

Supplementary information to:

**MOLECULAR CLONING AND CHARACTERIZATION OF PROTEIN
DISULFIDE ISOMERASE OF *BRUGIA MALAYI*,
A HUMAN LYMPHATIC FILARIAL PARASITE**

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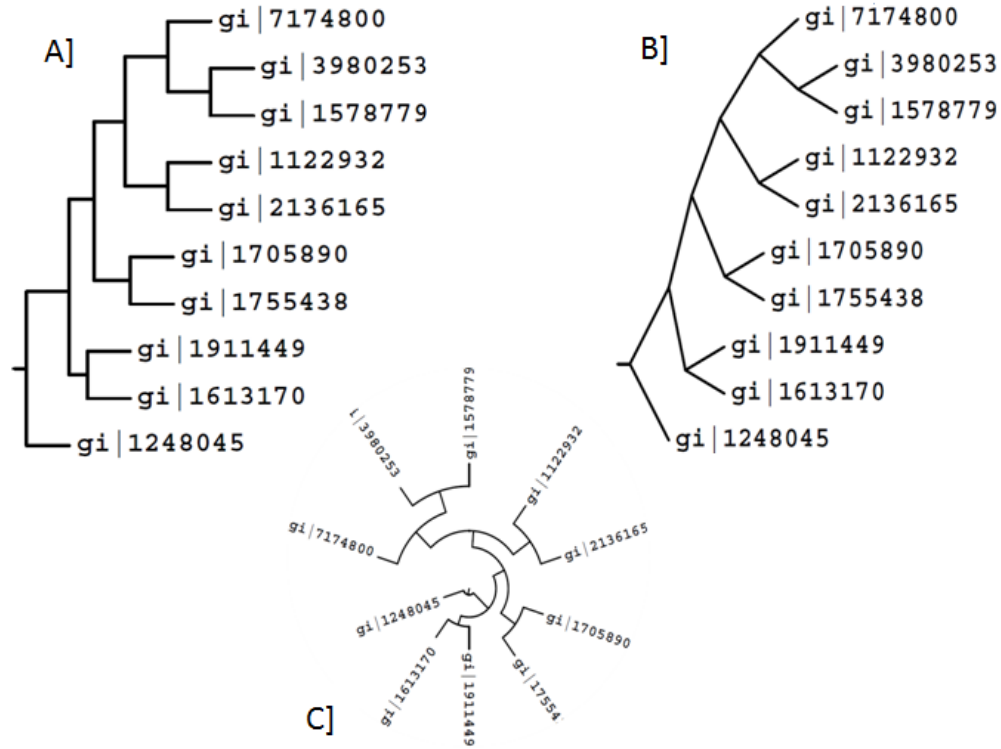
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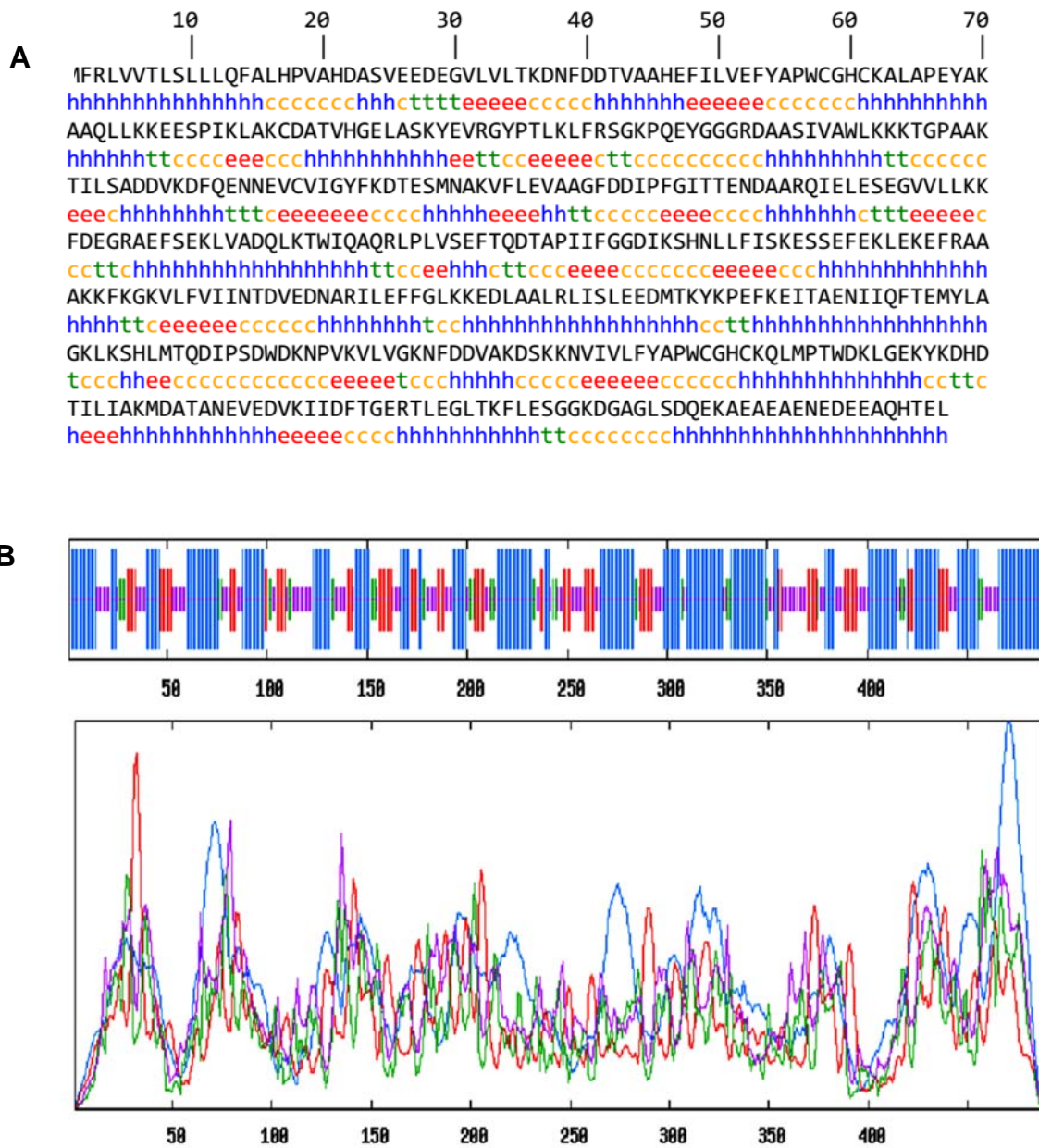
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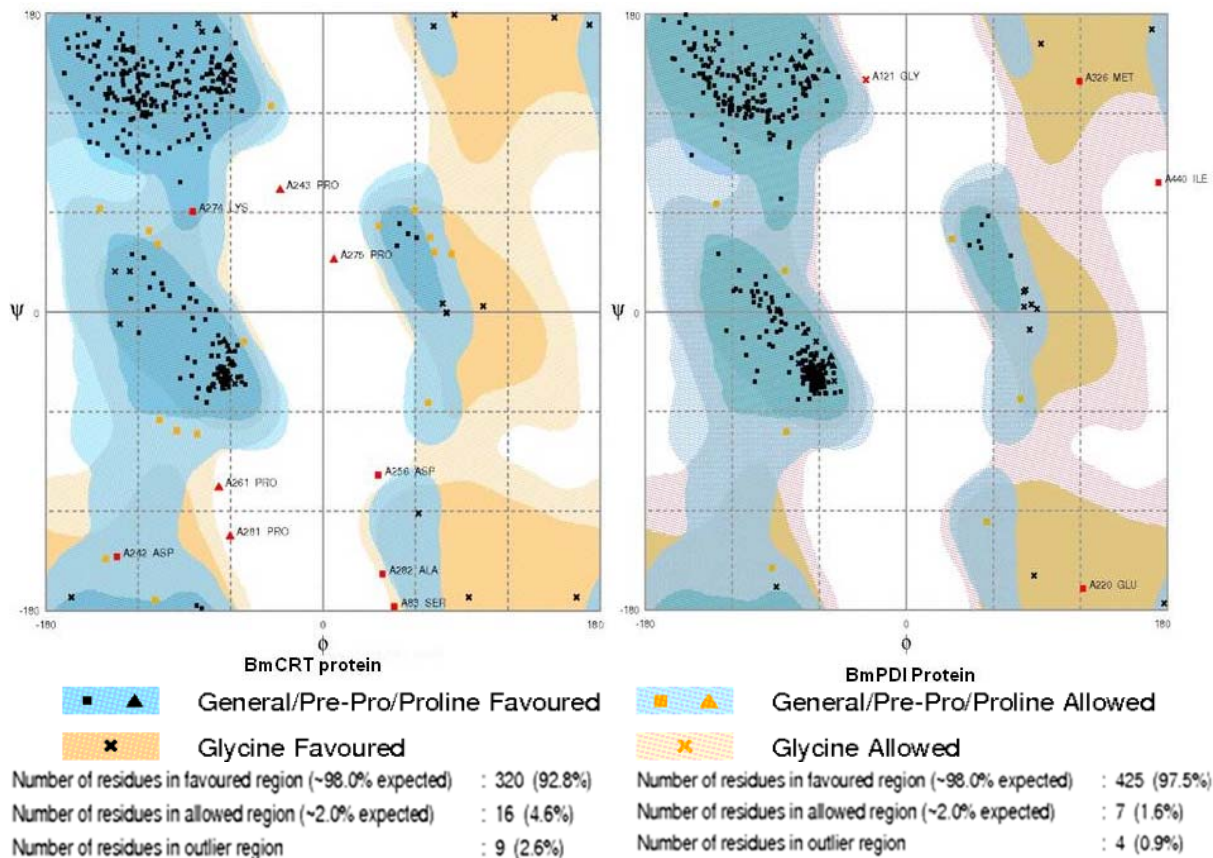
Supplementary Figure 1: Multiple alignment of the predicted amino acid sequences of Protein disulfide isomerases from *Brugia malayi* (XP_001899304.1), *Homo sapiens* (NP_005304), *Caenorhabditis elegans* (NP_497746), *Mus musculus* (NP_031978), *Schizosaccharomyces pombe* (NP_593584), *Leishmania major* (XP_001687289), *Leishmania donovani* (XP_003865838), *Plasmodium falciparum* (XP_001348023), *Trypanosoma brucei brucei* (XP_823057), *Escherichia coli* (NP_418297) were carried out by Clustal W program (<http://www.ch.embnet.org/software/ClustalW.html>) and absence of amino acid is shown by dash '-' in the sequences while the conserved and semi-conserved residues are shown in boxes. Signature motif and binding region were also shown.



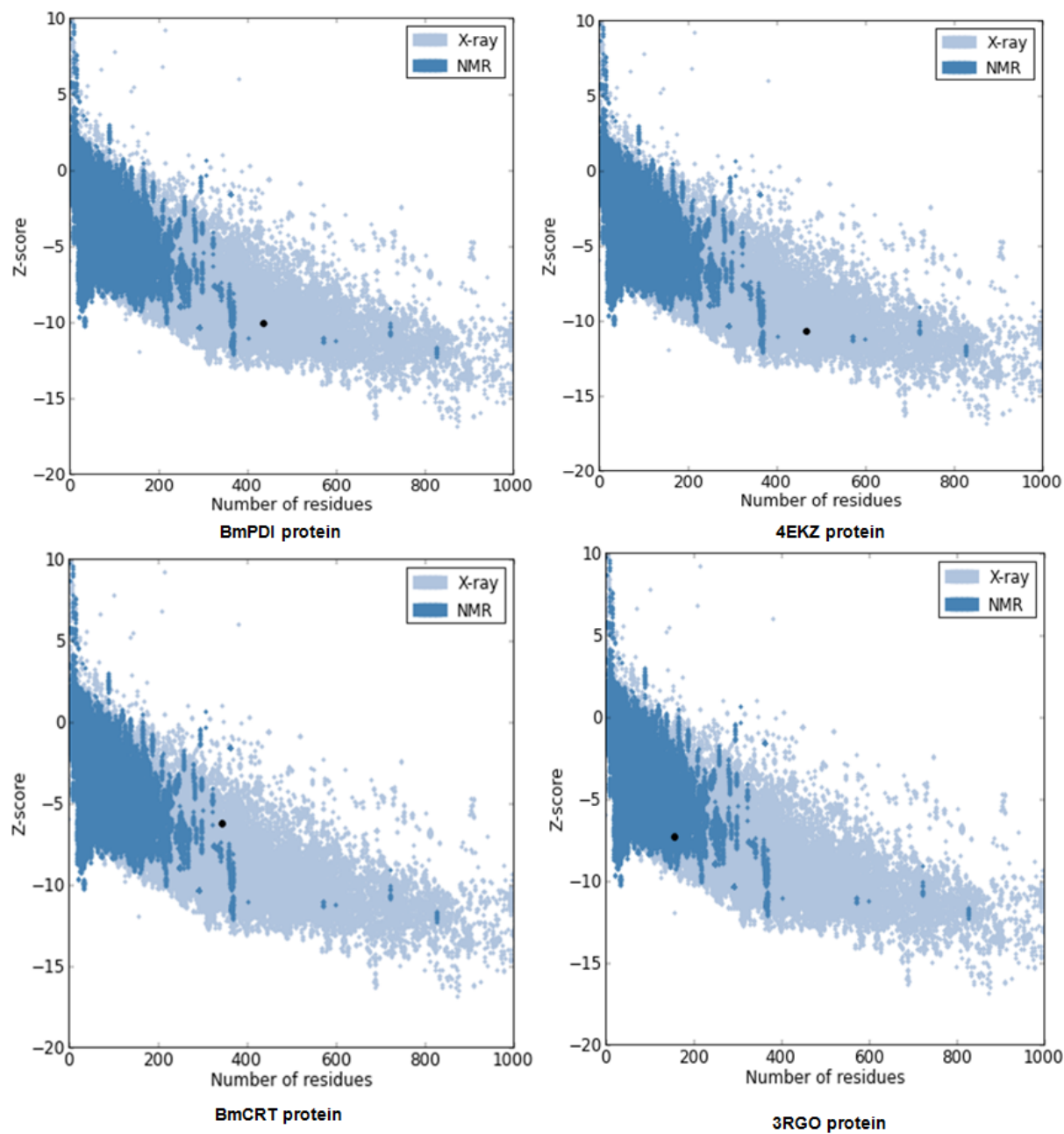
Supplementary Figure 2: Phylogenetic analysis of PDI protein sequence of *B. malayi* with PDI sequences of other organisms using PHYLIP: **A)** Phenogram of the sequences of PDI protein from different organisms; **A)** Phenogram; **B)** Cladogram; **C)** Circular tree [gi|170589085: BmPDI; gi|16131701: *Escherichia coli* str. K-12 substr. MG1655; gi|112293264: *Mus musculus*; gi|21361657: *Homo sapiens*; gi|157877997: *Leishmania major* strain Friedlin; gi|398025354: *Leishmania donovani*; gi|19114496: *Schizosaccharomyces pombe*; gi|17554386: *Caenorhabditis elegans*; gi|71748004: *Trypanosoma brucei brucei*; gi|124804507: *Plasmodium falciparum*].



Supplementary Figure 3: (A) Secondary structure of *Brugia malayi* Protein disulfide isomerase predicted by using SOPMA C= Random coil, H= Helix, E= extended strand. (B) Predicted secondary structure of *Brugia malayi* Protein disulfide isomerase. Here, helix is indicated by blue, while extended strands and beta turns are indicated by red and green, respectively.



Supplementary Figure 4: Ramachandran plot of modelled protein BmPDI & BmCART depicting most of the residues falling in the allowed region.



Supplementary Figure 5: Comparison of template PDB structures with modelled structures of BmCRT and BmPDI by using PROSA server.

Supplementary Table 1: Representing the calculated secondary structure elements of *Brugia malayi* Protein disulfide isomerase SOPMA

Alpha helix (Hh)	47.43 %
3₁₀ helix (Gg)	0.00 %
Pi helix (Ii)	0.00 %
Beta bridge (Bb)	0.00 %
Extended strand (Ee)	16.84 %
Beta turn (Tt)	7.60 %
Bend region (Ss)	0.00 %
Random coil (Cc)	28.13 %