

**Egress and Invasion Machinery of Malaria: An In-depth Look into The
Structural and Functional Features of The Flap Dynamics of Plasmeepsin**

IX and X

Supplementary Material

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<i>PLASMEPSIN</i>	<i>TEMPLATE</i>	<i>SEQUENCE IDENTITY</i>	<i>Z-SCORE</i>
IX	4OBZ	35%	-6.16
X	4OBZ	35%	-6.22

Table S1. The Z-score and sequence identity of 4OBZ template used for Plm IX-X

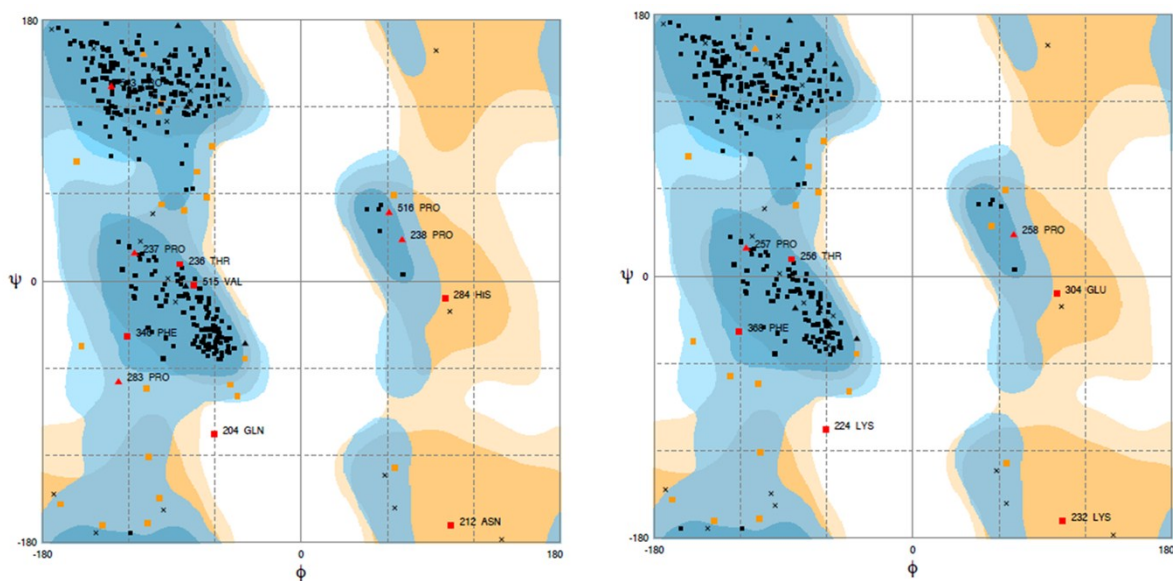


Figure S1. Ramachandran plots for models Plm IX (left) and Plm X (right).

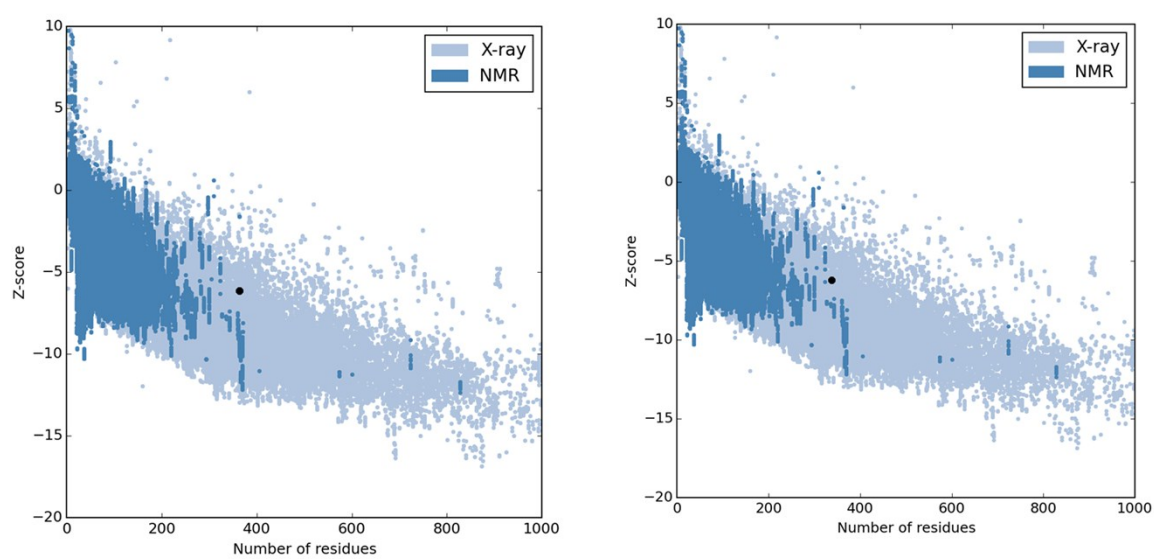


Figure S2. Overall model quality generated using ProSA-web of Plm IX (left) and Plm X (right).

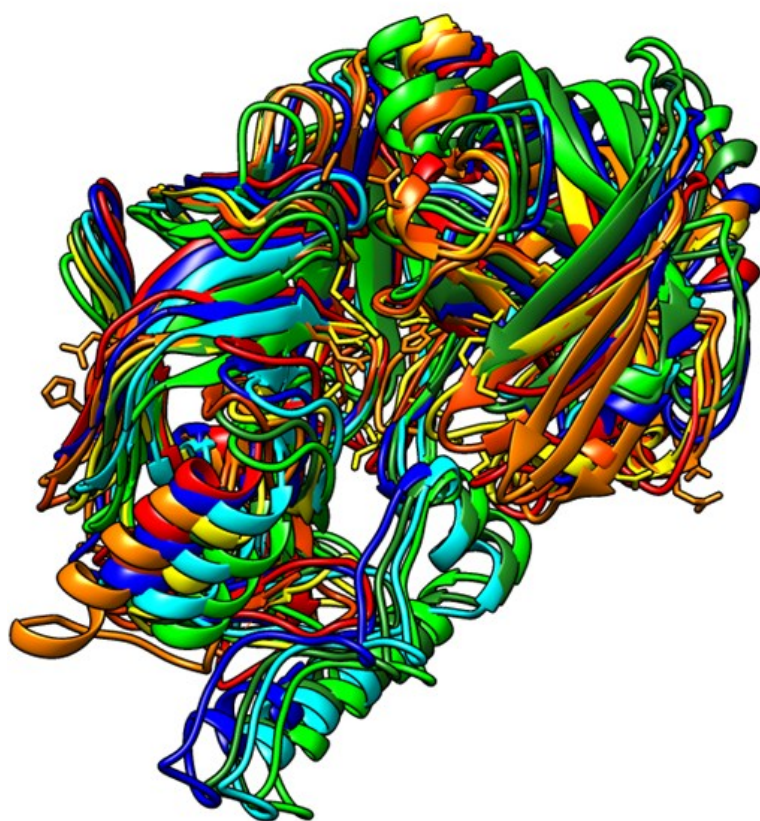


Figure S3. Superimposed image of Plasmepsins I (PDB: 3QRV; red), II (PDB:1LF4, orange red), III (PDB: 3FNS, orange), IV (1LS5, green), VI (dark green), VII (cyan), IX (sea green) and X (blue).

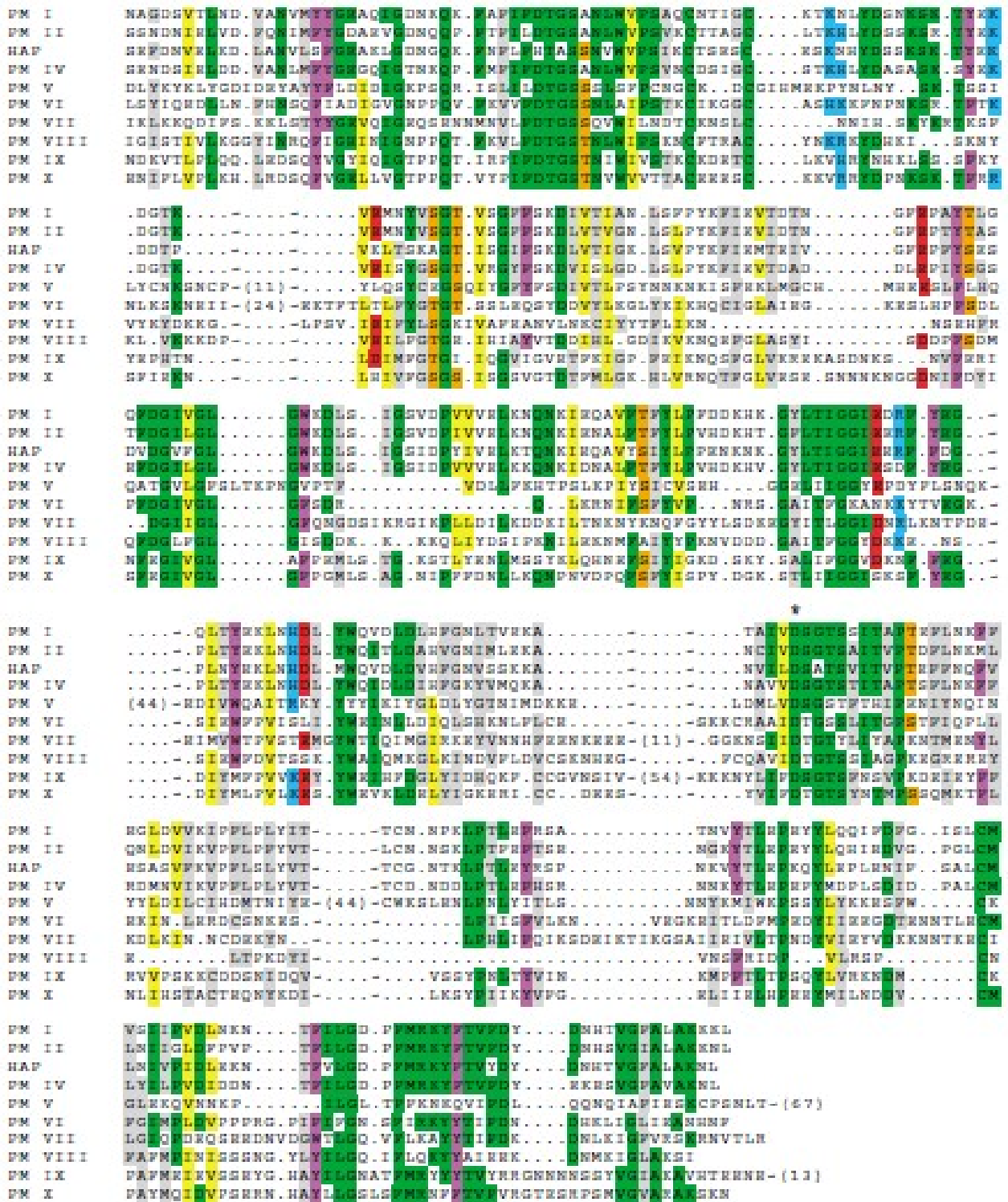


Figure S4. Sequence alignment of Plasmeprin I-X from *Plasmodium falciparum*.

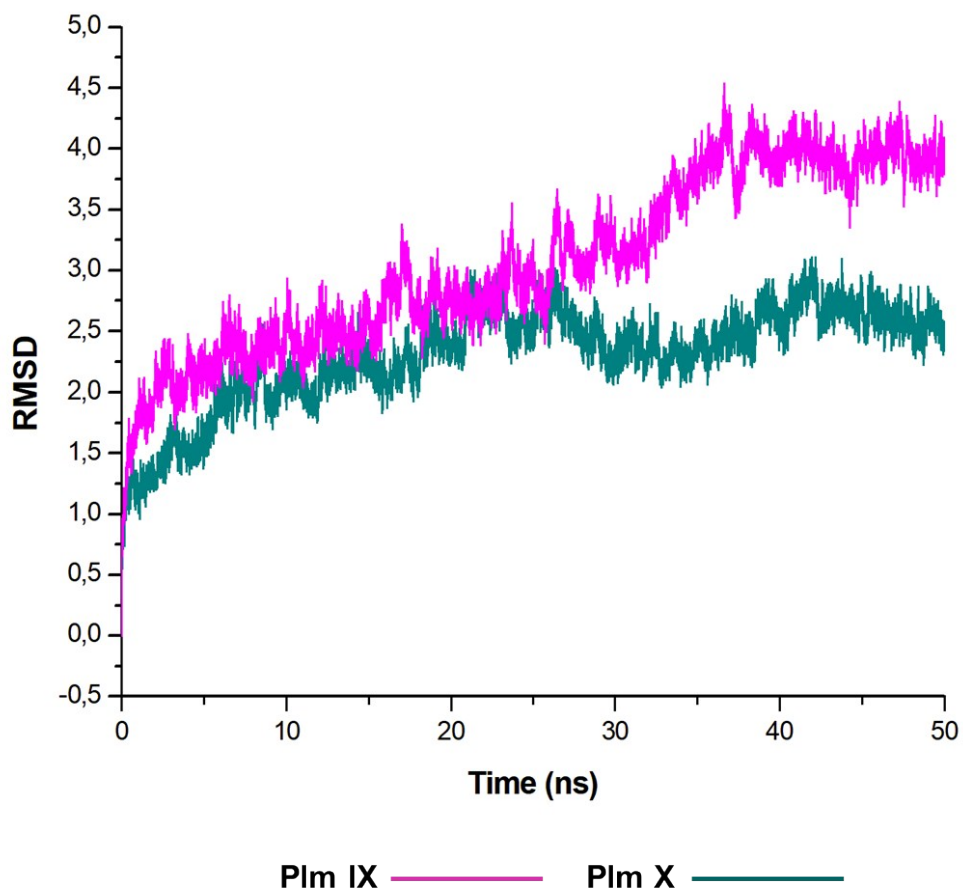
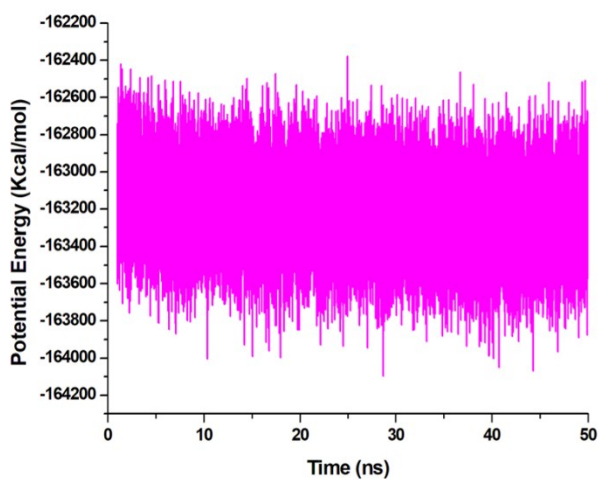
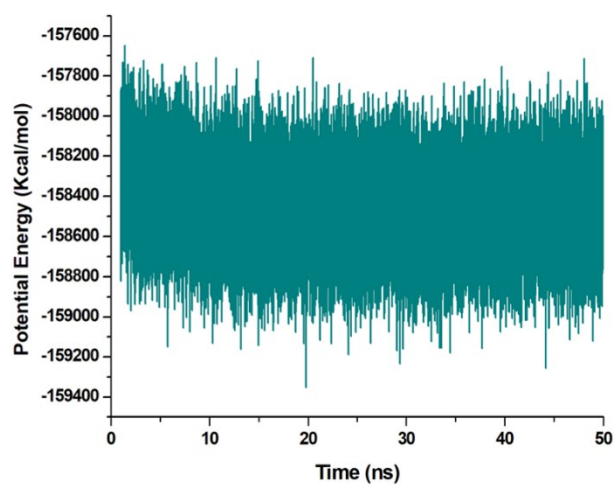


Figure S5. RMSD plot of plasmepsin IX and X, displaying system stability after 30ns.



PE= -163213,16136



PE= -158461,37335

Figure S6. Potential energy (PE) plots of Plm IX (left) and Plm X (right) with interaction cutoff of 12 Å. Mean values are presented below the respective plots.