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The ATAD2/Abo1/Yta7 homologue, Bromodomain Factor 7, is essential for macrophage infection by *Leishmania mexicana*.

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To facilitate processes such as transcription and replication, eukaryotes have evolved factors able to disassemble nucleosomes so that they do not present obstructions on the chromatin The conserved Type II AAA+ ATPases ATAD2/Abo1/Yta7 can remove nucleosomes from chromatin and perform such a function. Exemplified by Yta7 the H3 N-terminal tail is recognised by a crown of atypical bromodomains, before the homohexamer of the ATPase removes the H3 monomer from the nucleosome, resulting in its dissociation. *Leishmania* Bromodomain Factor 7 was identified as a potential homologue of these factors, based on its domain organisation. Alphafold modelling of the BDF7 bromodomain suggests it does not contain the canonical binding pocket to accommodate acetylated lysine residues. Live-cell imaging of mNeonGreen::BDF7 revealed it is a nuclear protein in *L. mexicana*. To explore BDF7 function a null mutant was generated in promastigote stage *L. mexicana* using the T7/Cas9 system. The null mutant strain exhibited normal growth in culture but lost viability when transitioned to amastigote differentiation conditions, a phenotype that was restored when an add-back BDF7 allele was integrated using the pRIB vector. The BDF7-null mutant could not establish productive infections in murine bone marrow-derived macrophages. RNA-seq was used to assess the BDF7-null strain under metacyclic enriching conditions and indicated a dysregulated transcriptome that may leave the cell unprepared the cell for infection. Many histone genes were differentially expressed as were protein components of the ribosome. XL-BioID was performed to identify proteins in spatial proximity to BDF7, using CRK9 as an organellar control; defining 82 proteins as significantly enriched. The GO terms describing these proteins indicate the enrichment of factors involved in the regulation of gene expression and factors also involved in ribosome biogenesis. Ongoing work seeks to identify the genomic loci, if any, at which BDF7 is enriched.