Egress and Invasion Machinery of Malaria: An In-depth Look into The Structural and Functional Features of The Flap Dynamics of Plasmepsin IX and X

Supplementary Material

Geraldene Munsamy, Pritika Ramharack and Mahmoud E. S. Soliman*

*Molecular Bio-computation and Drug Design Laboratory, School of Health Sciences, University of KwaZulu-Natal, Westville Campus, Durban 4001, South Africa

*Corresponding Author: Mahmoud E.S. Soliman
Email: soliman@ukzn.ac.za
Telephone: +27 (0) 31 260 8048, Fax: +27 (0) 31 260 7872
Table S1. The Z-score and sequence identity of 4OBZ template used for Plm IX-X

<table>
<thead>
<tr>
<th>PLASMEPSIN</th>
<th>TEMPLATE</th>
<th>SEQUENCE IDENTITY</th>
<th>Z-SCORE</th>
</tr>
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<tbody>
<tr>
<td>IX</td>
<td>4OBZ</td>
<td>35%</td>
<td>-6.16</td>
</tr>
<tr>
<td>X</td>
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<td>35%</td>
<td>-6.22</td>
</tr>
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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 Plasmepsin I-X from *Plasmodium falciparum*. 
**Figure S5.** RMSD plot of plasmepsin IX and X, displaying system stability after 30ns.
Figure S6. Potential energy (PE) plots of Plm IX (left) and Pllm X (right) with interaction cutoff of 12 Å. Mean values are presented below the respective plots.