

**A**

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QSTSGIGGDVVDIEETHPDFQPRVLSADLAEDEIAMV
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DAPPAMGGDT-DAEETHPDFQPRMVSSDLAQDEIAMI
DSEPTMGGDP-DLEETHPDFQPRIVGGDLAEDEIAMI
SRSDVVGGDVHDEWTHPDFQPRIVSTDLAEDEVMTV

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**SUPPLEMENTARY FIG. S1. Conservation and predicted secondary structure of the N-terminal extension of *Tb1-C-Grx1*.** (A) Multiple sequence alignment of the N-terminal stretch in trypanosomatid proteins identified by homology search with PSI-BLAST ([www.ebi.ac.uk/Tools/sss/psiblast](http://www.ebi.ac.uk/Tools/sss/psiblast)) using the sequence of *Tb1-C-Grx1* as the template. The 13 sequences retrieved were aligned with BioEdit ([www.mbio.ncsu.edu/bioedit/bioedit.html](http://www.mbio.ncsu.edu/bioedit/bioedit.html)), and are from top to bottom: *T. brucei brucei* strain 427 CAF02300.1, *T. b. gambiense* CBH14109.1, *T. brucei brucei* strain 927 XP\_803662.1, *T. brucei congolense* CCD12136.1, *T. cruzi* strain Silvio×10/1 EFZ28890.1, *T. cruzi* strain CL-Brener XP\_818148.1, *T. cruzi* strain CL-Brener XP\_807837.1, *Leishmania major* XP\_003721531.1, *L. donovani* CBZ31098.1, *L. infantum* XP\_001462624.1, *L. mexicana* CBZ22994.1, *L. braziliensis* XP\_001561455.1, and *T. vivax* XP\_001561455.1. (B) Residue conservation is represented as a logotype using the alignment data above and the WebLogo 3.0 server (<http://weblogo.threeplusone.com>). Green is for polar (G, S, T, Y, and C), purple for neutral (Q and N), blue for basic (K, R, and H), red for acidic (D and E), and black for hydrophobic residues (A, V, L, I, P, W, F, and M). (C) Qualitative predictions of disordered (red) and putative secondary structures (green) of the most conserved part of the sequence (*blue line*). The scheme was prepared based on the results obtained from several Web-based servers (DISEMBL: <http://dis.embl.de>; GlobPlot2: <http://globplot.embl.de>; AGADIR: <http://agadir.crg.es>; PSIPRED: <http://bioinf.cs.ucl.ac.uk/psipred>; PEP-FOLD: <http://bioserv.rpbs.univ-paris-diderot.fr/PEP-FOLD>; Parcoil2: <http://groups.csail.mit.edu/cb/parcoil2>; and COILS: [www.ch.embnet.org/software/COILS\\_form.html](http://www.ch.embnet.org/software/COILS_form.html)).