

5'-flanking sequence of a glutamine synthetase gene specifying the β subunit of the cytosolic enzyme from *Phaseolus vulgaris* L.Jane F.Turton⁺, Alison P.Hopley and Brian G.Forde*

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Glutamine synthetase (GS) in *Phaseolus vulgaris* L. is specified by a small differentially regulated multigene family which encodes at least three cytosolic subunits (α , β and γ) and one chloroplast subunit (δ) (1-3). The GS mRNA species represented by the cDNA clone pcGS- β 1 (formerly pR-1, ref. 2) codes for subunit β (4) and is about 20-fold more abundant in roots than in leaves (2). We have now isolated the gene for subunit β (*gln- β*) from a genomic library of *P. vulgaris* cv. Tendergreen (*Mbo*I partial digest) in Charon 34 (5). The *gln- β* clone (λ PvGSR4) contains a 10.7 kb insert and was initially identified by its strong hybridization to pcGS- β 1 at high stringency. An internal 1.7 kb *Hind*III/*Bgl*III fragment was sub-cloned in pUC8 and 1140 bp of the sequence adjacent to the *Bgl*III site was determined by methods described previously (6). The translation initiation codon is at base 1127 and a putative TATA box sequence is underlined. The 5' end of the mRNA was mapped by primer extension to the three bases indicated by dots. The sequence at bases 1006-1146 is identical to bases 2-42 of pcGS- β 1 (N.B. a computer-generated error in the published cDNA sequence means that the AG at bases 4-5 in ref. 2 should be replaced by TCAC). Mis-reading at the cap-site during cDNA synthesis probably accounts for the discrepancy between base 1 of the pcGS- β 1 sequence (G) and base 1005 in the genomic sequence (T).

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1  TGCTTTTAAT  TTATCTACAG  GAAAACTAA  AAGCAGAATA  ATTAATATTT  GACTGAAAAC  CTAATCATT  AATCGATTTA  ATTTTTTTAA
91  AGACTAAAAG  TACATTTTTT  TATAAATAAA  GATAATATTA  TACACAACGA  CTCTATCCGA  TAGATATTTT  TAACAAATTT  ATATTTTTTA
181  AGGTATTTTT  ATCAAATATA  TTTTGAATTT  CGAAAAAAT  CTCTTTAATT  ATCTGAATTT  ATATTTTAAG  AGAATGATAC  ACAGATGTAT
271  ATAAATAATA  TAATTATTA  TTTAGTATTC  ATTTGACTTT  AAAAAAAGC  TATGACAATA  AITTAATAAA  AAAAAATACAT  ATGAAAGTAT
361  CTTTTATAGA  ATCTAATGCT  TATATTAAG  TAATAAAGTA  TAATATTATA  AAAATGAAAC  AAGGAGATAT  AAAAAATTT  CAGGTTAGAT
451  ATGATGAAGT  AAAAAATACA  TATTTTTAGG  AAGAGGCCTT  AAAGTACCTA  CTGCATGACA  CAATAATTTA  ATAAATAAAT  AAAAGGAAAA
541  CCAGAAGAAG  CAGTACCCGG  TGAAGGGTTG  GTGGACCCCA  GCAATTTGAT  TCTCTGCCA  AACGCCATTT  TGAACCGGCC  ATGCCATTTG
631  GACTATTTAT  TATTTAACA  AAGTTAGTA  ATCCACCTA  ATATGATCAT  AGTTATGATT  ATATCTATAA  TAAAAACGAA  AAACATTTAA
721  TATTCACACA  TGGTTCATTG  TAAATCTGT  CTGTTACATA  TTAATAATCC  ATGATCTTAA  TGAGTATCTT  GATCATGTCA  TTTGAATAAT
811  TGTTTCTTTA  CCAATAATG  TTTTCTTTT  GATGAATCTA  AAAGAAATAA  GCATAATAGA  GTTAAAGTTT  AGGGTGGAAA  TTTGAATAAA
901  AGGCCTTTTT  TAGAGTGAAT  TAGCTATTGA  ATCTGAGGGA  GTACAATGTT  GTAGGGGAAC  AAGAACAACC  CACTATAAAA  TCCCACACAC
991  CTCTCTATT  CTGTGCTCA  CGTACGAGTT  GAATCTCAGG  ATTCAGAGAG  AAAAGGAGAC  AGAGAGAGAG  AAAGAGAGAT  TTTTTTTTTT
                                     M S L L S D
1081  TGTGAAGAAG  GGTCTTCTCT  TGTTTCTCTG  TCTCTTCATT  TCTACCATGT  CGCTGCTCTC  AGATCT

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