Retraction. We have discovered that a critical DNA sample used in performing experiments described in our paper "A precise termination site in the mouse β -major globin transcription unit", by M. Salditt-Georgieff and J. E. Darnell, Jr., which appeared in number 15, August 1983, of *Proc. Natl. Acad. Sci. USA* (80, 4694-4698), did not contain the sequences we thought it did. The sample in question was a single-stranded M13 bacteriophage preparation that we thought contained an insertion of ≈ 700 nucleotides of a region downstream from the mouse β -major globin gene (labeled F in Fig. 1, p. 4695) that we know to be transcribed in mouse erythroleukemia cells [for example, see Hofer, E., Hofer-Warbinek, R. & Darnell, J. E., Jr. (1982) *Cell* 29, 887-893, and Fig. 1 of the paper referenced above]. We find that instead, the bacteriophage DNA used in the experiments contained only between 150 and 200 nucleotides from the F region. This DNA sample therefore could only be complementary to a stretch of RNA from mouse erythroleukemia cell nuclei of 150-200 nucleotides. In our paper, we mistakenly interpreted this complementarity to indicate that RNA transcription terminated at a site 150 nucleotides within the border of the DNA region in question. New experiments with an M13 clone containing the full-length F fragment (actually 809 nucleotides by sequence analysis) and with additional M13 clones containing the full-length G and H fragments (these two clones cover an adjacent 600 and 300 nucleotides downstream; see Fig. 1, p. 4695) have been performed. These results show that transcription often (about one-half the time) goes across the F region and occasionally completely across the G fragment but there is no detectable transcription from the H region. We thus have clear evidence that transcription ceases within a region 2500-3500 nucleotides from the initiation site but does not do so at a discrete site. Further experiments are underway to determine the effectiveness of these β -globin sequences in stopping transcription when they are incorporated into another DNA setting. It hardly needs recording that we are among those least happy with this mistake and hope other workers studying termination have not been inconvenienced by our errant results.