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Supporting information for article:

Cysteine synthase: multiple structures of a key enzyme in cysteine synthesis and a potential drug target for Chagas disease and leishmaniasis

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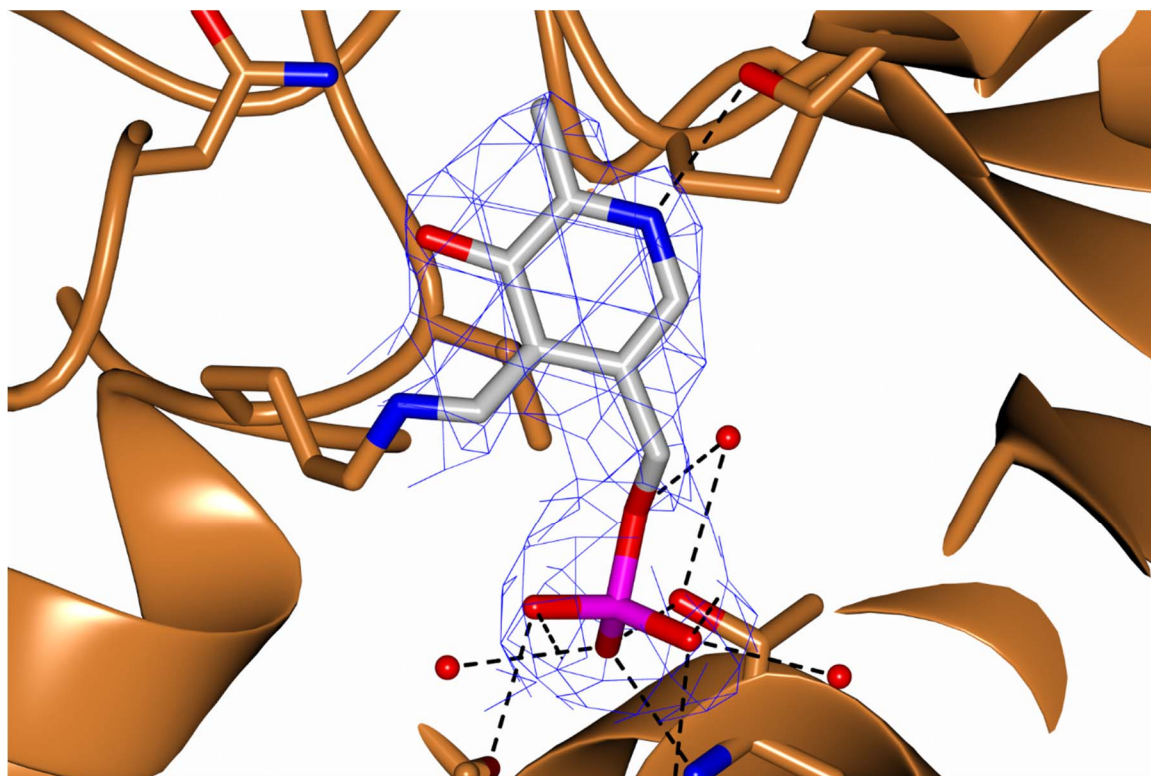


Figure S1 Closeup of the active site of *ThCS*, showing the protein chain in ribbon representation, the cofactor PLP and the side chains of Lys⁷¹, Thr²⁰⁷, Thr²¹⁰ and Ser²⁹⁴ in stick representation with N in blue, O in red, C in green and P in magenta. Key hydrogen bonds are indicated by dashed lines. Electron density is shown in blue at 1 σ level in a $2F_o-F_c$ map.

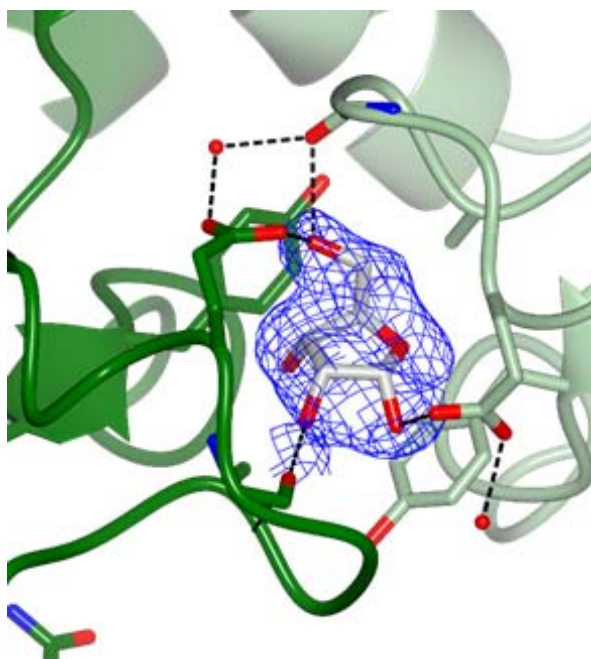


Figure S2 Ribbon diagram of the dimer interface of chain A and B of *TcCS* – Chain A in dark green, Chain B in light green, ribose shown in stick representation. O is shown in red and N is shown in blue. Residues forming hydrogen bonds and ribose are shown in stick representation with hydrogen bonds displayed as black dashed lines. Electron density is shown in a $2F_o - F_c$ map blue at 1σ level.

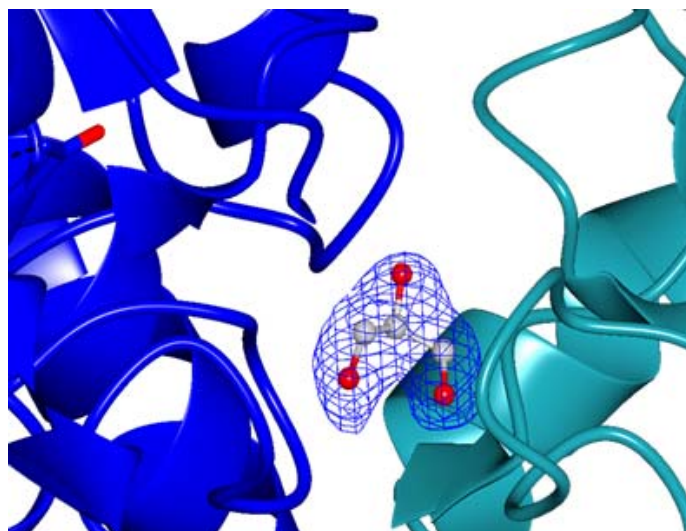


Figure S3 Ribbon diagram of the dimer interface of chain C and D in *TcCS* - Chain C in blue chain D in dark teal, glycerol is shown in stick representation. O is shown in red. Electron density is shown in a $2F_o-F_c$ map blue at 1σ level.

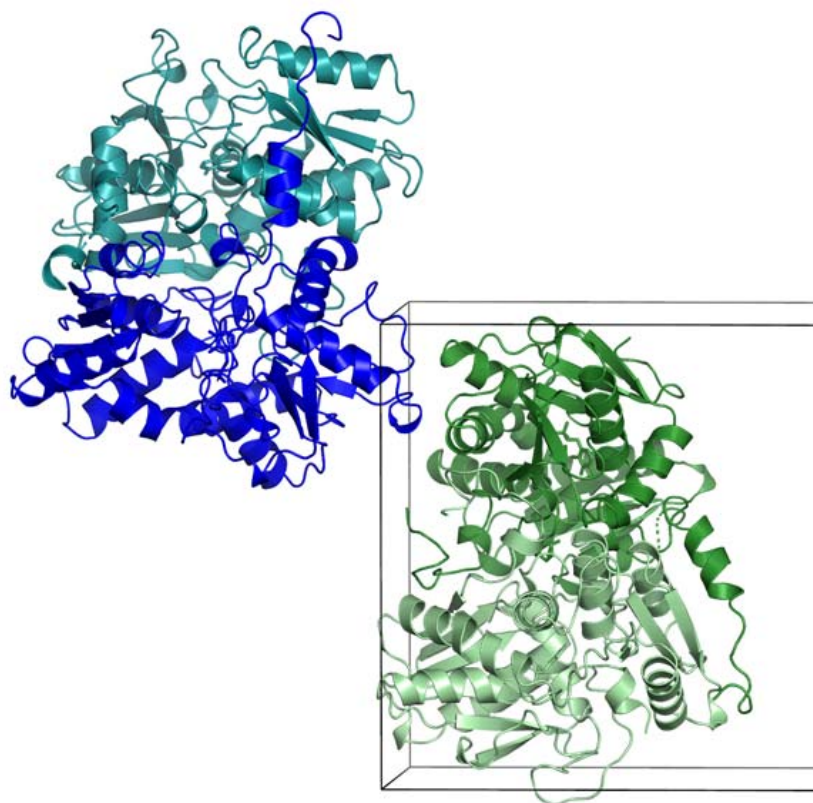


Figure S4 Ribbon diagram of the two crystallographically independent *TcCS* dimers with the unit cell shown in black: Chain A in dark green, Chain B in light green, Chain C in blue, Chain D in dark teal.

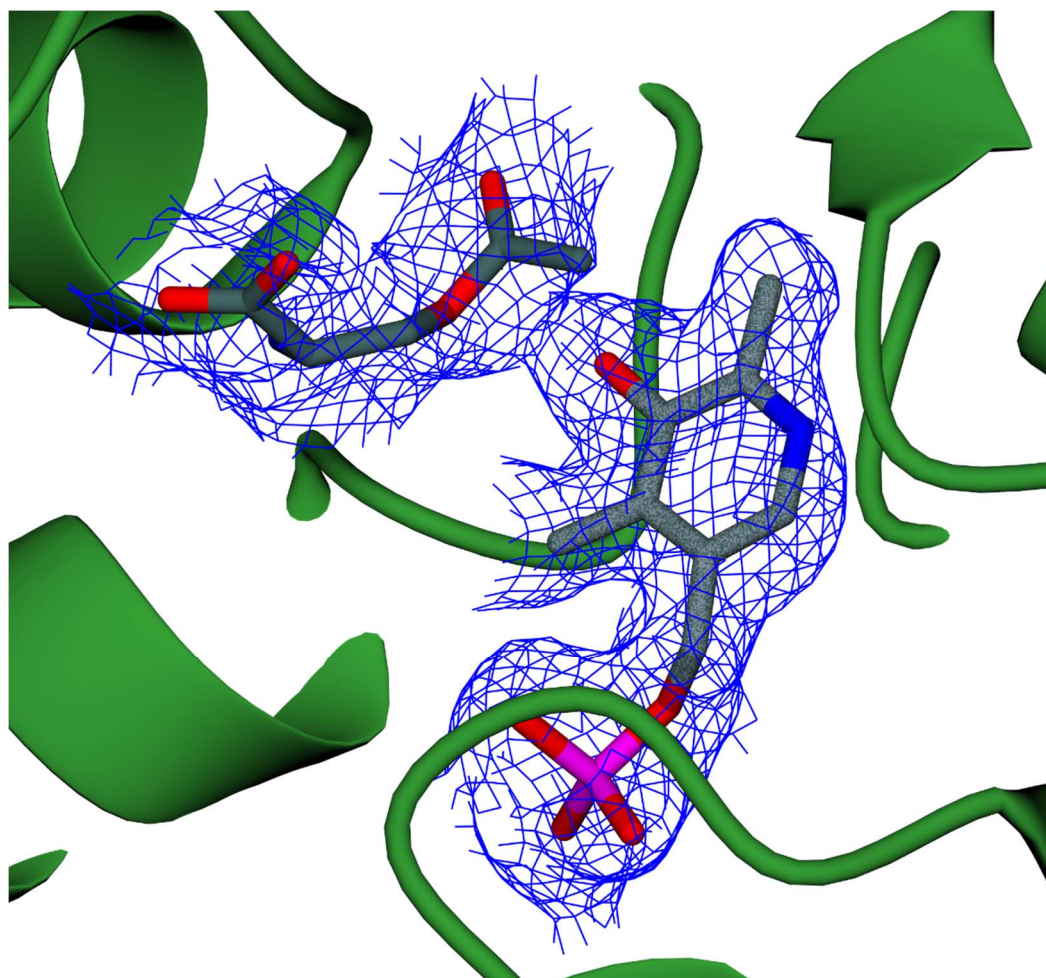


Figure S5 Close up showing active site of *TcCS* Chain A. Dashed lines indicate hydrogen bonds. Atoms are coloured as before. Electron density is shown in a $2F_o - F_c$ map blue at 1σ level with the electron density indicating the presence of OAS.

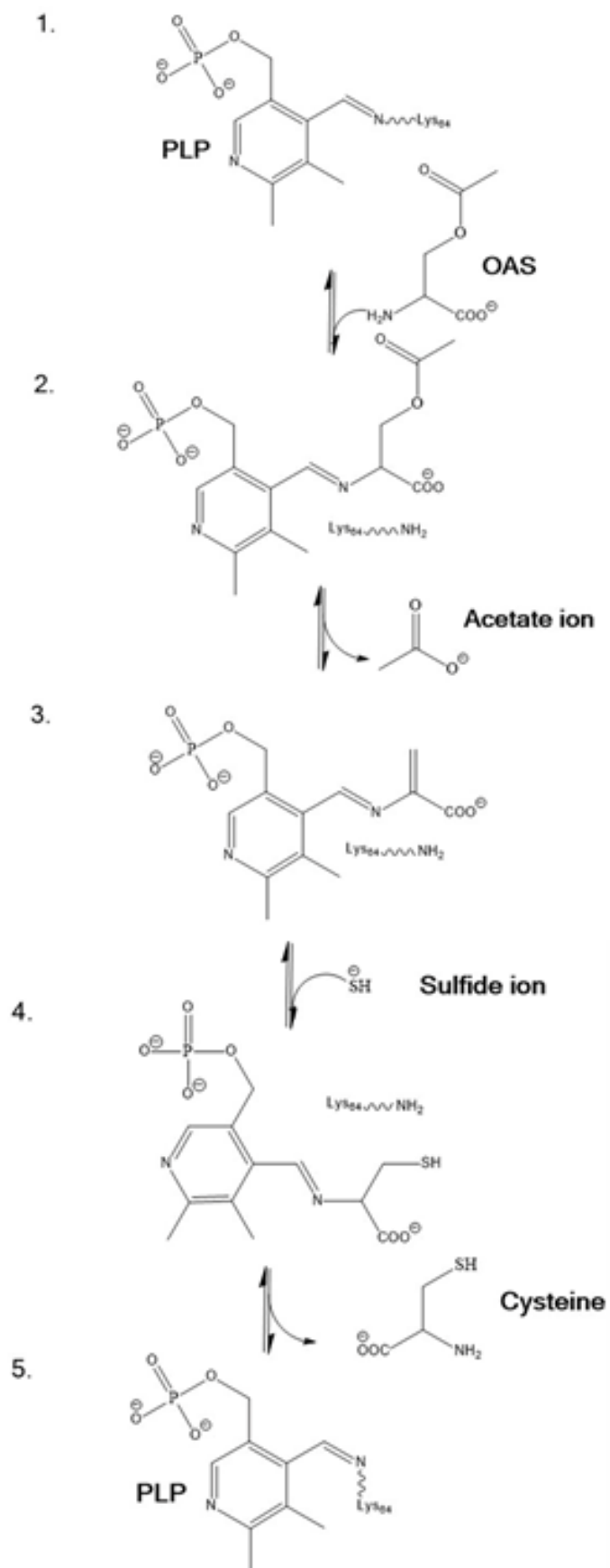


Figure S6 Schema showing reaction of PLP with OAS and a sulfide ion to produce cysteine.

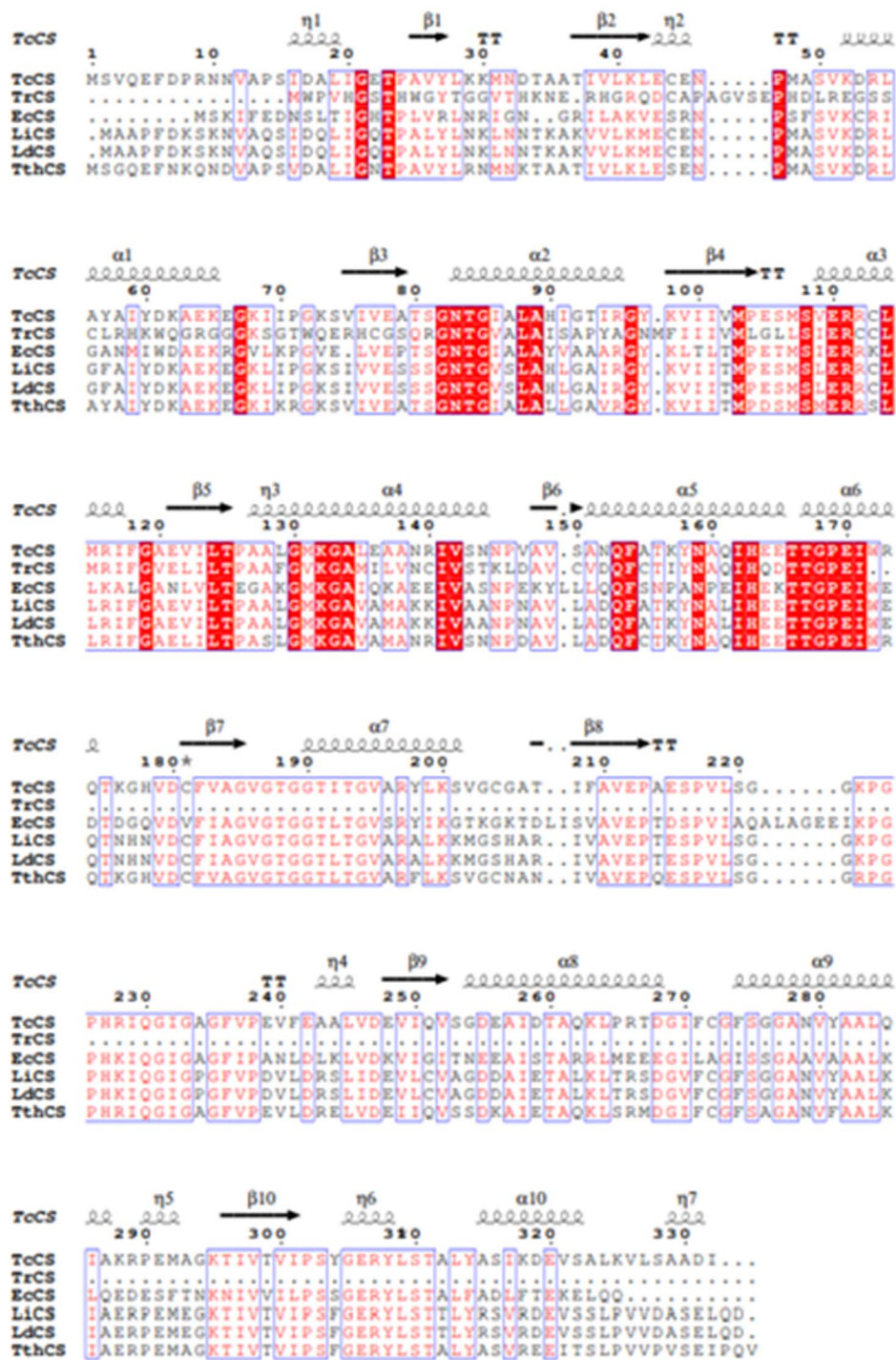


Figure S7 Multiple Alignment of the cysteine synthase sequences of *T. cruzi*, *T. rangeli*, *E. coli*, *L. infantum*, *L. donovani* and *T. theileri*. Identical residues are displayed in a red box, with similar residues in red text, similar or identical residues are framed in a blue box. The secondary structure annotation is based on the *TcCS* structure presented here.

Table S1 Summary of least-squares superpositions of all protein monomers of the three structures, from *TcCS*, *LiCS* and *TthCS*.

Residues 8 – 308 from *TcCS* and the corresponding residues 5 – 307 from *LiCS* and 6 – 308 from *TthCS* were used. RMSD values given in Å are presented on the upper right-hand side of table, while the lower left-hand side shows the number of C-alpha atoms used in each least-squares superposition. All calculations were performed with CCP4mg (McNicholas *et al.*, 2011)

	TcCS A	TcCS B	TcCS C	TcCS D	LiCS A	LiCS B	TthCS A	TthCS B
TcCS A		0.54	0.30	0.50	0.70	0.78	0.63	0.56
TcCS B	282		0.60	0.17	0.84	1.02	0.64	0.71
TcCS C	287	298		0.54	0.78	0.73	0.69	0.63
TcCS D	282	303	298		0.83	0.94	0.62	0.68
LiCS A	274	270	275	270		0.72	0.74	0.72
LiCS B	275	271	274	269	277		1.09	0.97
TthCS A	281	303	297	303	268	269		0.74
TthCS B	281	303	297	303	269	270	268	