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Nucleotide sequence of a field bean (*Vicia faba* L.var.minor) vicilin gene

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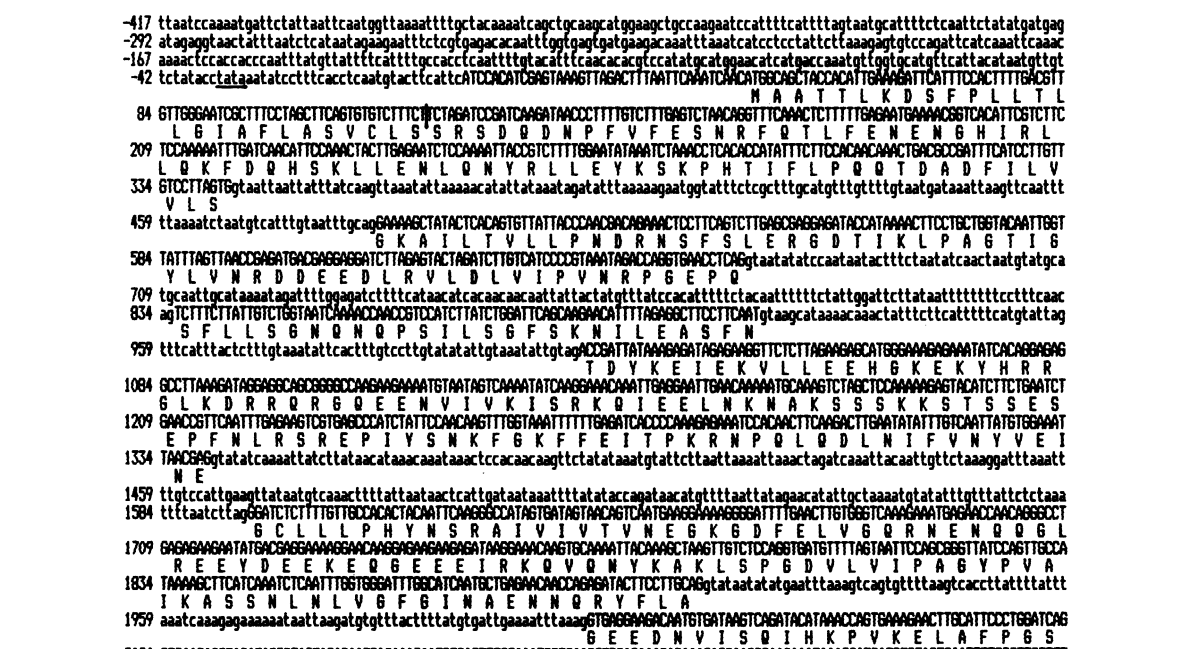
Vicilin, the 7S seed storage protein fraction of Vicia faba, is a polymorphic protein composed of three subunits. These subunits belong to two main classes: less abundant large polypeptides of M_r70,000 - 80,000 and dominant small polypeptides of M_r around 50,000. We have isolated and sequenced from a genomic library (1) with the help of cDNA clones (2) a charon 4 phage (λVfVic1) which carries on a 4kb EcoRI fragment a complete and most probably functioning gene coding for an abundant 50 kD vicilin polypeptide in field bean (Vicia faba L.var.minor) seeds. The determined sequence and its conceptual translation is given. Exon/intron bounderies and the poly(A)-addition site (black triangle) were defined by comparison with a quasi identical cDNA sequence (R.Bassüner and N.Van Hai, pers.comm.), the transcription start site (+1) deduced by analogy to published vicilin-type gene sequences of other legumes(3). TATA box and AATAAA-sites are underlined, the most likely signal peptide cleavage site marked by a vertical line. (1) Bäumlein, H., et al. (1986) Nucleic Acids Res. 14, 2707-2720; (2) Wobus, U., et al. (1984) Kulturpflanze (Bln.) 32, 117- 126; (3) Doyle, J.J., et al. (1986) J.Biol.Chem. 261, 9228-9238.



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