Corrigenda

Differential utilization of poly (A) signals between DHFR alleles in CHL cells

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The authors wish to correct a mistake which appeared in the abstract to the above paper concerning the number of transcripts produced by DHFR alleles. The correct abstract is printed below.

The Chinese hamster cell line, DC-3F, is heterozygous at the DHFR locus, and each allele can be distinguished on the basis of a unique DNA pattern, protein isoelectric profile and in the abundancy of the DHFR and mRNAs it expresses. Although each allele produces transcripts 1000, 1650 and 2150 nucleotides in length, the relative distribution of these RNAs differs for each; the 2150 nt mRNA represents the major (60%) species generated from one allele, while the 1000 nt mRNA is the major species generated from the other. The allele that predominantly expresses the 2150 nt transcript is preferentially overexpressed when DC-3F cells are subjected to selection in methotrexate. We have analyzed the 3′ ends of both DHFR alleles and have found that the three major mRNAs arise by readthrough of multiple polyadenylation signals. A four base deletion in one allele changes the consensus polyadenylation signal AAUAAA to AAUAAU, resulting in the utilization of a cryptic polyadenylation signal lying 21 bp upstream. Surprisingly, this mutation in the third polyadenylation signal appears to affect not only the utilization of this signal, but also the efficiency with which the first signal, located 1171 bp upstream from the third site is utilized.

Evidence for opposite groove-directed curvature of GGGCCC and AAAAA sequence elements

by I.Brukner, M.Dlakic, A.Savic, S.Susic, S.Ponger and D.Suck

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The authors wish to substitute an amended figure 7 for the one that appears in the above paper. The changes affect only the two absolute R_L values and therefore do not affect the conclusions drawn from the ∂ values. The amended version of figure 7 with its legend is shown below.

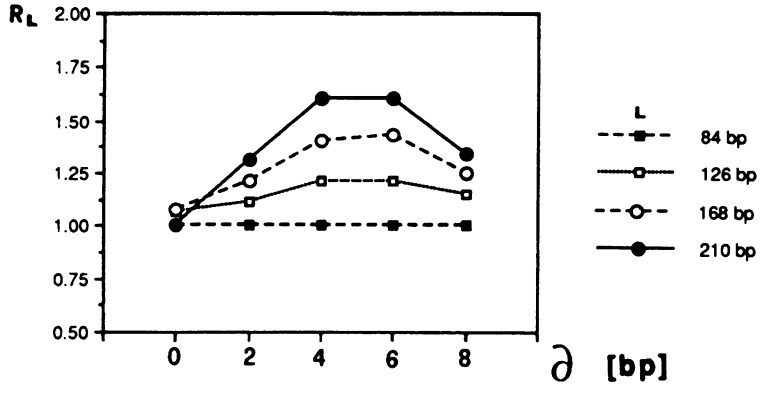

Figure 7. Plot of relative mobility of 5 ligated 42-mers, versus deviation ∂ from the helical turn distance between the GGGCCC and AAAAA motifs. The multimers with the same actual size (L) are connected into a curve. The data point for multimers with the same actual size L are connected. The mobility anomaly is the largest for $\partial=5$, corresponding to a separation of motifs by odd multiples of half a helical turn. In the case $\partial=0$, i.e. with the motifs separated by multiples of a full helical turn, the curvatures are cancelling each others and no mobility anomaly is found.