Article

Design and Synthesis of New Anthranyl Phenylhydrazides: Antileishmanial Activity and Structure–Activity Relationship

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Supporting Information

Table S1. Targets predicted by chemogenomics.

Uniprot	Target name	Organism
Q01782	Pteridine reductase 1	Leishmania major
Q27686	Pyruvate kinase	Leishmania mexicana
O96394	Arginase	Leishmania amazonensis

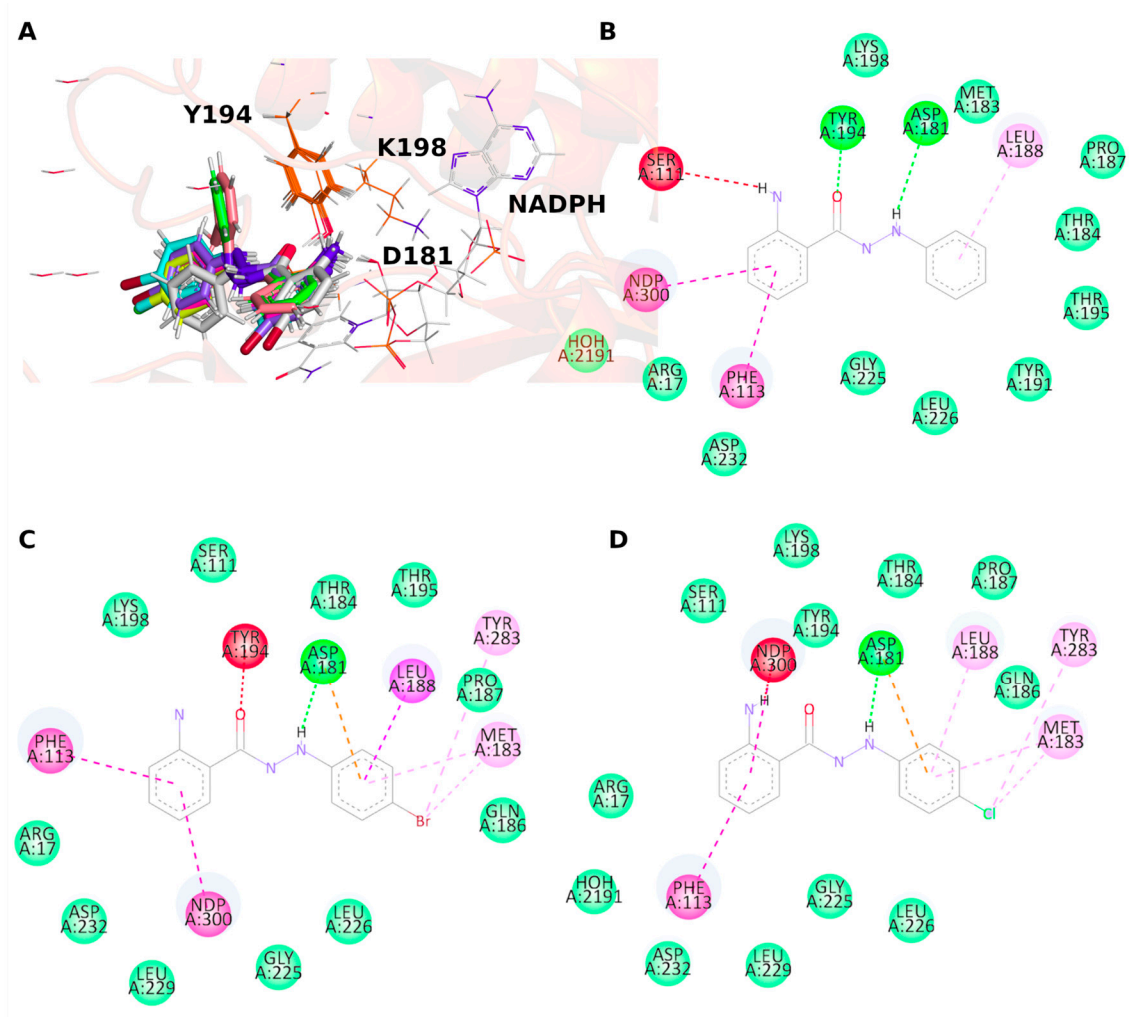Figure S1. Alignment between PTR1 of *L.amazonensis* and *L. major*.

Figure S2. (**A**) Overlay of Putative binding pose. Docking analysis of inhibitors (**B**) 1a (**C**) 1d and (**D**) 1e. Interactions are colored by type: hydrogen bond, van der Waals, alkyl, Pi-stacked, halogen, unfavorable donor-donor, and Pi-anion/cation are shown by colors green, light green, light pink, pink, cyan, red, and gold, respectively.

Figure S3.(**A**) Docking analysis of inhibitors 1f (**B**) 1j (**C**) 1c and (**D**) 1g. Interactions are colored by type: hydrogen bond, van der Waals, alkyl, Pi-stacked, halogen, unfavorable donor-donor, and Pi-anion/cation are shown by colors green, light green, light pink, pink, cyan, red, and gold, respectively.
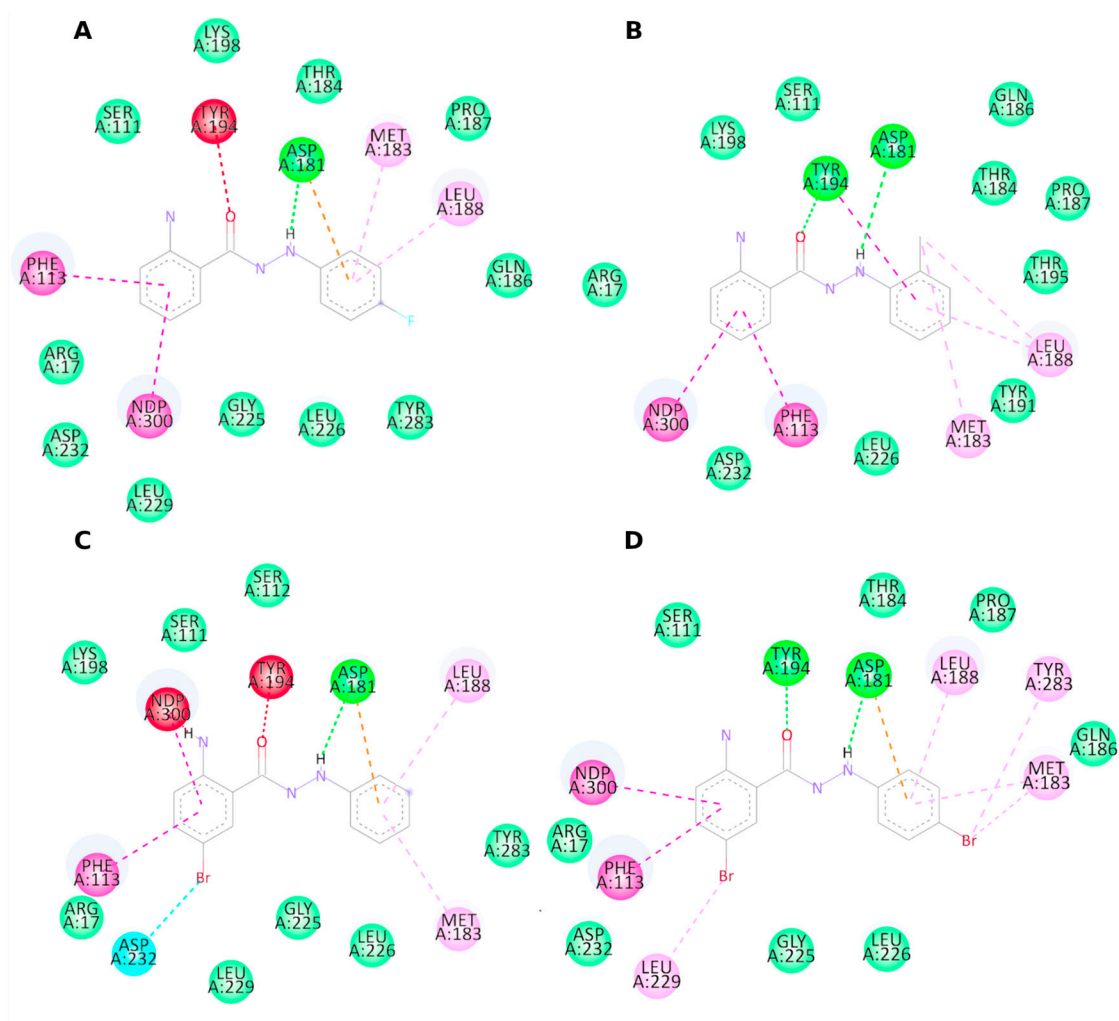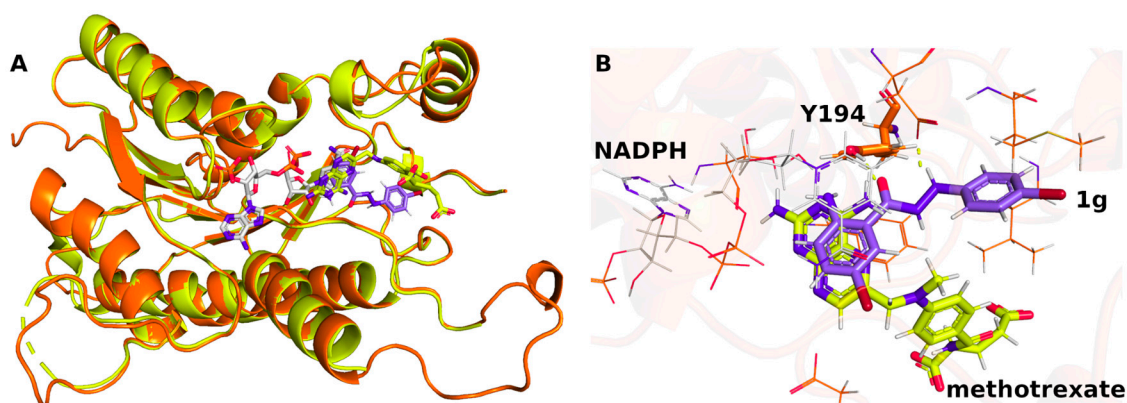
Figure S4. (**A**) Structural alignment between PTR1 from *L. major* (yellow) and *L. amazonensis* (orange). (**B**) Comparison between docking pose of inhibitor 1g and methotrexate co-crystallized in PTR1

Ramachandran Plot
saves

Plot statistics

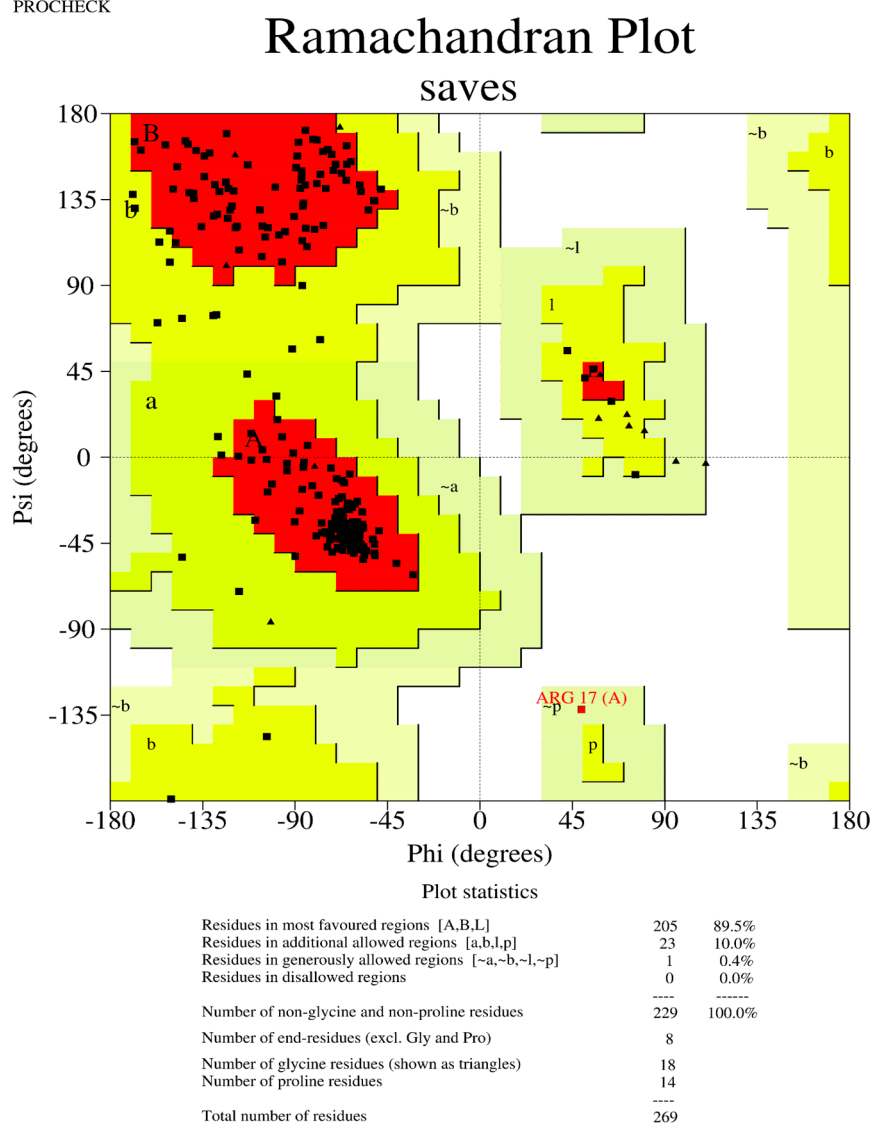|		
Residues in most favoured regions [A,B,L]	205	89.5%
Residues in additional allowed regions [a,b,l,p]	23	10.0%
Residues in generously allowed regions [~a,~b,~l,~p]	1	0.4%
Residues in disallowed regions	0	0.0%
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Number of non-glycine and non-proline residues	229	100.0%
Number of end-residues (excl. Gly and Pro)	8	
Number of glycine residues (shown as triangles)	18	
Number of proline residues	14	

Total number of residues	269	

Figure S5. Ramachandran plot of PTR1 model from *L. amazonensis* obtained in AlphaFold.
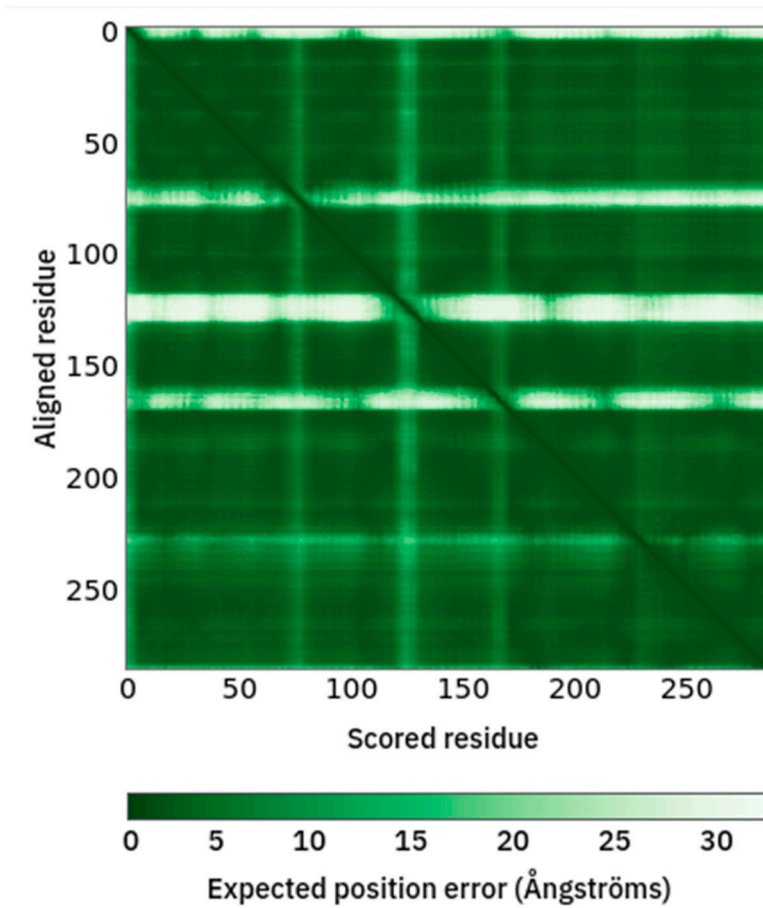
Figure S6. Predicted error of PTR1 model from *L. amazonensis* obtained in AlphaFold.
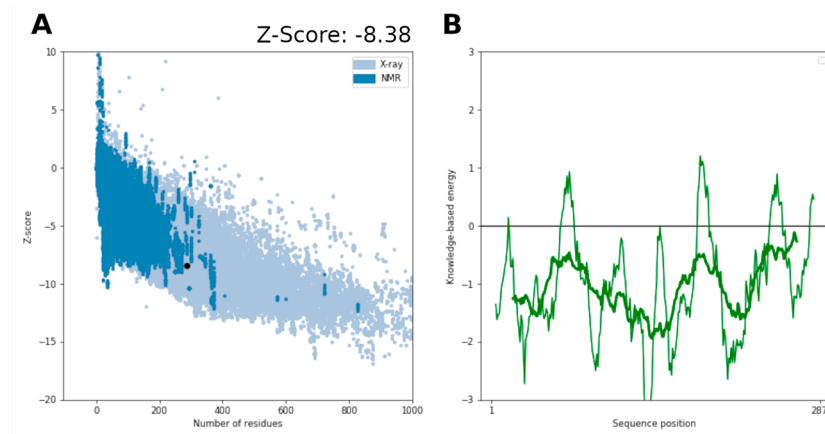

Figure S7. (A) Comparison of z-score of our model against all protein chains in PDB determined by X-ray crystallography (light blue) or NMR spectroscopy (dark blue). (B) Local model quality observed by residue energies averaged in two windows size 10 (light green) and 40 (green).