Pharmacology. In the article "Molecular cloning of bullfrog saxiphilin: A unique relative of the transferrin family that binds saxitoxin" by Maria A. Morabito and Edward Moczydlowski, which appeared in number 7, March 29, 1994, of *Proc. Natl. Acad. Sci. USA* (**91,** 2478–2482), the authors request that the following corrections be noted. In the course of studies that involved resequencing saxiphilin cDNA, a few errors in the published sequence were discovered. The most significant error was an inadvertent insertion of three noncontiguous nucleotide bases. Correction of this error results in a revised translation of the coding sequence within the previously identified 144-residue insertion domain. This latter region is actually a sequence of 143 residues that is absent in other members of the transferrin protein family as previously noted. Furthermore, 31 consecutive amino acids within the insertion domain have been revised as shown below in a corrected Fig. 4. Analysis of the revised sequence indicates that the insertion domain is a tandem duplication with 67% identity (instead of the previously reported 35% identity) for an alignment of residues 90–159 with 160–232. As shown in Fig. 4, this insertion domain of saxiphilin contains two type 1 thyroglobulin module domains (Thyr-1) instead of one, as reported previously. The 143-residue revised insertion does not contain a consensus site for N-linked glycosylation suggested previously. Two additional nucleotide bases in the sequence were corrected. One of these changes did not affect the translation and the other one resulted in a change of the previous saxiphilin residue Thr-238 to corrected Ala-237. In summary, the reported saxiphilin cDNA contains an open reading frame of 844 residues. Removal of the 19-residue secretory signal sequence gives a predicted molecular weight of 90,901 for this 825-residue secreted protein. The saxiphilin sequence has been corrected in the Genbank data base (accession no. U05246).

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Sax (90-159)    KCLKERQQALA--KKMIGHYIPQCDEKGNYQPQQCHGSTGHCWCVNAMGEKISGTNTPPGQTRATCERHELP-
                ||||||| ||:   |::|:::|||||||||:||| ||||| :|||||:|| | || ||||   |||::|:|
Sax (160-232)   KCLKERQVALGGDEKVLGRFVPQCDEKGNYEPQQFHGSTGYSWCVNAIGEEIAGTKTPPGKIPATCQKHDLVT

nidogen (842-889)              GMFVPQCDEYGHYVPTQCHHSTGYCWCVDRDGRELEGSRTPPGMRPP-C
invariant chain (210-248)      GAFRPKCDENGNYMPLQCHGSTGYCWCVFPNGTEVPHTK
EGP (93-123)                   GLYDPDCDESGLFKAKQCNG-TSMCWCVNTAG
thyroglobulin 1.1 (29-73)        YVPQCAEDGSFQTVQCQNDGRSCWCVGANGSEVLGSRQP-GR-PVAC
thyroglobulin 1.2 (97-141)       YLPQCQDSGDYAPVQCDVQHVQCWCVDAEGMEVYGTRQL-GR-PKRC
thyroglobulin 1.5 (597-639)      FVPSCTTEGSYEDVQCFSGE--CWCVNSWGKELPGSRVRDGQ-PR-C
thyroglobulin 1.6 (664-707)      FVPACTSEGHFLPVQCFNSE--CYCVDAEGQAIPGTRSAIGK-PKKC
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FIG. 4. Homology relationships of the 143-residue insertion unique to saxiphilin. The upper two sequences are a pairwise alignment of saxiphilin residues 90–159 and 160–232 showing significant twofold internal homology within the 143-residue insertion. A vertical line marks an identity and a colon marks a conservative substitution. The lower seven sequences illustrate homology between residues 105–153 and 177–225 within the saxiphilin insertion and a domain observed in other proteins that is known as a type 1 repetitive module of thyroglobulin (22). The comparison sequences are mouse nidogen (23), rat invariant chain (24), human epithelial glycoprotein (EGP) (25), and human thyroglobulin (22). Residues in boldface type are identical to those in saxiphilin and are present in at least four of the nine sequences.