Erratum

Complex pattern of alternative splicing generates unusual diversity in the leader sequence of the chicken link protein mRNA

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Nucleic Acids Research, **19**, pp. 4983–4990 (1991)

The publishers wish to apologize for the incorrect legends accompanying Figures 1, 2 and 3 of this article. Supplementary data not intended for publication was inadvertantly included. The correct legends are published below.

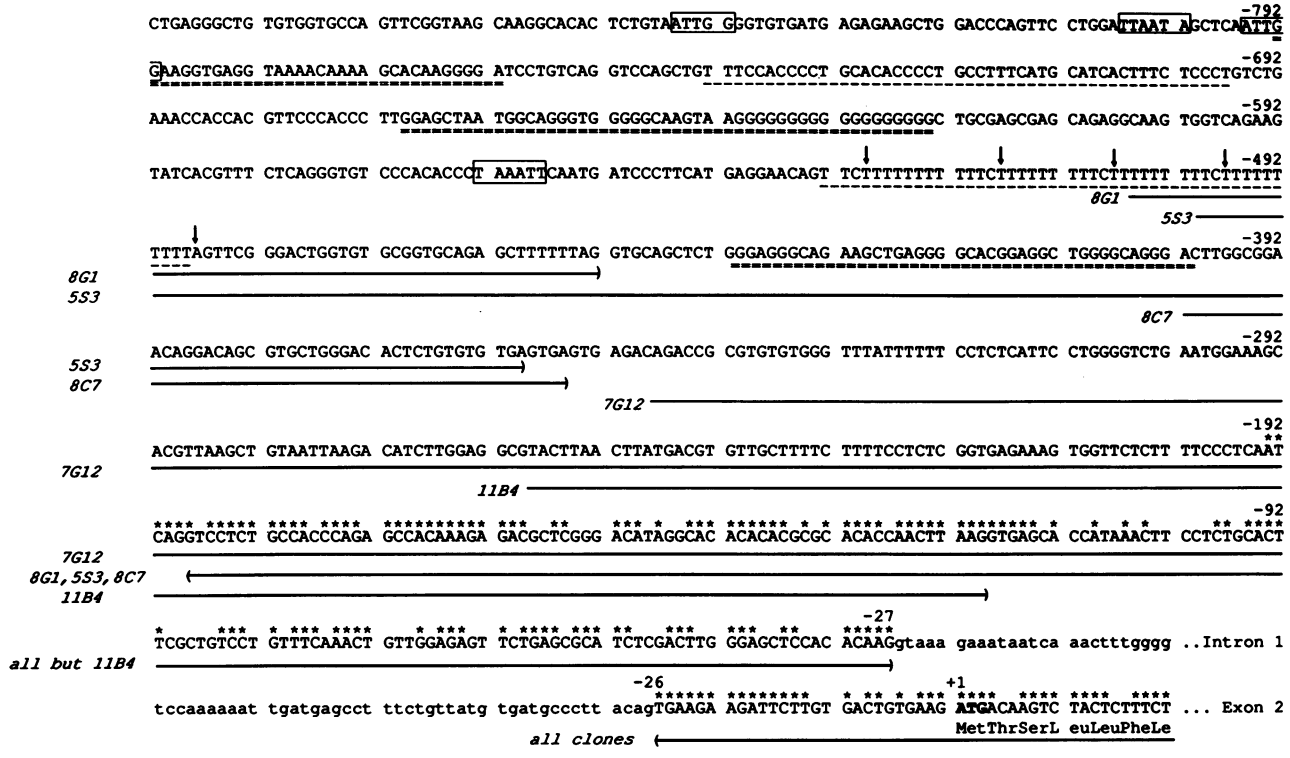

Fig. 1. Nucleotide sequence of the 5′ end of the chicken LP gene. Positions are given from the translation start site within exon 2, not including intron 1 (nucleotides in lower case letters). Nucleotide sequences represented by cDNA clones are indicated by solid lines. All sequences were determined from both directions. TATA and CCAAT motifs are boxed. Homopurine and homopyrimidine tracts longer than 30 nt are denoted by double and single broken lines, respectively. Arrows point to the major transcription start sites. Nucleotides identical with the human sequence (31) are marked with asterisks above the sequence.

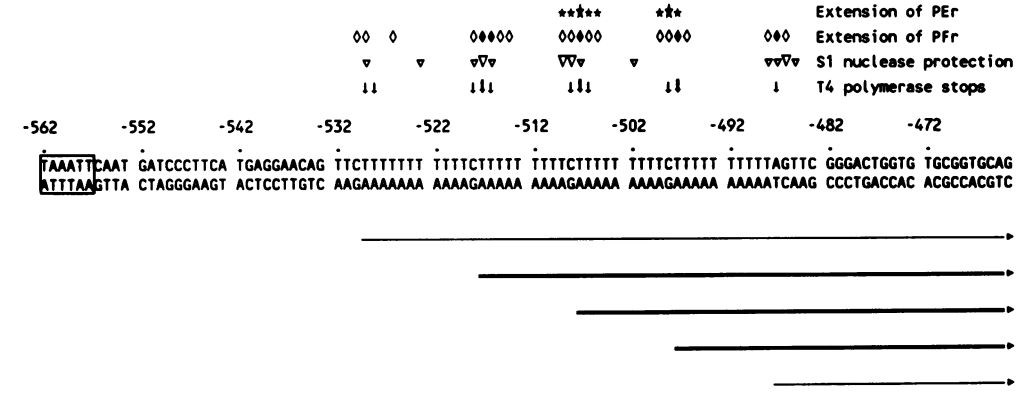

Fig. 2. Composite representation of the transcription initiation sites determined by various techniques. The TATA-like sequence is boxed. Thickness of the horizontal arrows below the sequence reflects the relative frequency of initiation.

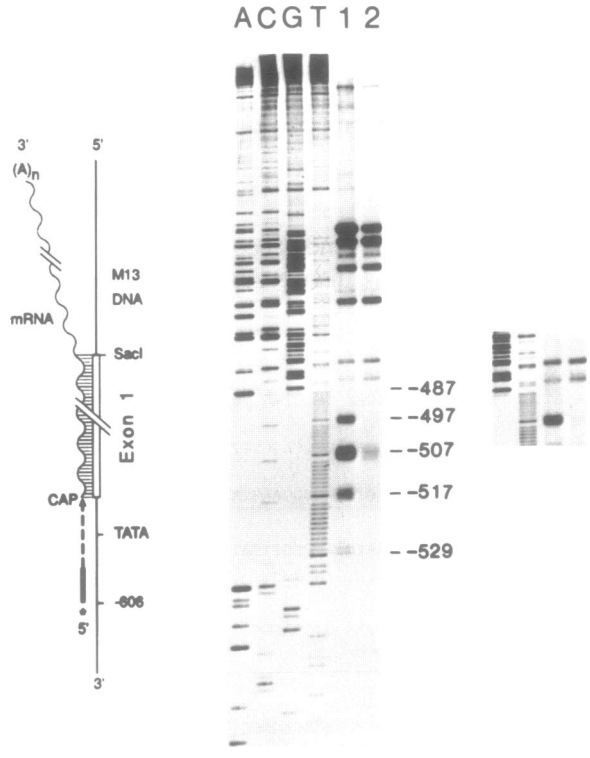

Fig. 3. Mapping of transcription start sites by T4 DNA polymerase. The diagram to the left depicts the experimental strategy. An M13 DNA carrying the RNA-complementary strand of exon 1 and the promoter region was used as template. Solid bar with asterisk represents the ^{32}P end-labeled PA primer, broken arrow indicates the primer extension products. Lanes A, C, G and T, dideoxy sequencing ladders of the same template DNA from unlabeled PA primer in the presence of [^{35}S]dATP. Lane 1, 4 μg poly(A)$^+$ RNA was hybridized to the template before primer extension. Lane 2, primer extension in the absence of hybridized mRNA. The numbers at the right margin of the autoradiogram denote the nucleotide positions. That part of the autoradiogram which carries the extension product at position −487 is shown after prolonged exposure, in an inlet to the right.

Hypervariable polymorphism in the APOC3 gene

by S.Bhattacharya, T.M.E.Wilson, A.P.Wojciechowski, C.P.Volpe and J.Scott

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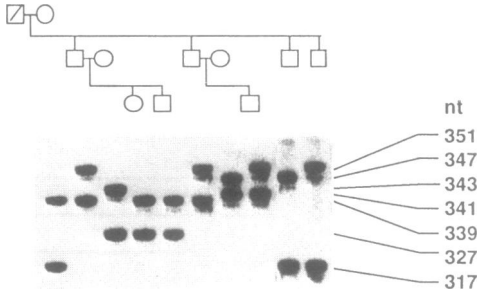
An incorrect figure was inadvertantly supplied with this paper. The correct figure is reprinted below



Frequency was estimated in 30 unrelated Caucasian English individuals, in whom 24 alleles could be distinguished. Only one of the 30 individuals was homozygous. The heterozygosity index was 0.95, and the polymorphic information content 0.94. Further alleles e.g. 317 nt have also been noted. A constant band measuring 340 nt was seen in 4 of 30 individuals.