

**Supplementary Materials**

**Figure S1.** Multiple sequence alignment analysis of SlDnaJ20. AtDjA3 (At3g44110) and PeJ3 (XM\_002316443.2) are known as type I J-proteins. SlDnaJ20 lacks a glycine- and phenylalanine-rich region (G/F) domain, zinc finger, and C-terminal domain. The protein sequence of PeJ3 and AtDjA3 contains a J-domain (gold box), a proximal G/F domain (blue box), and a distal zinc finger (CxxCxGxG) domain (red box), followed by less conserved C-terminal sequences (green box).

AtDjA3	.....MFGRGESKRSNDTRFYEILGVPPFSASPEDIKFA	33
PeJ3	.....MFGRAE.KKSDNRYEILGVSPFSASQDDIKFA	32
SlDnaJ20	MCCNSNGVIPTSEFRLPLFSTHPPTIISFNPRLFFLNPNHGVIRTKFVSYRAKSNLNDVVSYDTDGKSFYDLLGIPENGSLLEIKQA	88
	<b>J-domain</b> <span style="margin-left: 150px;"><b>G/F-domain</b></span>	
AtDjA3	YRKAATKHPKGGDPEKFKELAQAIEVLSDEPKRDIYDQYGEIATKEGMDGGGGG..HDPFDIIFSSFFGGG.PFEG.NISKRRQRERGE	119
PeJ3	YRKAATKHPKGGDPEKFKELAQAIEVLSDEPKRDIYDQYGEIATKEGMDGGGGGGGADHDFDIIFCSFFGGGNPFSGGSSRGRQRERGE	122
SlDnaJ20	YKQLVRFKHPDVSPPDR...VEEYIQRFRVQIAYITLSDKMFALYIIDMAKGLHFGFSARSHEAMEE.....RGEWRKRWQSCLSL	169
	<b>zinc finger (CxxCxGxG) domain</b>	
AtDjA3	DVVHPIKWSLEDVYLGIMKKLSLSRNAICSKCNGKSGKSGASLRCCGCGSGMKVSIHQLGFGMIQQMQHACNECKGTGETINDRDRCPQ	209
PeJ3	DVIHPIKWSLEDIYNCTSKKLSLSRNVICSKCKGKSGKSGASLRCCGCGSGMKVSIHQLGFGSMIQQMQHPCNDCKGTGEAINDKDRCPQ	212
SlDnaJ20	KRRRTYKSSNSMSWCAARMRKQRDDA.....	196
	<b>conserved C-terminal sequences</b>	
AtDjA3	CRGDKV IPEKRVLEVNVVERGMQHSQKITFEQCDAEAPDIVTGDIVFVLQKREHPKFRKKGEDLFVEHTLSLIEALCGFQFVTLHLDGRSL	299
PeJ3	CRGKERVQEKRVLEVNVVERGMQNAQRITFPGEADEAPDIVTGDIVFVLQKREHPKFRKKGEDLFVEHTLSLAEALCGFQFVTLHLDGRQL	302
SlDnaJ20	.....	196
AtDjA3	LIKSNGEVVVRPDSYKAISDEGMPIYQRPFMRGKLYIHFTVEFFDLSLSPDQTKALEAVLKPSTAQSLDMEIDECEETTLHDVNIEEMR	389
PeJ3	LIKSQFGEVVRPDCFRAINDEGMPIYQRPFMRGKLYIHFTVDFDLSLSDQCKALETVLFPRTSALITDMELDECEETTLHDVNIEEMR	392
SlDnaJ20	.....	196
AtDjA3	RKAQAQR.EAYDDDEDDDHGGGAQRVQCAQC.....	420
PeJ3	RKCCQAQAEAYDEDEDE..MHGGGGQRVQCAQC.....	422
SlDnaJ20	.....	196

**Table S1.** Prediction of subcellular localization of SIDnaJ20 using software program TargetP 1.1 ([http://www.cbs.dtu.dk/services /TargetP/](http://www.cbs.dtu.dk/services/TargetP/)). Sequence is the amino-acid sequence of SIDnaJ20. Length is the length of the submitted sequence. Numbers given under the cTP, mTP, SP, and other categories represent the probabilities of protein localization in different subcellular regions (cTP, chloroplast transit peptide; mTP, mitochondrial targeting peptide; SP, secretory pathway signal peptide).

Sequence	Length	cTP	mTP	SP	other
SIDnaJ20	196	0.808	0.110	0.048	0.184

**Table S2.** Prediction of subcellular localization of SIDnaJ20 using software program ChloroP 1.1 (<http://www.cbs.dtu.dk/services/ChloroP/>). Sequence is the amino-acid sequence of *SIDnaJ20*. Length is the length of the submitted sequence. Score is the output score for the probability of protein localization in the chloroplast. cTP predicts whether a sequence is a cTP-containing sequence, wherein “Y” signifies that the sequence is predicted to contain a cTP. cTP-length is the predicted length of the presequence. cTP, chloroplast transit peptide.

Sequence	Length	Score	cTP	cTP-length
SIDnaJ20	196	0.531	Y	50

**Table S3.** The primers used for the qPCR reactions.

<i>Gene name</i>	<i>Sequence (5'–3')</i>
<i>EF1-1<math>\alpha</math></i>	Forward, GGAACTTGAGAAGGAGCCTAAG
	Reverse, CAACACCAACAGCAACAGTCT
<i>SlDnaJ20</i>	Forward, AGATCGGGTTGAAGAGTAT
	Reverse, ATAGCTGAGACTGCCAACGGT
<i>SlCuZnSOD</i>	Forward, TCTTACCACAACCAGCACT
	Reverse, CAGTAAGGGGTTTAGGGGTAGT
<i>SlFeSOD</i>	Forward, GGAAGTATCACAGGGCGTATG
	Reverse, GGCTCTCCTCCTCCGTTGG
<i>SlAPX1</i>	Forward, TGCTGGTACCTACGATGTGTG
	Reverse, CTGGTGGCTCTGGCTTGTG
<i>SlAPX2</i>	Forward, GGCTGGTGTTGTTGCTGTTG
	Reverse, TCAGGCAAGCGACCTTCAAC
<i>SlAPX</i>	Forward, GAATTCATGACTTCCCTCACAGGC
	Reverse, AATGCTGATATAAAGCGCAC
<i>HsfA1</i>	Forward, AGACAACAGCAGCAATCCACT
	Reverse, ATGTCCTGCTTAATCCTTCGT
<i>HsfA2</i>	Forward, AATGTTGGTCAGAGTATGAAT
	Reverse, ATGGCAATGATCTGATTCCT
<i>HsfB1</i>	Forward, ACTGACGATGTGATATCTT
	Reverse, AGTTCTCATTGGCGAATTCCCAT