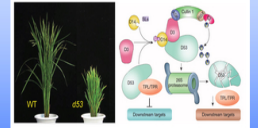




植物基因组学国家重点实验室

State Key Laboratory of Plant Genomics (SKLPG)
Institute of Genetics and Developmental Biology, Institute of Microbiology
Chinese Academy of Sciences



DWARF 53 acts as a repressor of strigolactone signalling in rice (*Nature* 504: 401-405, 2013)

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2016年

序号	作者	文章题目	杂志	年卷期	5年平 均影响 因子	类型
1	Cui, X.#, Lu, F.#, Qiu, Q.#, Zhou, B.#, Gu, L., Zhang, S., Kang, Y., Cui, X., Ma, X., Yao, Q., Ma, J., Zhang, X., and Cao, X.*	REF6 recognizes a specific DNA sequence to demethylate H3K27me3 and regulate organ boundary formation in <i>Arabidopsis</i>	<i>Nat Genet</i>	2016, 48: 694-701	32.197	A
2	Li, L.#*, Kim, P.#, Yu, L.#, Cai, G.#, Chen, S., Alfano, J., and Zhou, J.M.*	Activation-dependent destruction of a co-receptor by a <i>Pseudomonas syringae</i> effector dampens plant immunity	<i>Cell Microbe</i>	<i>Host</i> 2016, 504-514	20: 12.944	A
3	Jia, W.#, Li, B.#, Li, S.#, Liang, Y., Wu, X., Ma, M., Wang, J., Gao, J., Cai, Y., Zhang, Y., Wang, Y., Li, J.*, and Wang, Y.*	Mitogen-activated protein kinase cascade MKK7-MPK6 plays important roles in plant development and regulates shoot branching by phosphorylating PIN1 in <i>Arabidopsis</i>	<i>PLoS Biol</i>	2016, 14: e1002550	10.731	A
4	Deng, X.#, Lu, T.#, Wang, L.#, Gu, L., Sun, J., Kong, X., Liu, C.*, and Cao, X.*	Recruitment of the NineTeen Complex to the activated spliceosome requires AtPRMT5	<i>Proc Natl Acad Sci USA</i>	2016, 113: 5447-5452	10.285	A
5	Ji, J.#, Tang, D.#, Shen, Y.#, Xue, Z., Wang, H., Shi, W., Zhang, C., Du, G., Li, Y., and Cheng, Z.*	p31 ^{comet} , a member of the synaptonemal complex, participates in meiotic DSB formation in rice	<i>Proc Natl Acad Sci USA</i>	2016, 113: 10577-10582	10.285	A
6	Zhou, H.#, Wang, L.#, Liu, G.#, Meng, X., Jing, Y., Shu, X., Kong, X., Sun, J., Yu, H., Smith, S., Wu, D., and Li, J.*	Critical roles of soluble starch synthase SSIIIa and granule-bound starch synthase Waxy in synthesizing resistant starch in rice	<i>Proc Natl Acad Sci USA</i>	2016, 113: 12844-12849	10.285	A
7	Li, D.#, Huang, Z.#, Song, S.#*, Xin, Y.#*, Mao, D.#, Lv, Q.#, Zhou, M., Tian, D., Tang, M., Wu, Q., Liu, X., Chen, T., Song, X., Fu, X., Zhao, B., Liang, C., Li, A., Liu, G., Li, S., Hu, S., Cao, X., Yu, J., Yuan, L.*, Chen, C.*, and Zhu, L.*	Integrated analysis of phenome, genome, and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase	<i>Proc Natl Acad Sci USA</i>	2016, 113: E6026-E6035	10.285	A
8	Li, S.#, Wang, W.#, Gao, J., Yin, K., Wang, R., Wang, C., Pertersen, M., Mundy, J., and Qiu, J.*	MYB75 phosphorylation by MPK4 is required for light-induced anthocyanin accumulation in <i>Arabidopsis</i>	<i>Plant Cell</i>	2016, 28: 2866-2883	9.88	A
9	Gao, S., Fang, J., Xu, F., Wang, W., and Chu, C.*	Rice HOX12 regulates panicle exertion by directly modulating the expression of <i>ELONGATED UPPERMOST INTERNODE1</i>	<i>Plant Cell</i>	2016, 28: 680-695	9.88	A
10	Zhou, J.M.*	Plant pathology: A life and death struggle in rice blast disease	<i>Curr Biol</i>	2016, 26: R843-R845	9.733	A
11	Liang, X.#, Ding, P.#, Lian, K., Wang, J., Ma, M., Li, L., Li, L., Li, M., Zhang, X., Chen, S., Zhang, Y.*, and Zhou, J.M.*	<i>Arabidopsis</i> heterotrimeric G proteins regulate immunity by directly coupling to the FLS2 receptor	<i>eLife</i>	2016, 5: e13568	8.533	A
12	Li, J.*	Rice breeding: never off the table	<i>Natl Sci Rev</i>	2016, 3: 275	8	A
13	Deng, X., Song, X., Wei, L., Liu, C., and Cao, X.*	Epigenetic regulation and the epigenomic landscape in rice	<i>Natl Sci Rev</i>	2016, 3: 309-327	8	A
14	Zhao, Y., Zhou, T., and Guo, H.*	Hyphopodium-specific VdNoxB/VdPls1-dependent ROS-Ca ²⁺ signaling is required for plant infection by <i>Verticillium dahliae</i>	<i>PLoS Pathog</i>	2016, 12: e1005793	7.758	A
15	Wang, L., Pan, Y., Yuan, Z., Zhang, H., Peng B., Wang, F., Qian, W*.	Two-component signaling system VgrRS directly senses extracytoplasmic and intracellular iron to control bacterial adaptation under iron depleted stress	<i>PLoS Pathog</i>	2016, 12:e1006133	7.758	A
16	Shi, B.#, Zhang, C.#, Tian, C., Wang, J., Wang, Q., Xu, T., Xu, Y., Ohno, C., Sablowski, R., Heisler, M., Theres, K., Wang, Y.*, and Jiao, Y.*	Two-step regulation of a meristematic cell population acting in shoot branching in <i>Arabidopsis</i>	<i>PLoS Genet</i>	2016, 12: e1006168	7.481	A
17	Jiao, Y.*	Trichome formation: Gibberellins on the move	<i>Plant Physiol</i>	2016, 170: 1174-1175	7.367	A
18	Li, Y.#, Han, L.#, Wang, H., Zhang, J., Sun, S., Feng, D., Yang, C., Sun, Y., Zhong, N.*, and Xia, G.*	The thioredoxin GbNRX1 plays a crucial role in homeostasis of apoplastic reactive oxygen species in response to <i>Verticillium dahliae</i> infection in cotton	<i>Plant Physiol</i>	2016, 170: 2392-2406	7.367	A
19	Wang, H.#, Hu, Q., Tang, D., Liu, X., Du, G., She, Y., Li, Y., and Cheng, Z.*	OsDMC1 is not required for homologous pairing in rice meiosis	<i>Plant Physiol</i>	2016, 171: 230-241	7.367	A

20	Hu, Q.#, Tang, D.#, Wang, H.#, Shen, Y., Chen, X., Ji, J., Du, G., Li, Y., and Cheng Z.*	The exonuclease homolog OsRAD1 promotes accurate meiotic double-strand break repair by suppressing nonhomologous end joining	<i>Plant Physiol</i>	2016, 172: 7.367-1105-1116	A
21	Wei, G., Tian, P., Zhang, F., Qin, H., Miao, H., Chen, Q., Hu, Z., Cao, L., Wang, M., Gu, X., Huang, S., Chen, M., and Wang, G.*	Integrative analyses of non-targeted volatile profiling and transcriptome data provide molecular insight into VOC diversity in cucumber plants (<i>Cucumis sativus</i> L.)	<i>Plant Physiol</i>	2016, 172: 603-618	A
22	Wang, H., Jiao, X., Kong, X., Hamera, S., Wu, Y., Chen, X., Fang, R., and Yan, Y.*	A signaling cascade from miR444 to RDR1 in rice antiviral RNA silencing pathway	<i>Plant Physiol</i>	2016, 172: 413-421	A
23	Zhang, G., Song, X., Guo, H., Wu, Y., Chen, X.*, and Fang, R.*	A small G protein as a novel component of the rice brassinosteroid signal transduction	<i>Mol Plant</i>	2016, 9: 1260-1271	A
24	Li, C.*, Li, J.*, Harter, K., Lee, Y., Leung, J., Martinoia, E., Matsuoka, M., Offring, R., Qu, L., Schroeder, J., and Zhao, Y.	Toward a molecular understanding of plant hormone actions	<i>Mol Plant</i>	2016, 9: 1-3	A
25	Pan, W.#, Tao, J.#, Cheng, T., Bian, X., Wei, W., Zhang, W., Ma, B., Chen, S.*, and Zhang, J.*	Soybean <i>miR172a</i> improves salt tolerance and can function as a long distance signal	<i>Mol Plant</i>	2016, 9: 1337-1340	A
26	Wang, Y., Liang, C., Wu, S., Zhang, X., Tang, J., Jian, G., Jiao, G., Li, F., and Chu, C.*	Significant improvement of cotton <i>Verticillium</i> wilt resistance by manipulating the expression of <i>Gastrodia</i> antifungal proteins	<i>Mol Plant</i>	2016, 9: 1436-1439	A
27	Yang, X.#, Nian, J.#, Xie, Q., Feng, J., Zhang, F., Jing, H., Zhang, J., Dong, G., Liang, Y., Peng, J., Wang, G., Qian, Q., and Zuo, J.*	Rice ferredoxin-dependent glutamate synthase regulates nitrogen-carbon metabolomes and is genetically differentiated between <i>japonica</i> and <i>indica</i> subspecies	<i>Mol Plant</i>	2016, 9: 1520-1534	A
28	Xue, Z.#, Li, Y.#, Zhang, L., Shi, W., Zhang, C., Feng, M., Zhang, F., Tang, D., Yu, H., Gu, M., and Cheng, Z.*	OsMTPVIB promotes meiotic DNA double-strand break formation in rice	<i>Mol Plant</i>	2016, 9: 1535-1538	A
29	Yu, F., Lou, L., Tian, M., Li, Q., Ding, Y., Cao, X., Wu, Y., Belda-Palazon, B., Rodriguez, P., Yang, S., and Xie, Q.*	ESCRT-I component VPS23A affects ABA signaling by recognizing ABA receptors for endosomal degradation	<i>Mol Plant</i>	2016, 9: 1570-1582	A
30	Yu, F.#, Wu, Y.#, and Xie, Q.*	Ubiquitin-proteasome system in ABA signaling: From perception to action	<i>Mol Plant</i>	2016, 9: 21-33	A
31	Shu, K., Liu, X., Xie, Q.*, and He, Z.*	Two faces of one seed: hormonal regulation of dormancy and germination	<i>Mol Plant</i>	2016, 9: 34-45	A
32	Yu, H.#, Tian, C.#, Yu, Y., and Jiao, Y.*	Transcriptome survey of the contribution of alternative splicing to proteome diversity in <i>Arabidopsis thaliana</i>	<i>Mol Plant</i>	2016, 9: 749-752	A
33	Zhang, T., Jin, Y., Zhao, J., Gao, F., Zhou, B., Fang, Y., and Guo, H.*	Host-induced gene silencing of the target gene in fungal cells confers effective resistance to the cotton wilt disease pathogen <i>Verticillium dahliae</i>	<i>Mol Plant</i>	2016, 9: 939-942	A
34	Wang, H., Xu, X., Vieira, F., Xiao, Y., Li, Z., Wang, J.*, Nielsen, R.*, and Chu, C.*	The power of inbreeding: NGS based GWAS of rice reveals convergent evolution during rice domestication	<i>Mol Plant</i>	2016, 9: 975-985	A
35	Jiao, Y.#, Hamant, O.#, Ding, Z.#, and Zhang, X.*	Meristem biology flourishes under Mt. Tai	<i>Mol Plant</i>	2016, 9: 1224-1227	A
36	Lu, X., Li, Q., Xiong, Q., Li, W., Bi, Y., Lai, Y., Liu, X., Man, W., Zhang, W., Ma, B., Chen, S.*, and Zhang, J.*	The transcriptomic signature of developing soybean seeds reveals genetic basis of seed trait adaptation during domestication	<i>Plant J</i>	2016, 86: 530-544	A
37	Song, L., Wang, R., Zhang, L., Wang, Y., and Yao, S.*	<i>CRR1</i> encoding callose synthase functions in ovary expansion by affecting vascular cell patterning in rice	<i>Plant J</i>	2016, 88: 620-632	A
38	Cheng, H., Han, L., Yang, C., Wu, X., Zhong, N., Wu, J., Wang, F., Wang, H.*, and Xia, G.*	The cotton MYB108 forms a positive feedback regulation loop with CML11 and participates in the defense response against <i>Verticillium dahliae</i> infection	<i>J Exp Bot</i>	2016, 67: 1935-1950	A
39	Shu, K., Chen, Q., Wu, Y., Liu, R., Zhang, H., Wang, S., Tang, S., Yang, W., and Xie, Q.*	ABSCISIC ACID-INSENSITIVE 4 negatively regulates flowering through directly promoting <i>Arabidopsis</i> <i>FLOWERING LOCUS C</i> transcription	<i>J Exp Bot</i>	2016, 67: 195-205	A
40	Liu, X.#, Li, M.#, Liu, K., Tang, D., Sun, M., Li, Y., Shen, Y., Du, G., and Cheng, Z.*	<i>Semi-Rolled Leaf2</i> modulates rice leaf rolling by regulating abaxial side cell differentiatio	<i>J Exp Bot</i>	2016, 67: 2139-2150	A
41	Zhao, J., Hua, C., Fang, Y., and Guo, H.*	The dual edge of RNA silencing suppressors in the virus-host interactions	<i>Curr Opin Virol</i>	2016, 17: 39-44	A
42	Zhao, J.*, Fang, Y., Duan, C., Fang, R., Ding, S., and Guo, H.*	Genome-wide identification of endogenous RNA-directed DNA methylation loci associated with abundant 21-nucleotide siRNAs in <i>Arabidopsis</i>	<i>Sci Rep</i>	2016, 6: 1-13	A
43	Zhang, Y.#, Lu, X.#, Zhao, F., Li, Q., Niu, S., Wei, W., Zhang, W., Ma, B., Chen, S.*, and Zhang, J.*	Soybean GmDREBL increases lipid content in seeds of transgenic <i>Arabidopsis</i>	<i>Sci Rep</i>	2016, 6: 34307	A
44	Zhou, Z.#, Pang, Z.#, Li, G., Lin, C., Wang, J., Lv, Q., He, C.*, and Zhu, L.*	Endoplasmic reticulum membrane-bound MoSec62 is involved in the suppression of rice immunity and is essential for the pathogenicity of <i>Magnaporthe oryzae</i>	<i>Mol Plant Pathol</i>	2016, 17: 1211-1222	A
45	Min, H.#, Chen, C.#, Wei, S.#,	Identification of drought tolerant	<i>Front Plant Sci</i>	2016, 7: 4.461	A

	Shang, X., Sun, M., Xia, R., Liu, X., Hao, D., Chen, H., and Xie, Q.*	mechanisms in maize seedlings based on transcriptome analysis of recombination inbred lines							1080-1090	
46	Yang, M., and Jiao, Y.*	Regulation of axillary meristem initiation by transcription factors and plant hormones	<i>Front Plant Sci</i>	2016, 7:	183	4.461				A
47	Fang, Y.#, Zhao, J.#, Liu, S., Wang, S., Duan, C., and Guo, H.*	CMV2b-AGO interaction is required for the suppression of RDR-dependent antiviral silencing in <i>Arabidopsis</i>	<i>Front Microbiol</i>	2016, 7:	1-11	4.36				A
48	Cao, J., Yang, C., Li, L., Jiang, L., Wu, Y., Wu, C., Bu, Q., Xia, G., Liu, X., Luo, Y.,* and Liu, J.*	Rice plasma membrane proteomics reveals <i>Magnaporthe oryzae</i> promotes susceptibility by sequential activation of host hormone signaling pathways	<i>Mol Plant Microbe Interact</i>	2016, 29:	902-913	4.328				A
49	Bai, Z., Chen, J., Liao, Y., Wang, M., Liu, R., Ge, S., Wing, R. and Chen, M.*	The impact and origin of copy number variations in the <i>Oryza</i> species	<i>BMC Genomics</i>	2016, 17:	261-272	4.278				A
50	Zhao, W., Guan, C., Feng, J., Liang, Y., Zhan, N., Zuo, J., and Ren, B.*	The <i>Arabidopsis</i> CROWDED NUCLEI genes regulate seed germination by modulating degradation of ABI5 protein	<i>J Integr Biol</i>	2016, 58:	669-678	3.993				A
51	Wang, S., Xing, H., Hua, C., Guo, H.*, and Zhang, J.*	An improved single-step cloning strategy simplifies the <i>Agrobacterium tumefaciens</i> -mediated transformation (ATMT)-based gene-disruption method for <i>Verticillium dahliae</i>	<i>Phytopathology</i>	2016, 106:	645-652	3.248				A
52	Guo, W.#, Wang, Z.#, Luo, X., Jin, X., Chang, J., He, J., Tu, E., Tian, Y., Si, H.*, and Wu, J.*	Development of selectable marker-free transgenic potato plants expressing cry3A against the Colorado potato beetle (<i>Leptinotarsa decemlineata</i> Say)	<i>Pest Manag Sci</i>	2016, 72:	497-504	3.116				A
53	Zhang, F., Li, Q., Chen, X., Huo, Y., Guo, H., Song, Z., Cui, F., Zhang, L.*, and Fang, R.*	Roles of the <i>Laodelphax striatellus</i> Down syndrome cell adhesion molecule in Rice stripe virus infection of its insect vector	<i>Insect Mol Biol</i>	2016, 25:	413-421	3.025				A
54	Xie, Q.#, Liang, Y.#, Zhang, J., Zheng, H., Dong, G., Qian, Q., and Zuo, J.*	Involvement of a putative bipartite transit peptide in targeting rice pheophorbide a oxygenase into chloroplasts for chlorophyll degradation during leaf senescence	<i>J Genomics</i>	2016, 43:	145-154	3.013				A
55	Li, H., Hu, B., Wang, W., Zhang, Z., Liang, Y., Gao, X., Li, P., Liu, Y., Zhang, L., and Chu, C.*	Identification of microRNAs in rice root in response to nitrate and ammonium	<i>J Genomics</i>	2016, 43:	651-661	3.013				A
56	Wang, L.#, Zhu, Y.#, Wang, P., Fan, Q., Wu, Y., Peng, Q., Xia, G., and Wu, J.*	Functional characterization of a dihydroflavanol 4-reductase from the fiber of upland cotton (<i>Gossypium hirsutum</i>)	<i>Molecules</i>	2016, 21:	32	2.749				A
57	Han, L.*, Li, Y., Sun, Y., Wang, H., Kong, Z., and Xia, G.	The two domains of cotton WLIM1a protein are functionally divergent	<i>Sci China Life Sci</i>	2016, 59:	206-212	1.772				A
58	Wei, L., and Cao, X.*	The effect of transposable elements on phenotypic variation: insights from plants to humans	<i>Sci China Life Sci</i>	2016, 59:	24-47	1.772				A
59	Wang, S., Sun, J., Fan, F., Tan, Z., Zou, Y., and Lu, D.*	A <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> effector, XopR, associates with receptor-like cytoplasmic kinases and suppresses PAMP-triggered stomatal closure.	<i>Sci China Life Sci</i>	2016, 59:	897-905	1.772				A
60	Huo, Y.#, Chen, L.#, Su, L., Wu, Y., Chen, X., Fang, R.*, and Zhang, L.*	Artificial feeding Rice stripe virus enables efficient virus infection of <i>Laodelphax striatellus</i>	<i>J Virol Methods</i>	2016, 235:	139-143	1.642				A
61	Wu, D., Huang, L., Gao, J., and Wang, Y.*	The molecular mechanism of plant gravitropism	<i>Hereditas</i>	2016, 38:	589-602	0.966				A
62	Che, R., Tong, H., Shi, B., Liu, Y., Fang, S., Liu, D., Xiao, Y., Hu, B., Liu, L., Wang, H., Zhao, M., and Chu, C.	Control of grain size and rice yield by GL2-mediated brassinosteroid responses	<i>Nat Plants</i>	2016, 2:	1-7	0				A
63	Zhang, T.#, Zhao, Y.#, Zhao, J.#, Wang, S., Jin, Y., Chen, Z., Fang, Y., Hua, C., Ding, S., and Guo, H.*	Cotton plants export microRNAs to inhibit virulence gene expression in a fungal pathogen	<i>Nat Plants</i>	2016, 2:	16153	0				A
64	Chen, Q., Zhong, Y., Wu, Y., Liu, L., Wang, P., Liu, R., Cui, F., Li, Q., Yang, X., Fang, S., and Xie, Q.*	HRD1-mediated ERAD tuning of ER-bound E2 is conserved between plants and mammals	<i>Nat Plants</i>	2016, 2:	16094	0				A
65	Song, X., and Cao, X.*	Small RNA extraction and detection in rice (<i>Oryza sativa</i>)	<i>Curr Protoc Plant Biol</i>	2016, 1:	79-87					A
66	Wang, N.#, Yao, Y.#, Zhu, C., Wen, F.*, and Ye, J.*	Towards sustainable protection against insect-borne plant viral diseases: phytohormones and beyond	<i>Science Foundation in China</i>	2016, 24:	69-80					A
67	Liang, Y., and Wang, Y.*	The genes controlling rice architecture and its application in breeding	<i>Chin Bull Life Sci</i>	2016, 28:	1156-1167					A
68	赵赫, 陈受宜, 张劲松*	乙烯信号转导与植物非生物胁迫反应调控研究进展	<i>生物技术通报</i>	2016, 32:	1-10					A
69	沈鸣, 陈受宜, 张劲松*	乙烯对豆科植物生长发育和根瘤形成的影响	<i>大豆科学</i>	2016, 35:	330-336					A
70	Liu, Y., Hu, B., and Chu, C.*	¹⁵ N-nitrate uptake activity and root-to-shoot transport assay	<i>Bio Protoc</i>	2016, 6:	e1897					A
71	Tao, J., Chen, S., and Zhang, J.*	Simple methods for screening and statistical analysis of leaf epidermal cells in dicotyledonous plants	<i>Bio Protoc</i>	2016, 6:	e1916					A
72	Huang, S.*, Weigel, D.*, Beachy, R.*, and Li, J.*	A proposed regulatory framework for genome-edited crops	<i>Nat Genet</i>	2016, 48:	109-111	32.197				B
73	Xu, Y., Jin, W., Li, N., Zhang, W., Liu, C., Li, C.*, and Li, Y.*	UBIQUITIN-SPECIFIC PROTEASE14 interacts with ULTRAVIOLET-B INSENSITIVE4 to regulate endoreduplication and cell and organ growth in <i>Arabidopsis</i>	<i>Plant Cell</i>	2016, 28:	1200-1214	9.88				B

74	Xin, Q.#, Shen, Y.#, Li, X., Lu, W., Wang, X., Han, X., Dong, F., Wan, L., Yang, G., Hong, D.*, and Cheng, Z.*	MS5 mediates early meiotic progression and its natural variants may have applications for hybrid production in <i>Brassica napus</i>	<i>Plant Cell</i>	2016, 28: 1263-1278	9.88	B
75	Tang D.*, and Zhou J.M.*	PEPRs spice up plant immunity	<i>EMBO J</i>	2016, 35: 4-5	9.387	B
76	Li, S.#, Le, B.#, Ma, X.#, Li, S.#, You, C., Yu, Y., Zhang, B., Liu, L., Gao, L., Shi, T., Zhao, Y., Mo, B., Cao, X., and Chen, X.*	Biogenesis of phased siRNAs on membrane-bound polysomes in <i>Arabidopsis</i>	<i>eLife</i>	2016, e22750	5: 8.533	B
77	Qian, Q., Guo, L., Smith, S.*, and Li, J.*	Breeding high-yield superior quality hybrid super rice by rational design	<i>Natl Sci Rev</i>	2016, 3: 283-294	8	B
78	Wang, D.#, Qin, B.#, Li, X.#, Tang, D., Zhang, Y., Cheng, Z., and Xue, Y.*	Nucleolar DEAD-box RNA helicase TOGR1 regulates thermotolerant growth as a pre-rRNA chaperone in rice	<i>PLoS Genet</i>	2016, e1005844	12: 7.481	B
79	Qiu, Z.#, Li, R.#, Zhang, S.#, Wang, K., Xu, M., Li, J., Du, Y.*, Yu, H.*, and Cui, X.*	Identification of regulatory DNA elements using genome-wide mapping of DNase I hypersensitive sites during tomato fruit development	<i>Mol Plant</i>	2016, 1168-1182	9: 6.885	B
80	Wang, C.#, Chen, Q.#, Fan, D., Li, J., Wang, G.*, and Zhang, P.*	Structural analyses of short-chain prenyltransferases identify an evolutionarily conserved GFPPS clade in Brassicaceae plants	<i>Mol Plant</i>	2016, 9: 195-204	6.885	B
81	Xiong, G.#, Li, J., and Smith, S.*	Evolution of strigolactone perception by seeds of parasitic plants: reinventing the wheel	<i>Mol Plant</i>	2016, 9: 493-495	6.885	B
82	Shu, K.#, Chen, Q.#, Wu, Y., Liu, R., Zhang, H., Wang, P., Li, Y., Wang, S., Tang, S., Liu, C., Yang, W., Cao, X., Serino, G., and Xie, Q.*	ABI4 mediates antagonistic effects of abscisic acid and gibberellins transcript and protein levels	<i>Plant J</i>	2016, 348-361	85: 6.468	B
83	Lv, D.#, Liu, S.#, Zhao, J., Zhou, B., Wang, S., Guo, H., and Fang, Y.*	Replication of a pathogenic non-coding RNA increases DNA methylation in plants associated with a bromodomain-containing viroid-binding protein	<i>Sci Rep</i>	2016, 6: 1-9	5.525	B
84	Li, D.#, Zeng, R.#, Li, Y.#, Zhao, M., Chao, J., Li, Y., Wang, K., Zhu, L.*, Tian, W.*, and Liang, C.*	Gene expression analysis and SNP/InDel discovery to investigate yield heterosis of two rubber tree F1 hybrids	<i>Sci Rep</i>	2016, 24984	6: 5.525	B
85	Li, Q., Zhang, M., Shen, D., Liu, T., Chen, Y., Zhou, J.M.*, and Dou, D.*	A <i>Phytophthora sojae</i> effector PsCRN63 forms homo-/hetero-dimers to suppress plant immunity via an inverted association manner	<i>Sci Rep</i>	2016, 26951	6: 5.525	B
86	Jin, J.#, Lee, M.#, Bai, B.#, Sun, Y.#, Qu, J., Rahmadsyah, A., Lim, C., Suwanto, A., Sugiharti, M., Wong, L., Ye, J.*, Chua, N.*, and Yue, G.*	Draft genome sequence of an elite <i>Dura</i> palm and whole-genome patterns of DNA variation in oil palm	<i>DNA Res</i>	2016, 0: 1-7	5.235	B
87	Zhang, G.#, Zhu, Y.#, Fu, W., Wang, P., Zhang, R., Zhang, Y., Song, Z., Xia, G., and Wu, J.*	iTRAQ protein profile differential analysis of dormant and germinated grassbur twin seeds reveals that ribosomal synthesis and carbohydrate metabolism promote germination possibly through the PI3K pathway	<i>Plant Physiol</i>	Cell 2016, 1244-1256	57: 4.847	B
88	Zheng, L.#, Wang, F.#, Ren, B., Liu, W., Liu, Z.*, and Qian, W.*	Systematic mutational analysis of histidine kinase genes in nosocomial pathogen <i>Stenotrophomonas maltophilia</i> identifies BfmAK system controlling biofilm development	<i>Appl Environ Microbiol</i>	2016, 2444-2456	82: 4.303	B
89	Chen, J., Deng, C., Zhang, Y., Liu, Z., Wang, P., Liu, L., Qian, W.*, Yang, D.*	Cloning, expression, and characterization of a four-component O-demethylase from human intestinal bacetrium <i>Eubacterium limosum</i> ZL-II	<i>Appl Microbiol Biotechnol</i>	2016, 9111-9124	21: 3.882	B
90	Yang, R.#, Li, Y.#, Su, Y., Tang, D., Luo, Q.*, and Cheng, Z.*	A functional centromere lacking CentO sequences in a newly formed ring chromosome in rice	<i>J Genet Genomics</i>	2016, 694-701	43: 3.013	B
91	Hamera, S.*, Yan, Y., Song, X., Chaudhary, S., Murtaza, I., Su, L., Tariq, M., Chen, X.*, and Fang, R.*	Expression of Cucumber mosaic virus suppressor 2b alters FWA methylation and its siRNA accumulation in <i>Arabidopsis thaliana</i>	<i>Biol Open</i>	2016, 1727-1734	5: 2.33	B
92	Lian, L., Wang, F., Zhang, Y., Fang, R.*, and Liu, Q.*	Isolation, identification and expression patterns of <i>RoLEAFY</i> in non-recurrent and recurrent flowering roses	<i>Eur J Horticult Sci</i>	2016, 122-132	81: 0.423	B
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97	Muller, D., Vogel, C., Bai, Y., and The	plant microbiota: systems-level	<i>Annu Rev Genet</i>	2016, 60: 16.738		C

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99	Zhang, Y., Liang, Z., Zong, Y., Wang, Y., Liu, J., Chen, K., Qiu, J., and Gao, C.*	Efficient and transgene-free genome editing in wheat through transient expression of CRISPR/Cas9 DNA or RNA	<i>Nat Commun</i>	2016, 12617	7:	12.001	C	
100	Wicker, T.*, Yu, Y., Haberer, G., Mayer, K., Marri, P., Rounsley, S., Chen, M., Zuccolo, A., Panaud, O., Wing, R. and Roffler, S.	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses	<i>Nat Commun</i>	2016, 12790	7:	12.001	C	
101	Li, S., Bashline, L., Zheng, Y., Xin, X., Huang, S., Kong, Z., Kim, S., Cosgrove, D., and Gu, Y.*	Cellulose synthase complexes act in a concerted fashion to synthesize highly aggregated cellulose in secondary cell walls of plants	<i>Proc Natl Acad Sci USA</i>	2016, 11348-11353	113:	10.285	C	
102	Chi, W.#, Li, J.#, He, B., Chai, X., Xu, X., Sun, X., Jiang, J., Feng, P., Zuo, J., Lin, R., Rochaix, J., and Zhang, L.*	DEG9, a serine protease, modulates cytokinin and light signaling by regulating the level of <i>ARABIDOPSIS RESPONSE REGULATOR 4</i>	<i>Proc Natl Acad Sci USA</i>	2016, E3568-E3576	113:	10.285	C	
103	Wu, Z.#, Zhu, D.#, Lin, X.#, Miao, J.#, Gu, L., Deng, X., Yang, Q., Sun, K., Zhu, D., Cao, X., Tsuge, T., Dean, C., Aoyama, T., Gu, H., and Qu, L.*	RNA binding proteins RZ-1B and RZ-1C play critical roles in regulating pre-mRNA splicing and gene expression during development in <i>Arabidopsis</i>	<i>Plant Cell</i>	2016, 59-73	28:	9.88	C	
104	Li, S., Yu, H., Dong, J., Che, X., Jiao, Y., and Liu, D.*	The molecular mechanism of ethylene-mediated root hair development induced by phosphate starvation	<i>PLoS Genet</i>	2016, e1006194	12:	7.481	C	
105	Chen, L.#, Peng, Y.#, Tian, J., Wang, X., Kong, Z., Mao, T., Yuan, M., and Li, Y.*	TCS1, a microtubule-binding protein, interacts with KCBP/ZWICHEL to regulate trichome cell shape in <i>Arabidopsis thaliana</i>	<i>PLoS Genet</i>	2016, e1006266	12:	7.481	C	
106	Zhu, X.#, Yin, J.#, Liang, S., Liang, R., Zhou, X., Chen, Z., Zhao, W., Wang, J., Li, W., He, M., Yuan, C., Miyamoto, K., Ma, B., Wang, J., Qin, P., Chen, W., Wang, Y., Wang, W., Wu, X., Yamane, H., Zhu, L., Li, S., and Chen, X.*	The multivesicular bodies (MVBs)-localized AAA ATPase LRD6-6 inhibits immunity and cell death likely through regulating MVBs-mediated vesicular trafficking in rice	<i>PLoS Genet</i>	2016, e1006311	12:	7.481	C	
107	Luo, C.#, Cai, X.#, Du, J., Zhao, T., Wang, P., Zhao, P., Liu, R., Xie, Q., Cao, X., and Xiang, C.*	PARAQUAT TOLERANCE3 is an E3 ligase that switches off activated oxidative response by targeting histone-modifying PROTEIN METHYLTRANSFERASE4b	<i>PLoS Genet</i>	2016, e1006332	12:	7.481	C	
108	Liu, J.#, Zhang, C.#, Wei, C., Liu, X., Wang, M., Yu, F., Xie, Q., and Tu, J.*	The RING finger ubiquitin E3 ligase OsHTAS enhances heat tolerance by promoting H ₂ O ₂ -induced stomatal closure in rice	<i>Plant Physiol</i>	2016, 429-443	170:	7.367	C	
109	Liu, J.#, Deng, S.#, Wang, H.#, Ye, J., Wu, H., Sun, H., and Chua, N.*	<i>CURLY LEAF</i> regulates gene sets coordinatng seed size and lipid biosynthesis	<i>Plant Physiol</i>	2016, 424-436	171:	7.367	C	
110	Wang, T., Chang, C., Gu, C., Tang, S., Xie, Q., and Shen, Q.*	An E3 ligase affects the NLR receptor stability and immunity to powdery mildew	<i>Plant Physiol</i>	2016, 2504-2515	172:	7.367	C	
111	Shen, Q., Hu, T., Bao, M., Cao, L., Zhang, H., Song, F., Xie, Q., and Zhou, X.*	Tobacco RING E3 ligase NTRFP1 mediates ubiquitination and proteasomal degradation of a geminivirus-encoded β C1	<i>Mol Plant</i>	2016, 9: 911-925	9: 111-925	6.885	C	
112	Xie, T.#, Chen, D., Wu, J., Huang, X., Wang, Y., Tang, K., Li, J., Sun, M., and Peng, X.*	<i>Growing Slowly 1</i> locus encodes a PLS-type PPR protein required for RNA editing and plant development in <i>Arabidopsis</i>	<i>J Exp Bot</i>	2016, 5687-5698	67:	6.229	C	
113	Chen, Y.*, Ma, J., Miller, A., Luo, B., Wang, M., Zhu, Z., and Ouwkerk, P.*	OsCHX14 is involved in the K ⁺ homeostasis in rice (<i>Oryza sativa</i>) flowers	<i>Plant Physiol</i>	2016, 1530-1543	57:	4.847	C	
114	Tang, W.#, Wu, T.#, Ye, J., Sun, J., Jiang, Y., Yu, J., Tang, J., Chen, G., Wang, C.*, and Wan, J.	SNP-based analysis of genetic diversity reveals important alleles associated with seed size in rice	<i>BMC Plant Biol</i>	2016, 16: 93	93	4.604	C	
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118	刘于, 毛传淦*, 储成才	水稻养分利用功能基因组研究进展	<i>生命科学</i>	2016, 1230-1242	28:		C	
119	郭庆华*, 吴芳芳, 庞树鑫, 赵晓倩, 陈琳海, 刘瑾, 薛宝林, 徐光彩, 李乐, 景海春, 储成才	Crop 3D——基于激光雷达技术的作物高通量三维表型测量平台	<i>中国科学</i>	2016, 1210-1221	46:		C	
120	Song, Q., Chu, C., Parry, M., and Zhu, X.*	Genetics-based dynamic systems model of canopy photosynthesis: The key to improve light and resource use efficiencies for crops	<i>Food Energy Secur</i>	2016, 5: 18-25	5: 18-25		C	



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