Hongyong Fu

List of Publications by Year
in descending order

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33 papers	2,143 citations	304368 22 h-index	414034 32 g-index
33 all docs	33 docs citations	33 times ranked	2264 citing authors

#	Article	IF	Citations
1	The Deubiquitinase OTU5 Regulates Root Responses to Phosphate Starvation. Plant Physiology, 2018, 176, 2441-2455.	2.3	19
2	Deubiquitinating Enzyme OTU5 Contributes to DNA Methylation Patterns and Is Critical for Phosphate Nutrition Signals. Plant Physiology, 2017, 175, 1826-1838.	2.3	26
3	Distinct phylogenetic relationships and biochemical properties of Arabidopsis ovarian tumor-related deubiquitinases support their functional differentiation. Frontiers in Plant Science, 2014, 5, 84.	1.7	25
4	Reversible ubiquitylation in plant biology. Frontiers in Plant Science, 2014, 5, 707.	1.7	2
5	IRT1 DEGRADATION FACTOR1, a RING E3 Ubiquitin Ligase, Regulates the Degradation of IRON-REGULATED TRANSPORTER1 in <i>Arabidopsis</i>. Plant Cell, 2013, 25, 3039-3051.	3.1	151
6	In vivo relevance of substrate recognition function of major Arabidopsis ubiquitin receptors. Plant Signaling and Behavior, 2012, 7, 722-727.	1.2	3
7	The Defective Proteasome but Not Substrate Recognition Function Is Responsible for the Null Phenotypes of the <i>Arabidopsis</i> Proteasome Subunit RPN10. Plant Cell, 2011, 23, 2754-2773.	3.1	52
8	Crossâ€species divergence of the major recognition pathways of ubiquitylated substrates for ubiquitin/26<i>S</i> proteasomeâ€mediated proteolysis. FEBS Journal, 2010, 277, 796-816.	2.2	42
9	The RAD23 Family Provides an Essential Connection between the 26S Proteasome and Ubiquitylated Proteins in<i>Arabidopsis</i>Â. Plant Cell, 2010, 22, 124-142.	3.1	113
10	Proteasomal recognition of ubiquitylated substrates. Trends in Plant Science, 2010, 15, 375-386.	4.3	36
11	Pollen-Specific SKP1-Like Proteins are Components of Functional SCF Complexes and Essential for Lily Pollen Tube Elongation. Plant and Cell Physiology, 2009, 50, 1558-1572.	1.5	23
12	Generation and analyses of the transgenic potatoes expressing heterologous thermostable Î²-amylase. Plant Science, 2008, 174, 649-657.	1.7	10
13	Abscisic acid-inducible nuclear proteins bind to bipartite promoter elements required for ABA response and embryo-regulated expression of the carrot Dc3 gene. Planta, 2005, 220, 424-433.	1.6	20
14	Purification of the Arabidopsis 26 S Proteasome. Journal of Biological Chemistry, 2004, 279, 6401-6413.	1.6	153
15	Molecular cloning of the carboxylesterase gene and biochemical characterization of the encoded protein from Pseudomonas citronellolis ATCC 13674. Research in Microbiology, 2003, 154, 521-526.	1.0	12
16	Monomeric NarB Is a Dual-Affinity Nitrate Reductase, and Its Activity Is Regulated Differently from That of Nitrate Uptake in the Unicellular Diazotrophic Cyanobacterium Synechococcus sp. Strain RF-1. Journal of Bacteriology, 2003, 185, 5838-5846.	1.0	3
17	Construction and characterization of thermo-inducible vectors derived from heat-sensitivelacI genes in combination with the T7 A1 promoter. Biotechnology and Bioengineering, 2002, 79, 1-8.	1.7	23
18	Subunit interaction maps for the regulatory particle of the 26S proteasome and the COP9 signalosome. EMBO Journal, 2001, 20, 7096-7107.	3.5	219

#	ARTICLE	IF	CITATIONS
19	Overproduction of d -hydantoinase and carbamoylase in a soluble form in Escherichia coli. Applied Microbiology and Biotechnology, 2000, 54, 348-353.	1.7	33
20	Multiubiquitin Chain Binding Subunit MCB1 (RPN10) of the 26S Proteasome Is Essential for Developmental Progression in Physcomitrella patens. Plant Cell, 1999, 11, 1457.	3.1	0
21	Multiubiquitin Chain Binding Subunit MCB1 (RPN10) of the 26S Proteasome Is Essential for Developmental Progression in Physcomitrella patens. Plant Cell, 1999, 11, 1457-1471.	3.1	94
22	Structural and functional analysis of the six regulatory particle triple-A ATPase subunits from the Arabidopsis 26S proteasome. Plant Journal, 1999, 18, 529-539.	2.8	80
23	One-Step Production of D-p-Hydroxyphenylglycine by Recombinant Escherichia coli Strains. Biotechnology Progress, 1999, 15, 1039-1045.	1.3	36
24	Structure and functional analysis of the 26S proteasome subunits from plants. Molecular Biology Reports, 1999, 26, 137-146.	1.0	48
25	Functional analysis of the proteasome regulatory particle. Molecular Biology Reports, 1999, 26, 21-28.	1.0	97
26	Use of alternate splice sites in granule-bound starch synthase mRNA from low-amylose rice varieties. Plant Molecular Biology, 1998, 38, 407-415.	2.0	98
27	Anchor probes for comparative mapping of grass genera. Theoretical and Applied Genetics, 1998, 97, 356-369.	1.8	123
28	Multiubiquitin Chain Binding and Protein Degradation Are Mediated by Distinct Domains within the 26 S Proteasome Subunit Mcb1. Journal of Biological Chemistry, 1998, 273, 1970-1981.	1.6	168
29	Molecular Organization of the 20S Proteasome Gene Family from Arabidopsis thaliana. Genetics, 1998, 149, 677-692.	1.2	103
30	ATPase and ubiquitin-binding proteins of the yeast proteasome. Molecular Biology Reports, 1997, 24, 17-26.	1.0	22
31	A Potato Sus3 Sucrose Synthase Gene Contains a Context-Dependent 3' Element and a Leader Intron with Both Positive and Negative Tissue-Specific Effects. Plant Cell, 1995, 7, 1395.	3.1	1
32	Sink- and vascular-associated sucrose synthase functions are encoded by different gene classes in potato.. Plant Cell, 1995, 7, 1369-1385.	3.1	178
33	High-level tuber expression and sucrose inducibility of a potato Sus4 sucrose synthase gene require 5' and 3' flanking sequences and the leader intron.. Plant Cell, 1995, 7, 1387-1394.	3.1	130