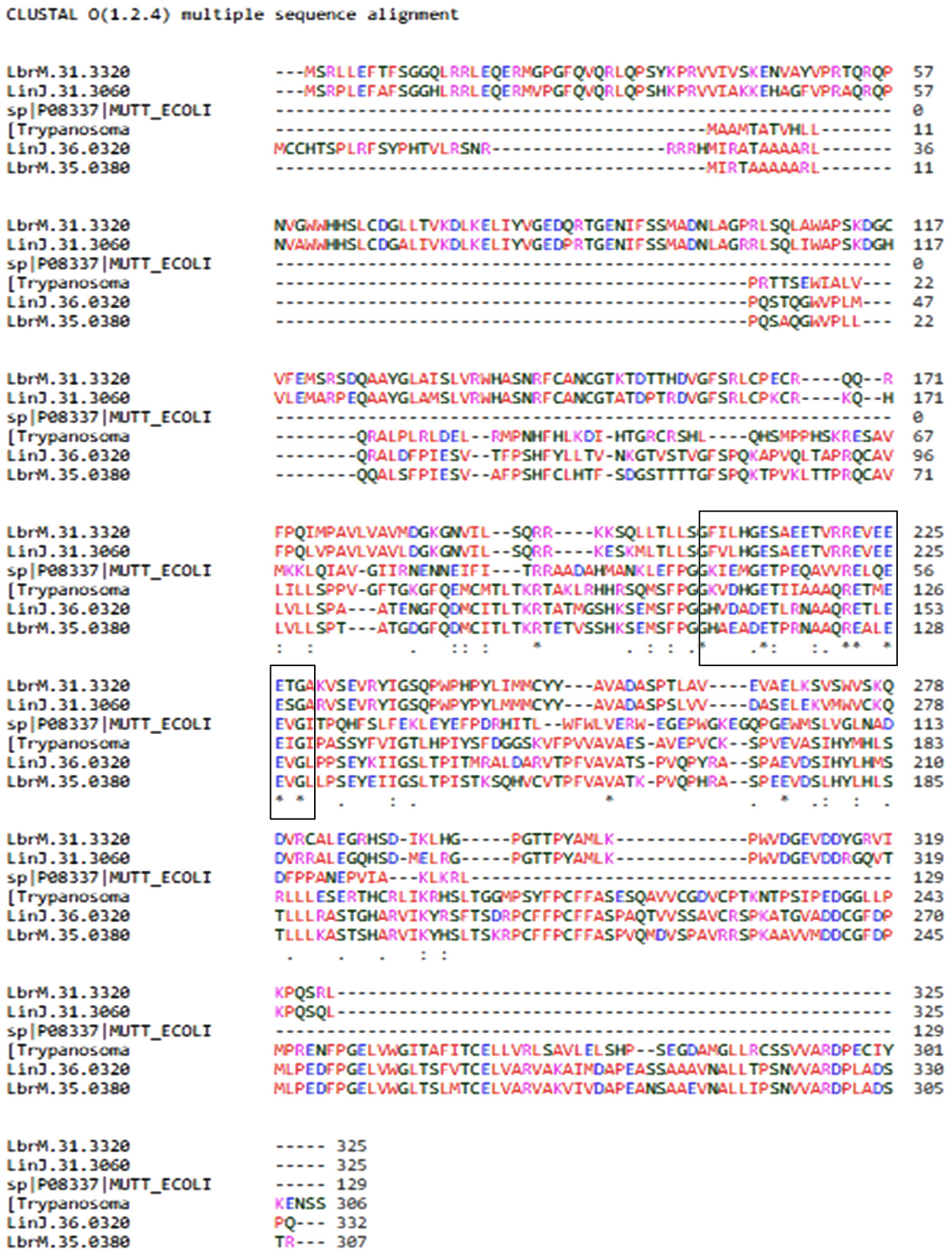

Fig. 1: multiple sequence alignment of the *mutT* amino acid sequences from *Escherichia coli* (P08337), *Trypanosoma cruzi* (AGM37761.1), *Leishmania infantum* (LinJ.31.3060 and LinJ.36.0320) and *L. braziliensis* (LbrM.31.3320 and LbrM.35.0380). The black box encloses the Nudix motif. The asterisks (*) represents the maximum identity between sequences analised; the two point mark (:) represents change of two amino acids; the end point (.) represents change of amino acid residue.

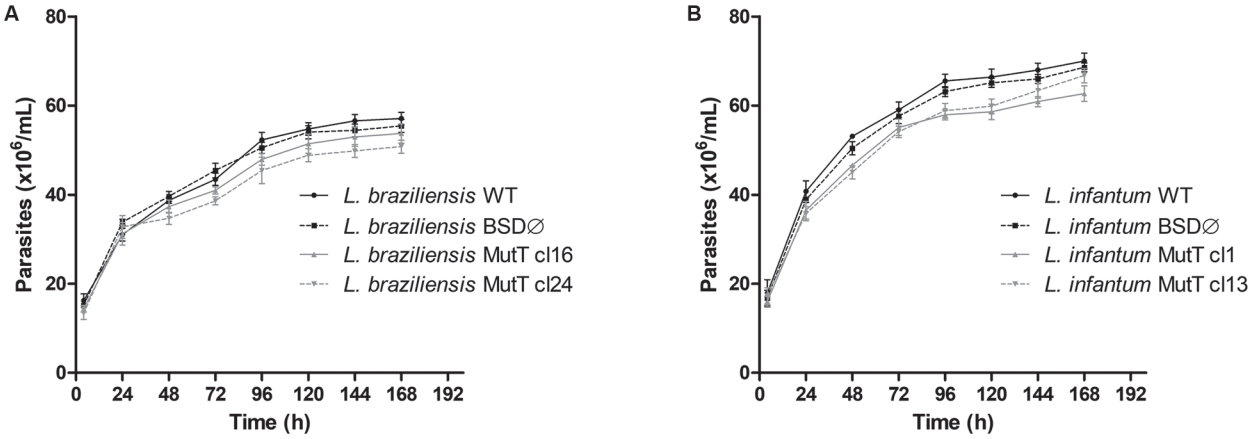

Fig. 2: MutT heterologous expression did not alter *Leishmania braziliensis* (A) and *L. infantum* (B) growth. Wild-type (WT), parasites transfected only with pIR1-BSD plasmid (BSDØ) and clones transfected with pIR1-BSD-MutT were growth in M199 medium and followed for 4 to 168 h until stationary phase. The parasite number was determined using a model Z1 Coulter counter. Experiments were performed three times in triplicate.

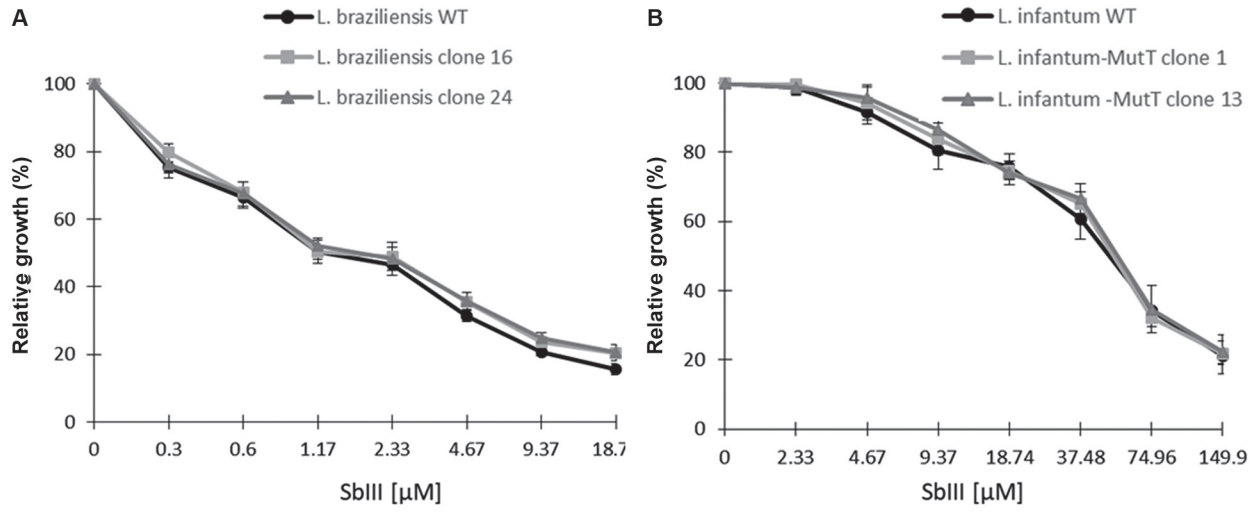

Fig. 3: EcMutT heterologous expression did not affect SbIII susceptibility in *Leishmania braziliensis* (A) and *L. infantum* (B). Susceptibility to SbIII was evaluated in wild-type (WT) and transfected with pIR1-BSD-MutT *L. braziliensis* (A) and *L. infantum* (B) lines. Parasites were incubated in the absence or presence of SbIII (0.3 to 149.9 µM) for 48 h and the percentages of parasites were determined using a model Z1 Coulter Counter. Mean values ± standard deviations of three independent experiments in triplicate are indicated.