

## *Supporting Information*

### **The Reaction Mechanism of Loganic Acid Methyltransferase: A Molecular Dynamics Simulation and Quantum Mechanics Study**

**Mateusz Jędrzejewski, Łukasz Szeleszczuk and Dariusz Maciej Pisklak \***

Department of Organic and Physical Chemistry, Faculty of Pharmacy, Medical

University of Warsaw, Banacha 1, 02-093 Warsaw, Poland;

s078210@student.wum.edu.pl (M.J.); lukasz.szeleszczuk@wum.edu.pl (Ł.S.)

\* Correspondence: [dariusz.pisklak@wum.edu.pl](mailto:dariusz.pisklak@wum.edu.pl)

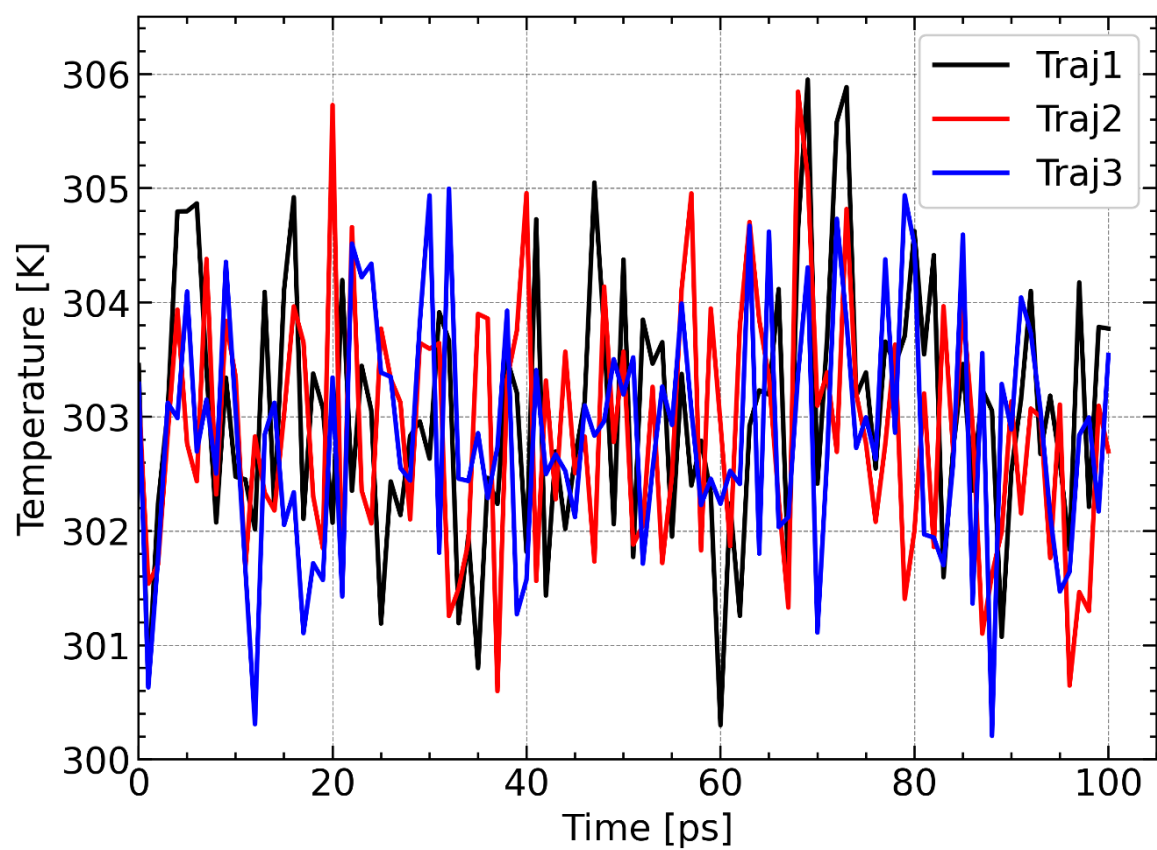


Figure S1. System temperature changes during NVT simulation for 3 different trajectories (Traj1, Traj2, Traj3).

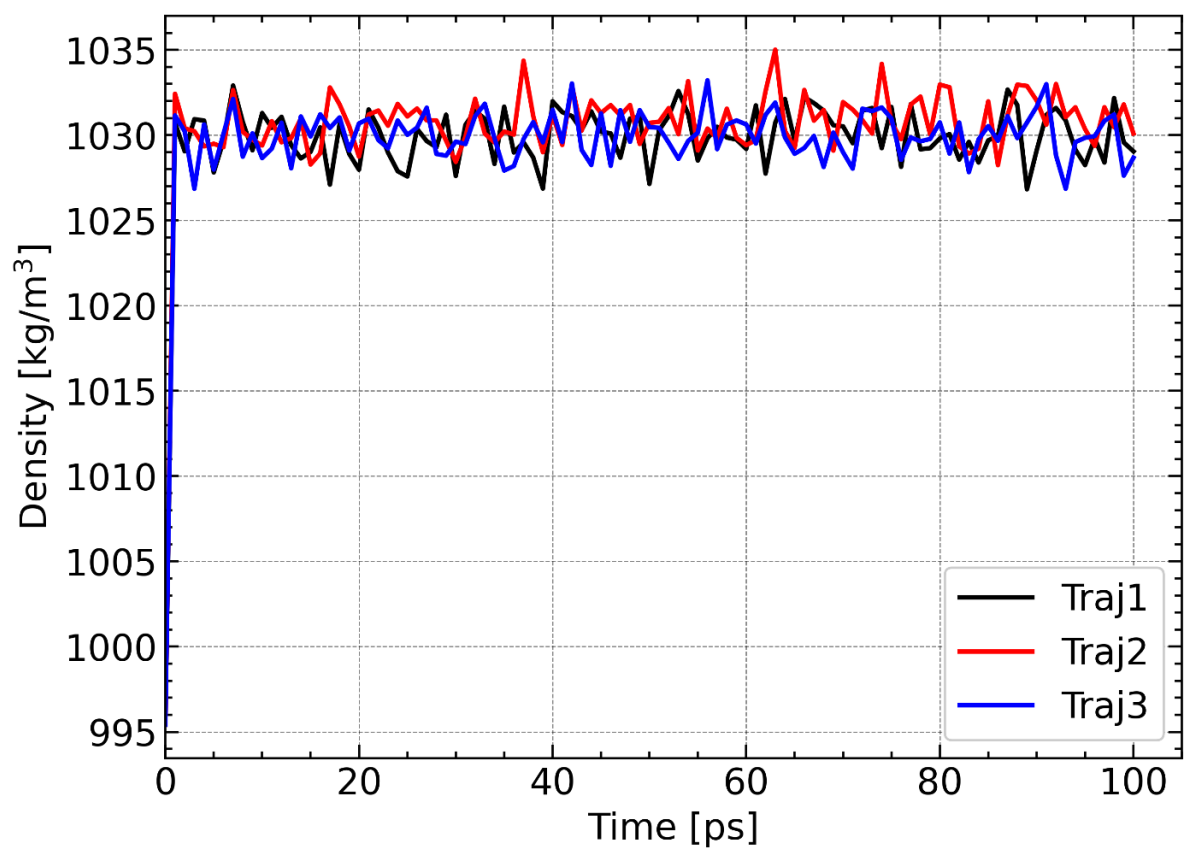


Figure S2. Changes in system density during NPT simulation for 3 different trajectories (Traj1, Traj2, Traj3).

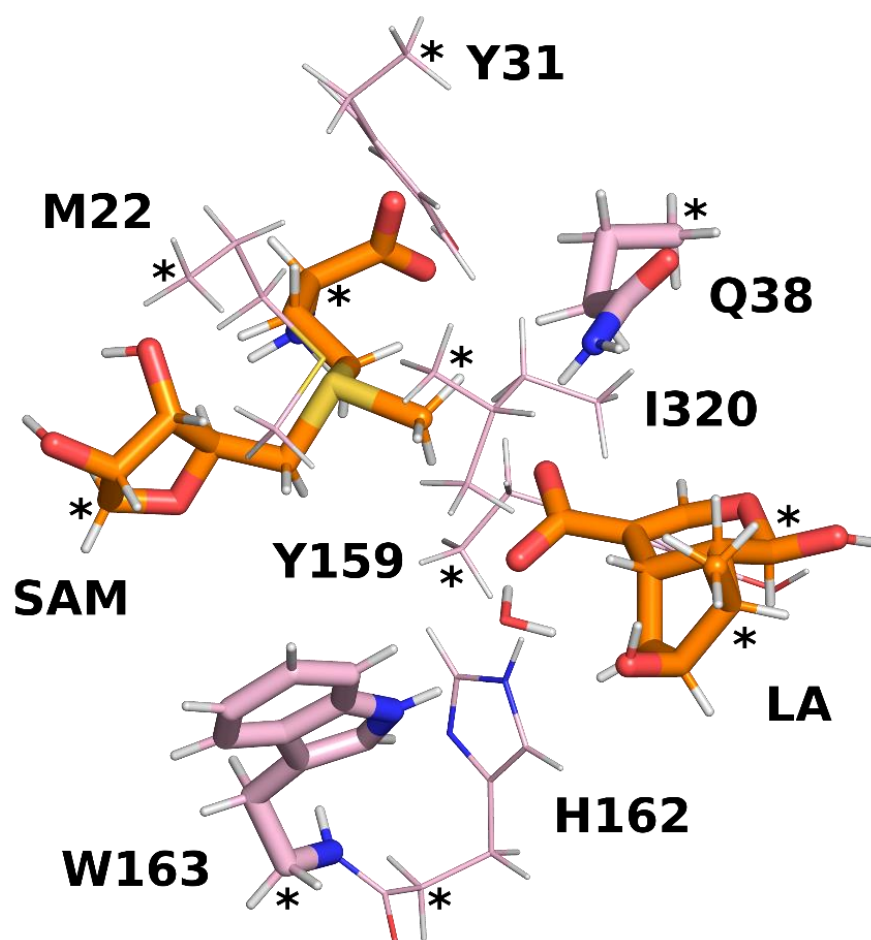


Figure S3. The structure of **Model 1** with water-mediated hydrogen bond between W163 and loganic acid. The fixed atoms are marked with an asterisk.

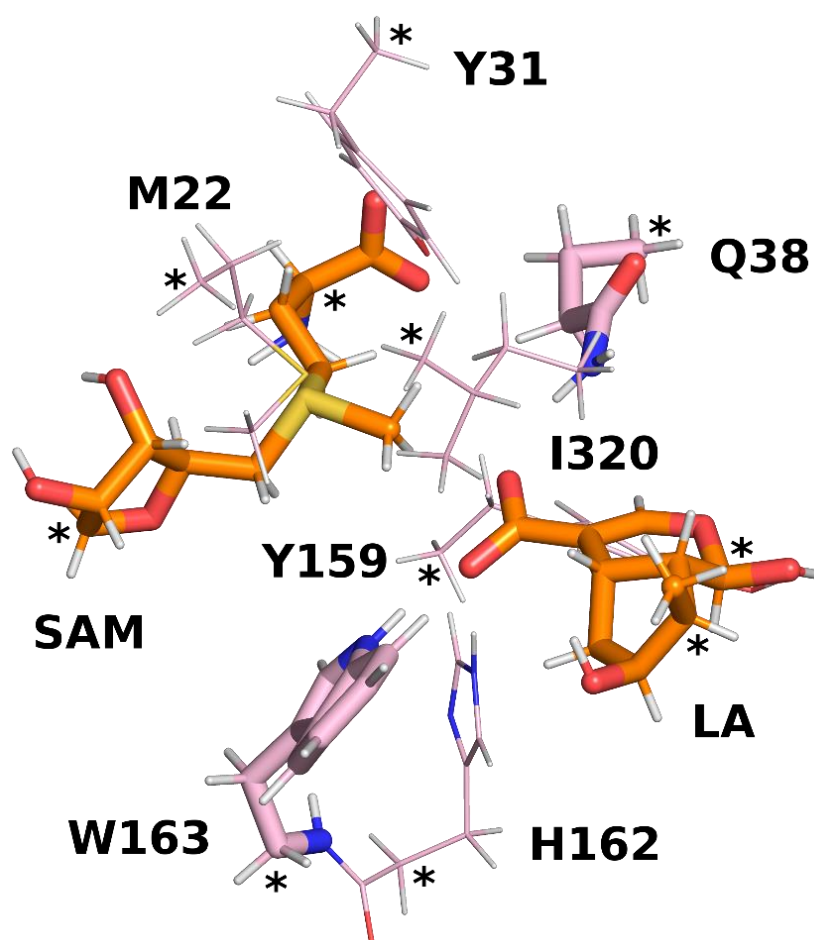


Figure S4. The structure of Model 2 with a direct hydrogen bond between W163 and loganic acid. The fixed atoms are indicated with an asterisk.

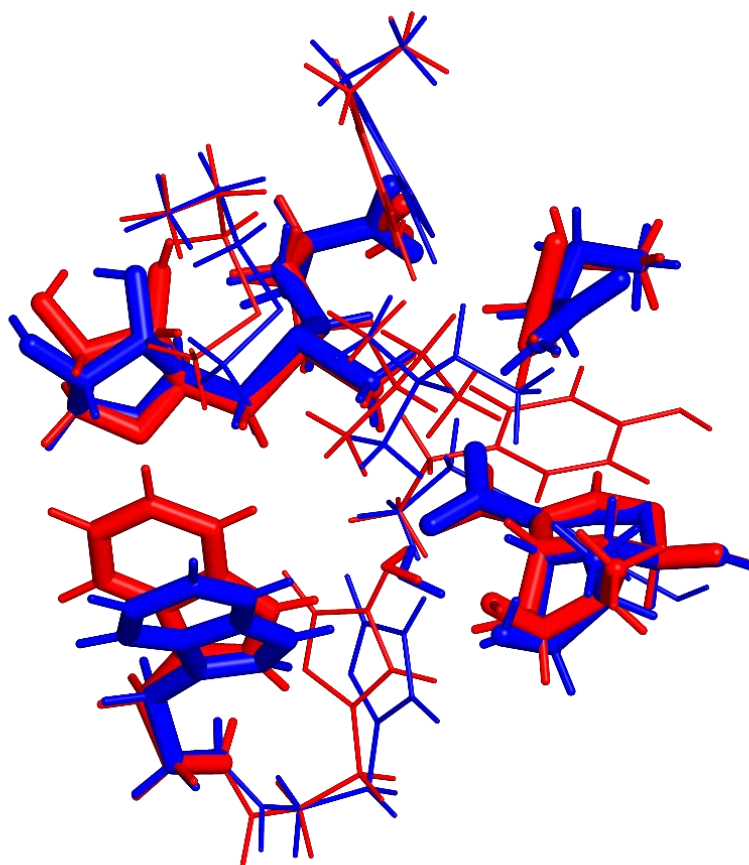


Figure S5. The initial structure from the optimization for Model 1 (in blue) superimposed on the structure of the found energy minimum (in red).

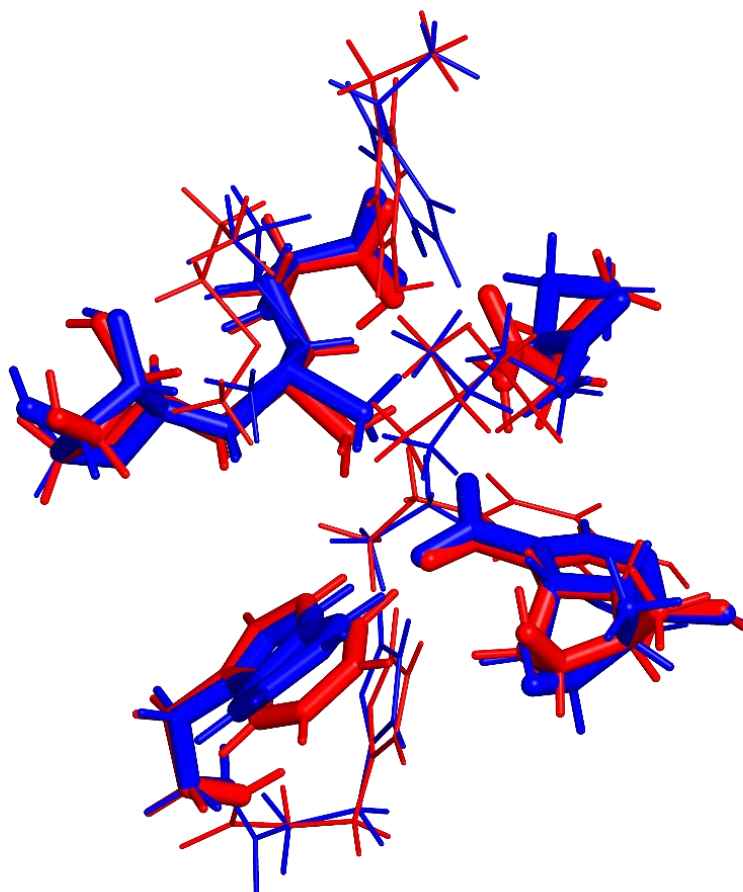


Figure S6. The initial structure from the optimization for Model 2 (in blue) superimposed on the structure of the found energy minimum (in red).

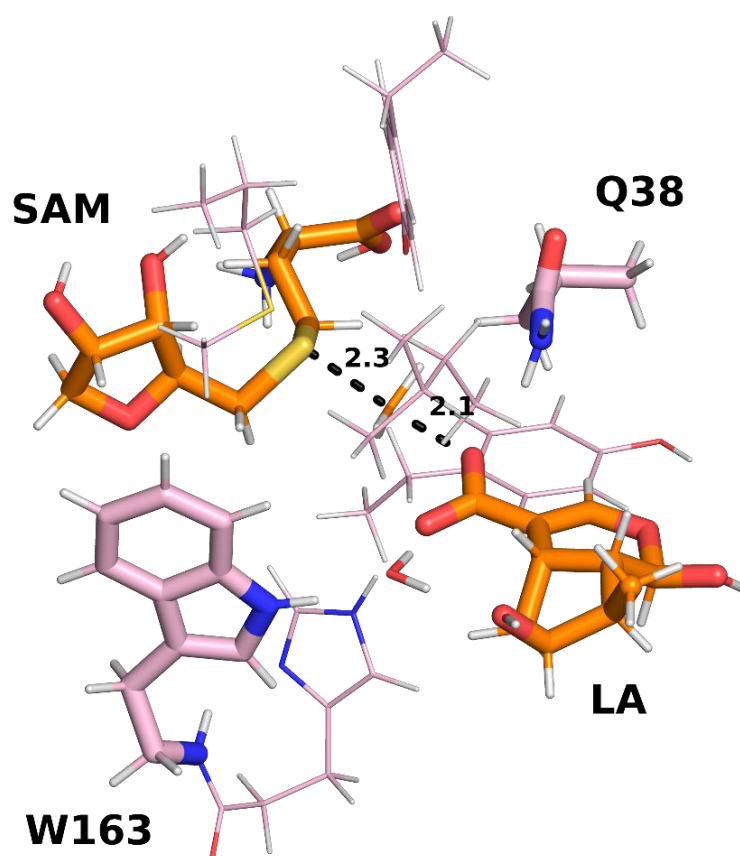


Figure S7. Optimized transition state structure for Model 1.



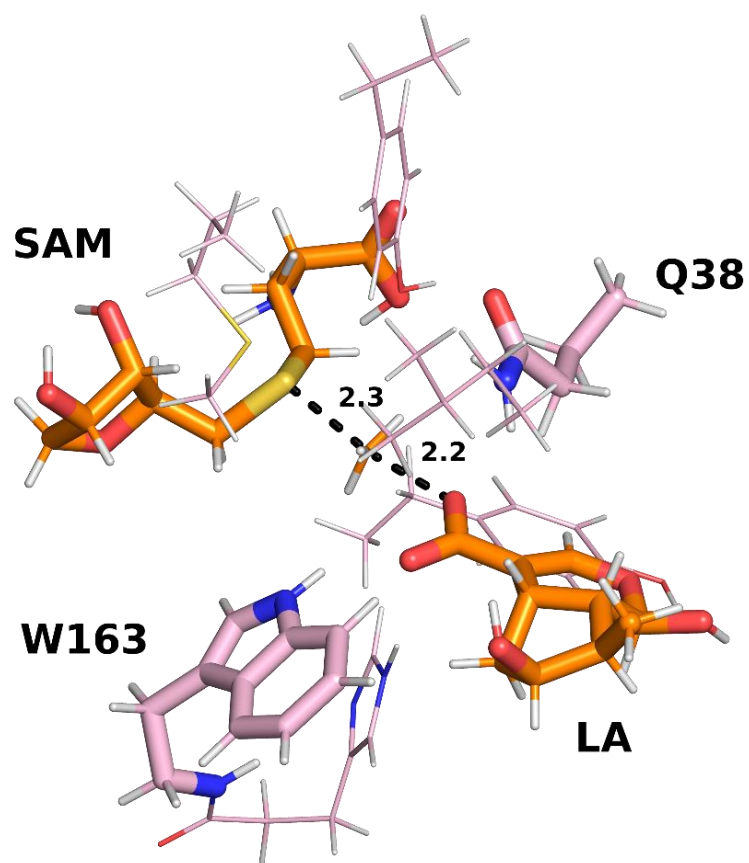


Figure S8. Optimized transition state structure for Model 2.