

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.

1182	1218
GAG GTG GAG GAC CAG GGC GGT GCG <u>GGC</u> TCC GCC GGG TCG CAC ATC AAG ATG <u>CGC</u> AAC GCG	
Glu Val Glu Asp Gln Gly Gly Ala <u>Gly Ser Ala Gly Ser His Ile Lys Met Arg Asn Ala</u>	
328	
	1278
CAG GAC GAG CTC ATG GCG CCT GCT GCA GCT GCC GGG TAC TAC ACC GCC CTG ACC ATG GCC	
<u>Gln Asp Glu Leu Met Ala Pro Ala Ala Ala Ala Gly Tyr Tyr Thr Ala Leu Thr Met Ala</u>	
	1338
ATC TTC CAG GAC CTC GGC TTC TAC CAG GCG GAC TTC AGC AAG GCC GAG GTG ATG CCG TGG	
<u>Ile Phe Gln Asp Leu Gly Phe Tyr Gln Ala Asp Phe Ser Lys Ala Glu Val Met Pro Trp</u>	
	1398
GGC CAG AAC GCG GGC TGC GCC TTC CTC ACC AAC AAG TGC ATG GAG CAG AGC GTC ACG CAG	
<u>Gly Gln Asn Ala</u> 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.