Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

Molecular dynamics of dibenz[a,h]anthracene and its metabolite interacting with lung surfactant phospholipid bilayers

(Supporting information material)

Helmut I. Padilla-Chavarria, Teobaldo R. C. Guizado, and Andre S. Pimentel*

Departamento de Química, Pontifícia Universidade Católica do Rio de Janeiro, Rua Marques de São Vicente, 225, Gávea, CP 38097, 22451-900, Rio de Janeiro, RJ, Brazil

*Corresponding author: a_pimentel@puc-rio.br

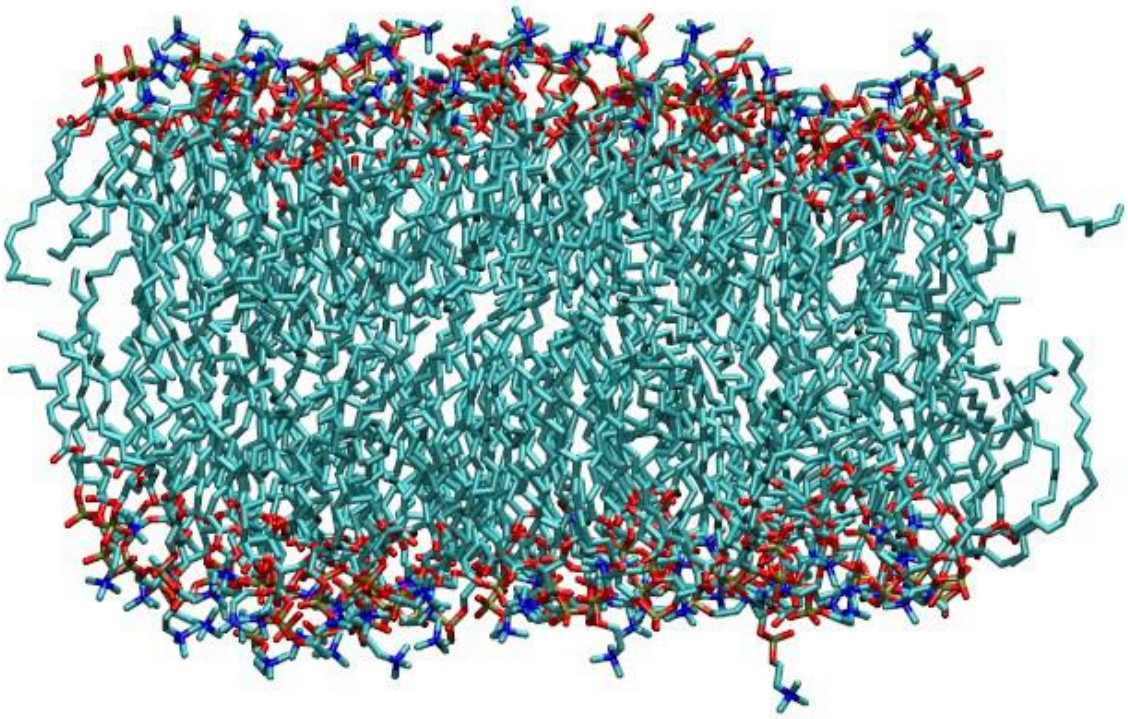

Figure 1S. The representation of the DPPC model (reference system). Light blue represents the hydrocarbon chain. The phosphate groups are shown in red and yellow. Dark blue represents the choline group.

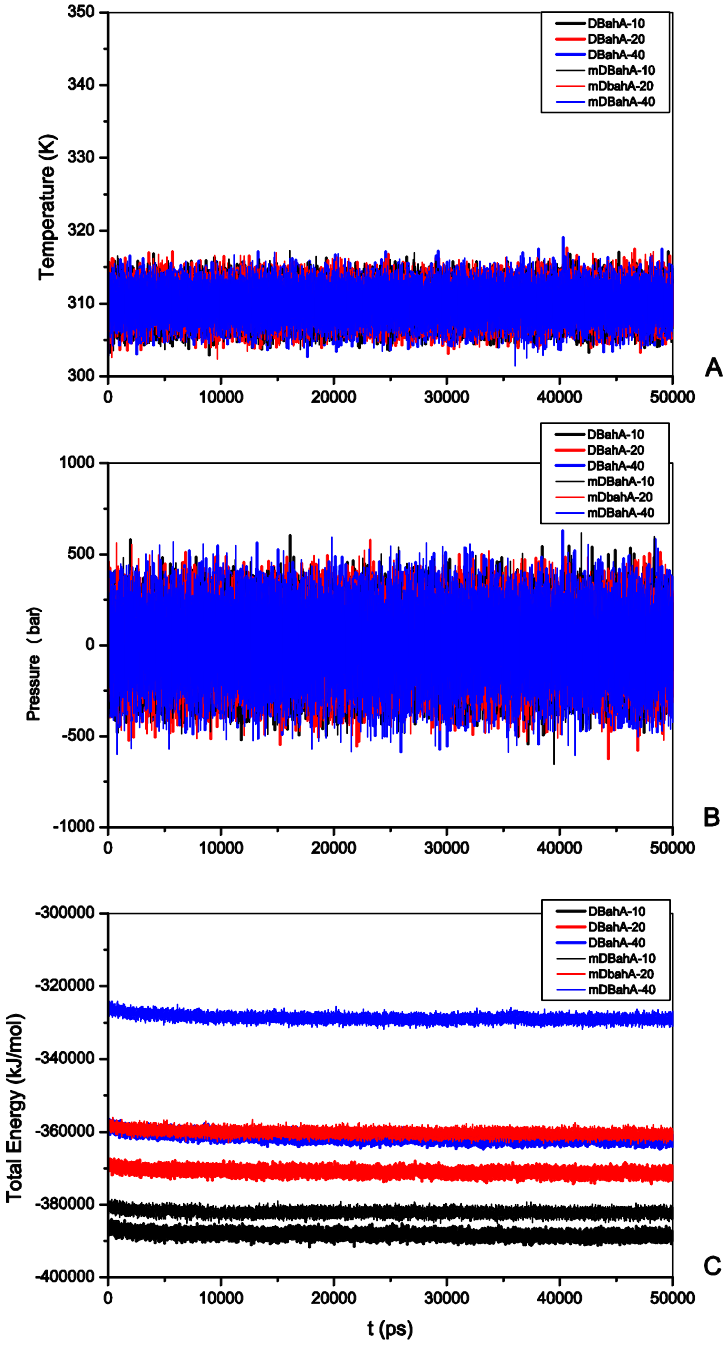

Figure 2S. The temperature (A), pressure (B), and total energy (C) during the simulations for the DPPC model with 10, 20, and 40 molecules of DBahA or mDBahA.

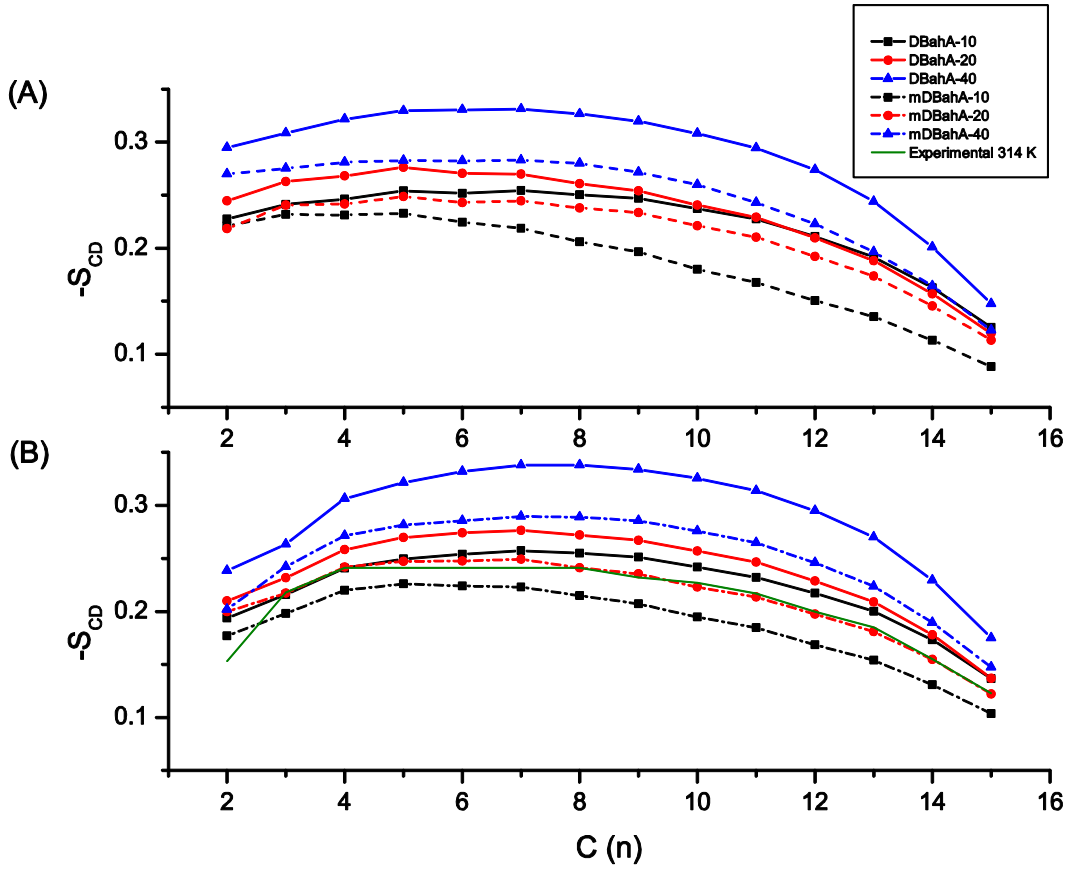

Figure 3S. The order parameter $-S_{CD}$ for the hydrocarbon chain of mixed DBahA-DPPC and mDBahA-DPPC bilayers at 310 K as a function of the carbon atom index. $-S_{CD}$ sn-1 (A) and $-S_{CD}$ sn-2 (B) stands for hydrocarbon chains 1 and 2, respectively. The experimental order parameter for pure DPPC at 314 K is given as reference in the green line. (Ref. 63).

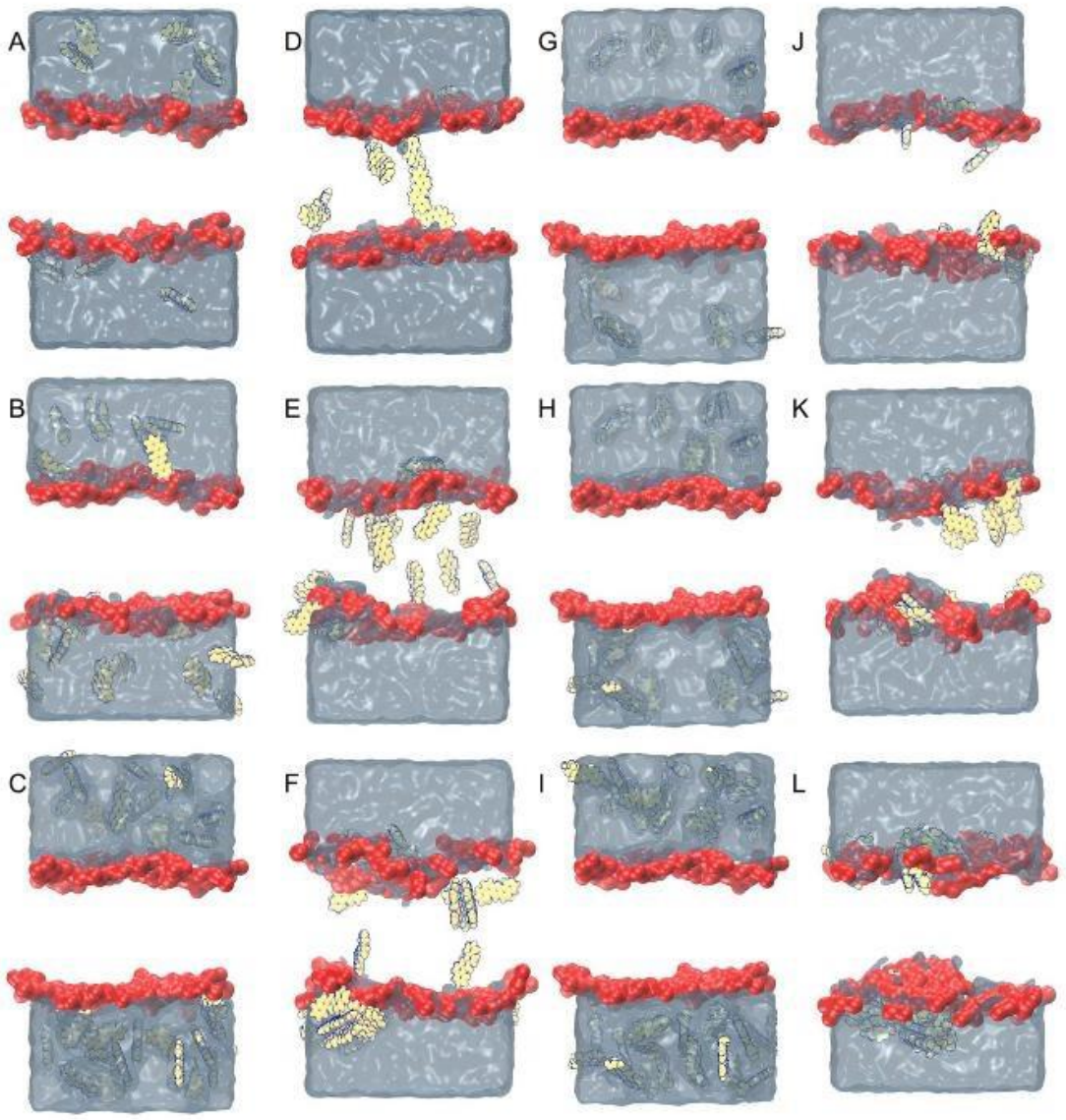

Figure 4S. Snapshots of DBahA/DPPC system: (A), (B), (C) are 10, 20, and 40 molecules of DBahA at the starting position, respectively, and (D), (E) e (F) are 10, 20, and 40 molecules of DBahA at 200 ns, respectively. Snapshots of mDBahA/DPPC system: (G), (H), (I) are 10, 20, and 40 molecules of mDBahA at the starting position, respectively, and (J), (K) e (L) are 10, 20, and 40 molecules of DBahA at 200 ns, respectively. For better clarity the gray region is filled by water molecules, the red balls are N and P atoms, and the atoms of DBahA and mDBahA molecules are yellow balls. The DPPC molecules were omitted for better clarity.

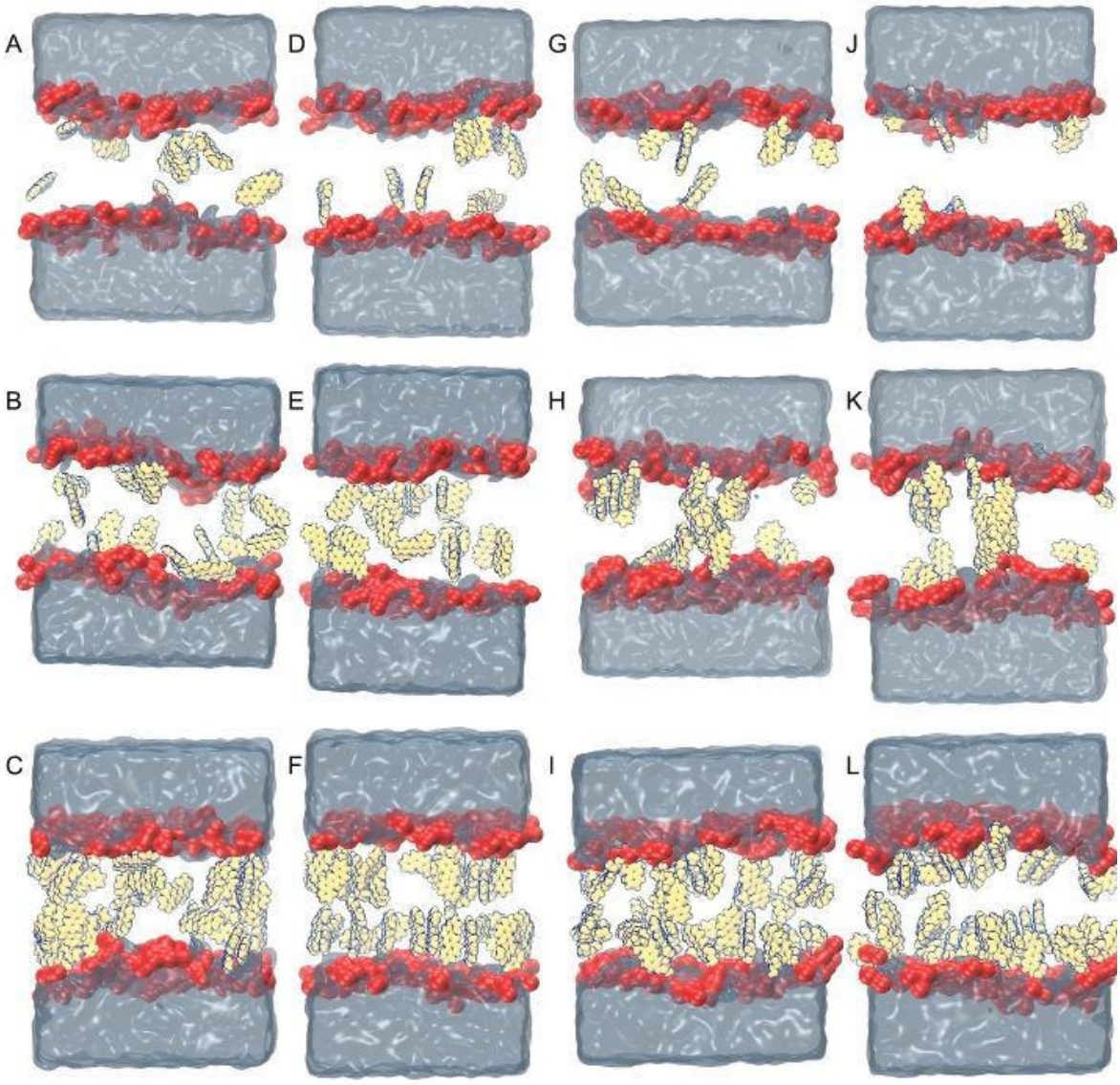

Figure 5S. Snapshots of DBahA/DPPC system: (A), (B), (C) are 10, 20, and 40 molecules of DBahA at the starting position, respectively, and (D), (E) e (F) are 10, 20, and 40 molecules of DBahA at 50 ns, respectively. Snapshots of mDBahA/DPPC system. (G), (H), (I) are 10, 20, and 40 molecules of mDBahA at the starting position, respectively, and (J), (K) e (L) are 10, 20, and 40 molecules of DBahA at 50 ns, respectively. For better clarity the gray region is filled by water molecules, the red balls are N and P atoms, and the atoms of DBahA and mDBahA molecules are yellow balls. The DPPC molecules were omitted for better clarity.

Figure 5S presents the snap shots in 0 and 50 ns for the DPPC model with DBahA and mDBahA starting in the lipid phase. The snap shots A, B, and C are the starting positions (0 ns) for 10, 20, and 40 molecules of DBahA, respectively, in the lipid phase. The DBahA molecules translate and achieve the final snap shots D, E, and F representing the configurations for 10, 20, and 40 molecules of DBahA, respectively. As it is observed, there is no transfer to the water phase within 50 ns. Also, the DBahA molecules prefer to be located in the interior of the phospholipid bilayer as presented previously in the trajectories. The snap shots G, H, and I are the starting configurations (0 ns) for 10, 20, and 40 molecules of mDBahA, respectively, in the water phase. On the other hand, the mDBahA molecules prefer to be located in the region of the polar head in 50 ns as presented in the snap shots J, K, and L.

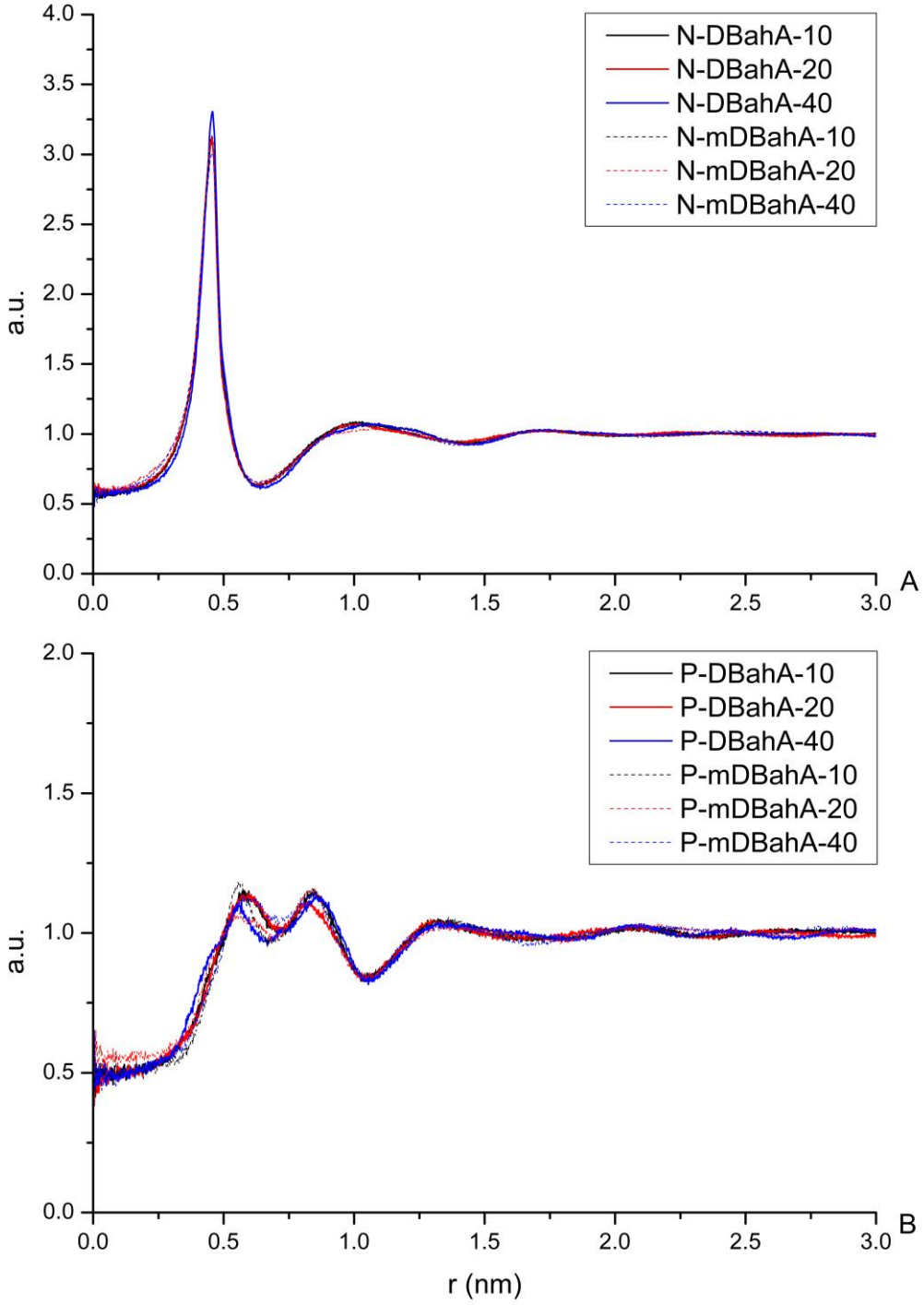

Figure 6S. (A) The radial distribution function between the atoms N and P in the polar heads of the DPPC molecules for the system of 10, 20, and 40 molecules of DBahA (or mDBahA) interacting with the pure DPPC bilayer. (B) The radial distribution function between two P atoms in the polar heads of the DPPC in the same system.

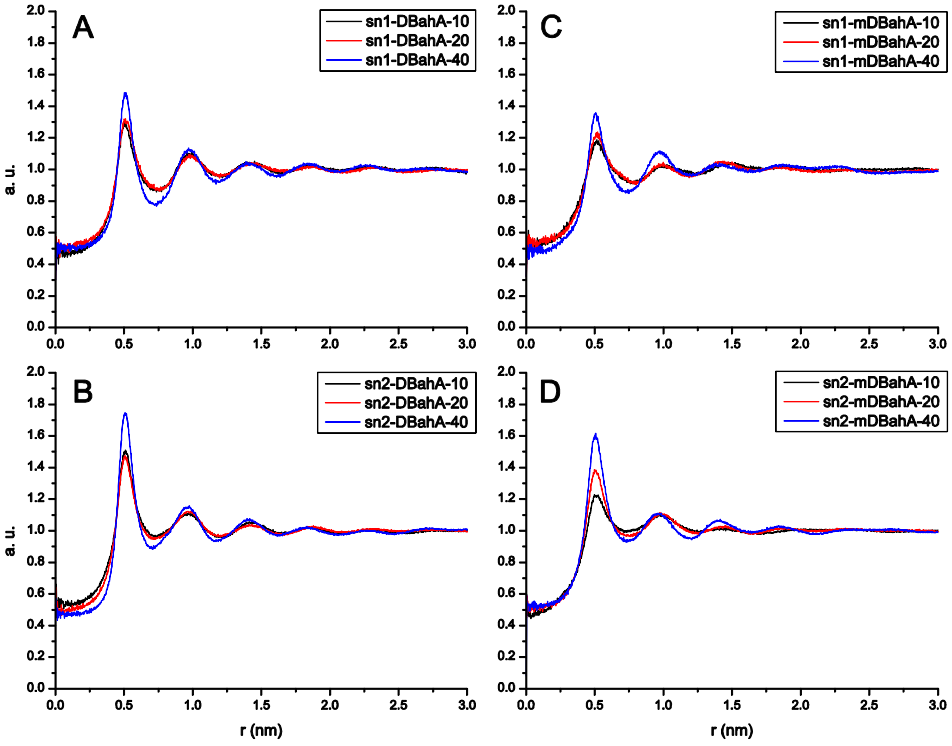

Figure 7S. The radial distribution function between the two centers of mass of the hydrocarbon chains sn-1 (A and C) and sn-2 (B and D) for the systems with 10, 20, and 40 molecules of DBahA (A and B) and mDBahA (C and D) distributed randomly inside the DPPC bilayer.

The RDF between the two centers of mass of the hydrocarbon chains sn-1 and sn-2 for the systems with 10, 20, and 40 molecules of DBahA and mDBahA distributed randomly inside the DPPC bilayer are presented in the Figure 7S. It is observed that the peak intensity increases as the number of DBahA and mDBahA molecules is raised, which means a greater ordering, lesser fluidity, and consequently, less freedom of motion of the hydrocarbon chain. This ordering is greater in the systems with DBahA compared with those ones with mDBahA because DBahA is located near to (or between) the hydrocarbon chains. Thus, DBahA interacts more with the hydrocarbon chains, decreasing the freedom of them.

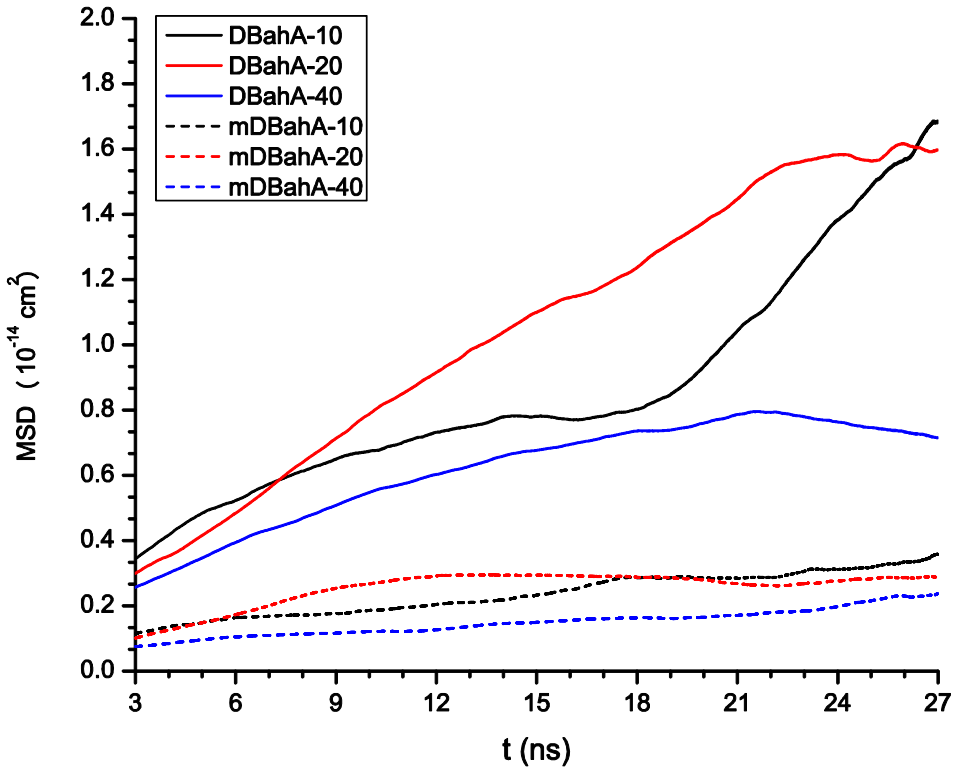

Figure 8S. The mean square displacement of the center of mass for DBahA and mDBahA under the plane xy of the DPPC bilayer with 10, 20, and 40 molecules of DBahA or mDBahA.

It is important to emphasize here that these diffusion coefficients calculated from Figures 8S and 9S are estimated from fits of non-straight lines, and consequently, have large errors because of the random movement of aggregates inside the water and lipid phases. For example, the MSD for 10 molecules of DBahA (black solid line in Figure 9S) shows different slopes at different times. Thus, these MSDs are not meaningful, just indicating a rough estimate for the diffusion process. It seems that these MSDs are not equilibrated yet, and if so, one cannot calculate diffusion coefficients from them.

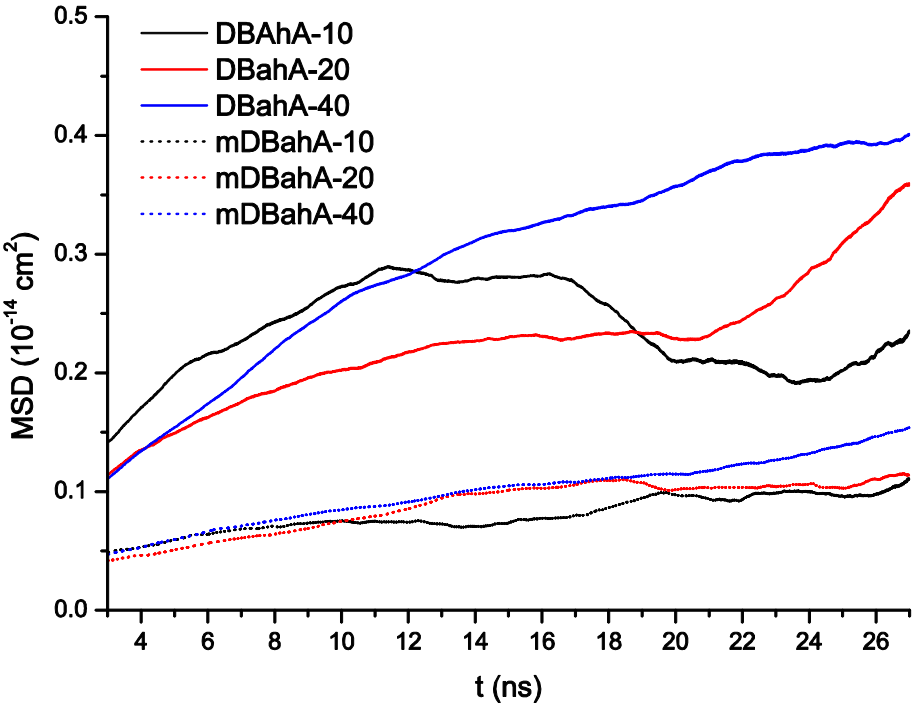

Figure 9S. The mean square displacement of the center of mass of DBahA and mDBahA in the z-axis of the DPPC bilayer with 10, 20, and 40 molecules of DBahA or mDBahA.

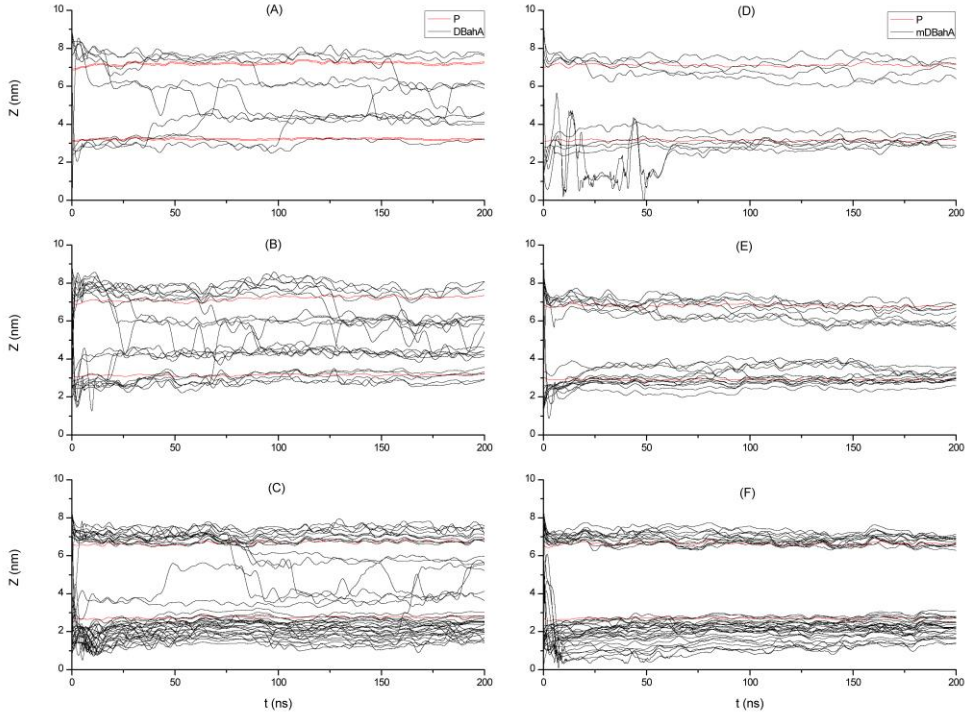

Figure 10S. Trajectories of 10 (A), 20 (B), and 40 (C) molecules of DBahA, and 10 (D), 20 (E), and 40 (F) molecules of mDBahA during 200 ns. The red lines are the center of mass of P atoms in the DPPC polar head, and the black lines are the center of mass of each DBahA and mDBahA molecules.

Figure 10S shows the trajectories of 10, 20, and 40 molecules of DBahA (or mDBahA) during 200 ns of simulation of the DPPC bilayer with these molecules starting in the water phase. It is important to observe that the DBahA molecules reside in the water/lipid interface for long times, >200 ns, and some of them are transferred to the lipid phase, crossing the region of the polar heads. On the other hand, mDBahA molecules prefer to interact with the polar heads due to its polar groups, so all of them reside much longer times (> 200 ns) in the water/lipid interface.

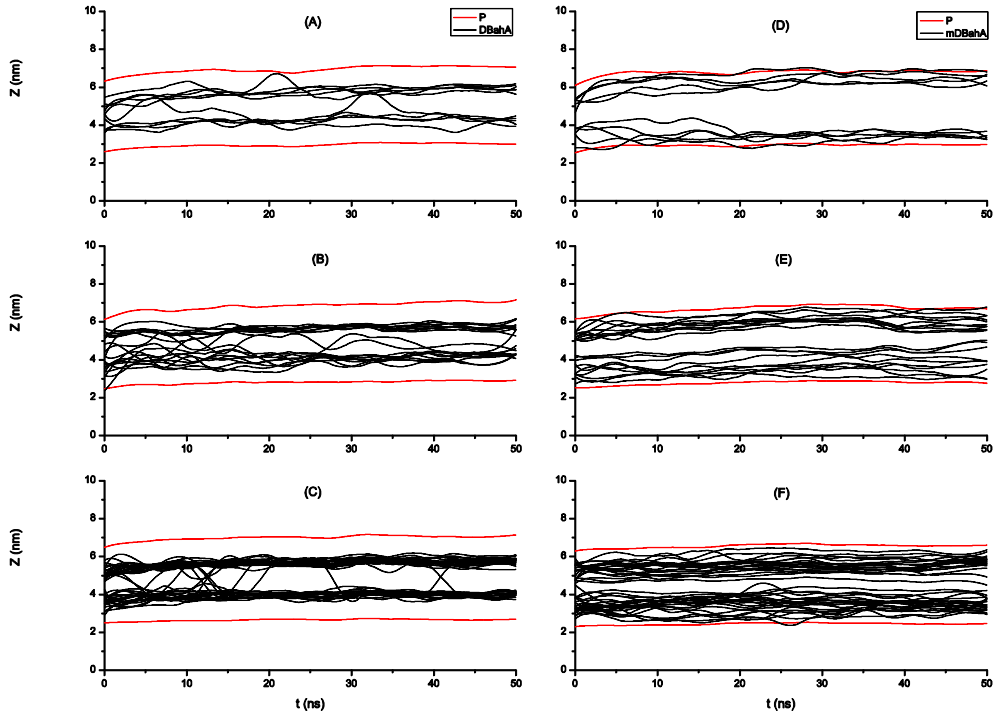

Figure 11S. Trajectories of 10 (A), 20 (B), and 40 (C) molecules of DBahA, and 10 (D), 20 (E), and 40 (F) molecules of mDBahA during 50 ns. The red lines are the center of mass of P atoms in the DPPC polar head, and the black lines are the center of mass of each DBahA and mDBahA molecules.