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Supporting information for article:

Structural insights into novel inhibition mechanism of *Trypanosoma cruzi* spermidine synthase

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Table S1 List of the amino acid residues in outliers of Ramachandran plot.

Compound	dcSAM	dcSAM + 4MCHA	dcSAM + Fragment 1	dcSAM + Fragment 2	dcSAM + Fragment 3	dcSAM + Fragment 4	dcSAM + Fragment 5	dcSAM + Fragment 6
PDB ID	4YUV	4YUW	4YUX	4YUY	4YUZ	4YU0	4YU1	4YU2
Ramachandran plot (%)								
Preferred	95.6	96.2	95.5	95.4	96.1	96.4	96	95
Allowed	3.8	3.1	3.6	4.1	3.3	3	3.3	4.6
Outliers	0.5	0.7	0.9	0.5	0.6	0.6	0.6	0.4
Residues in outliers	A, K87	A, K87	A, G3	A, E203	A, K87	A, K87	A, K87	A, E70
(Chain ID, Residue ID)	A, E203	A, E203	A, K87	B, K87	A, E203	A, E203	A, E203	A, E203
	B, E203	B, K87	A, E203	B, E203	A, V253	B, E203	B, E203	
		B, E203	B, K87		C, K30	C, S8	C, Q18	
			B, E203		C, K87	C, E203	C, K87	
					C, E203	D, T170	C, E203	
						D, E203		

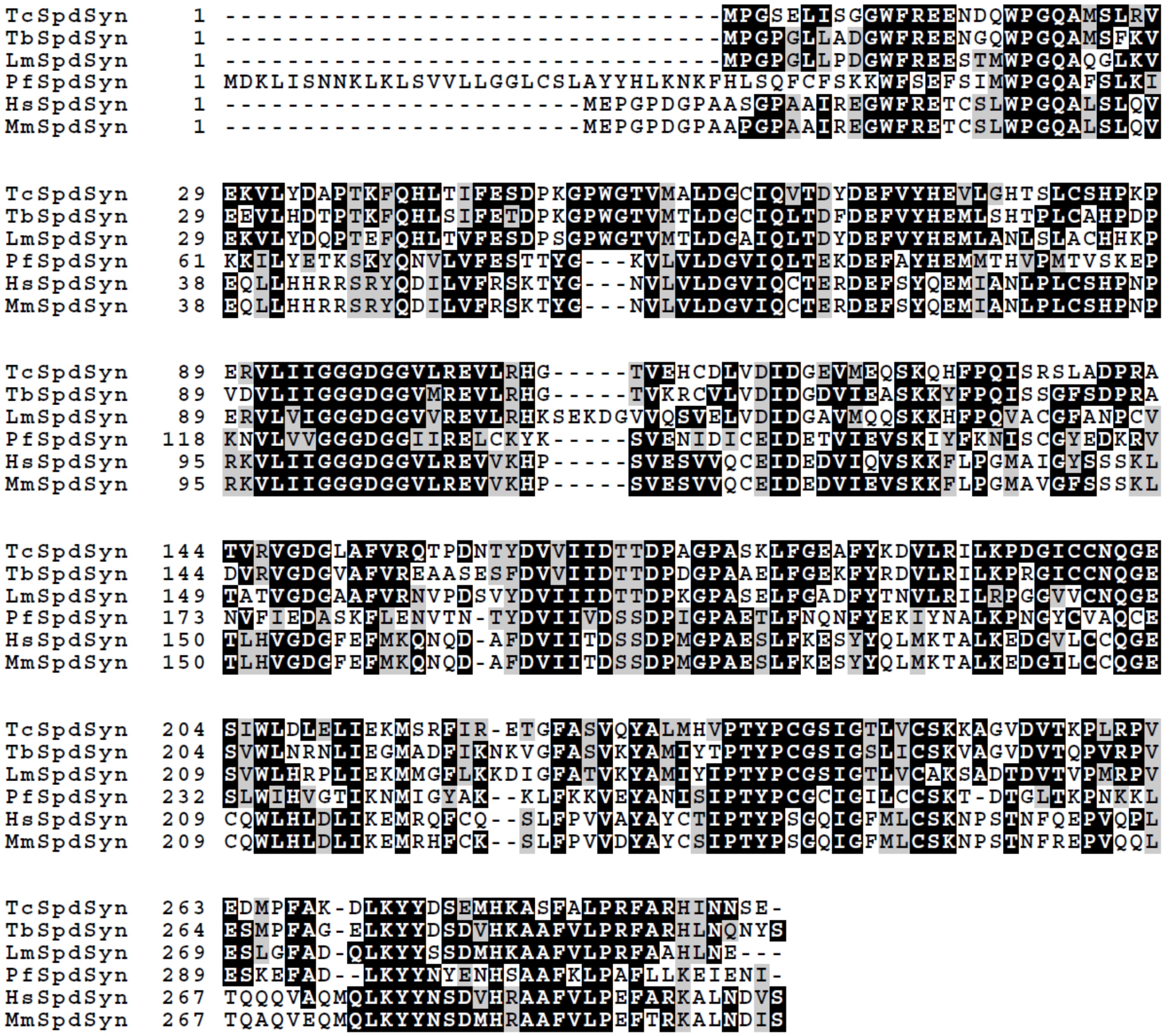

Figure S1 Sequence alignment of SpdSyn from *Trypanosoma cruzi* (Tc), *Trypanosoma brucei* (Tb), *Leishmania major* (Lm), *Plasmodium falciparum* (Pf), human (Hs), and mouse (Mm). Identical residues are boxed in black and similar residues are boxed in gray.