Supporting Information

Discovery of monoacylglycerol lipase (MAGL) inhibitors based on a pharmacophore-guided virtual screening study

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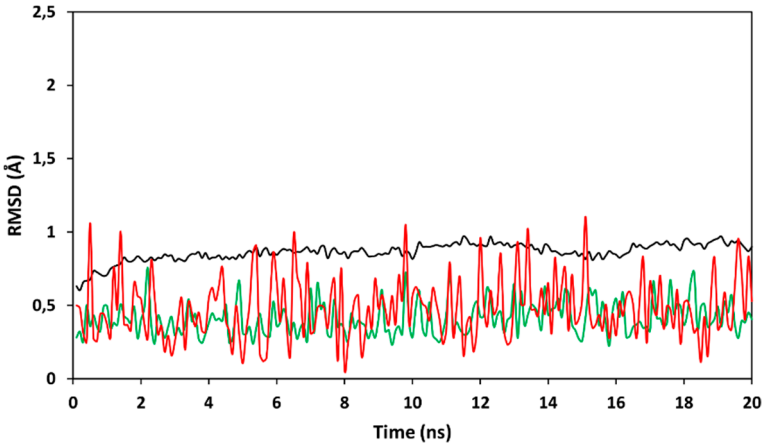

Figure S1. MD simulation analysis of the reference MAGL-inhibitor X-ray-complex (PDB code 5ZUN). The RMSD of the ligand during the 20 ns of simulation, with respect to the crystallographic coordinates, is shown in red, confirming the stability of the ligand binding mode (average RMSD = 0.4 Å). The RMSD of the structural water molecule during the MD is shown in green: the low RMSD fluctuation and the small average RMSD value (0.5 Å) indicate a strong stability of the water disposition and thus its importance for the ligand binding mode. Finally, the RMSD of the receptor heavy atoms during the MD is shown in black, indicating a high conformation stability (average RMSD = 0.9 Å) and thus confirming the reliability of the MD protocol.

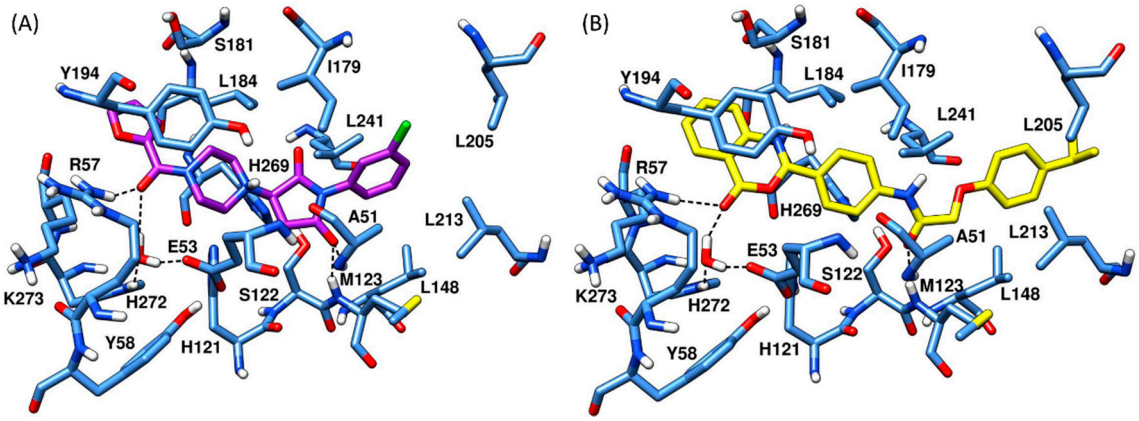

Figure S2. Minimized average structure of compounds **VS3** (A) and **VS4** (B) within MAGL binding site.