SUPPORTING INFORMATION

Title: Molecular Determinants of Topoisomerase I Poisoning by Lamellarins: Comparison with Camptothecin and Structure-Activity Relationships

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Figure S1. Time evolution of the root-mean-square deviations (rmsd) of heavy atoms of Top1-DNA-CPT complex (red) and Top1-DNA-LAMD complexes (TG in black and CG in green), with respect to the initial structure (thick) and the calculated average structure (thin). Each line is made up of 700 individual points from the MD trajectory.

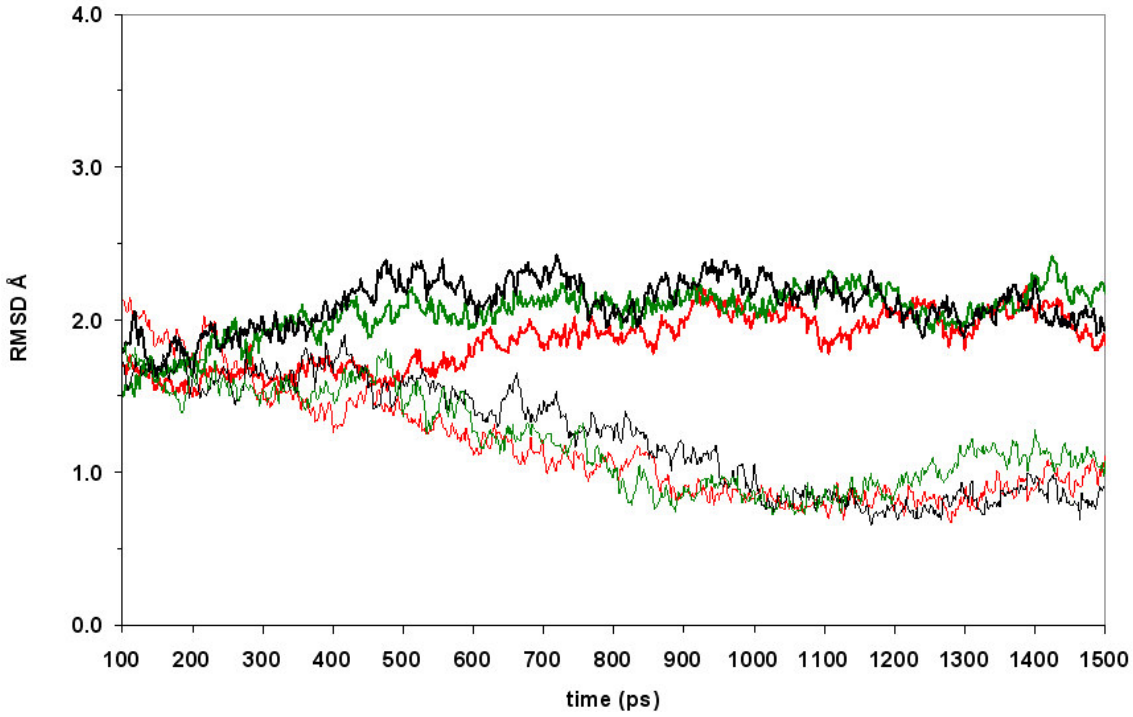

Figure S2. Time evolution of the distance (Å) between the ring B nitrogen (N1) of CPT and NH1 of Arg364 as measured in 700 consecutive snapshots taken every 2 ps from the last 1.4 ns of the molecular dynamics simulation. The red lines represent the lower and upper limits for hydrogen bonding distances (2.8–3.2 Å).

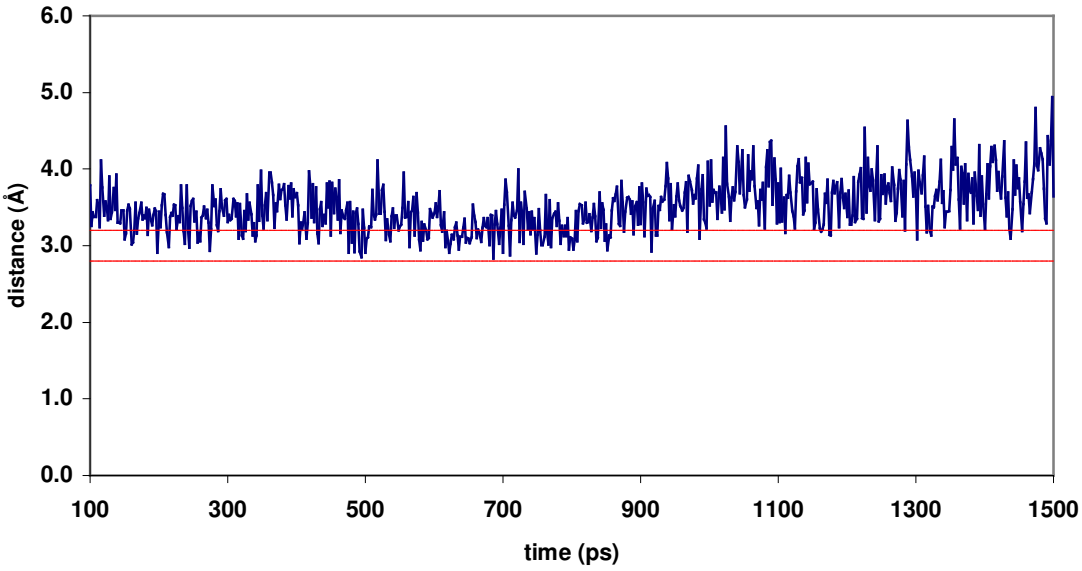

Figure S3. Molecular electrostatic potential (MEP) calculated for the open form of CPT and represented as two semitransparent contours surrounding a stick model of the molecule. Negative (–0.2 to –4.84 kcal mol^{-1}) and positive MEP regions (0.05 to 1.27 kcal mol^{-1}) are colored in pink and cyan, respectively.