1	Trypanosoma cruzi Bromodomain Factor 3 (\textit{Tc} BDF3) binds acetylated α tubulin and
2	concentrates in the flagellum during metacyclogenesis
3	
4	
5	Victoria Lucia Alonso ^{a,b} , Gabriela Vanina Villanova ^{a,b} , Carla Ritagliati ^b , María Cristina
6	Machado Motta ^c , Pamela Cribb ^{a,b} and Esteban Carlos Serra ^{a,b} #
7	
8	Facultad de Ciencias Bioquímicas y Farmacéuticas, Universidad Nacional de Rosario (UNR).
9	Rosario, Argentina ^a ; Instituto de Biología Molecular y Celular de Rosario (IBR), CONICET.
10	Rosario, Argentina ^b ; Laboratório de Ultraestrutura Celular Hertha Meyer, Instituto de Biofísica
11	Carlos Chagas Filho, Universidade Federal do Rio de Janeiro. Rio de Janeiro, Brazil ^c .
12	
13	Running head: <i>T. cruzi</i> bromodomain 3 binds acetylated α tubulin
14	
15	#Address correspondence to Esteban C. Serra: eserra@fbioyf.unr.edu.ar
16	
17	
18	
19	
20	
21	
22	
23	
24	
	1

Abstract

25

26

27

28

29

30

31

32

33

34

35

36

37

38

39

40

41

Bromodomains are highly conserved acetyl-lysine binding domains found mainly in proteins associated with chromatin and nuclear acetyltransferases. The Trypanosoma cruzi genome encodes at least four Bromodomain Factors (TcBDFs). We describe here Bromodomain Factor 3 (TcBDF3), a bromodomain-containing protein localized in the cytoplasm. TcBDF3 cytolocalization was determined using purified antibodies by western blot analysis (WB) and immunofluorescence (IF) in all life cycle stages of T. cruzi. In epimastigotes and amastigotes it was detected in the cytoplasm, the flagellum and the flagellar pocket and in trypomastigotes only in the flagellum. Subcellular localization of TcBDF3 was also determined by digitonin extraction, ultrastructural immunocytochemistry and expression of TcBDF3 fused to Cyan Fluorescent Protein (CFP). Tubulin can acquire different posttranslational modifications (PTMs), which modulate microtubules functions. Acetylated α tubulin has been found in the axoneme of flagella and cilia as well as in the subpellicular microtubules of Trypanosomatids. TcBDF3 and acetylated α tubulin partially co-localized in isolated cytoskeletons and flagella from T. cruzi epimastigotes and trypomastigotes. Interaction between the two proteins was confirmed by co-immunoprecipitation and far western blot assays with synthetic acetylated a tubulin peptides and recombinant *Tc*BDF3.

42

43

44

45

46

47

Introduction

49

50

51

52

53

54

55

56

57

58

59

60

61

62

63

64

65

66

67

68

69

70

71

72

Trypanosoma cruzi is a protozoan parasite and the causative agent of Chagas disease. It has a complex life cycle that alternates between two hosts and at least four distinct developmental stages. Amastigotes and bloodstream trypomastigotes are present in the mammalian host whereas epimastigotes and the infective metacyclic trypomastigotes are present in the insect vector (from the Triatominae and Reduviidae family). The differentiation event, from epimastigotes to metacyclic trypomastigotes occurring inside the insect, is called metacyclogenesis. This process can be induced in vitro using artificial media that resemble the conditions inside the vector and occurs spontaneously in old epimastigote cultures (1). Trypanosomatids are characterized by the presence of a particular cytoskeleton responsible for the modulation of cell shape between the different life cycle stages and for motility and attachment to the host cell surface (2). These parasites present a layer of microtubules (MT), the subpellicular microtubules, located below the plasma membrane and a flagellum with a typical 9+2 pattern of axonemal microtubules. The flagellum emerges from a membrane invagination called the flagellar pocket (FP). Four cytoplasmic microtubules are nucleated close to the basal body and run around the FP and along the entire flagellum attachment zone (FAZ) to the anterior cellular pole. The FP lacks the layer of subpellicular microtubules and is the place where endocytosis and exocytosis occur (3). Microtubules can acquire a variety of evolutionary conserved posttranslational modifications (PTM). It was proposed that these modifications dictate the recruitment of protein complexes that might regulate microtubule-based functions in different cellular locations (Reviewed by (4-7)). Acetylation occurs on Lysine 40 of α tubulin (4-5) and it was thought that MT stabilization was a consequence of this PTM (6-7). However, it was recently demonstrated that acetylation of MTs do not necessarily affect their stability (8-9).

73 In Trypanosomatids, acetylated α tubulin is found in the subpellicular microtubules and in the flagella of T. cruzi and T. brucei (10-11). This PTM is also present in the ephemeral 74 75 microtubules of the mitotic spindle of T. brucei (11). The presence of acetylated α tubulin in 76 early mitotic spindles in several organisms and the fact that protozoa like T. brucei and T. 77 cruzi exhibit global α tubulin acetylation reinforces the idea that this PTM is not restricted to 78 stable MTs (Reviewed by (12)). 79 Although tubulin acetylation has been described a long time ago, the enzymes responsible for this reversible modification have recently started to emerge. The first tubulin deacetylase 80 81 described in mammals was HDAC6 (class II histone deacetylase), which can also modify 82 other non-nuclear proteins (13). SIRT2, is a NAD-dependent deacetylase (class III histone 83 deacetylase or Sirtuin) capable of modifiying α tubulin (14). In the *Trypanosoma cruzi* genome 84 (http://tritrypdb.org/tritrypdb/) there are two coding sequences (CDSs) for histone deacetylases homologous to HDAC6 and two CDSs for Sirtuins. The Leishmania infantum 85 Sirtuin (LiSIR2RP1) is a NAD-dependent deacetylase and ADP-ribosyltransferase capable of 86 87 deacetylating α tubulin (15). Also, there are two tubulin acetyltransferases described until 88 now. The ELP3 subunit of the Elongator complex is known to modify microtubules of the 89 cortical neurons (16) and αTAT-1, which has recently been proposed as the mayor α tubulin 90 K40 acetyltransferase in mammals and nematodes (17). The Trypanosoma cruzi genome 91 contains two sequences homologous to ELP3. In Trypanosoma brucei, TbELPa and b have 92 been reported (18). Also, a putative sequence homologous to αTAT-1 is present in 93 trypanosomatids but has not been characterized yet. 94 Bromodomains are conserved protein modules, capable of binding acetylated lysines and 95 found in proteins associated with chromatin and in nearly every nuclear histone 96 acetyltransferase. They have an atypical left-handed four-helix bundle structure (helixes α_A ,

 α_B , α_C , and α_Z) connected by two loops (loop ZA and loop BC) that constitute the surface 97 98 accessible hydrophobic pocket where the acetyl-lysine binding site is located (19). 99 Bromodomains can interact with other proteins in an acetylation-dependent manner and form 100 multi-subunit complexes (20). The Bromodomain is considered a nuclear domain but a small 101 number of bromodomain-containing proteins have a dual nuclear-cytosolic localization (21-102 23). 103 Genes coding for putative bromodomain containing factors (BDFs) were found in the TriTryp 104 genomes (Trypanosoma brucei, Trypanosoma cruzi and Leishmania ssp.) (24). We have 105 previously characterized TcBDF2, which binds histone H4 (25). Here we describe 106 Bromodomain Factor 3 from Trypanosoma cruzi (TcBDF3), the first exclusively non-nuclear 107 bromodomain-containing protein reported so far. TcBDF3 is expressed in all life cycle stages 108 and interacts with acetylated α tubulin, the major component of the flagellar and subpellicular 109 microtubules. In both metacyclic and bloodstream trypomastigotes, TcBDF3 was found 110 concentrated in the flagellum and in the flagellar pocket region. Even though the precise 111 function of TcBDF3 remains unrevealed, the results presented herein suggest a participation 112 of this bromodomain factor in cytoskeleton dynamics.

113

114

Materials and Methods

- 115 Ethics Statement
- 116 All experiments were approved by the Institutional Animal Care and Use Committee of the
- 117 School of Biochemical and Pharmaceutical Sciences (National University of Rosario,
- 118 Argentina) and conducted according to specifications of the US National Institutes
- of Health guidelines for the care and use of laboratory animals.
- 120 Cell culture

6

121 The Vero cell line was routinely cultivated in DMEM medium (Gibco) supplemented with 10% heat inactivated Fetal Calf Serum (FCS), 0.15% (w/v) NaHCO₃, 100 U ml⁻¹ penicillin and 100 122 123 mg ml⁻¹ streptomycin at 37°C in a humid atmosphere containing 5% CO₂. 124 Parasites 125 Epimastigotes of T. cruzi Dm28c strain were cultured in liver infusion-tryptose medium (LIT) 126 (26) supplemented with 10% FCS at 28°C. The parasites were kept in exponential growth 127 phase by sub-culturing every three days. Intracellular forms and trypomastigotes were 128 obtained by infecting Vero cells with trypomastigotes as previously described (27-28). 129 To obtain metacyclic trypomastigotes, epimastigotes were differentiated in vitro following the 130 procedure described by Contreras and co-workers (1) using chemically defined conditions 131 (TAU3AAG medium). Culture supernatants were collected after 24, 48 and 72 h of incubation 132 in TAU3AAG medium. 133 Plasmid construction and expression of *Tc*BDF3 PCR 134 *Tc*BDF3 gene amplified by using BDF3Fw was 135 (5'AAGGATCCATGGGCTCTACGGGTCGG) and BDF3Rv (5'AACTCGAGCCTCGTCCTCCACCGCC) oligonucleotides. TcBDF3ΔC fragment was 136 137 amplified using BDF3Fw and BDF3ΔCRv (5'AACTCGAGTGCTCTTCCGCAAGACGCTCC) 138 oligonucleotides. Proofreading DNA polymerase was used. DNA purified from cultured T. 139 cruzi epimastigotes served as template. 140 PCR products were inserted into pCR 2.1TOPO® vector (Invitrogen) and sequenced. 141 TcBDF3 and TcBDF3∆C coding regions were inserted into a pENTR3C vector (Gateway system® Invitrogen) and then transferred by recombination to pDEST17 (Gateway system® 142 143 Invitrogen) and pTcCFPN (29) using LR clonase II enzyme mix (Invitrogen) to generate

Histidine tag and cyan fluorescent protein (CFP) fusions. pDEST17-TcBDF3 was transformed

145 into Escherichia coli BL21 pLysS and the recombinant protein (fused to a His-tag) was 146 obtained by induction with 0.5 mM IPTG for 3 h at 37°C. The protein was purified by affinity 147 chromatography using a Ni-NTA agarose resin (Qiagen) following the manufacturer's 148 instructions. The secondary structure of recombinant TcBDF3 was measured by circular 149 dicroism. 150 Polyclonal antibodies 151 Rabbit and mouse polyclonal antisera against TcBDF3 were obtained by inoculating 152 subcutaneously recombinant TcBDF3 three times. First using complete Freund's adjuvant 153 and with incomplete adjuvant the following times. Specific antibodies were purified from the 154 antisera obtained by chromatography through a Ni-NTA agarose column containing cross-155 linked TcBDF3-His. Antibodies were eluted with 100 mM triethylamine pH 11, neutralized to pH 7 and stored at 4°C or at -20°C with 50% glycerol. The purified antibodies specificity was 156 157 tested by western blot assays. 158 Protein extracts 159 Exponentially growing epimastigotes were washed twice with cold PBS, pellets were resuspended in lysis buffer (20 mM Hepes, 8M Urea) and incubated for 30 minutes at room 160 161 temperature with gentle agitation. Insoluble debris was eliminated by centrifugation. The 162 same procedure was applied to amastigote and trypomastigote cellular pellets. To obtain 163 nuclear extracts, exponentially growing epimastigotes were washed with PBS, lysed in hypotonic buffer A (10 mM HEPES pH 8, 50 mM NaCl, 1 mM EDTA, 5 mM MgCl₂, 1% v/v 164 165 Nonidet P-40, 1 mM phenylmethylsulphonyl fluoride (PMSF), aprotinin, 0.25% Triton X-100), 5% v/v glycerol was added and the pellet was collected by centrifugation. Pellets were 166 167 washed with buffer B (10 mM HEPES pH 8, 140 mM NaCl, 1 mM EDTA, 5 mM MgCl2 5% v/v

glycerol, 1 mM PMSF, 10 µg ml⁻¹ aprotinin) and incubated for 10 min on ice. Nuclei were

8

169 collected by centrifugation and resuspended in Buffer C (10 mM HEPES pH 8, 400 mM NaCl, 0.1 mM EDTA, 0.5 mM DTT, 5% v/v glycerol, 1 mM PMSF, 10 µg ml⁻¹ aprotinin), incubated 170 171 for 1 h on ice and sonicated. This extraction was repeated three times and supernatants were 172 precipitated with 20% trichloroacetic acid (TCA) overnight at 4 C°. 173 Trypanosoma cruzi cytoskeleton enriched extracts were prepared as previously described by 174 Schneider and co-workers (11). Briefly, cells were harvested, washed twice with PBS and 175 incubated with EB buffer (50 mM HEPES, 5 mM EGTA, 1 mM MgSO₄, 0,1 mM EDTA, 2 mM 176 MgCl₂, 0.1% Triton-X100 and Protease Inhibitor Cocktail set I, Calbiochem) on ice for 30 177 minutes. The lysate was centrifuged at 10,000 x g for 15 minutes and the supernatant, which 178 contained soluble proteins, was named Sn1. The remaining pellet was incubated with EB 179 buffer supplemented with 1M NaCl on ice for 5 minutes, sonicated and centrifuged at 20,000 180 x q for 15 minutes. The supernatant obtained contained soluble flagellar and cytoskeletal proteins (Sn2). The remaining pellet (P) contained insoluble flagellar and cytoskeletal 181 182 proteins. Supernatants were precipitated with 20% TCA overnight at 4 °C. 183 immunoprecipitation cells mΜ DSP assays were incubated with 184 (dithiobis[succinimidylpropionate]) (Thermo Scientific) for 2 hours on ice. This reagent was 185 used to cross-link protein complexes within the cell. After incubation the reaction was stopped 186 with 20 mM Tris, pH 7.5. Then the cells were harvested and incubated with EB buffer 187 supplemented with 1 M NaCl on ice for 30 minutes. The lysate was centrifuged at 10,000 x g 188 for 15 minutes and the supernatant obtained was used to perform co-immunoprecipitation 189 experiments. 190 Western blot and slot blot 191 Protein extracts (30-50 µg per well) were separated by SDS-PAGE and transferred to

nitrocellulose membranes. Transferred proteins were visualized with Ponceau S. Membranes

193 were treated with 10 % non-fat milk in PBS for 2 hours and then incubated with specific 194 antibodies diluted in PBS for 3 hours. The antibodies used were: polyclonal rabbit and mouse 195 anti-TcBDF3; monoclonal mouse anti-acetylated α tubulin antibody clone 6-11B-1 (Sigma 196 Aldrich); monoclonal mouse anti-trypanosome α tubulin clone TAT-1 (gift from K. Gull, 197 University of Oxford, England, UK.); mouse anti-paraflagellar rod protein 2 (gift from Ariel 198 Silber, University of São Pablo, Brazil); mouse anti-Trypanosoma cruzi Histone H4 (gift from 199 Sergio Shenkman, Universidade Federal de São Paulo, Brazil); rabbit anti-Trypanosoma cruzi 200 High Mobility Group B (TcHMGB) (30) and anti- Trypanosoma cruzi Bromodomain factor 2 201 (TcBDF2) (25). Bound antibodies were detected using peroxidase labelled anti-mouse or anti-202 rabbit IgGs (GE Healthcare) and ECL Prime (GE Healthcare) according to manufactures 203 protocol. 204 Slot Blot was performed immobilizing 10 μg of α tubulin (PDGAMPSDKTIGVEDDA; 205 Genscript), α tubulin acetylated on lysine 40 (PDGAMPSDKacTIGVEDDA; Genscript) and 206 histone H4 acetylated on lysine 14 (AKGKKSGEAKGTQKacRQ; (31)) synthetic peptides onto 207 nitrocellulose membranes. The membranes were incubated with recombinant His-tagged 208 TcBDF3 or TcBDF2 for 3 hours (0.5 µg/ml). Bound proteins were visualized using anti-209 Histidine antibodies (GE Healthcare) and detected as mentioned above. 210 Subcellular localization of *Tc*BDF3 by digitonin extraction 211 Parasites in exponential phase were collected, washed and resuspended in buffer A (20 mM Tris-HCl, pH 7.2 with 225 mM sucrose, 20 mM KCl, 10 mM KH₂PO₄, 5 mM MgCl₂, 1 mM 212 Na₂EDTA and 1 mM DTT) at a concentration of 1 mg ml⁻¹ protein and supplemented with 213 214 digitonin (0-1 mg) (final volume of 1 ml for each digitonin concentration). The resuspended 215 parasites were incubated at 28 °C for 20 min before being centrifuged at 14,000 x g for 2 min 216 at 4 °C. The enzymatic activities of Alpha-hydroxiacid dehydrogenase (αHAdH) (cytosolic 9

217 marker) and Malate dehydrogenase (MdH) (glycosomal and mitochondrial marker) were 218 determined in the supernatant (S) and occasionally in the cell pellet (P) in the presence of 219 0.1% (v/v) Triton X-100 and 150 mM NaCl. To measure the enzymatic activity of αHAdH the 220 extracts were incubated with 4 ul of 0.5 mM NADH, 7 ul of 1 mM Phenilpyruvate, 2 ul 20% 221 (v/v) Tritón X-100 and 40 ul of the protein extract in 10 mM Tris-HCl pH 8. The percentage of activity was determined spectrophotometrically by measuring the oxidation of NADH 222 (£339nm=6220 M⁻¹ cm⁻¹) at 340 nm. To measure the enzymatic activity of MdH the extracts 223 224 were incubated with 5 ul of 0.5 mM NADH, 10 ul of 1 mM Oxalacetate, 2 ul 20% (v/v) Tritón 225 X-100 and 20 ul of the protein extract in 10 mM Tris-HCl pH 8. The percentage of activity was 226 determined spectrophotometrically by measuring the oxidation of NADH (ε339nm=6220 M⁻¹ 227 cm⁻¹) at 340 nm. 228 Equal volumes of selected S and P fractions were subjected to SDS-PAGE, blotted onto 229 nitrocellulose membranes and probed with specific antibodies. The antibodies used were: 230 Anti-Tyrosine Amino Transferase antibodies (TcTAT), anti-Glycosomal 231 Dehydrogenase (TcMdHqlyc), anti-Mitochondrial Malate Dehydrogenase (TcMdHmit) 232 antibodies (all of them where a gift from Cristina Nowicki, Universidad de Buenos Aires, 233 Argentina), anti-paraflagellar rod 2 (TcPAR2) antibodies and mouse monoclonal anti-234 trypanosome α tubulin clone TAT-1 (α tubulin). 235 Ultrastructural Immunocytochemistry 236 Parasites were fixed in 0.3% glutaraldehyde, 4% formaldehyde and 1% picric acid diluted in 0.1 M cacodylate buffer at pH 7.2 and then dehydrated at 20 °C using a graded acetone series 237 238 and progressively infiltrated with Unicryl at lower temperatures. The polymerization of the resin was carried out in BEEM capsules at 20 °C for 5 days under UV light. Ultra-thin sections 239 240 were obtained in a Leica ultramicrotome (Reichert Ultracuts) and the grids containing the 10

sections were incubated with 50 mM NH₄Cl for 30 min. The grids were then incubated with blocking solution (3.5% BSA, 0.5% teleostean gelatine, 0.02% Tween -20 diluted in PBS, pH 8.0) for 30 min and finally with goat serum diluted in blocking solution (1:200). Grids containing ultra-thin sections were incubated for 1 h with anti-*Tc*BDF3 antibodies diluted in blocking solution (1:1) and washed with PBS. Grids were then incubated with gold-labelled goat anti-rabbit IgG diluted 1:200 for 45 min, washed with blocking solution and stained with uranyl acetate and lead citrate for further observation using a Zeiss 900 transmission electron microscope. In control assays, sections were not incubated with the primary anti-serum.

Immunocytolocalization

Trypomastigotes and exponentially growing epimastigotes were centrifuged, washed twice with PBS, settled on polylisine-coated coverslips and fixed with 4% para-formaldehyde in PBS at room temperature for 20 minutes. Fixed parasites were washed with PBS and permeabilized with 0.2% Triton X-100 in PBS for 10 minutes. After washing with PBS, parasites were incubated with the appropriate primary antibody diluted in 1% BSA in PBS for 3 hours at room temperature. In co-localization experiments both antibodies were incubated together. Non-bound antibodies were washed with 0.01% Tween 20 in PBS and then the slides were incubated with fluorescent-conjugated anti-rabbit (Fluorescein, Jackson Immuno Research) or anti-mouse (Rodhamine, Calbiochem) IgG antibodies and 2 µg ml⁻¹ of DAPI for 1 hour. Alternatively DNA was stained with Propidium Iodide (Invitrogen) according to manufacturer's instructions. The slides were washed with 0.01% Tween 20 in PBS and finally mounted with VectaShield (Vector Laboratories). To analyze intracellular amastigotes, Vero cells monolayers were grown on coverslips and infected with *T. cruzi* trypomastigotes as described above. Three days post infection cultures were washed with PBS and fixed with 4% para-formaldehyde in PBS at room temperature for 20 minutes. The same procedure

265	described above was followed for immunodetection. Images were acquired with a confocal
266	Nikon Eclipse TE-2000-E2 microscope using Nikon EZ-C1 Software or an epifluorescence
267	Nikon Eclipse Ni-U microscope. Adobe Photoshop CS and Image J software (32) were used
268	to pseudo-color and process all images.
269	Isolated cytoskeletons and flagellar complexes were obtained for immunocytolocalization as
270	previously described by Sasse and Gull (33) and prepared for immunofluorescence as
271	described above.
272	Transfection of parasites
273	Epimastigotes were grown at 28°C in LIT medium supplemented with 10% FCS, to a density
274	of approximately 3×10^7 cells ml ⁻¹ . Parasites were then harvested by centrifugation at 4,000 x
275	g for 5 min at room temperature, washed once with PBS and resuspended in 0.35 ml of
276	transfection buffer pH 7.5 (0.5 mM MgCl $_2$, 0.1 mM CaCl $_2$ in PBS) to a density of 1 x 10 8 cells
277	$\text{ml}^{\text{-1}}.$ Cells were then transferred to a 0.2 cm gap cuvette (Biorad) and 15 to 100 μg of DNA
278	was added in a final volume of 40 μ l. The mixture was placed on ice for 15 min and then
279	subjected to a pulse of 450 V and 500 μF using GenePulser II (Bio-Rad, Hercules, USA).
280	After electroporation, cells were transferred into 5 ml of LIT medium containing 10% FCS and
281	maintained at room temperature for 15 minutes. Then the cells were incubated at 28°C. After
282	24 h the antibiotic G418 (Genbiotech) was added to an initial concentration of 125 $\mu g \ ml^{-1}$.
283	Then, 72 to 96 hours after electroporation, cultures were diluted 1:5 and antibiotic
284	concentration was doubled. Stable resistant cells were obtained approximately 30 days after
285	transfection.
286	Co-Immunoprecipitation
287	Epimastigotes were grown up to 10 ⁷ parasites ml ⁻¹ and 10 ¹⁰ parasites were used per co-
288	immunoprecipitation experiment. Antibodies anti- <i>Tc</i> BDF3 and total IgGs purified from non-12

immunized rabbits were immobilized to magnetic beads (Dynabeads® Invitrogen) following the manufacturer's instructions. The antibody-coupled beads were incubated with the protein extracts for 3 hours at 4 °C with gentle shaking. Then the beads were washed three times with MME buffer (50 mM HEPES, 5 mM EGTA, 1 mM MgSO₄, 0,1 mM EDTA, 2 mM MgCl₂) and two times with Last Wash Buffer (30 mM Tris, pH 7.5, 0.02% Tween 20). The protein complexes were eluted with 0,5 M HN₄OH and neutralized. The eluted proteins were separated by SDS-PAGE and then transferred to nitrocellulose membrane for western blot analysis. Molecular exclusion chromatography

297

Molecular exclusion chromatography was carried out using a Superdex 75 column (GE Healthcare) equilibrated with 10 mM sodium phosphate buffer pH 8 at the recommended flow rate of 0.25 ml/min, and the absorbance at 280 nm continuously monitored using an ÄKTA FPLC system (GE Healthcare). The standard curve was constructed using: Lisozime (14,7 kDa), GST (27 kDa for the monomeric form and 54 kDa for the dimeric form) and Bovine Serum Albumin (67 kDa). All buffers and samples were filtered (0.45 µm) before use.

304

305

307

308

309

310

311

289

290

291

292

293

294

295

296

298

299

300

301

302

303

Results and Discussion

306 *Trypanosoma cruzi* Bromodomain factor 3 (*Tc*BDF3)

> Trypanosoma cruzi Bromodomain factor 3 (TcBDF3) coding sequence has two almost identical variant haplotypes in the T. cruzi genome (TcCLB.510719.70 and TcCLB.509747.110, http://tritrypdb.org/tritrypdb) that encode for a 223 amino acid polypeptide. This coding sequence contains a bromodomain (pfam: PF00439) in its N-terminal portion from R37 to L141 (Supplementary Figure S1A). TcBDF3 has a predicted molecular weight of 24.7 kDa

312 and an isolelectric point of 5.2. The C-terminal portion of the sequence shows no similarity 313 with any domain present in databases. However, it is enriched in acidic amino acids (30% 314 glutamic acid + aspartic acid), basic amino acids (37% lysine + arginine) and serine (14%) 315 (Figure S1A). These highly charged low complexity sequences are generally involved in 316 protein-protein interactions. 317 Orthologous genes are present in other trypanosomatids, the T. brucei (Tb927.11.10070) and 318 Leishmania major (LmjF.36.3360) proteins have a percentage sequence identity of 63% and 319 42% and a similarity of 75.9% and 54.9% respectively with TcBDF3. The similarity between 320 the four Trypanosoma cruzi BDFs and bromodomains from other organisms is low, with a 321 percentage of sequence identities always below 20%. However, the amino acids involved in 322 binding the acetyl-lysine are conserved or conservatively substituted, supporting the 323 hypothesis that TcBDF3 has a functional bromodomain (Figure S1B). The secondary 324 structure of TcBDF3 bromodomain region was modelled with the Phyre2 server (34) retriving 325 the characteristic four α-helix pattern of these domains (Figure S1C). When analysed by 326 molecular exclusion chromatography, most of the recombinant TcBDF3 was found to be a 327 dimmer in solution (figure S1D). 328 TcBDF3 is a cytoplasmatic protein 329 To study the expression of TcBDF3 in Trypanosoma cruzi, antibodies raised against 330 recombinant protein were purified by affinity chromatography. Western blot analysis with 331 rabbit and mouse antibodies showed a single band of the expected molecular weight in total 332 lysates of T. cruzi epimastigotes (Figure S2A). To test the specificity of the anti-TcBDF3 333 antibodies, they were competed with recombinant TcBDF3 and then used in western blot 334 (Figure S2B) and immunofluorescence (Figure S2C) assays.

336

337

338

339

340

341

342

343

344

345

346

347

348

349

350

351

352

353

354

355

356

357

358

TcBDF3 subcellular localization was predicted using pSORTII (http://psort.hgc.jp/form2.html) and Wolf pSORT (http://wolfpsort.org/). Surprisingly, the highest score was assigned to a nonnuclear localization. Also, the TFPP server (Tool for recognizing flagellar proteins in Trypanosoma brucei) (35) predicted a flagellar localization for TcBDF3 and its orthologue in T. brucei (Tb927.11.10070). Although Tb927.11.10070 has not been identified in the flagellar proteome of *T. brucei* (36-38), it is worth mentioning that due to technical limitations many flagellar proteins fail to be detected or cannot be assigned to the flagellum with certainty by proteomic studies. Then, we evaluated the expression of TcBDF3 in nuclear and non-nuclear epimastigote extracts by western blot analysis. The TcBDF3-specific immunoreactive band was observed only in the non-nuclear fraction. Tyrosine Amino Transferase (TcTAT) (39) is a cytosolic protein and TcHMGB (Trypanosoma cruzi High Mobility Group B) (30), TcBDF2 (25) and Histone H4 (40) are all nuclear proteins (Figure 1A). We decided to confirm the non-nuclear localization of this protein through several approaches. First, we performed western blot analysis in subcellular fractions of epimastigotes obtained by digitonin extraction (39). By this approach plasma membranes with high sterol content are specifically permeabilized at low concentration of digitonin, whereas higher concentrations are required to permeabilize glycosomal and mitochondrial membranes (41). Measuring the activity of alpha Hydroxyacid Dehydrogenase (αHAdH) (cytosolic protein) we determined in which fractions the cytosolic (C) content was released (starting at 0.04 mg of digitonin). The Malate Dehydrogenase (MdH) presents a glycosomal and a mitochondrial isoform. Measuring the activity of this enzyme we determined when the glycosomal content (G, starting at 0.2 mg of digitonin) and the mitochondrial content (M, starting at 0.4 mg of digitonin) were released (Figure 1B). The extraction pattern of TcBDF3 was monitored by western blot analysis of 15

360

361

362

363

364

365

366

367

368

369

370

371

372

373

374

375

376

377

378

379

380

381

382

selected soluble (S) and insoluble (P) fractions (Figure 1C, 0-0.7 mg of digitonin). In agreement with our previous results, TcBDF3 was released at low digitonin concentrations. However, TcBDF3 was not completely extracted in the soluble fraction and an immunoreactive band was observed in all the insoluble fractions, showing a pattern similar to that of PAR2 (a flagellar protein) and α tubulin. These results suggest that TcBDF3 is a cytoplasmatic protein that could also be associated with insoluble proteins in the membrane or cytoskeleton of *T. cruzi*. Then, TcBDF3 was immunolocalized in thin sections of epimastigotes by transmission electron microscopy (TEM). TcBDF3 was not observed over DNA containing structures, such as the nucleus (N) or kinetoplast (K) (Figure 2A-C). TcBDF3 was immunolocalized at the flagellum (F) (Figure 2B, D and F, white arrows), especially in its inner part, which is attached to the cell body. Labelling was also observed dispersed in the cytoplasm and close to the flagellar pocket (FP) (Figure 2A-D, black arrows). In control assays with no primary antibody no immunogold particles were detected (data not shown). Next, TcBDF3 expression during T. cruzi life cycle was addressed using epimastigotes, trypomastigotes and amastigotes total protein extracts. A single band of the expected molecular weight was observed for all developmental stages (Figure 3A). The subcellular localization of TcBDF3 was assessed by immunofluorescence microscopy in different stages (Figure 3B). In epimastigotes (E) TcBDF3 was present in the cytoplasm, the flagellum and the flagellar pocket region similar to the pattern obtained by TEM. In amastigotes (A and Ac) we observed an expression pattern similar to epimastigotes. However, the flagellar pocket region was more deeply marked and the plasma membrane appeared to be labelled. Surprisingly, in infective trypomastigotes (T and Tm) TcBDF3 expression pattern changed and was localized exclusively in the flagellum.

384

385

386

387

388

389

390

391

392

393

394

395

396

397

398

399

400

401

402

403

404

405

406

This change in TcBDF3 localization during the epimastigote-trypomastigote transition was also analysed using N-terminal fusions to the Cyan Fluorescent Protein (CFP). A full length (pTcCFPN-TcBDF3) and a truncated form of TcBDF3, containing the first 131 amino acids (pTcCFPN-TcBDF3ΔC), were over-expressed in epimastigotes. Both fusion proteins were detected in the whole cell body of epimastigotes, in a pattern similar to that observed for TcBDF3 by immunocytolocalization (Figure S3). When transfected parasites were differentiated in vitro to trypomastigotes, CFPN-TcBDF3 was found concentrated at the flagellum, as did wild type *Tc*BDF3 (Figure S3A). However, truncated CFPN-*Tc*BDF3∆C remained dispersed in the cell body (Figure S3B). Expression of CFPN-TcBDF3 and CFPN-TcBDF3ΔC was corroborated by western blot analysis with anti-TcBDF3 antibodies (Figure S3C). These results suggest that the C-terminal portion of TcBDF3 could be important for the flagellar localization of *Tc*BDF3 in trypomastigotes. The presence of a bromodomain containing protein outside the nucleus has been described in other models but always with a dual cytoplasmic-nuclear localization and restricted to some specific mammalian cells (21-23). The existence of a bromodomain factor in the flagellum as described herein, suggests a completely new role for these protein modules. Given that in the last few years several authors, using high resolution mass spectrometry, identified thousands of acetylated proteins involved in a wide variety of cellular processes in different organisms (42-45) it is not unrealistic to think that bromodomains could be playing regulatory roles outside the nuclear compartment. In 2000, Kouzarides proposed that acetylation might rival phosphorylation as a regulator of cell function and that the bromodomain may be analogous to the phosphotyrosine-recognizing SH2 domain (46). The presence of TcBDF3 outside the nucleus opens new perspectives for a possible role of lysine acetylation as a regulatory switch in complex cellular processes as proposed by many authors (47-50).

408

409

410

411

412

413

414

415

416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

To study in further detail the differential localization of TcBDF3, in vitro metacyclic trypomastigotes were obtained using TAU medium. During the differentiation process between epimastigotes and trypomastigotes, intermediate stages were distinguished and classified based on the position of the kinetoplast, the nucleus and the flagellum as described by Ferreira and co-workers (51) (a schematic representation is shown in Figure 4, right panel). The immunocytolocalization of TcBDF3 and acetylated α tubulin was analyzed in the intermediate differentiation stages (1a, b and c). As it is shown in figure 4, TcBDF3 concentrates in the flagellum during metacyclogenesis. As previously reported (10), acetylated a tubulin was detected in the whole cell body in the intermediate stages with no significant changes. However, we observed a partial co-localization of TcBDF3 and acetylated a tubulin in the flagella of the intermediate stages (Figure 4), which strongly suggested that *Tc*BDF3 was associated to the flagellar microtubule structure. TcBDF3 binds to acetylated α tubulin The former results as well as the known ability of bromodomain-containing proteins to bind acetylated proteins led us to think that TcBDF3 could be binding acetylated proteins in the cytoskeleton and flagellum of *T. cruzi*. As already mentioned, microtubules are components of the subpellicular corset, the axoneme, the flagellar pocket and the flagellum attachment zone in trypanosomatids (52). Multiple tubulin isotypes are present in microtubules due to a series of posttranslational modifications. Among all isoforms of α tubulin associated with the *T. cruzi* subpellicular and axonemal microtubules, the acetylated form seems to be predominant (10). Isolated subpellicular microtubules and flagellar complexes from epimastigotes and trypomastigotes were obtained in order to verify the presence of TcBDF3 in these cellular components. TcBDF3 as well as acetylated α tubulin and PAR2 (a-PFR, para flagellar rod 2 protein) were

432

433

434

435

436

437

438

439

440

441

442

443

444

445

446

447

448

449

450

451

452

453

454

detected by immunofluorescence (Figure 5). In epimastigotes (E), TcBDF3 was present in discrete regions of the cytoskeleton with a stronger signal in the flagellar pocket region (Figure 5A upper panel). Also it was observed in the flagellum, where it partially co-localized with acetylated α tubulin (Figure 5A lower panel). The protocol performed to obtain isolated flagella, as Sasse and Gull stated in 1988, did not always lead to complete solubilization and a group of subpeculliar MTs attached to basal bodies and forming the flagellar pocket appeared to be resistant to treatment (33). In the enlarged images of the isolated flagella we observed the presence of TcBDF3 and acetylated α tubulin in these resistant structures (Figure 5A, green and red arrows heads), which further corroborated the results obtained by TEM. These results suggest that TcBDF3 localization correlates to acetylated α tubulin, although the opposite is not necessarily true. In trypomastigotes (T), TcBDF3 was present only in the flagellum, as it was previously determined using intact parasites, where it colocalized partially with acetylated α tubulin (Figure 5A). Localization of TcBDF3 and PAR2 was compared in detail to determine if TcBDF3 was present in the paraflagellar rod. The paraflagellar rod is present from the point where the flagellum exits the flagellar pocket and runs alongside the axoneme right to the distal tip. We observed that in the flagellum of epimastigotes and trypomastigotes the two proteins did not co-localize but they seemed to run side by side, supporting the hypothesis that TcBDF3 is present in the flagellar axoneme of T. cruzi but not in the paraflagellar rod (Figure 5B). The presence of TcBDF3 but not of PAR2 in the flagellar pocket region is clearly observed in the enlarged images of the isolated flagella (Figure 5B, green and red arrow heads). Next, western blot assays with anti-TcBDF3 and anti-acetylated α tubulin were performed using protein extracts enriched in cytoskeletal and flagellar proteins (Figure 6A). Three enriched fractions which corresponded to soluble proteins (Sn1), soluble cytoskeletal and 19

455 flagellar proteins (Sn2) and insoluble cytoskeletal and flagellar proteins (P) were obtained by 456 differential extraction with detergent as described by Schneider and co-workers (11). TcBDF3 457 and acetylated α tubulin seemed to be fractionated together from soluble protein pools and 458 from insoluble flagellar and cytoskeletal protein complexes. These results suggested that the 459 interaction between these proteins is restricted to some specific cellular compartments. 460 Immuno-precipitation assays were performed to study the interaction of TcBDF3 with 461 acetylated α tubulin (Figure 6B). We used anti-TcBDF3 antibodies coupled to magnetic beads. Both TcBDF3 and acetylated α tubulin were detected by western blot analysis in the 462 463 immunoprecipitated complexes. These results demonstrated that these two proteins interact 464 in vivo. We did not detect any immunoreactive band using magnetic beads coupled to purified 465 IgG (negative control). To test TcBDF3 binding specificity for acetylated α tubulin, we blotted acetylated, non-466 467 acetylated α tubulin (Ac α tubulin and α tubulin) and histone H4 acetylated in lysine 14 468 (H4K14Ac) peptides onto a nitrocellulose membrane. Then, the membrane was incubated 469 with recombinant TcBDF3 and TcBDF2 (fused to a Histidine tag) and the bound proteins were 470 visualized by western blot analysis with anti-Histidine antibodies (Figure 6C). There was no 471 cross reactivity between bromodomain factors, recombinant TcBDF2 only recognized the 472 H4K14Ac peptide (25) and TcBDF3 only the acetylated α tubulin peptide. This suggests that 473 each BDF can recognize and bind to one (or a limited number of) specific acetylated lysine 474 residues. 475 Although tubulin acetylation is a widespread modification present in all eukaryotic cells, its 476 precise function on cytoskeleton dynamics has not been completely elucidated yet. Recent 477 reports suggested a function for this PTM in axonemal-related cell structures. The acetylation 478 of α tubulin at K40 by the specific enzyme MEC-17 was associated to ciliogenesis and 20

480

481

482

483

484

485

486

487

488

489

490

491

492

493

494

495

496

497

498

499

500

501

502

efficient mechanosensation in Caenorhabditis elegans (17, 53). Trypanosomes are evolutionary early-branched species that have some unique characteristics. The participation of a bromodomain-containing protein complex during metacyclogenesis could also be a unique feature of these particular eukaryotic cells. It has been proposed that cilia and flagella emerged early in eukaryotic evolution, and that in primitive eukaryotes microtubule PTMs existed as a cilia and flagella specific phenomenon, which was later adapted to other microtubule structures (6). The results presented herein show that TcBDB3 binds to acetylated α tubulin both ex vivo and in vivo. This interaction seems to be associated with changes in the amount of TcBDF3 in the flagellum during metacyclogenesis. Although the exact meaning of this observation cannot be understood yet, it is important to mention that TcBDF3 is the first described bromodomaincontaining protein that recognizes a modification in tubulin and, hence, the first candidate to be able to read a tubulin PTM. At least two basic models can be proposed for its mode of action. In analogy to those already proposed for histone-binding bromodomains, a TcBDF3containg complex could be carrying an enzymatic activity to the flagellum to modify tubulin or any other cytoskeletal component. Another hypothesis is that TcBDF3 might carry acetylated a tubulin from the cell body to the flagellum. However, we cannot rule out the possibility that TcBDF3 simply binds to the acetylated lysine residue to protect it from the action of modifying enzymes. A bromodomain-containing protein complex involved in the remodelling of the cytoskeleton in T. cruzi may also be a new quimotherapeutic target for Chagas' disease. Recently, two inhibitors that target bromodomains from the BET family have shown selective activity in a squamous cell carcinoma model (54). Many other inhibitors of the bromodomain-acetyl lysine interaction were developed later, putting bromodomains alongside KATs (Lysine 21

503	Acetyltransferases) and KDACs (Lysine Deacetylases) as interesting targets for diseases
504	caused by aberrant acetylation of lysine residues (55). The presence of an exclusively
505	cytoplasmic bromodomain, as TcBDF3, could be another feature of trypanosomatids absent
506	in mammalian host cells and hence could be considered as potential targets for the
507	development of new drugs against trypanosomiasis.
508	
509	Acknowledgements
510	This work was supported by the National Research Council (CONICET) grant PIP2010-0685
511	and the National Agency of Scientific and Technological Promotion (ANPCyT) and Glaxo
512	SmithKline joint grant PICTO2011-0046.
513	V.L Alonso, and C. Ritagliati are fellows and E.C. Serra, P. Cribb and G.V. Villanova are
514	researchers of the National Research Council (CONICET), Argentina.
515	Authors would like to thank to Dr. K. Gull for his generous gift of anti- <i>T. brucei</i> α tubulin
516	antibodies; Dr. C. Nowiki for the anti-T. cruzi Tyrosine Amino Transferase and anti-T.cruzi
517	Malate Dehydrogenase antibodies; Dr. A. Silver for the anti-PAR2 antibodies; Dr. Sergio
518	Schenkman for the anti-Histone H4 antibodies and H4K14 acetylated peptides, and Dr.
519	Lisvane Silva for helping to rise the mouse anti-TcBDF3 antisera.
520	
521	
522	
523	
524	
525	
526	
527	
528	

529 530		References
531	1.	Contreras VT, Araujo-Jorge TC, Bonaldo MC, Thomaz N, Barbosa HS, Meirelles Mde N,
532		Goldenberg S. 1988. Biological aspects of the Dm 28c clone of Trypanosoma cruzi after
533		metacyclogenesis in chemically defined media. Mem Inst Oswaldo Cruz 83:123-133.
534	2.	Hill KL. 2010. Parasites in motion: flagellum-driven cell motility in African trypanosomes. Curr
535		Opin Microbiol 13: 459-465.
536	3.	Field MC, Carrington M. 2009. The trypanosome flagellar pocket. Nat Rev Microbiol 7:775-
537		786.
538	4.	Hammond JW, Cai D, Verhey KJ. 2008. Tubulin modifications and their cellular functions.
539		Curr Opin Cell Biol 20:71-76.
540	5.	Verhey KJ, Gaertig J. 2007. The tubulin code. Cell Cycle 6:2152-2160.
541	6.	Janke C, Bulinski JC. 2011. Post-translational regulation of the microtubule cytoskeleton:
542		mechanisms and functions. Nat Rev Mol Cell Biol 12:773-786.
543	7.	Cambray-Deakin MA, Burgoyne RD. 1987. Acetylated and detyrosinated alpha-tubulins are
544		co-localized in stable microtubules in rat meningeal fibroblasts. Cell Motil Cytoskeleton 8:284-
545		291.
546	8.	Belmadani S, Pous C, Fischmeister R, Mery PF. 2004. Post-translational modifications of
547		tubulin and microtubule stability in adult rat ventricular myocytes and immortalized HL-1
548		cardiomyocytes. Mol Cell Biochem 258: 35-48.
549	9.	Janke C, Kneussel M. 2010. Tubulin post-translational modifications: encoding functions on
550		the neuronal microtubule cytoskeleton. Trends Neurosci 33: 362-372.
551	10.	Souto-Padron T, Cunha e Silva NL, de Souza W. 1993. Acetylated alpha-tubulin in
552		Trypanosoma cruzi: immunocytochemical localization. Mem Inst Oswaldo Cruz 88:517-528.
553	11.	Schneider A, Sherwin T, Sasse R, Russell DG, Gull K, Seebeck T. 1987. Subpellicular and
554		flagellar microtubules of Trypanosoma brucei brucei contain the same alpha-tubulin isoforms. J
555	23	Cell Biol 104: 431-438.

556	12.	Alonso VL, Serra EC. 2012. Lysine acetylation: elucidating the components of an emerging
557		global signaling pathway in trypanosomes. J Biomed Biotechnol 2012:452934.
558	13.	Hubbert C, Guardiola A, Shao R, Kawaguchi Y, Ito A, Nixon A, Yoshida M, Wang XF, Yao
559		TP. 2002. HDAC6 is a microtubule-associated deacetylase. Nature 417:455-458.
560	14.	North BJ, Marshall BL, Borra MT, Denu JM, Verdin E. 2003. The human Sir2 ortholog,
561		SIRT2, is an NAD+-dependent tubulin deacetylase. Mol Cell 11:437-444.
562	15.	Tavares J, Ouaissi A, Santarem N, Sereno D, Vergnes B, Sampaio P, Cordeiro-da-Silva
563		A. 2008. The Leishmania infantum cytosolic SIR2-related protein 1 (LiSIR2RP1) is an NAD+ -
564		dependent deacetylase and ADP-ribosyltransferase. Biochem J 415:377-386.
565	16.	Creppe C, Malinouskaya L, Volvert ML, Gillard M, Close P, Malaise O, Laguesse S,
566		Cornez I, Rahmouni S, Ormenese S, Belachew S, Malgrange B, Chapelle JP, Siebenlist
567		U, Moonen G, Chariot A, Nguyen L. 2009. Elongator controls the migration and differentiation
568		of cortical neurons through acetylation of alpha-tubulin. Cell 136:551-564.
569	17.	Shida T, Cueva JG, Xu Z, Goodman MB, Nachury MV. 2010. The major {alpha}-tubulin K40
570		acetyltransferase {alpha}TAT1 promotes rapid ciliogenesis and efficient mechanosensation.
571		Proc Natl Acad Sci U S A.
572	18.	Alsford S, Horn D. 2011. Elongator protein 3b negatively regulates ribosomal DNA
573		transcription in african trypanosomes. Mol Cell Biol 31:1822-1832.
574	19.	Zeng L, Zhou MM. 2002. Bromodomain: an acetyl-lysine binding domain. FEBS Lett 513:124-
575		128.
576	20.	Yang XJ. 2004. Lysine acetylation and the bromodomain: a new partnership for signaling.
577		Bioessays 26: 1076-1087.
578	21.	Crowley T, Brunori M, Rhee K, Wang X, Wolgemuth DJ. 2004. Change in nuclear-
579		cytoplasmic localization of a double-bromodomain protein during proliferation and

differentiation of mouse spinal cord and dorsal root ganglia. Brain Res Dev Brain Res 149:93-

101.

580

582	22.	Crowley TE, Kaine EM, Yoshida M, Nandi A, Wolgemuth DJ. 2002. Reproductive cycle
583		regulation of nuclear import, euchromatic localization, and association with components of Pol
584		Il mediator of a mammalian double-bromodomain protein. Mol Endocrinol 16: 1727-1737.
585	23.	Trousdale RK, Wolgemuth DJ. 2004. Bromodomain containing 2 (Brd2) is expressed in
586		distinct patterns during ovarian folliculogenesis independent of FSH or GDF9 action. Mol
587		Reprod Dev 68: 261-268.
588	24.	Ivens AC, Peacock CS, Worthey EA, Murphy L, Aggarwal G, Berriman M, Sisk E,
589		Rajandream MA, Adlem E, Aert R, Anupama A, Apostolou Z, Attipoe P, Bason N, Bauser
590		C, Beck A, Beverley SM, Bianchettin G, Borzym K, Bothe G, Bruschi CV, Collins M,
591		Cadag E, Ciarloni L, Clayton C, Coulson RM, Cronin A, Cruz AK, Davies RM, De
592		Gaudenzi J, Dobson DE, Duesterhoeft A, Fazelina G, Fosker N, Frasch AC, Fraser A,
593		Fuchs M, Gabel C, Goble A, Goffeau A, Harris D, Hertz-Fowler C, Hilbert H, Horn D,
594		Huang Y, Klages S, Knights A, Kube M, Larke N, Litvin L, Lord A, Louie T, Marra M,
595		Masuy D, Matthews K, Michaeli S, Mottram JC, Muller-Auer S, Munden H, Nelson S,
596		Norbertczak H, Oliver K, O'Neil S, Pentony M, Pohl TM, Price C, Purnelle B, Quail MA,
597		Rabbinowitsch E, Reinhardt R, Rieger M, Rinta J, Robben J, Robertson L, Ruiz JC,
598		Rutter S, Saunders D, Schafer M, Schein J, Schwartz DC, Seeger K, Seyler A, Sharp S,
599		Shin H, Sivam D, Squares R, Squares S, Tosato V, Vogt C, Volckaert G, Wambutt R,
600		Warren T, Wedler H, Woodward J, Zhou S, Zimmermann W, Smith DF, Blackwell JM,
601		Stuart KD, Barrell B, Myler PJ. 2005. The genome of the kinetoplastid parasite, Leishmania
602		major. Science 309: 436-442.
603	25.	Villanova GV, Nardelli SC, Cribb P, Magdaleno A, Silber AM, Motta MC, Schenkman S,
604		Serra E. 2009. Trypanosoma cruzi bromodomain factor 2 (BDF2) binds to acetylated histones
605		and is accumulated after UV irradiation. Int J Parasitol 39:665-673.

606	26.	Camargo ME, Segura EL, Kagan IG, Souza JM, Carvalheiro Jda R, Yanovsky JF,
607		Guimaraes MC. 1986. Three years of collaboration on the standardization of Chagas' disease
608		serodiagnosis in the Americas: an appraisal. Bull Pan Am Health Organ 20:233-244.
609	27.	Tonelli RR, Silber AM, Almeida-de-Faria M, Hirata IY, Colli W, Alves MJ. 2004. L-proline is
610		essential for the intracellular differentiation of Trypanosoma cruzi. Cell Microbiol 6: 733-741.
611	28.	Yoshida N, Mortara RA, Araguth MF, Gonzalez JC, Russo M. 1989. Metacyclic neutralizing
612		effect of monoclonal antibody 10D8 directed to the 35- and 50-kilodalton surface
613		glycoconjugates of Trypanosoma cruzi. Infect Immun 57:1663-1667.
614	29.	Batista M, Marchini FK, Celedon PA, Fragoso SP, Probst CM, Preti H, Ozaki LS, Buck
615		GA, Goldenberg S, Krieger MA. 2010. A high-throughput cloning system for reverse genetics
616		in Trypanosoma cruzi. BMC Microbiol 10: 259.
617	30.	Cribb P, Perozzi M, Villanova GV, Trochine A, Serra E. 2011. Characterization of TcHMGB,
618		a high mobility group B family member protein from Trypanosoma cruzi. Int J Parasitol
619		41: 1149-1156.
620	31.	da Cunha JP, Nakayasu ES, de Almeida IC, Schenkman S. 2006. Post-translational
621		modifications of Trypanosoma cruzi histone H4. Mol Biochem Parasitol 150:268-277.
622	32.	Rasband WS. 1997-2011. ImageJ software. In U. S. National Institutes of Health B, Maryland,
623		USA (ed.), http://imagej.nih.gov/ij/ .
624	33.	Sasse R, Gull K. 1988. Tubulin post-translational modifications and the construction of
625		microtubular organelles in Trypanosoma brucei. J Cell Sci 90 (Pt 4):577-589.
626	34.	Kelley LA, Sternberg MJ. 2009. Protein structure prediction on the Web: a case study using
627		the Phyre server. Nat Protoc 4: 363-371.

Zhang X, Shen Y, Ding G, Tian Y, Liu Z, Li B, Wang Y, Jiang C. 2013. TFPP: an SVM-

based tool for recognizing flagellar proteins in Trypanosoma brucei. PLoS One 8:e54032.

35.

628

630	36.	Broadhead R, Dawe HR, Farr H, Griffiths S, Hart SR, Portman N, Shaw MK, Ginger ML,
631		Gaskell SJ, McKean PG, Gull K. 2006. Flagellar motility is required for the viability of the
632		bloodstream trypanosome. Nature 440: 224-227.
633	37.	Hart SR, Lau KW, Hao Z, Broadhead R, Portman N, Huhmer A, Gull K, McKean PG,
634		Hubbard SJ, Gaskell SJ. 2009. Analysis of the trypanosome flagellar proteome using a
635		combined electron transfer/collisionally activated dissociation strategy. J Am Soc Mass
636		Spectrom 20: 167-175.
637	38.	Oberholzer M, Langousis G, Nguyen HT, Saada EA, Shimogawa MM, Jonsson ZO,
638		Nguyen SM, Wohlschlegel JA, Hill KL. 2011. Independent analysis of the flagellum surface
639		and matrix proteomes provides insight into flagellum signaling in mammalian-infectious
640		Trypanosoma brucei. Mol Cell Proteomics 10: M111 010538.
641	39.	Nowicki C, Montemartini M, Duschak V, Santome JA, Cazzulo JJ. 1992. Presence and
642		subcellular localization of tyrosine aminotransferase and p-hydroxyphenyllactate
643		dehydrogenase in epimastigotes of Trypanosoma cruzi. FEMS Microbiol Lett 71:119-124.
644	40.	Marciano D, Maugeri DA, Cazzulo JJ, Nowicki C. 2009. Functional characterization of stage
645		specific aminotransferases from trypanosomatids. Mol Biochem Parasitol 166: 172-182.
646	41.	Marciano D, Llorente C, Maugeri DA, de la Fuente C, Opperdoes F, Cazzulo JJ, Nowicki
647		C. 2008. Biochemical characterization of stage-specific isoforms of aspartate
648		aminotransferases from Trypanosoma cruzi and Trypanosoma brucei. Mol Biochem Parasitol
649		161 :12-20.
650	42.	Choudhary C, Kumar C, Gnad F, Nielsen ML, Rehman M, Walther TC, Olsen JV, Mann M
651		2009. Lysine acetylation targets protein complexes and co-regulates major cellular functions.
652		Science 325: 834-840.
653	43.	Kim SC, Sprung R, Chen Y, Xu Y, Ball H, Pei J, Cheng T, Kho Y, Xiao H, Xiao L, Grishin
654		NV, White M, Yang XJ, Zhao Y. 2006. Substrate and functional diversity of lysine acetylation
655		revealed by a proteomics survey. Mol Cell 23:607-618.

- 656 44. Yu BJ, Kim JA, Moon JH, Ryu SE, Pan JG. 2008. The diversity of lysine-acetylated proteins 657 in Escherichia coli. J Microbiol Biotechnol 18:1529-1536.
- 658 45. Zhao S, Xu W, Jiang W, Yu W, Lin Y, Zhang T, Yao J, Zhou L, Zeng Y, Li H, Li Y, Shi J, An
- 659 W, Hancock SM, He F, Qin L, Chin J, Yang P, Chen X, Lei Q, Xiong Y, Guan KL. 2010.
- 660 Regulation of cellular metabolism by protein lysine acetylation. Science 327:1000-1004.
- 661 46. Kouzarides T. 2000. Acetylation: a regulatory modification to rival phosphorylation? EMBO J 662 **19:**1176-1179.
- 47. 663 Polevoda B, Sherman F. 2002. The diversity of acetylated proteins. Genome Biol 664 3:reviews0006.
- 665 48. Norvell A, McMahon SB. 2010. Cell biology. Rise of the rival. Science 327:964-965.
- 666 49. Close P, Creppe C, Gillard M, Ladang A, Chapelle JP, Nguyen L, Chariot A. 2010. The emerging role of lysine acetylation of non-nuclear proteins. Cell Mol Life Sci 67:1255-1264. 667
- 668 50. Kim GW, Yang XJ. 2010. Comprehensive lysine acetylomes emerging from bacteria to 669 humans. Trends Biochem Sci 36:211-220.
- 670 51. Ferreira LR, Dossin Fde M, Ramos TC, Freymuller E, Schenkman S. 2008. Active 671 transcription and ultrastructural changes during Trypanosoma cruzi metacyclogenesis. An 672 Acad Bras Cienc 80:157-166.
- 673 52. Kohl L, Gull K. 1998. Molecular architecture of the trypanosome cytoskeleton. Mol Biochem 674 Parasitol 93:1-9.
- 675 53. Akella JS, Wloga D, Kim J, Starostina NG, Lyons-Abbott S, Morrissette NS, Dougan ST, 676 Kipreos ET, Gaertig J. 2010. MEC-17 is an alpha-tubulin acetyltransferase. Nature 467:218-677
- 678 54. Filippakopoulos P, Qi J, Picaud S, Shen Y, Smith WB, Fedorov O, Morse EM, Keates T,
- 679 Hickman TT, Felletar I, Philpott M, Munro S, McKeown MR, Wang Y, Christie AL, West N,
- 680 Cameron MJ, Schwartz B, Heightman TD, La Thangue N, French CA, Wiest O, Kung AL,

222.

Knapp S, Bradner JE. 2010. Selective inhibition of BET bromodomains. Nature 468:1067 1073.

683 55. **Muller S, Filippakopoulos P, Knapp S.** 2011. Bromodomains as therapeutic targets. Expert Rev Mol Med **13:**e29.

685

686

687

688

689

690

691

692

693

694

695

696

697

698

699

700

701

Figure TcBDF3 is a cytoplasmatic bromodomain-containing epimastigotes. (A) Nuclear (N) and Non-nuclear (NN) protein extracts (30 μg per well) were subjected to western blot analysis using rabbit anti-TcBDF3 antibodies, anti-Tyrosine aminotransferase (TcTAT) (cytosolic), anti-T.cruzi High Mobility Group B (TcHMGB) (nuclear). anti-T.cruzi Bromodomain Factor 2 (TcBDF2) (nuclear) and anti-T.cruzi H4 histone (TcH4) (nuclear). The first panel shows the Coomassie-stained gel. (B) Enzymatic activity of Alpha Hydroxyacid Dehydrogenase (aHAdH) and Malate Dehydrogenase (MdH) in epimastigotes treated with increasing concentrations of digitonin. Activities were measured and normalized to the protein concentration in the extracts. The arrows below the graph indicate the digitonin concentration at which cytosolic (C) glycosomal (G) and mitochondrial (M) proteins are released. (C) Equal volumes of selected soluble (S) and insoluble (P) fractions obtained at different digitonin amounts (0-0.7 mg) were subjected to western blot analysis using anti-TcBDF3 antibodies (TcBDF3) and known markers for different organelles. The antibodies used were: anti-T. cruzi Tyrosine Amino Transferase (TcTAT) (cytosolic), anti-T. cruzi glycosomal Malate Dehydrogenase (TcMdHglyc) (glycosomal), anti-T. cruzi mitochondrial Malate Dehidrogenase (TcMdHmit) (mitochondrial), anti-T. cruzi paraflagellar rod 2 protein (*Tc*PAR2) (flagellar) and anti-α tubulin (α tubulin) (cytoskeletal). TL, total lisate.

703

Figure 2: TcBDF3 is localized at the cytoplasm, the flagellum and the flagellar pocket of epimastigotes. (A-E) Immunoelectron microscopy of TcBDF3 in T. cruzi epimastigotes using purified rabbit anti-TcBDF3 antibodies. The nucleus (N), kinetoplast (K), flagellar pocket (FP) and flagellum (F) are indicated. Gold particles are indicated with black and white arrows. White arrows indicate flagellar labelling. (D) Enlarged image of the marked area in (C). (F) Enlarged image of the marked area in (E). Bar = 1 μ m.

Figure 3: *Tc*BDF3 is expressed throughout the *T. cruzi* life cycle *in vitro*. (A) Western blot analysis using purified rabbit anti-*Tc*BDF3 antibodies (*a-Tc*BDF3) and mouse anti-α tubulin (*a*-α tubulin) as a loading control. A, amastigotes total protein extracts; E, epimastigotes total protein extracts; T, trypomastigotes total protein extracts (30 μg per well). (B) Immuno-fluorescence assay using purified anti-*Tc*BDF3 and parasites at different stages of the *T. cruzi* life cycle. A, free amastigote; Ac, amastigotes inside a Vero cell; E, epimastigote; T, trypomastigote from infected Vero cells; Tm, metacyclic trypomastigote obtained *in vitro*. Anti-rabbit IgG conjugated to Fluorescein was used as secondary antibody. Nucleus and kinetoplast were labelled with DAPI. Bars = 2 μm.

Figure 4: *Tc*BDF3 changes its location during *in vitro* metacyclogenesis. Immunofluorescence assays using purified rabbit anti-*Tc*BDF3 (*a-Tc*BDF3) and mouse monoclonal anti-acetylated α tubulin (*a*-AcTub) antibodies in intermediate stages 1a, 1b and 1c as defiened by (51). On the right side a schematic diagram of the position of the flagellum (F), nucleus (N) and kinetoplast (K) in the three selected intermediate differentiation stages is shown. Anti-rabbit IgG conjugated to Fluorescein (green) and anti-mouse IgG conjugated to

Rodhamine (red) were used as secondary antibodies. Nucleus and kinetoplast were labelled with DAPI (blue).

Figure 5: TcBDF3 is detected in the cytoskeleton and flagellum of epimastigotes and only in the flagellum of metacyclic trypomastigotes. Immunofluorescence assays using purified rabbit anti-TcBDF3 (a-TcBDF3), mouse monoclonal anti-acetylated α tubulin (a-AcTub) (A) and mouse anti-PAR2 (a-PFR) (B) antibodies on isolated cytoskeletons and flagella of epimastigotes and metacyclic trypomastigotes. Anti-rabbit IgG conjugated to Fluorescein (green) and anti-mouse IgG conjugated to Rodhamine (red) were used as secondary antibodies. Panels on the right of A and B show enlarged images of the detergent resistant structures that correspond to MTs attached to basal bodies and forming the flagellar pocket. Green arrow heads show TcBDF3 localization and red arrow heads show acetylated α tubulin (A) and PAR2 (B) localization in these structures.

Figure 6: *TcBDF3* interacts with acetylated α tubulin. (A) Coomassie stained SDS-PAGE and western blot analysis of epimastigotes protein extracts enriched in cytoskeletal and flagellar proteins. Sn1, soluble protein extracts; Sn2, soluble cytoskeletal and flagellar protein extracts; P, insoluble cytoskeletal and flagellar protein extracts (50 μ g per well). Rabbit anti-*Tc*BDF3 antibodies (*a-Tc*BDF3) and mouse anti-acetylated α tubulin antibodies (*a*-AcTub) were used. (B) Co-immunoprecipitation assay using purified anti-*Tc*BDF3 antibodies covalently coupled to magnetic beads (*Tc*BDF3 beads). Magnetic beads coupled to IgGs (purified from antisera of non-immunized rabbits) were used as a negative control (Control beads). Left panel shows a silver stained SDS-PAGE of total cytoskeletal extracts and the elutions obtained after the immunoprecipitation experiment. Right panel shows a western blot

analysis of the eluted proteins after coimmunoprecipitation using purified rabbit anti-TcBDF3 antibodies (a-TcBDF3) and mouse monoclonal anti-acetylated α tubulin antibodies (a-AcTub). (C) Slot far western blot assay. Acetylated tubulin (TubK40Ac), non-acetylated tubulin (Tub) or acetylated histone H4 (H4K14Ac) peptides were blotted onto a nitrocellulose membrane and incubated with His-tagged recombinant TcBDF3 (BDF3-His) or TcBDF2 (BDF2-His). Bound recombinant proteins were detected with anti-Histidine antibodies (a-His). Signals were quantified by densitometry and normalized using the interaction with acetylated α tubulin peptide as a reference (assigned the arbitrary value of 1). Error bars indicate means \pm S.D. from results of three independent experiments.











