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Gutierrez et al. Vol. 139, No. 4, November 17, 1997. Pages 895–905.

The cDNA sequence coding for SFT (stimulator of Fe transport) published in the article by Gutierrez et al. contains several errors. Corrected sequence data are available from GenBank under accession number AF020761. These changes indicate that the open reading frame originally predicted to encode the SFT protein is incorrect; several potential but smaller open reading frames are present in the corrected nucleotide sequence. The functional activity associated with SFT cDNA, i.e., stimulation of Fe transport in transfected cells, has been reconfirmed as described in this article and resequencing of the pGL2-SFT construct used for these functional studies confirms the sequence changes except for an A→T conversion at position 725 and a nucleotide deletion at position 883. Recent BLAST analysis of the nonredundant GenBank/EMBL/DDBJ/PDB sequences indicates a 46-base pair stretch of identity between nucleotides 530–573 of human SFT and nucleotides 414–457 of human ubiquitin-conjugating enzyme E2131 (UBE2D1, accession number X78140) and a search of human EST sequences identifies at least two GenBank entries, accession numbers AA188127 and AA146924, that overlap with both UBE2D1 and SFT. Our laboratory is currently determining the true open reading frame responsible for SFT function and evaluating the potential relationship between UBE2D1 and SFT. We wish to apologize for any additional work that the sequencing errors may have caused other investigators.

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