertion mutagenesis as an efficient tool to produce diverse variations for rice breeding. <i>Plant Molecular Biology</i> , 2007, 65, 385-402.	3.9	39
14	A genome-wide gain-of-function analysis of rice genes using the FOX-hunting system. <i>Plant Molecular Biology</i> , 2007, 65, 357-371.	3.9	103
15	Rice Metabolomics. <i>Rice</i> , 2008, 1, 63-71.	4.0	55
16	Towards a better bowl of rice: assigning function to tens of thousands of rice genes. <i>Nature Reviews Genetics</i> , 2008, 9, 91-101.	16.3	143
17	Mutagenesis and Highâ€™Throughput Functional Genomics in Cereal Crops: Current Status. <i>Advances in Agronomy</i> , 2008, 98, 357-414.	5.2	4
18	Systems Approaches to Identifying Gene Regulatory Networks in Plants. <i>Annual Review of Cell and Developmental Biology</i> , 2008, 24, 81-103.	9.4	96
19	Engineering with Precision: Tools for the New Generation of Transgenic Crops. <i>BioScience</i> , 2008, 58, 391-401.	4.9	24

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20	A Novel Class of Gibberellin 2-Oxidases Control Semidwarfism, Tillering, and Root Development in Rice. <i>Plant Cell</i> , 2008, 20, 2603-2618.	6.6	410
21	A Versatile Transposon-Based Activation Tag Vector System for Functional Genomics in Cereals and Other Monocot Plants. <i>Plant Physiology</i> , 2008, 146, 189-199.	4.8	64
23	Transposon-based activation tagging in cereals. <i>Functional Plant Biology</i> , 2009, 36, 915.	2.1	12
24	Mutant Resources in Rice for Functional Genomics of the Grasses. <i>Plant Physiology</i> , 2009, 149, 165-170.	4.8	167
25	Development of an activation tagging system for the basidiomycetous medicinal fungus <i>Antrodia cinnamomea</i> . <i>Mycological Research</i> , 2009, 113, 290-297.	2.5	22
26	Activation tagging, an efficient tool for functional analysis of the rice genome. <i>Plant Molecular Biology</i> , 2009, 69, 69-80.	3.9	88
27	Systematic approaches to using the FOX hunting system to identify useful rice genes. <i>Plant Journal</i> , 2009, 57, 883-894.	5.7	121
28	Specific features of T-DNA insertion regions in transgenic plants. <i>Russian Journal of Genetics</i> , 2009, 45, 1289-1301.	0.6	3
29	Rice germination and seedling growth in the absence of oxygen. <i>Annals of Botany</i> , 2009, 103, 181-196.	2.9	238
30	Molecular analysis of rice plants harboring a multi-functional T-DNA tagging system. <i>Journal of Genetics and Genomics</i> , 2009, 36, 267-276.	3.9	31
31	Genetic technologies for the identification of plant genes controlling environmental stress responses. <i>Functional Plant Biology</i> , 2009, 36, 696.	2.1	11
32	Phenome Analysis in Plant Species Using Loss-of-Function and Gain-of-Function Mutants. <i>Plant and Cell Physiology</i> , 2009, 50, 1215-1231.	3.1	83
33	A rice DEAD-box protein, OsRH36, can complement an <i>Arabidopsis</i> <i>atrh36</i> mutant, but cannot functionally replace its yeast homolog <i>Dbp8p</i> . <i>Plant Molecular Biology</i> , 2010, 74, 119-128.	3.9	13
34	Comparative analyses of linkage maps and segregation distortion of two F2 populations derived from japonica crossed with indica rice. <i>Hereditas</i> , 2010, 147, 225-236.	1.4	22
35	Proteomic approaches to study plant-pathogen interactions. <i>Phytochemistry</i> , 2010, 71, 351-362.	2.9	90
36	Transgenic rice plants carrying RNA interference constructs of <i>AOS</i> (<i>allene oxide synthase</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	2.9	21
37	Natural and artificial mutants as valuable resources for functional genomics and molecular breeding. <i>International Journal of Biological Sciences</i> , 2010, 6, 228-251.	6.4	54
38	Insertional mutagenesis with Tos17 for functional analysis of rice genes. <i>Breeding Science</i> , 2010, 60, 486-492.	1.9	25

#	ARTICLE	IF	CITATIONS
39	Production and characterization of a large population of cDNA-overexpressing transgenic rice plants using Gateway-based full-length cDNA expression libraries. <i>Breeding Science</i> , 2010, 60, 575-585.	1.9	31
40	Rice transgenic resources with gain-of-function phenotypes. <i>Breeding Science</i> , 2010, 60, 493-501.	1.9	15
41	Abscisic Acid-Induced Resistance against the Brown Spot Pathogen <i>Cochliobolus miyabeanus</i> in Rice Involves MAP Kinase-Mediated Repression of Ethylene Signaling. <i>Plant Physiology</i> , 2010, 152, 2036-2052.	4.8	186
42	Transgene Integration, Expression and Stability in Plants: Strategies for Improvements. , 2010, , 201-237.		24
43	High-Throughput Characterization of Plant Gene Functions by Using Gain-of-Function Technology. <i>Annual Review of Plant Biology</i> , 2010, 61, 373-393.	18.7	40
44	Comparing Genetic Characteristics of Retrotransposon TOS17 During Different Tissue Culture Processes in the Rice Cultivars Nipponbare and Shishoubaimao. <i>Agricultural Sciences in China</i> , 2010, 9, 157-162.	0.6	1
45	TTRSIS: A Cloud Computing Platform for Rice Functional Genomics Research through a Reverse Genetics Approach. , 2011, , .		1
46	Development of an Efficient Inverse PCR Method for Isolating Gene Tags from T-DNA Insertional Mutants in Rice. <i>Methods in Molecular Biology</i> , 2011, 678, 139-146.	0.9	21
47	FOX-superroots of <i>Lotus corniculatus</i> , overexpressing <i>Arabidopsis</i> full-length cDNA, show stable variations in morphological traits. <i>Journal of Plant Physiology</i> , 2011, 168, 181-187.	3.5	13
48	Functional Genomics of Rice Pollen and Seed Development by Genome-wide Transcript Profiling and <i>Ds</i> Insertion Mutagenesis. <i>International Journal of Biological Sciences</i> , 2011, 7, 28-40.	6.4	8
49	Screening for resistance against <i>Pseudomonas syringae</i> in rice-FOX <i>Arabidopsis</i> lines identified a putative receptor-like cytoplasmic kinase gene that confers resistance to major bacterial and fungal pathogens in <i>Arabidopsis</i> and rice. <i>Plant Biotechnology Journal</i> , 2011, 9, 466-485.	8.3	68
50	Rice <i>SIZ1</i> , a SUMO E3 ligase, controls spikelet fertility through regulation of anther dehiscence. <i>New Phytologist</i> , 2011, 189, 869-882.	7.3	65
51	Genome walking in eukaryotes. <i>FEBS Journal</i> , 2011, 278, 3953-3977.	4.7	45
52	Activation Tagging. <i>Methods in Molecular Biology</i> , 2011, 876, 117-133.	0.9	11
53	Functional characterisation of OsCPK21, a calcium-dependent protein kinase that confers salt tolerance in rice. <i>Plant Molecular Biology</i> , 2011, 75, 179-191.	3.9	141
54	RiceFOX: A Database of <i>Arabidopsis</i> Mutant Lines Overexpressing Rice Full-Length cDNA that Contains a Wide Range of Trait Information to Facilitate Analysis of Gene Function. <i>Plant and Cell Physiology</i> , 2011, 52, 265-273.	3.1	72
55	Strategies for Silencing and Escape. <i>International Review of Cell and Molecular Biology</i> , 2011, 292, 119-152.	3.2	39
56	RiceXPro: a platform for monitoring gene expression in japonica rice grown under natural field conditions. <i>Nucleic Acids Research</i> , 2011, 39, D1141-D1148.	14.5	227

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57	Clone DB: an integrated NCBI resource for clone-associated data. <i>Nucleic Acids Research</i> , 2012, 41, D1070-D1078.	14.5	14
58	Effort and Contribution of T-DNA Insertion Mutant Library for Rice Functional Genomics Research in China: Review and Perspective. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 953-966.	8.5	17
59	Rice functional genomics research: Progress and implications for crop genetic improvement. <i>Biotechnology Advances</i> , 2012, 30, 1059-1070.	11.7	100
60	Transformation Using Controlled cDNA Overexpression System. <i>Methods in Molecular Biology</i> , 2012, 913, 277-290.	0.9	5
61	Plant Salt Tolerance. <i>Methods in Molecular Biology</i> , 2012, , .	0.9	9
62	Transgenic Plants as Gene-Discovery Tools. , 0, , .		0
63	Serotonin accumulation in transgenic rice by over-expressing tryptophan decarboxylase results in a dark brown phenotype and stunted growth. <i>Plant Molecular Biology</i> , 2012, 78, 525-543.	3.9	56
64	Ac/Ds-transposon activation tagging in poplar: a powerful tool for gene discovery. <i>BMC Genomics</i> , 2012, 13, 61.	2.8	33
65	Genome-wide <i>LORE1</i> retrotransposon mutagenesis and high-throughput insertion detection in <i>Lotus japonicus</i> . <i>Plant Journal</i> , 2012, 69, 731-741.	5.7	149
66	Rice LGD1 containing RNA binding activity affects growth and development through alternative promoters. <i>Plant Journal</i> , 2012, 71, 288-302.	5.7	21
67	Magnetic nanoparticle-based immunosensor for electrochemical detection of hepatitis B surface antigen. <i>Analytical Biochemistry</i> , 2013, 441, 1-7.	2.4	41
68	Transgenic Cotton. <i>Methods in Molecular Biology</i> , 2013, , .	0.9	2
70	Analysis of the early-flowering mechanisms and generation of T-DNA tagging lines in Kitaake, a model rice cultivar. <i>Journal of Experimental Botany</i> , 2013, 64, 4169-4182.	4.8	48
71	Mutant Resources for the Functional Analysis of the Rice Genome. <i>Molecular Plant</i> , 2013, 6, 596-604.	8.3	112
72	Activation tagging in <i>Salvia miltiorrhiza</i> can cause increased leaf size and accumulation of tanshinone I and IIA in its roots. , 2013, 54, 37.		6
73	How important are transposons for plant evolution?. <i>Nature Reviews Genetics</i> , 2013, 14, 49-61.	16.3	711
75	Investigating Transgene Integration and Organization in Cotton (<i>Gossypium hirsutum</i> L.) Genome. <i>Methods in Molecular Biology</i> , 2013, 958, 95-107.	0.9	2
76	RiceFRIEND: a platform for retrieving coexpressed gene networks in rice. <i>Nucleic Acids Research</i> , 2013, 41, D1214-D1221.	14.5	163

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77	RiceXPro Version 3.0: expanding the informatics resource for rice transcriptome. <i>Nucleic Acids Research</i> , 2013, 41, D1206-D1213.	14.5	312
78	International Consortium of Rice Mutagenesis: resources and beyond. <i>Rice</i> , 2013, 6, 39.	4.0	53
79	High-throughput analysis of rice genes by means of the heterologous full-length cDNA overexpressor (FOX)-hunting system. <i>International Journal of Developmental Biology</i> , 2013, 57, 517-523.	0.6	6
80	Overexpression of DWARF AND LESION FORMATION 1 (DLE1) causes altered activation of plant defense system in <i>Arabidopsis thaliana</i> . <i>Plant Biotechnology</i> , 2013, 30, 385-392.	1.0	5
81	Increasing Leaf Vein Density by Mutagenesis: Laying the Foundations for C4 Rice. <i>PLoS ONE</i> , 2014, 9, e94947.	2.5	36
82	Discovery and Characterization of Two Novel Salt-Tolerance Genes in <i>Puccinellia tenuiflora</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 16469-16483.	4.1	6
83	Phenotype to genotype using forward-genetic Mu-seq for identification and functional classification of maize mutants. <i>Frontiers in Plant Science</i> , 2014, 4, 545.	3.6	20
84	The bHLH142 Transcription Factor Coordinates with TDR1 to Modulate the Expression of <i>EAT1</i> and Regulate Pollen Development in Rice. <i>Plant Cell</i> , 2014, 26, 2486-2504.	6.6	142
85	Genome-wide patterns of large size presence/absence variants in sorghum. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 24-37.	8.5	22
87	Application of T-DNA activation tagging to identify glutamate receptor-like genes that enhance drought tolerance in plants. <i>Plant Cell Reports</i> , 2014, 33, 617-631.	5.6	36
88	A Positive Feedback Loop between HEAT SHOCK PROTEIN101 and HEAT STRESS-ASSOCIATED 32-KD PROTEIN Modulates Long-Term Acquired Thermotolerance Illustrating Diverse Heat Stress Responses in Rice Varieties. <i>Plant Physiology</i> , 2014, 164, 2045-2053.	4.8	120
89	Progress in TILLING as a tool for functional genomics and improvement of crops. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 425-443.	8.5	84
90	17. Induced mutagenesis for improving plant abiotic stress tolerance. , 2014, , 345-376.		21
91	Action of multiple intra-QTL genes concerted around a co-localized transcription factor underpins a large effect QTL. <i>Scientific Reports</i> , 2015, 5, 15183.	3.3	58
92	Non-canonical structure, function and phylogeny of the B sister MADS box gene OsMADS30 of rice. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 16-23.	8.7	16
93	Alteration of osa-miR156e expression affects rice plant architecture and strigolactones (SLs) pathway. <i>Plant Cell Reports</i> , 2015, 34, 767-781.	5.6	44
94	Identification of differentially expressed transcripts associated with bast fibre development in <i>Corchorus capsularis</i> by suppression subtractive hybridization. <i>Planta</i> , 2015, 241, 371-385.	3.2	14
95	Characterization of a potato activation-tagged mutant, nikku, and its partial revertant. <i>Planta</i> , 2015, 241, 1481-1495.	3.2	3

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97	High-throughput generation of an activation-tagged mutant library for functional genomic analyses in tobacco. <i>Planta</i> , 2015, 241, 629-640.	3.2	9
98	Expression of eggplant ascorbate peroxidase increases the tolerance of transgenic rice plants to flooding stress. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2015, 24, 257-267.	1.7	21
99	Overexpression of <i>BSR1</i> confers broad-spectrum resistance against two bacterial diseases and two major fungal diseases in rice. <i>Breeding Science</i> , 2016, 66, 396-406.	1.9	26
100	Lack of Genotype and Phenotype Correlation in a Rice T-DNA Tagged Line Is Likely Caused by Introgression in the Seed Source. <i>PLoS ONE</i> , 2016, 11, e0155768.	2.5	7
101	Gene Overexpression Resources in Cereals for Functional Genomics and Discovery of Useful Genes. <i>Frontiers in Plant Science</i> , 2016, 7, 1359.	3.6	16
102	Genetic resources offer efficient tools for rice functional genomics research. <i>Plant, Cell and Environment</i> , 2016, 39, 998-1013.	5.7	42
103	Somaclonal variation does not preclude the use of rice transformants for genetic screening. <i>Plant Journal</i> , 2016, 85, 648-659.	5.7	34
104	Transposon Ds Mediated Insertional Mutagenesis in Rice (<i>Oryza sativa</i>). <i>Current Protocols in Plant Biology</i> , 2016, 1, 466-487.	2.8	6
105	Nitrogen recycling from the xylem in rice leaves: dependence upon metabolism and associated changes in xylem hydraulics. <i>Journal of Experimental Botany</i> , 2016, 67, 2901-2911.	4.8	35
106	An Indexed, Mapped Mutant Library Enables Reverse Genetics Studies of Biological Processes in <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2016, 28, 367-387.	6.6	336
107	A New Enzyme-Free Electrochemical Immunoassay for <i>Escherichia coli</i> Detection using Magnetic Nanoparticles. <i>Analytical Letters</i> , 2016, 49, 245-257.	1.8	18
108	The phenome analysis of mutant alleles in Leucine-Rich Repeat Receptor-Like Kinase genes in rice reveals new potential targets for stress tolerant cereals. <i>Plant Science</i> , 2016, 242, 240-249.	3.6	27
109	Sustainable Agriculture Reviews. <i>Sustainable Agriculture Reviews</i> , 2017, , .	1.1	12
110	Bioengineering Hairy Roots: Phytoremediation, Secondary Metabolism, Molecular Pharming, Plant-Plant Interactions and Biofuels. <i>Sustainable Agriculture Reviews</i> , 2017, , 213-251.	1.1	17
111	Role of Biotechnology in Rice Production. , 2017, , 487-547.		7
112	Overexpression of the ascorbate peroxidase gene from eggplant and sponge gourd enhances flood tolerance in transgenic Arabidopsis. <i>Journal of Plant Research</i> , 2017, 130, 373-386.	2.4	17
113	Characterization of Transgenic <i>Kalanchoe</i> and <i>Petunia</i> with Organ-Specific Expression of GUS or GA 2 ox Genes Led by the Deletion BOX-I Version (dBI) of the PAL1 Promoter. <i>Journal of Plant Growth Regulation</i> , 2017, 36, 424-435.	5.1	5
114	Gain-of-function mutagenesis approaches in rice for functional genomics and improvement of crop productivity. <i>Briefings in Functional Genomics</i> , 2017, 16, elw041.	2.7	8

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115	Auxin transport and response requirements for root hydrotropism differ between plant species. <i>Journal of Experimental Botany</i> , 2017, 68, 3441-3456.	4.8	19
116	The Sequences of 1504 Mutants in the Model Rice Variety Kitaake Facilitate Rapid Functional Genomic Studies. <i>Plant Cell</i> , 2017, 29, 1218-1231.	6.6	138
117	A collection of enhancer trap insertional mutants for functional genomics in tomato. <i>Plant Biotechnology Journal</i> , 2017, 15, 1439-1452.	8.3	33
118	Integration of <i>Agrobacterium</i> T-DNA into the Plant Genome. <i>Annual Review of Genetics</i> , 2017, 51, 195-217.	7.6	214
119	Biotechnology of Medicinal Plants and Fungi in Taiwan: Production of Bioactive Secondary Metabolites in In Vitro Culture Systems. <i>Medicinal and Aromatic Plants of the World</i> , 2017, , 459-483.	0.2	0
120	Ectopic Expression of WINDING 1 Leads to Asymmetrical Distribution of Auxin and a Spiral Phenotype in Rice. <i>Plant and Cell Physiology</i> , 2017, 58, 1494-1506.	3.1	3
121	Large-scale phenomics analysis of a T-DNA tagged mutant population. <i>GigaScience</i> , 2017, 6, 1-7.	6.4	15
122	A novel method for sensitive, low-cost and portable detection of hepatitis B surface antigen using a personal glucose meter. <i>Journal of Immunological Methods</i> , 2018, 458, 26-32.	1.4	21
123	The COMPASS-Like Complex Promotes Flowering and Panicle Branching in Rice. <i>Plant Physiology</i> , 2018, 176, 2761-2771.	4.8	43
124	Comparative Analysis of Flanking Sequence Tags of T-DNA/Transposon Insertional Mutants and Genetic Variations of Fast-neutron Treated Mutants in Rice. <i>Journal of Plant Biology</i> , 2018, 61, 80-84.	2.1	8
125	Responses of contrasting rice genotypes to excess manganese and their implications for lignin synthesis. <i>Plant Physiology and Biochemistry</i> , 2018, 123, 252-259.	5.8	33
126	Pervasive read-through transcription of T-DNAs is frequent in tobacco BY-2 cells and can effectively induce silencing. <i>BMC Plant Biology</i> , 2018, 18, 252.	3.6	3
127	Cas9/sgRNA-based genome editing and other reverse genetic approaches for functional genomic studies in rice. <i>Briefings in Functional Genomics</i> , 2018, 17, 339-351.	2.7	5
128	Whole Genome Characterization of a Few EMS-Induced Mutants of Upland Rice Variety Nagina 22 Reveals a Staggeringly High Frequency of SNPs Which Show High Phenotypic Plasticity Towards the Wild-Type. <i>Frontiers in Plant Science</i> , 2018, 9, 1179.	3.6	40
129	The Polycistronic miR166k-166h Positively Regulates Rice Immunity via Post-transcriptional Control of EIN2. <i>Frontiers in Plant Science</i> , 2018, 9, 337.	3.6	83
130	<i>OsDCL1a</i> activation impairs phytoalexin biosynthesis and compromises disease resistance in rice. <i>Annals of Botany</i> , 2019, 123, 79-93.	2.9	15
131	Insertional Mutagenesis Approaches and Their Use in Rice for Functional Genomics. <i>Plants</i> , 2019, 8, 310.	3.5	25
132	Mutagenesis in Rice: The Basis for Breeding a New Super Plant. <i>Frontiers in Plant Science</i> , 2019, 10, 1326.	3.6	82

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133	A Sequence-Indexed <i>Mutator</i> Insertional Library for Maize Functional Genomics Study. <i>Plant Physiology</i> , 2019, 181, 1404-1414.	4.8	28
134	Climate-Resilient Future Crop: Development of C4 Rice. , 2019, , 111-124.		7
135	Type-B response regulators of rice play key roles in growth, development, and cytokinin signaling. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	38
136	EAT-Rice: A predictive model for flanking gene expression of T-DNA insertion activation-tagged rice mutants by machine learning approaches. <i>PLoS Computational Biology</i> , 2019, 15, e1006942.	3.2	4
137	Identification of sugar response complex in the metallothionein OsMT2b gene promoter for enhancement of foreign protein production in transgenic rice. <i>Plant Cell Reports</i> , 2019, 38, 899-914.	5.6	1
138	Development of an activation tagging system for maize. <i>Plant Direct</i> , 2019, 3, e00118.	1.9	4
139	Osa-miR7695 enhances transcriptional priming in defense responses against the rice blast fungus. <i>BMC Plant Biology</i> , 2019, 19, 563.	3.6	34
140	Comparative transcriptome analysis of two common wheat varieties induced by 7Li-ion beam irradiation reveals mutation hotspot regions and associated pathways. <i>Radiation Physics and Chemistry</i> , 2020, 170, 108650.	2.8	9
141	Development of a large population of activation-tagged mutants in an elite <i>indica</i> rice variety. <i>Plant Breeding</i> , 2020, 139, 328-343.	1.9	6
142	<i>BonnMu</i> : A Sequence-Indexed Resource of Transposon-Induced Maize Mutations for Functional Genomics Studies. <i>Plant Physiology</i> , 2020, 184, 620-631.	4.8	25
143	An ethyl methanesulfonate-induced neutral mutant bridging method efficiently identifies spontaneously mutated genes in rice. <i>Plant Journal</i> , 2020, 104, 1129-1141.	5.7	3
144	Expression of Human papillomavirus type 52 L1 capsid gene in <i>Oryza sativa</i> involved in cytoprotective activities. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2020, 48, 40-52.	1.1	0
146	<i>Rice Big Grain 1</i> promotes cell division to enhance organ development, stress tolerance and grain yield. <i>Plant Biotechnology Journal</i> , 2020, 18, 1969-1983.	8.3	25
147	PAP90, a novel rice protein plays a critical role in regulation of D1 protein stability of PSII. <i>Journal of Advanced Research</i> , 2021, 30, 197-211.	9.5	6
149	Collection, preservation and distribution of <i>Oryza</i> genetic resources by the National Bioresource Project RICE (NBRP-RICE). <i>Breeding Science</i> , 2021, 71, 291-298.	1.9	5
150	Metabolomics in Rice Improvement. , 2021, , 83-103.		0
151	OsARF11 Promotes Growth, Meristem, Seed, and Vein Formation during Rice Plant Development. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4089.	4.1	18
152	A drought-responsive rice amidohydrolase is the elusive plant guanine deaminase with the potential to modulate the epigenome. <i>Physiologia Plantarum</i> , 2021, 172, 1853-1866.	5.2	2

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153	Comparisons within the Rice GA 2-Oxidase Gene Family Revealed Three Dominant Paralogs and a Functional Attenuated Gene that Led to the Identification of Four Amino Acid Variants Associated with GA Deactivation Capability. <i>Rice</i> , 2021, 14, 70.	4.0	5
154	SET DOMAIN GROUP 721 protein functions in saline alkaline stress tolerance in the model rice variety Kitaake. <i>Plant Biotechnology Journal</i> , 2021, 19, 2576-2588.	8.3	29
155	Characterization and Evaluation of Transgenic Rice Pyramided with the Pi Genes Pib, Pi25 and Pi54. <i>Rice</i> , 2021, 14, 78.	4.0	9
156	Era-like GTP protein gene expression in rice. <i>Brazilian Journal of Biology</i> , 2021, 82, e250700.	0.9	0
157	Mutant Resources for Functional Analysis of the Rice Genome. , 2013, , 81-115.		6
158	Methods for Rice Phenomics Studies. <i>Methods in Molecular Biology</i> , 2011, 678, 129-138.	0.9	5
159	Activation Tagging and Insertional Mutagenesis in Barley. <i>Methods in Molecular Biology</i> , 2011, 678, 107-128.	0.9	11
160	Reverse Genetics in Rice Using Tos17. <i>Methods in Molecular Biology</i> , 2013, 1057, 205-221.	0.9	6
162	Overexpression of OsSAP16 Regulates Photosynthesis and the Expression of a Broad Range of Stress Response Genes in Rice (<i>Oryza sativa</i> L.). <i>PLoS ONE</i> , 2016, 11, e0157244.	2.5	14
163	Development of pollen mediated activation tagging system for Phalaenopsis and Doritaenopsis. <i>Electronic Journal of Biotechnology</i> , 2012, 15, .	2.2	3
164	Towards a C4 Rice. <i>Asian Journal of Cell Biology</i> , 2012, 7, 13-31.	0.4	11
165	Activation of CDC48 and acetyltransferase encoding genes contributes to enhanced abiotic stress tolerance and improved productivity traits in rice. <i>Plant Physiology and Biochemistry</i> , 2021, 168, 329-339.	5.8	3
166	Unravelling Gene Function Through Mutagenesis. , 2010, , 437-467.		0
167	Feasibility analysis of leaf disc samples produced via agroinfiltration for promoter trapping studies. <i>Emirates Journal of Food and Agriculture</i> , 2010, 22, 448.	1.0	0
168	Rice functional genomics using T-DNA mutants. <i>Journal of Plant Biotechnology</i> , 2010, 37, 133-143.	0.4	1
169	Concepts and Strategies for Reverse Genetics in Field, Forest and Bioenergy Crop Species. , 2010, , 354-398.		1
170	A comprehensive and efficient genomic PCR analysis for the identification of transgenes in rice full-length cDNA-overexpressing lines. <i>Ikushugaku Kenkyu</i> , 2013, 15, 160-166.	0.3	0
171	High-level gene expression in differentiating xylem of tobacco driven by a 2.0 [^] kb Poplar COMT2 promoter and a 4 [^] times35S enhancer. <i>Plant Biotechnology</i> , 2013, 30, 191-198.	1.0	0

#	ARTICLE	IF	CITATIONS
172	Biotechnological Approaches for Improvement and Conservation of Prunus Species. , 2014, , 456-478.		0
173	Plant functional genomics: Approaches and applications. , 2016, , 157-186.		2
174	Induction of Male-Sterility by Controlling of Gibberellin Biosynthesis in Rice (<i>Oryza sativa</i>). Plant Breeding and Biotechnology, 2018, 6, 19-29.	0.9	0
175	Investigating Transgene Integration and Organization in Cotton (<i>Gossypium hirsutum</i> L.) Genome. Methods in Molecular Biology, 2019, 1902, 123-136.	0.9	1
176	Enhancing Crop Breeding Using Population Genomics Approaches. Population Genomics, 2020, , 1.	0.5	0
177	Phalaenopsis orchid miniaturization by overexpression of OsGA2ox6, a rice GA2-oxidase gene. , 2020, 61, 10.		9
178	Closer vein spacing by ectopic expression of nucleotide-binding and leucine-rich repeat proteins in rice leaves. Plant Cell Reports, 2022, 41, 319-335.	5.6	1
179	Using Machine Learning Approaches to Predict Target Gene Expression in Rice T-DNA Insertional Mutants. Frontiers in Genetics, 2021, 12, 798107.	2.3	2
188	Simultaneous detection of <scp>miRNA</scp> and <scp>mRNA</scp> at the singleâ€cell level in plant tissues. Plant Biotechnology Journal, 2023, 21, 136-149.	8.3	2
189	Retrotransposons: How the continuous evolutionary front shapes plant genomes for response to heat stress. Frontiers in Plant Science, 0, 13, .	3.6	5
190	Proof of concept and early development stage of market-oriented high iron and zinc rice expressing dicot ferritin and rice nicotianamine synthase genes. Scientific Reports, 2023, 13, .	3.3	4
191	Developments of Plant-Based Emulsion-Type Sausage by Using Grey Oyster Mushrooms and Chickpeas. Foods, 2023, 12, 1564.	4.3	6
193	Introduction/Review. , 2023, , 1-73.		0
194	Rice transformation treatments leave specific epigenome changes beyond tissue culture. Plant Physiology, 2023, 193, 1297-1312.	4.8	1
195	Plant Functional Genomics Based on Highâ€Throughput CRISPR Library Knockout Screening: A Perspective. Genetics & Genomics Next, 2024, 5, .	1.5	0
196	Catalase associated with antagonistic changes of abscisic acid and gibberellin response, biosynthesis and catabolism is involved in eugenol-inhibited seed germination in rice. Plant Cell Reports, 2024, 43, .	5.6	0
197	A newly evolved riceâ€specific gene <i>JAUP1</i> regulates jasmonate biosynthesis and signalling to promote root development and multiâ€stress tolerance. Plant Biotechnology Journal, 2024, 22, 1417-1432.	8.3	1