

**TO270, 3.0 cM**

Guatamine-dependent asparagine synthetase, T21L8.90

(Good hits with same gene from beans, rice, tobacco and tomato from NCBI)

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**Primers:**

TO270F1            CTG AAC AGT GAA GTG AAA CTC GTG GT

TO270R2           CTG ATG TCC CCT TTG GTG TTC TGC TCT CG

**GERMPLASM:** 19a = GMh8632; 113a = Gc2711; 228-2 = GMp6330; Heinz = Heinz 1706  
(1-83 = exon; 191-329 = exon; two SNPs occur in intron)

19a	CTGAACAGTGAAGTGAAACTCGTGGTGAACGGTTCCTAAAAAGTCAGCAACTTCTTTTCGC	60
113a	CTGAACAGTGAAGTGAAACTCGTGGTGAACGGTTCCTAAAAAGTCAGCAACTTCTTTTCGC	60
228-2	CTGAACAGTGAAGTGAAACTCGTGGTGAACGGTTCCTAAAAAGTCAGCAACTTCTTTTCGC	60
Heinz	CTGAACAGTGAAGTGAAACTCGTGGTGAACGGTTCCTAAAAAGTCAGCAACTTCTTTTCGC	60
Cons	ctgaacagtgaagtgaaactcgtgggtaacggttcctaaaaagtcagcaacttctttcgc	
19a	AGCCTTAAGATCTGGTGAACCCCTGTTCAATCATAAAACACACAGATTATAGATGCACAA	120
113a	AGCCTTAAGATCTGGTGAACCCCTGTTCAATCATAAAACACACAtATTATAGATGCACAA	120
228-2	AGCCTTAAGATCTGGTGAACCCCTGTTCAATCATAAAACACACAtATTATAGATGCACAA	120
Heinz	AGCCTTAAGATCTGGTGAACCCCTGTTCAATCATAAAACACACAtATTATAGATGCACAA	120
Cons	agccttaagatctgggtaaccctgttcaatcataaaaacacaca atttatagatgcacaa	
19a	GTGA <del>A</del> AAAAACGGGCACGTATAGGTTGAAACCATCAAGTTTAAATTCCTTGATCCGCTTCTG	180
113a	GTGA <del>t</del> AAAAACGGGCACGTATAGGTTGAAACCATCAAGTTTAAATTCCTTGATCCGCTTCTG	180
228-2	GTGA <del>t</del> AAAAACGGGCACGTATAGGTTGAAACCATCAAGTTTAAATTCCTTGATCCGCTTCTG	180
Heinz	GTGA <del>t</del> AAAAACGGGCACGTATAGGTTGAAACCATCAAGTTTAAATTCCTTGATCCGCTTCTG	180
Cons	gtga aaaacgggacggtataggttgaaaccatcaagtttaaattccttgatccgcttctg	
19a	AACTGACTCACCTCGAGACCAACACAGAATGAATGAAGTTGTGCTCCCCATTGCTTAGCA	240
113a	AACTGACTCACCTCGAGACCAACACAGAATGAATGAAGTTGT.....	222
228-2	AACTGACTCACCTCGAGACCAACACAGAATGAATGAAGTTGT.....	223
Heinz	A.....	181
Cons	a	
19a	GCTTTCGTTCCAGCCAAGTATCGAGCAGTTACAGAAGCAACCAAAGACGAATCAAGTCCC	300
19a	CCCGAGAGCAGAACACCAAAGGGGACATCAG	331

**Comments:**

The sequence for GMh8632 is the complete sequence for the PCR fragment, and others are partial sequences.

BLAST search of NCBI: Match with asparagine synthetase mRNA, AY240926, 1-83 and 191-329 nt (exons)

BLAST search of SGN: BAC ends, no match; BAC full-length Sequences, no match; tomato ESTs, several matches, eg. SGN-E316705.

Jan. 7, 2007