Yasushi Yukawa

List of Publications by Year in descending order

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516710 477307 34 860 16 29 citations g-index h-index papers 34 34 34 974 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The AtGSTU7 gene influences glutathione-dependent seed germination under ABA and osmotic stress in Arabidopsis. Biochemical and Biophysical Research Communications, 2020, 528, 538-544.	2.1	15
2	Novel in vivo system to monitor tRNA expression based on the recovery of GFP fluorescence and its application for the determination of plant tRNA expression. Gene, 2019, 703, 145-152.	2.2	1
3	Pol III-Dependent Cabbage i>BoNR8 / i>Long ncRNA Affects Seed Germination and Growth in Arabidopsis. Plant and Cell Physiology, 2019, 60, 421-435.	3.1	19
4	Arabidopsis Pol II-Dependent in Vitro Transcription System Reveals Role of Chromatin for Light-Inducible <i>rbcS</i> Gene Transcription. Plant Physiology, 2016, 170, 642-652.	4.8	4
5	The context of transcription start site regions is crucial for transcription of a plant tRNALys(UUU) gene group both in vitro and in vivo. Gene, 2013, 512, 286-293.	2.2	6
6	Translation of partially overlapping psbD-psbC mRNAs in chloroplasts: the role of 5′-processing and translational coupling. Nucleic Acids Research, 2012, 40, 3152-3158.	14.5	25
7	A novel hypoxic stress-responsive long non-coding RNA transcribed by RNA polymerase III in Arabidopsis. RNA Biology, 2012, 9, 302-313.	3.1	94
8	Transcript levels, alternative splicing and proteolytic cleavage of TFIIIA control 5S rRNA accumulation during <i>Arabidopsis thaliana</i> development. Plant Journal, 2012, 71, 35-44.	5.7	16
9	ppGpp inhibits peptide elongation cycle of chloroplast translation system in vitro. Plant Molecular Biology, 2012, 78, 185-196.	3.9	17
10	A common sequence motif involved in selection of transcription start sites of Arabidopsis and budding yeast tRNA genes. Genomics, 2011, 97, 166-172.	2.9	12
11	The downstream atpE cistron is efficiently translated via its own cis-element in partially overlapping atpB–atpE dicistronic mRNAs in chloroplasts. Nucleic Acids Research, 2011, 39, 9405-9412.	14.5	20
12	Translation of psbC mRNAs Starts from the Downstream GUG, not the Upstream AUG, and Requires the Extended Shine–Dalgarno Sequence in Tobacco Chloroplasts. Plant and Cell Physiology, 2007, 48, 1374-1378.	3.1	49
13	A survey of expressed tRNA genes in the chromosome I of Arabidopsis using an RNA polymerase III-dependent in vitro transcription system. Gene, 2007, 392, 7-13.	2.2	7
14	The complete structure of the cucumber (Cucumis sativus L.) chloroplast genome: Its composition and comparative analysis. Cellular and Molecular Biology Letters, 2007, 12, 584-94.	7.0	41
15	Distinct modes of TATA box utilization by the RNA polymerase III transcription machineries from budding yeast and higher plants. Gene, 2006, 379, 12-25.	2.2	14
16	A simpleinÂvitroRNA editing assay for chloroplast transcripts using fluorescent dideoxynucleotides: distinct types of sequence elements required for editing ofndhtranscripts. Plant Journal, 2006, 47, 802-810.	5.7	50
17	Plant 7SL RNA genes belong to type 4 of RNA polymerase III- dependent genes that are composed of mixed promoters. Plant Journal, 2005, 43, 97-106.	5. 7	10
18	In Vitro Transcription Systems from BY-2 Cells. Biotechnology in Agriculture and Forestry, 2004, , 265-282.	0.2	2

#	Article	IF	CITATIONS
19	Inâ€fvitro analysis of the sequences required for transcription of the Arabidopsis thaliana 5S rRNA genes. Plant Journal, 2003, 35, 251-261.	5.7	35
20	A tRNA Leu -like sequence located immediately upstream of an Arabidopsis clock-regulated gene is transcriptionally active: efficient transcription by an RNA polymerase III-dependent in vitro transcription system. Gene, 2003, 307, 133-139.	2.2	3
21	Identification and characterization of transcription factor IIIA and ribosomal protein L5 from Arabidopsis thaliana. Nucleic Acids Research, 2003, 31, 2424-2433.	14.5	42
22	Identification of RNA Editing Sites in Chloroplast Transcripts from the Maternal and Paternal Progenitors of Tobacco (Nicotiana tabacum): Comparative Analysis Shows the Involvement of Distinct Trans-Factors for ndhB Editing. Molecular Biology and Evolution, 2003, 20, 1028-1035.	8.9	99
23	Analysis of the 5S RNA Pool in Arabidopsis thaliana: RNAs Are Heterogeneous and Only Two of the Genomic 5S Loci Produce Mature 5S RNA. Genome Research, 2002, 12, 132-144.	5.5	59
24	Organization and transcription of the gene family encoding chlorophyll a/b -binding proteins in Nicotiana sylvestris. Gene, 2002, 289, 161-168.	2.2	9
25	5S rRNA genes expression is not inhibited by DNA methylation inArabidopsis. Plant Journal, 2002, 29, 313-323.	5.7	30
26	Plant 7SL RNA and tRNA(Tyr) genes with inserted antisense sequences are efficiently expressed in an in vitro transcription system from Nicotiana tabacum cells. Plant Molecular Biology, 2002, 50, 713-723.	3.9	7
27	Analysis of the SINE S1 Pol III promoter from Brassica; impact of methylation and influence of external sequences. Plant Journal, 2001, 26, 295-305.	5.7	30
28	A tobacco nuclear extract supporting transcription, processing, splicing and modification of plant intron-containing tRNA precursors. Plant Journal, 2001, 28, 583-594.	5.7	14
29	The TATA motif, the CAA motif and the poly(T) transcription termination motif are all important for transcription re-initiation on plant tRNA genes. Plant Journal, 2000, 22, 439-447.	5.7	43
30	Splicing of arabidopsis tRNA(Met) precursors in tobacco cell and wheat germ extracts. Plant Molecular Biology, 2000, 44, 155-165.	3.9	12
31	Plant cytosolic tRNAHis possesses an exceptional C54 in the canonical TPsiC loop. Nucleic Acids Research, 1998, 26, 2708-2714.	14.5	5
32	In Vitro Transcription Analysis of the rbcS Gene. , 1998, , 2963-2966.		0
33	Efficient in vitro transcription of plant nuclear tRNASer genes in a nuclear extract from tobacco cultured cells. Plant Journal, 1997, 12, 965-970.	5.7	28
34	Structure and Expression of Two Seed-Specific cDNA Clones Encoding Stearoyl-Acyl Carrier Protein Desaturase from Sesame, Sesamum indicum L Plant and Cell Physiology, 1996, 37, 201-205.	3.1	42