Biochemistry. In the article "Adherence to the first-AUG rule when a second AUG codon follows closely upon the first" by Marilyn Kozak, which appeared in number 7, March 28, 1995, of Proc. Natl. Acad. Sci. USA (92, 2662–2666), the reproduction of Figs. 2–4 was too dark. The figures and accompanying legends are shown below.

**Fig. 2.** Test for dual initiation with an mRNA designed to preclude leaky scanning. The key construct is K44(5) in which both AUGout and the nearby AUGprecat occur in an optimal context. One or both of these upstream AUG codons were deleted from the control constructs K440, K44, and K44. In K45(5), K46(5), and K47(5), nucleotides that differ from K44(5) are underlined. Downstream from the BamHI site, all constructs are identical to K440. Divergent arrows mark a stem–loop structure within oligonucleotide 8336. The autoradiograms show protein products from a reticulocyte (A and C) or wheat germ (B) translation system.

**Fig. 3.** Modulation of initiator codon selection by context and downstream secondary structure. For each mRNA in which the second AUG codon (AUGprecat) occurs close to AUGout, there is a matched control (K47, K46, and so forth) in which the second AUG codon (AUGcat) occurs far downstream from AUGout. Each mRNA was tested with either a structured sequence (oligonucleotide 8336) (A) or an unstructured sequence (oligonucleotide 8335) (B) downstream from AUGout. Upstream from the ellipse (…) and downstream from oligonucleotide 8336 or 8335 the sequences were the same as in Fig. 2. Protein yields in B may be directly compared with those seen in A, inasmuch as aliquots of a common transcription reaction mixture were used to synthesize 21 of the mRNAs tested here [excluding K440(8335), which had to be remade], and aliquots of a master mix were used for all 22 translation assays.

**Fig. 4.** Primer-extension analysis of initiation complexes. The mRNAs indicated at the top of the autoradiogram were incubated in a reticulocyte lysate supplemented with sparsomycin. Bracketed lanes show analyses on adjacent fractions from a Sepharose column used to purify ribosome–mRNA complexes. A 32P-labeled primer (P) annealed within the CAT coding domain was extended by reverse transcriptase as described in Materials and Methods. Extension stop–sites labeled AUGout, AUGprecat, and AUGcat occur 15 or 16 nt downstream from the stated AUG codon. A control reaction (lane 0) lacking ribosomes shows only the full-length extension product (E). Reference lanes labeled G, A, U, or C depict the minus-strand sequence of construct K460(8334). All other mRNAs used here had oligonucleotide 8335 downstream.