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**Fig. S1**: **(A)** Sequence alignment of the template and the protein. Residues highlighted in red correspond to identical/conserved residues, while residues in red text are similar in the two proteins. **(B)** Superimposed structure of LdiPGAM (cyan) and template *Leishmania mexicana* co-factor independent phosphoglycerate mutase (LmiPGAM) (PDB ID: 3IGZ)3IGZ (*magenta*). **(C)** Ramachandran plot of the homology-modeled structure of LdiPGAM. The different colored areas indicate “disallowed” (*white*), “generously allowed” (*light yellow*), “additional allowed” (*yellow*), and “most favoured” (*red*) regions.

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**Fig. S2**: **(A)** Dose−response graph for the two potential enzyme inhibitors at four different concentrations. (B) Competitive inhibition of LdiPGAM activity by TL00638 and SPB00184 compounds. 20μg of LdiPGAM enzyme was preincubated with 10, 25, 50 μM of each of the compound for 1 h followed by addition of 3PGA at different concentration (0.05mM to 2mM) at each of the fixed concentration of the inhibitor. Finally kinetic inhibition as observed by Lineweaver-Burk plot.



**Fig. S3**: Docked conformation of compounds 3PGA (green) **(A)**, TL00638 (yellow) **(B)**, and SPB00184 (purple) **(C)** is showing interactions with neighboring residues through H-bonds in the LdiPGAM binding site. **(D)**-Molecular structure of 3PGA, TL00638 and SPB00184.

**Supplementary Table S1:** Identity of LdiPGAM gene sequence (in %) with other organisms

|  |  |
| --- | --- |
| **Organism** | **% of Homology** |
| *L. major* | 93% |
| *L. infantum* | 94% |
| *L. mexicana* | 90% |
| *T. cruzi* | 72% |