In the article "Molecular cloning of the major surface antigen of Leishmania" by Linda L. Button and W. Robert McMaster (February 1988, 167:724), please note the following DNA sequence corrections. The DNA sequence of a homologous GP63 gene from L. d. chagasi has recently been completed (Miller, R. A., S. G. Reed, and M. Parsons, Leishmania GP63 molecule implicated in cellular adhesion lacks an arg-gly-asp sequence, manuscript submitted for publication) and showed three additional nucleotides not found in the reported L. major gene sequence. The L. major gene was originally sequenced using the Klenow fragment of DNA polymerase I and 7-deaza-dGTP in the dideoxy sequencing reactions. The region of the L. major gene encompassing the three nucleotide differences was resequenced in our laboratory using T7 DNA polymerase and 7-deaza-dGTP and 7-deaza-dITP in the sequencing reactions. The revised sequence is in agreement with the L. d. chagasi sequence and shows that the original L. major sequence omitted a guanosine at positions 1182 and 1207 and a cytosine at position 1347. The revised DNA and predicted amino acid sequence of the L. major GP63 gene is shown in Fig. 1. The resulting frame shift changes the predicted amino acid sequence from codon 329 to 383, resulting in a change of 56 amino acids, and increases the predicted protein from 601 to 602 residues. Furthermore, the codon usage within this corrected region agrees with codon usage of the remainder of this gene.

2

GAG GTG GAG GAC CAG GGC GGT GCG GGC TCC GCC GGG TCG CAC ATC AAG ATG CGC GGU Val Glu Asp Gln Gly Gly Ala Gly Ser Ala Gly Ser His Ile Lys Met Arg Asn Ala

1278

1218

CAG GAC GAG CTC ATG GCG CCT GCT GCA GCT GCC GGG TAC TAC ACC GCC CTG ACC ATG GCC Gin Asp Glu Leu Met Ala Pro Ala Ala Ala Ala Gly Tyr Tyr Thr Ala Leu Thr Met Ala

1338

ATC TTC CAG GAC CTC GGC TTC TAC CAG GCG GAC TTC AGC AAG GCC GAG GTG ATG CCG TGG Ile Phe Gin Asp Leu Gly Phe Tyr Gin Ala Asp Phe Ser Lys Ala Glu Val Met Pro Trp

1398

GGC CAG AAC GCC GGC TGC GCC TTC CTC ACC AAC AAG TGC ATG GAG CAG AGC GTC ACG CAG Gly Gln Asn Ala Gly Cys Ala Phe Leu Thr Asn Lys Cys Met Glu Gln Ser Val Thr Gln

FIGURE 1. Revised DNA and predicted amino acid sequence of the L. major GP63 gene. Nucleotide positions are located above the sequence and amino acid positions are located below the sequence. The three insertions are indicated by a double underline. The revised predicted amino acid sequence is indicated by a single underline.