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The structure of a *Trypanosoma cruzi* glucose-6-phosphate dehydrogenase ternary complex with substrate and cofactor reveals differences from the mammalian enzyme

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**ABSTRACT**

The enzyme glucose-6-phosphate dehydrogenase from *Trypanosoma cruzi* (*Tc*G6PDH) catalyses the first step of the pentose phosphate pathway and is considered a promising target for the discovery of a new drug against Chagas Diseases. In the present work, we describe the crystal structure of *Tc*G6PDH obtained in a ternary complex with the substrate glucose-6-phosphate and the reduced ‘catalytic’ cofactor NADPH, which reveals the molecular basis of substrate and cofactor recognition. A comparison with the homologous human protein sheds light on differences in the cofactor-binding site that might be explored towards the design of new NADP<sup>+</sup> competitive inhibitors targeting the parasite enzyme.

**Keywords:** glucose-6-phosphate dehydrogenase; ternary-complex; Chagas disease; trypanosomatids; uncompetitive inhibitors; drug target.
1. Introduction

Glucose-6-phosphate dehydrogenase (G6PDH, EC 1.1.1.49) is a ubiquitous enzyme that catalyses the oxidation of β-D-glucose-6-phosphate (G6P) to 6-phosphoglucono-δ-lactone, with concomitant reduction of NADP⁺ to NADPH, in the first and rate limiting step of the pentose phosphate pathway (PPP). NADPH generated in the oxidative branch of the PPP is used as a reducing agent essential for redox balance maintenance and for lipid biosynthesis [1,2]. Furthermore, the non-oxidative branch of the PPP produces a variety of metabolic intermediates that includes ribose-5-phosphate, used in nucleotide biogenesis, and erythrose 4-phosphate, a precursor of coenzymes and aromatic amino acids [3].

The enzyme G6PDH plays a key functional role [2,4] with implications in human diseases such as cancer [5], metabolic disorders [6,7], and cardiovascular diseases [8]. G6PDH is associated with the most common human enzymopathy, affecting more than 400 million people worldwide [9]. Individuals with G6PDH deficiency may develop hemolytic anemia under oxidative stress, which can be triggered by factors like microbial infections, certain drugs or aspects of diet. In protozoan parasites, G6PDH has been shown to be essential for survival [10]. In bloodstream form Trypanosoma brucei, depletion of G6PDH levels by RNAi [11] or its inhibition by steroids, like dehydroepiandrosterone or epiandrosterone, kill parasites in vitro [12]. Additionally, steroids and quinazolinones were shown to inhibit the T. cruzi G6PDH and to kill the epimastigote forms of the parasite in vitro [13,14], suggesting that G6PDH is an attractive target for development of new trypanocidal drugs. Some efforts have already been made to develop G6PDH inhibitors with therapeutic utility against trypanosomiasis [11,13,14] and also cancer [15,16]. Steroids and quinazolinones represent the most potent G6PDH inhibitors known to date. These inhibitors act through an uncompetitive mechanism, but their binding site on G6PDH and the interactions relevant to inhibition are unknown.

At present, G6PDH structures of Leuconostoc mesenteroides (LmG6PDH), Mycobacterium avium (MaG6PDH), human (HsG6PDH) and Trypanosoma cruzi (TcG6PDH) are available in the Protein Data Bank. However, most of the structural knowledge about G6PDHs was established in the studies of Lm- and HsG6PDH enzymes. Studies with recombinant LmG6PDH revealed that the bacterial enzyme assemblies as a homodimer and that each subunit is composed of an NAD(P)-binding Rossmann-like domain and a β + α domain [17]. Site direct mutagenesis studies on LmG6PDH revealed the substrate and cofactor binding sites and informed on the mechanism of catalysis [18-20]. The crystal structure of HsG6PDH revealed an unprecedented tetrameric assembly and the binding of an additional NADP⁺ to the β + α domain, which became known as the structural NADP⁺ [21,22]. After a six-year gap, Ortíz and collaborators described the crystallization
of the short form of TcG6PDH (TcG6PDH-S; Met38 to Ala555) [23] and made available the coordinates of an apo and an enzyme-substrate complex (PDB entries: 4E9I and 4EM5, respectively). More recently the Seattle Structural Genomic Centre for Infectious Diseases deposited the structure of MaG6PDH at 2.3 Å resolution [24]. To date, no detailed discussion of the Ma- and Tc-G6PDH structures have been reported.

In the present work, we describe the crystal structure of TcG6PDH obtained in a ternary complex with G6P and NADPH and compare it to previous available G6PDH structures. A detailed analysis of the NADP-binding Rossmann-like domain revealed unique features that might be explored to the design of specific inhibitors against the parasite enzyme.

2. Methods

2.1. Truncated construct of G6PDH from T. cruzi

Based on the T. cruzi (CL Brener) G6PDH sequence available at the NCBI (entry: XP_820060.1), a nucleotide sequence, codon optimized for bacterial expression, was designed to produce a fragment of TcG6PDH spanning from Asp58 to Thr545 (TcΔG6PDH). The synthetic gene was purchased (GenScript USA Inc., Piscataway, New Jersey, USA) and sub-cloned into a modified pET28 vector in which the sequence encoding a thrombin recognition site, to allow for removal of a histidine-tag, was changed to that for tobacco etch virus (TEV) protease (pET28-TEV). The TcΔG6PDH gene was inserted within BamHI and XhoI sites of the pET28-TEV and the integrity of the pET28-TEV_TcΔG6PDH construct was confirmed by gene sequencing.

2.2. Recombinant Protein Production and Purification

Competent E. coli BL21 (DE3) cells were transformed with pET28-TEV_TcΔG6PDH and grown on auto-induction media ZYM-5052 (Studier, 2005) containing kanamycin 50 µg.mL⁻¹, under 200 rpm agitation, at 37 °C for 3h and then at 20 °C for 21h. Cells were harvested by centrifugation at 3,500 g for 30 minutes at 4 °C and resuspended in Buffer A (50 mM Tris-HCl pH 8.0, 0.5 M NaCl, 20 mM imidazole, 5% glycerol and 5 mM 2-mercaptoethanol). DNAse and EDTA-Free Protease Inhibitor Tablets (ThermoFisher) were added to the suspension and lysis performed with a cell disruptor (Pressure Cell Homogenizer, Stansted) using a pressure of 20,000 psi. The samples were centrifuged at 4 °C with a RCF equal to 40,000g for 30 min and the supernatant subjected to immobilized metal affinity chromatography (IMAC) using a 5 mL HisTrap HP (GE Healthcare). Buffer B (50 mM Tris-HCl pH 8.0, 0.5 M NaCl, 500 mM imidazole, 5%
glycerol and 5 mM 2-mercaptoethanol) was employed to generate an imidazole gradient and TcΔG6PDH eluted from the column with approximately 200 mM imidazole. Samples containing TcΔG6PDH were pooled and concentrated using an ultrafiltration unit (3.000 g at 4 °C, Vivaspin 20 MWCO 30 kDa, Sartorius). As a final purification step, size exclusion chromatography was performed using a HiLoad Superdex 200 26/60 column (GE Healthcare) and GF buffer (20 mM Tris-HCl and 0.2 M NaCl). Then, TcΔG6PDH was concentrated again in GF buffer (20 mM Tris-HCl and 0.2 M NaCl) containing 5 mM of 2-mercaptoethanol.

The gene of TcG6PDH long form (TcG6PDH-L; Met1 to Ala555) was sub-cloned from the previous reported pET28_TcG6PDH-L construct [25] to a pET28-TEV vector between NheI and XhoI restriction sites. The integrity of the pET28-TEV_TcG6PDH-L construct was confirmed by gene sequencing. TcG6PDH-L harboring a N-terminal His-tag was expressed in E. coli BL21 (DE3) cells transformed by pET28-TEV_TcG6PDH-L construct. The recombinant protein was purified by IMAC following the same procedure applied to the purification of TcΔG6PDH.

2.4. Enzyme Kinetics

TcΔG6PDH and TcG6PDH-L activities were measured following NADPH production in the forward reaction. NADPH fluorescence (λExc/Em: 340 nm / 460 nm) was monitored using the FLUOstar OPTIMA plate reader (BMG LABTECH). Enzyme activities were measured in a buffer containing 50 mM Tris-HCl pH 7.6, 0.5 M NaCl, 5% glycerol and 2 mM 2-mercaptoethanol. The reactions were performed in triplicate at 25 °C, using black 96 wells plates, with a final volume of 120 µL per well. Apparent Michaelis-Menten constants (Kmapp) and maximum velocity of reaction (Vmaxapp) values were calculated by non-linear regression of the data using the equation

\[ v = \frac{V_{\text{max}}^{\text{app}} [S]}{K_m^{\text{app}} + [S]} \]

in the software GraphPad Prism. The catalytic constant (kcat) were calculated using the equation

\[ k_{\text{cat}} = \frac{V_{\text{max}}}{E_0} \]

where E0 is the enzyme concentration used in the assay.

For the TcΔG6PDH, the Kmapp of G6P was measured varying the substrate concentration from 2 mM to 15.6 µM and keeping NADP+ at 1 mM. Likewise, Kmapp of NADP+ was measured varying its concentration from 1 mM to 7.8 µM and keeping G6P at 2 mM. In both assays TcΔG6PDH concentration was 2 nM. Values of kinetic parameters for TcG6PDH-L were obtained varying the G6P concentration between 2 mM to 15.6 µM and NADP+ between 1 mM and 7.8 µM, while keeping the other substrate at saturating concentrations, 600 µM and 2 mM for NADP+ and G6P, respectively. TcG6PDH-L concentration was kept at 2 nM.
2.5. Protein Crystallization and Data Collection

*TcΔG6PDH* crystallization screens used the sitting-drop vapor diffusion method. The protein samples had previously been filtered using a 0.1 µm Ultrafree-MC centrifugal filter (Millipore). Crystallization plates were prepared using a Phoenix/RE liquid handler (Art Robbins Instruments) and the JCSG-plus (Molecular Dimensions), Classics Suite (Qiagen), PEGs (Qiagen), and AmSO₄ (Qiagen) screens. The trial drops consisted of 100 nL of protein solution (10 mg.mL⁻¹ of His-tagged *TcΔG6PDH*, 2mM G6P, and 2 mM NADPH, 20 mM Tris-HCl pH 8.0, 0.2 M NaCl) and an equivalent volume of reservoir, equilibrated against 50 µL of reservoir at 20 °C in a CrystalMation Plate Hotel system (Rigaku).

Reproducible hits were obtained with condition G1 of the JCSG-plus screen (30% jeffamine ED-2003, 0.1 M HEPES pH 7.0) and this was optimized using hanging-drop vapor diffusion method at 18 °C. Suitable crystals of *TcΔG6PDH* were obtained when 2 µL of protein solution (10 mg.mL⁻¹ *TcΔG6PDH*, 5 mM G6P, 2 mM NADPH, 20 mM Tris-HCl pH 8.0, 0.2 M NaCl and 5 mM 2-mercaptoethanol) was mixed with 1 µL of reservoir solution (27-32 % jeffamine ED2003 and 0.1 M HEPES pH 6.8-7.2). Crystals were cryo-protected in 45% jeffamine ED2003 with 0.1 M HEPES pH 6.8, and then flash-cooled in liquid nitrogen before in-house screening using a Rigaku MicroMax-007 HF rotating-anode X-ray source equipped with a Saturn 944 HG+ CCD detector with sample maintained at about -170 °C. Several crystals were sent for full data collection at the Diamond Light Source, beamline I04-1 and the best dataset, as judged by data processing statistics (see below) was identified.

2.6. X-ray Data Processing and *TcΔG6PDH* Structure Determination and Refinement

Data were indexed and integrated using XDS [26] and scaled using AIMLESS [27]. The structure was solved by molecular replacement with PHASER [28] using chain A of the PDB entry 4E91 as search model. The program COOT [29] was used for model manipulation and incorporation of solvent and ligands. REFMAC5 [30] was used to perform restrained refinements, using Translation/Libration/Screw [31] and non-crystallographic symmetry restraints. MOLPROBITY [32] was used to inspect model geometry in combination with the validation tools provided by COOT. Molecular figures were prepared in PyMOL v.1.8 (Schrödinger, LLC). Electrostatic potential surfaces were computed with PDB2PQR [33] and APBS [34]. Crystallographic statistics are presented in Table 1.

3. Results and Discussion
We have significantly advanced the characterization of T. cruzi G6PDH. The new structural data on this validated target has potential to inform the development of new drugs with therapeutic utility. The truncated construct TcΔG6PDH, lacking 57 N-term and 10 C-terminal residues, was designed to improve the crystallizability of this protein. This approach was chosen in account the success attained in the crystallization the TcG6PDH-S, missing the first 37 residues [23]. His-tagged TcΔG6PDH was produced in E. coli and purified to homogeneity in two steps using affinity and size exclusion chromatography (Figures S1.A and S1.B, Suppl. Material). The size exclusion chromatography result indicates that TcΔG6PDH forms a tetramer, in agreement to previous published datwork [23]. When TcG6PDH-L is expressed in E. coli cells, almost all the protein appeared in inclusion bodies [25]. Nonetheless, the small amount of soluble TcG6PDH-L recovered by IMAC was enough to perform the intended kinetic analyses. In measuring the TcG6PDH activity, The NaCl and glycerol present in the reaction buffer showed to improved essential to keep the enzyme stable. The calculated $K_{m}^{app}$ values of G6P and NADP$^+$ were 306.1 ± 20.3 and 80.1 ± 5.9 μM, respectively (Figure S2.A, Suppl. Material). The $k_{cat}$ values obtained when varying the concentrations of G6P and NADP$^+$ were 53.6 ± 1.2 and 51.8 ± 1.1 s$^{-1}$, respectively. The $K_{m}^{app}$ values obtained for the TcG6PDH-L, using the same assay conditions, were 210.3 ± 21.6 and 47.4 ± 4.3 μM for G6P and NADP$^+$, respectively (Figure S2.B, Suppl. Material). Additionally, $k_{cat}$ values for the long form of the enzyme were 61.6 ± 1.9 for G6P and 52.8 ± 1.3 s$^{-1}$ for NADP$^+$. Thus, despite a reduced stability, the truncated enzyme remains functional and has an affinity for both substrate and cofactor that are only slightly higher (around 1.5 times) than those of the TcG6PDH-L.

3.1. TcΔG6PDH Overall Structure

Bipyramidal crystals of TcΔG6PDH obtained in the presence of both G6P and NADPH attained a maximum dimension of 0.3 mm within 15 days and diffracted to a resolution limit of 2.65 Å using synchrotron radiation (Figure S3, Suppl. Material). Molecular replacement calculations positioned three polypeptide chains, labelled A, B and C, in the asymmetric unit. In the refined structure (PDB ID 5AQ1), each polypeptide chain comprises residues P62 to T545, plus one molecule of G6P and NADPH. There are no outliers in the Ramachandran plot, which returned 98% and 2% of the residues in favoured and allowed regions, respectively. Two solvent exposed loops found in the final model, spanning from residues R129 to H136 and A290 to Y295, showed to be poorly ordered. Those loops do not participate in crystal contacts neither in ligands binding. The superposition of chains A, B and C did not reveal significant differences in the C$^\alpha$ trace (RMSD and

Commented [WH1]: There are no data relating to “stability”. The lack of soluble material might be simply the folding process which is distinct from whether the protein is stable or not.
number of atoms used in the alignment: AB, 0.10 Å and 434 Cα atoms; AC, 0.23 Å and 445 Cα atoms; BC, 0.17 Å and 448 Cα atoms). and no outliers were observed in Ramachandran analysis, which returned 98% and 2% of the residues in favoured and allowed regions, respectively. The topology of the TcΔG6PDH is very similar to the human and bacterial homologous enzymes [17,21], being composed by of an NAD(P)-binding Rossmann-like domain (residues P62 to I245) and a β + α domain (residues D246 to T545) (Figure 1A). The β + α domain has a large β-sheet with nine antiparallel strands that in HsG6PDH binds the a structural NADP+ in the HsG6PDH. In the present TcΔG6PDH structure there is no electron density to support the presence of a structural NADP+ in TcΔG6PDH. Although there are three polypeptide chains in the AU of TcΔG6PDH crystals and – the expected tetrameric biological unit can is be–reconstructed by crystallographic symmetry operations. The TcΔG6PDH tetramer can beis formed by the packing of two B:C dimers or-and by four A chains (Figure 1B). No significant differences were observed between those-tetramers. In the tetrameric assembly all inter-chain contacts are established by residues from the β + α domains burying about 12 % of each subunit surface area (equivalent to an area of approximately 3250 Å²).

3.2. G6P binding site

G6PDH catalyses the formation of a double bond between C1 and O1 of G6P to produce 6-phosphoglucono-δ-lactone with concomitant reduction of NADP+, by the transfer of a hydride ion to C4 of the nicotinamide (Scheme 1). In the TcΔG6PDH structure, the β-anomer of G6P is found in a chair 4C1 conformation establishing H-bonds with side-chains of K217, D246, H247, Y248, K251, E285, D304, H309, K403, R408 and Q437 (Figure 2A). These residues are highly conserved in the human and L. mesenteroides enzymes [19,22]. The conformation of the G6P observed in the TcΔG6PDH orients its the C1 hydroxyl group towards the H309 Nε2, and in turn the H309 Nε1 H-bonds to D246 Oδ1. These interactions are in agreement with the proposed mechanism of reaction for G6PDH [18,19], where a catalytic dyad, represented by H309 and D246 in the TcΔG6PDH, is responsible for proton abstraction of the substrate.

A comparison between the ternary complex of TcΔG6PDH-G6P-NADPH and the binary complex of TcG6PDH-G6P (PDB ID 4EM5; Buschiazzo, A., Botti, H., Ortiz, C., Comini, M.A., unpublished) reveals a striking and unexpected difference in the conformation of G6P. In the binary complex there are four polypeptide chains in the AU and in three of them, the pyranose ring of G6P is inverted, with the C4 hydroxyl group participating in an H-bond to H309 Nε2 (Figure 2B). This misposition of G6P, which is not compatible with the proposed mechanism, is observed in chains A, B and C. In but not in chain D, which presents the G6P is in the expected orientation with the
C1 hydroxyl group pointing to H309. The low resolution of the binary complex, 3.35 Å, might have led to a biased interpretation of the electron density and misorientation of the substrate may have complicated the analysis. In this way, we were fortunate to obtain much higher resolution diffraction data and therefore provide a more reliable model [our results represent a correction to the binary complex of the G6PDH from T. cruzi].

3.3. Catalytic NAD(P)(H) binding site

At the catalytic site, NADPH binds to the Rossmann-like domain forming H-bonds with S77, D79, L80, R109, S110, Y151, L186, and K217; in addition to forming a cation-π interaction between R109 and the adenine moiety (Figure 3A). The nicotinamide moiety is oriented in the syn conformation and with C4 oriented towards G6P C1 at a distance of 3.9 Å, compatible with hydride transfer (Figure S4, Suppl. Material). All of the residues involved in binding the catalytic NADPH are conserved in TcΔG6PDH and HsG6PDH structures, with one notable exception. In the human enzyme Y147 Oη donates its hydrogen to E170 carbonyl group forming an H-bond (Figure 3B). In TcΔG6PDH, Y147 is replaced by F191 with the χ1 angle rotated by almost 120°. This conformational difference, perhaps allowed by the loss of a restraining H-bond, leads to the formation of a cavity just below the nicotinamide riboside in TcΔG6PDH (Figures 3C). This cavity, with volume of about 220 Å³ calculated using the software KVFinder [35], would be large enough to accommodate cyclic substituents linked to a nicotinamide riboside (Figure S5, Suppl. Material). It is noteworthy that this cavity is absent in HsG6PDH (Figure 3D), and has not been found in other human proteins that, in accordance to CATH [36], also possess an NAD(P)-binding Rossmann-like domain (Table S3, Suppl. Material). The cavity in the T. cruzi enzyme offers opportunities for a structure-based approach to develop novel G6PDH inhibitors and since this structural feature represents a difference with respect to the human enzyme then also might assist the discovery of inhibitors selective for the trypanosomal G6PDH over the human enzyme.

3.4. Structural NADP⁺ binding site

A structural NADP⁺ site, located on the β + α domain, has been reported for HsG6PDH (PDBs entries 1QKI and 2BH9) and postulated as important for protein stability [21,22]. In the HsG6PDH, the structural NADP⁺ participates in H-bonds to K238, K366, R370, R393, Y401, K403, D421, T423, and R487 (Figure 4A). Additionally, W509 and Y503 establish π-stacking interactions with the nicotinamide and adenine rings, respectively. The comparison of the structural NADP⁺ binding site between the Hs- and TcΔG6PDH shows that K366, R487, and Y503 (in
HsG6PDH) are replaced by L409, C528, and T544 (in TcΔG6PDH), respectively (Figure 4B). L409 and C528 in the TcΔG6PDH would not be able to H-bond the 2'-phosphate of an NADP(H) possible that might occupying this site. Similarly, the T544 would not be able to make a π-stacking interaction with the adenine moiety. In addition to these natural occurring differences, the TcΔG6PDH C-terminus is artificially truncated. In the HsG6PDH, the C-terminus caps the structural NADP(H) providing an aromatic residue (W509) that stacks in on the adenine moiety. These changes differences might compromises the binding of a structural NADP(H) to TcΔG6PDH and so explain why it was not observed in the structure. Interestingly, in the kinetic assays performed with TcΔG6PDH an active enzyme requires the presence of NaCl and glycerol, additives that are known to improve protein stability.

The TcΔG6PDH structure is the first enzyme-substrate-cofactor complex of a eukaryotic G6PDH. Comparisons with other G6PDH structures resulted in several observations. Firstly, interactions made by G6P in TcΔG6PDH are in agreement with the proposed mechanism of reaction [18,19] and the substrate conformation is similar to those observed in complexes of the bacterial and human enzymes. In the binary TcG6PDH-G6P complex (PDB ID 4EM5), three (out of the four) chains of the asymmetric unit have the substrate is likely to be misoriented, with the pyranose ring of the substrate in an flipped orientation incompatible with a mechanism that involves proton abstraction from the C1-hydroxyl group by of the catalytic H309. Secondly, in the cofactor-binding site, the presence of a phenylalanine residue in the TcΔG6PDH (F191) instead of a tyrosine residue as in HsG6PDH (Y147), results in the formation of a cavity unique to the parasite enzyme. We believe this cavity might be further explored for the development of NADP(H) competitive inhibitors with selectivity against TcG6PDH enzyme.

Acknowledgments

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Authors Contributions

GFM conducted all experiments. AD assisted GFM with diffraction data collection, structure solution and refinement. WNH supervised GFM during his internship in Dundee. ATC was the project coordinator and supervisor of GFM Brazil. All authors reviewed and contributed to the
manuscript.


27 Evans PR & Murshudov GN (2013) How good are my data and what is the resolution? Acta


Figure Legends

Figure 1: Carton representation of TcΔG6PDH. A) Structure of a subunit, showing the N-term NAD(P)-binding Rossmann-like domain (orange), C-term β + α domain (gray), NADPH (magenta spheres) and G6P (green spheres). Site for structural NADP is highlighted (red ellipse). B) TcΔG6PDH biological unit: interface residues involved in the tetrameric assembly are exclusively located in the β + α domains. Two unique tetramers could be generated from TcΔG6PD subunits, one using chain A and its symmetry related neighbours (A', A'' and A'''') and the other using the dimer of chains B and C and a symmetry related dimer (B' and C').

Figure 2: Different orientations of G6P (green sticks) observed in the ternary complex (A) obtained in the present work (PDB ID 5AQ1) and in the binary complex (B) (PDB ID 4EM5). H309 and D246 (both yellow sticks) form the catalytic dyad responsible for proton abstraction from the C1-hydroxyl of the G6P pyranose ring. Residues in gray and yellow belong to the β + α domain, and K217 in orange is from the NAD(P)-binding Rossmann-like domain. Fo-Fc omit map for G6P contoured at 3.8 σ. Dashed lines represent H-bonds and distances observed in the TcΔG6PDH (present work) are reported in Table S1, Suppl. Material. Carbon atoms of the glucopyranose are numbered. Figure was prepared using chain A of both structures.

Figure 3: Comparison between the catalytic NADP(H) binding site of TcΔG6PDH (chain A; PDB ID 5AQ1) and HsG6PDH (chain A; PDB ID 2BH9) [22]. A) TcΔG6PDH residues (orange) making H-bonds (dashed lines) to the catalytic NADPH (magenta sticks). NADPH Fo-Fc omit map contoured at 2.5 σ. H-bond distances are reported in Table S2, Suppl. Material. B) HsG6PDH residues (cyan) making H-bonds (dashed lines) to the catalytic NADPH (yellow sticks). C) Electrostatic surface of TcΔG6PDH showing a cavity below the nicotinamide riboside. D) Electrostatic surface of the HsG6PDH displayed in the vicinity of NADP*.

Figure 4: Structural NADP* site from HsG6PDH (A) (PDB ID 2BH9) and comparison with TcΔG6PDH (B). Structural NADP* (yellow sticks) binds to residues of the β + α domain from the human enzyme through H-bonds (dashed lines) or π-stacking interactions. Residues K366, R487 and Y503 in HsG6PDH correspond to L409, C528 and T544 in TcΔG6PDH (labelled in red), respectively, and may compromises the binding of the structural NADP*. Figure prepared using chain A of both the human and T. cruzi enzyme structures.
Figure 1
Figure 3

(A) TcΔG6PDH

(B) HsG6PDH

(C) TcΔG6PDH

(D) HsG6PDH
Scheme 1 – Reaction catalysed by G6PDH.*

* H309 Nδ makes a hydrogen bond with D246 Oδ, forming the catalytic dyad of the G6PDH. H309 Nδ is the general base that abstracts the α-proton from the C1-OH of G6P, inducing the transfer of C1-hydride to C4 of the nicotinamide moiety of NADP+. 6-phosphoglucono-δ-lactone and NADPH are the reaction products. Only the nicotinamide moiety of NADP(H) is represented.
Table 1 – Crystallographic statistics for TcΔG6PDH-G6P-NADPH ternary complex.

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<td>Refinement</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rwork § (%)</td>
<td>19.99</td>
<td></td>
</tr>
<tr>
<td>Rfree ¶ (%)</td>
<td>22.55</td>
<td></td>
</tr>
<tr>
<td>R.m.s.d., bonds (Å)</td>
<td>0.0048</td>
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</tr>
<tr>
<td>R.m.s.d., angles (°)</td>
<td>1.0476</td>
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<tr>
<td>Total protein residues</td>
<td>1458</td>
<td></td>
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<tr>
<td>Total protein atoms</td>
<td>11571</td>
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<tr>
<td>No. of solvent atoms</td>
<td>253</td>
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<tr>
<td>Average B factors (Å²)</td>
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<tr>
<td>Protein – Chains A / B / C</td>
<td>43.0 / 46.9 / 54.2</td>
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<tr>
<td>BG6 – Chains A / B / C</td>
<td>29.2 / 32.7 / 37.1</td>
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<tr>
<td>NDP – Chains A / B / C</td>
<td>51.8 / 53.5 / 67.4</td>
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<tr>
<td>Waters</td>
<td>34.1</td>
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</tr>
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* - Values in parentheses refer to the highest resolution bin of 2.72-2.65 Å.
† Rmerge = Σhkl Σi |Ii(hkl)| - 〈I(hkl)〉 | Σhkl |I(hkl)|, where Ii(hkl) is the intensity of the ith measurement of reflection hkl and 〈I(hkl)〉 is the mean value of I(hkl) for all i measurements.
§ Rwork = Σhkl |Fobs| - |Fcalt| / Σhkl |Fobs|, where Fobs is the observed structure-factor amplitude and the Fcalc is the structure-factor amplitude calculated from the model.
¶ Rfree is the same as Rwork except calculated with a subset (5%) of data that were excluded from refinement calculations.