## CLUSTAL O(1.2.4) multiple sequence alignment

LbrM.31.3320 LinJ.31.3060 sp P08337 MUTT_ECOLI [Trypanosoma LinJ.36.0320 LbrM.35.0380	MSRLLEFTFSGGQLRRLEQERMGPGFQVQRLQPSYKPRVVIVSKENVAYVPRTQRQP MSRPLEFAFSGGHLRRLEQERMVPGFQVQRLQPSHKPRVVIAKKEHAGFVPRAQRQP MAAMTATVHLL	57 57 0 11 36 11
LbrM.31.3320 LinJ.31.3060 sp P08337 MUTT_ECOLI [Trypanosoma LinJ.36.0320 LbrM.35.0380	NVGWWHHSLCDGLLTVKDLKELIYVGEDQRTGENIFSSMADNLAGPRLSQLAWAPSKDGC NVAWWHHSLCDGALIVKDLKELIYVGEDPRTGENIFSSMADNLAGRRLSQLIWAPSKDGH PRTTSEWIALV	117 117 0 22 47 22
LbrM.31.3320 LinJ.31.3060 sp P08337 MUTT_ECOLI [Trypanosoma LinJ.36.0320 LbrM.35.0380	VFEMSRSDQAAYGLAISLVRWHASNRFCANCGTKTDTTHDVGFSRLCPECRQQR VLEMARPEQAAYGLAMSLVRWHASNRFCANCGTATDPTRDVGFSRLCPKCRKQH QRALPLRLDELRMPNHFHLKDI-HTGRCRSHLQHSMPPHSKRESAV QRALDFPIESVTFPSHFYLLTV-NKGTVSTVGFSPQKAPVQLTAPRQCAV QQALSFPIESVAFPSHFCLHTF-SDGSTTTTGFSPQKTPVKLTTPRQCAV	171 171 6 67 96 71
LbrM.31.3320 LinJ.31.3060 sp P08337 MUTT_ECOLI [Trypanosoma LinJ.36.0320 LbrM.35.0380	FPQIMPAVLVAVMDGKGNVILSQRRKKSQLLTLLSGFILHGESAEETVRREVEE FPQLVPAVLVAVLDGKGNVILSQRRKESKMLTLLSGFVLHGESAEETVRREVEE MKKLQIAV-GIIRNENNEIFITRRAADAHMANKLEFPGGKIEMGETPEQAVVRELQE LILLSPPV-GFTGKGFQEMCMTLTKRTAKLRHHRSQMSFPGGKVDHGETIIAAAQRETME LVLLSPAATENGFQDMCITLTKRTATMGSHKSEMSFPGGHAEADETPRNAAQRETLE LVLLSPTATGDGFQDMCITLTKRTETVSSHKSEMSFPGGHAEADETPRNAAQREALE : : . :: * . :: * . : * .** *	225 225 56 126 153 128
LbrM.31.3320 LinJ.31.3060 sp[P08337 MUTT_ECOLI [Trypanosoma LinJ.36.0320 LbrM.35.0380	ETGAKVSEVRYIGSQPWPHPYLIMMCYYAVADASPTLAVEVAELKSVSWVSKQ ESGARVSEVRYIGSQPWPYPYLMMCYYAVADASPSLVVDASELEKVMWVCKQ EVGITPQHFSLFEKLEYEFPDRHITLWFWLVERW-EGEPWGKEGQPGEWMSLVGLNAD EIGIPASSYFVIGTLHPIYSFDGGSKVFPVVAVAES-AVEPVCKSPVEVASIHYMHLS EVGLPPSEYKIIGSLTPITMRALDARVTPFVAVATS-PVQPYRASPAEVDSIHYLMMS EVGLLPSEYEIIGSLTPISTKSQHVCVTPFVAVATK-PVQPHRASPEEVDSLHYLHLS * *	278 278 113 183 210 185
LbrM.31.3320 LinJ.31.3060 sp P08337 MUTT_ECOLI [Trypanosoma LinJ.36.0320 LbrM.35.0380	DVRCALEGRHSD-IKLHGPGTTPYANLKPWVDGEVDDYGRVI DVRRALEGQHSD-MELRGPGTTPYANLKPWVDGEVDDRGQVT DFPPANEPVIAKLKRL	319 319 129 243 270 245
LbrM.31.3320 LinJ.31.3060 sp P08337 MUTT_ECOLI [Trypanosoma LinJ.36.0320 LbrM.35.0380	KPQSRL	325 325 129 301 330 305
LbrM.31.3320 LinJ.31.3060 sp[P08337 MUTT_ECOLI [Trypanosoma LinJ.36.0320 LbrM.35.0380	325 325 129 KENSS 306 PQ 332 TR 307	

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.

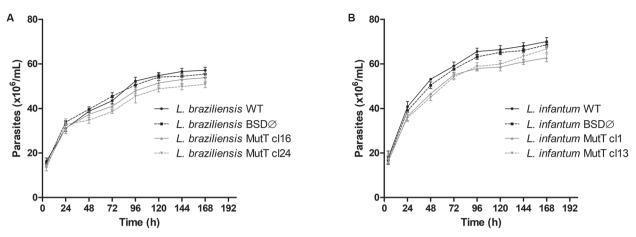


Fig. 2: MutT heterologous expression did not alter *Leishmania braziliensis* (A) and *L. infantum* (B) growth. Wild-type (WT), parasites transfected only with pIR1-BSD plasmid (BSDØ) and clones transfected with pIR1-BSD-MutT were growth in M199 medium and followed for 4 to 168 h until stationary phase.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

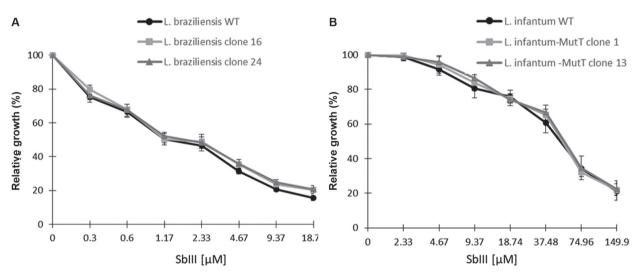


Fig. 3: EcMutT heterologous expression did not affect SbIII susceptibility in *Leishmania braziliensis* (A) and *L. infantum* (B). Susceptibility to SbIII was evaluated in wild-type (WT) and transfected with pIR1-BSD-MutT *L. braziliensis* (A) and *L. infantum* (B) lines. Parasites were incubated in the absence or presence of SbIII (0.3 to 149.9  $\mu$ M) 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.