Supplementary Material for:

The Protonation State of the Catalytic Aspartates in Plasmepsin II

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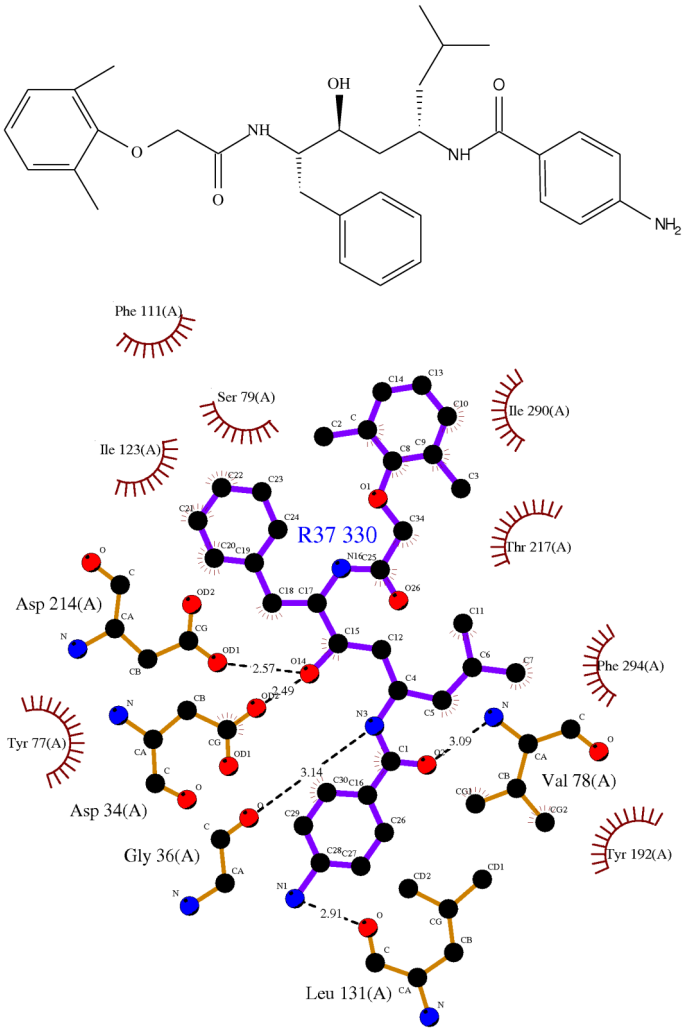

Supplementary Figure 1: The hydroxypropylamine inhibitor rs370
The structure of the inhibitor rs370 and its interactions with plasmepsin II as seen in the PDB structure 1LF2 [1]. The interactions were plotted with the computer program LIGPLOT [2]

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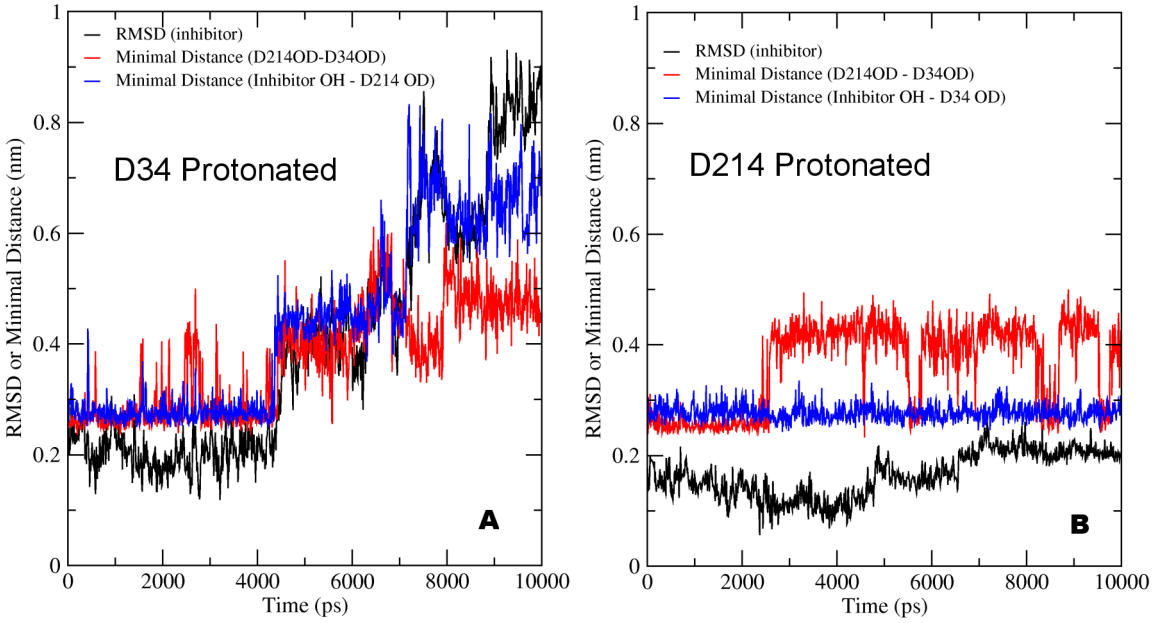

Supplementary Figure 2: The unbinding of the inhibitor with protonated D34.
Time series of the root mean square deviation of the inhibitor's heavy atoms, excluding the rings (due to their symmetry), upon alignment of the protein Cα atoms to the x-ray structure (black), the minimal distance between the catalytic aspartates Oδs (red) and the minimal distance between the inhibitor's hydroxyl oxygen and the catalytic dyad hydrogen bond acceptor (blue). (A) In a simulation with D34 protonated, the inhibitor starts to escape its binding site after 4.4ns of simulation time. (B) The same progress variables, monitored along one of the simulations where D214 was protonated, are plotted as a basis of comparison.

References

[1] Asojo, O. A., Afotina, A., Gulnik, S. V., Yu, B., Erickson, J. W., Randad, R., Medjahed, D., and Silva, A. M. (2002) Structures of Ser205 mutant plasmepsin II from Plasmodium falciparum at 1.8 angstrom in complex with the inhibitors rs367 and rs370. *Acta Crystallog. D*, **58**, 2001–2008.

[2] Wallace, A. C., Laskowski, R. A., and Thornton, J. M. (1995) LIGPLOT: a program to generate schematic diagrams of protein-ligand interactions. *Protein Eng*, **8**, 127–134.