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Chromatin from transcribed genes contains HMG17 only downstream from the starting point of transcription

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[illegible]

analyzed the DNA with respect to three active genes (Dorbic and [illegible]

Wittig, 1986). In employing this well-defined and highly specific tool we were able to locate HMG17 in the neighbourhood of the [illegible]

Fig. 1. Hybridization of nucleosomal DNA with RNA probes complementary to nucleotide sequences downstream from the respective transcription start of

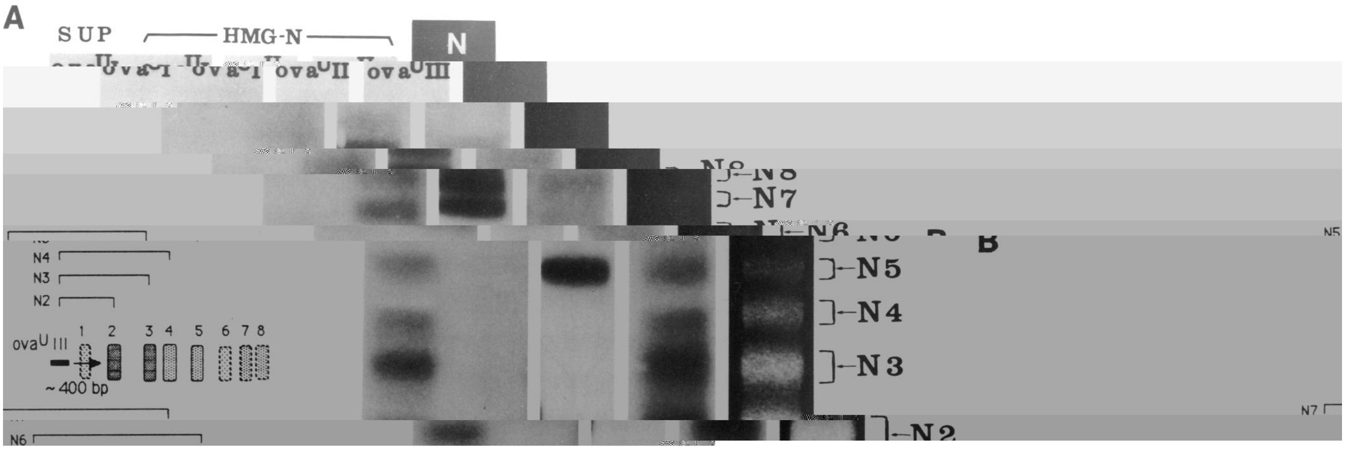
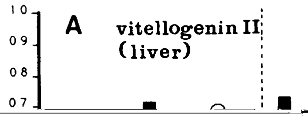


Fig. 2. (A) Hybridization of RNA probes complementary to different upstream locations (ova^{U}) with nucleosomal DNA from (laying hen) oviduct chromatin



the transcription start is also packed into nucleoprotein complexes (see the SUP fraction in Figure 2A). A short nucleoprotein-free gap in this region (McGhee *et al.*, 1981), indicated by the complete accessibility of DNA sequences from ~ −150 to +50 for

These experimental conditions yield mono- and oligonucleosomes which contain only small amounts or almost no histone H1 (depending on the oligonucleosome size class) since most of the H1-containing material precipitates at 0.15 M salt (analyzed quantitatively, but only at 0.1 M KCl, in Wittig and Wittig, 1977). The absence of H1 is essential for the subsequent enrichment of oligonucleosomes from active chromatin by immunoprecipitation since H1 binds unspecifically to

supplier and processed for hybridization as described for dot-blots.

Five microgram aliquots of DNA from the HMG-N, 'released' or 'non-released' fraction were precipitated with ethanol and processed as for dot-blotting on GeneScreenPlus membranes (Maniatis *et al.*, 1982); quantitative scintillation counting of hybridized samples was used instead of scanning X-ray photographs. The membranes were covered with 'Frischhaltefolie' Frappan (an equivalent to Saran

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