

Figure S1. Isotropic pressure coupling simulations ($t = 50$ ns, last 10ns have been used for density analysis). **(A)** DOPC lipids density at 1 bar with various molar concentrations of dissolved argon: 0%; 0,375%; 0,750% and 1.5%; **(B)** The dissolved argon at 1 bar with various molar concentrations: 0,375%, 0,750% and 1.5%; The liposome's center of mass located at $x = 0$ at the origin of the x axis. .

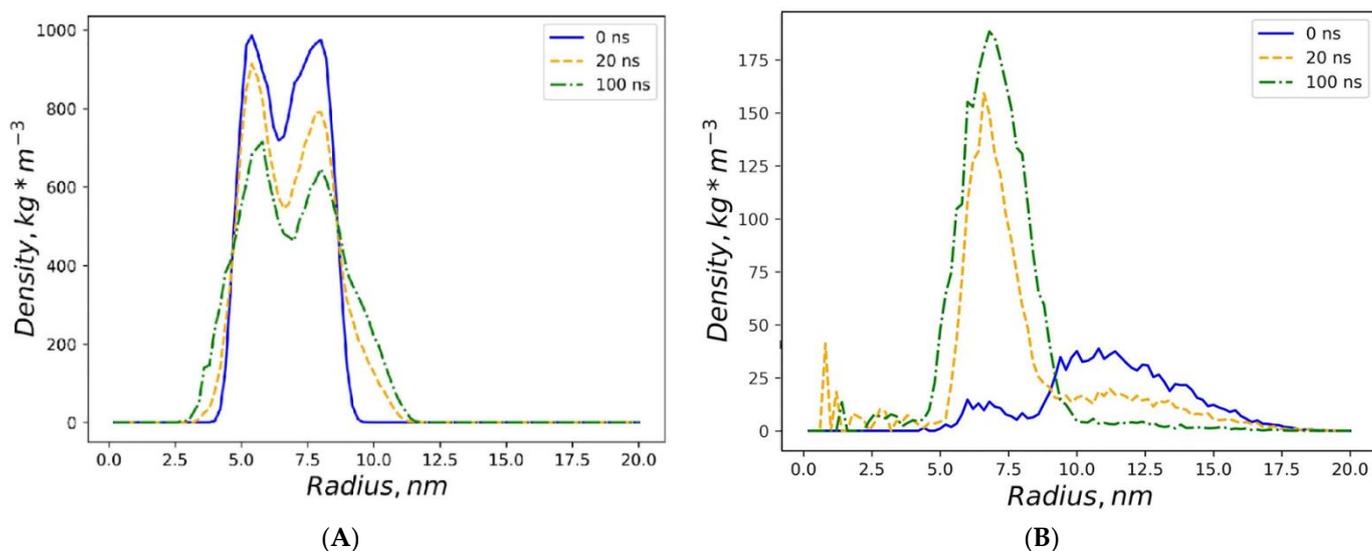


Figure S2. Isotropic pressure coupling simulations. **(A)** DOPC lipids density at 25 bar with 1.5% argon concentrations, MD frames: $t = 0, 20, 100$ ns; **(B)** The dissolved argon density at 25 bar with 1.5% concentrations, MD frames: $t = 0, 20, 100$ ns. The liposome's center of mass located at $x = 0$ at the origin of the x axis.

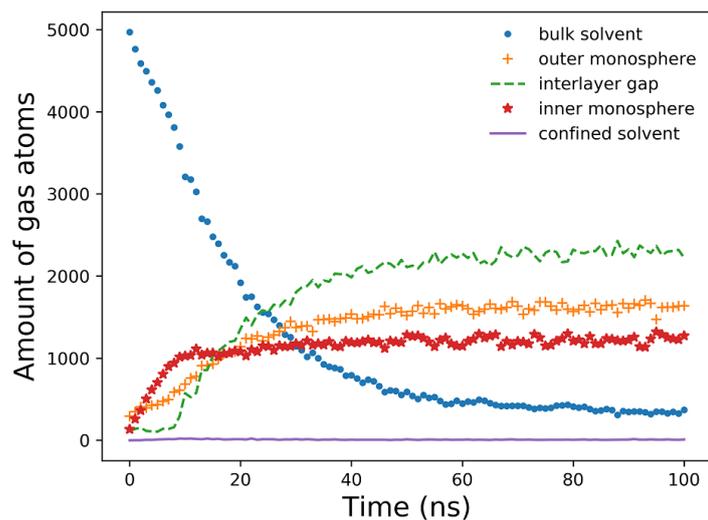


Figure S3. Isotropic pressure coupling simulation. Argon atoms counter is presented at 25 bar for 5 compartments of the simulation box vs. MD time (100 ns).

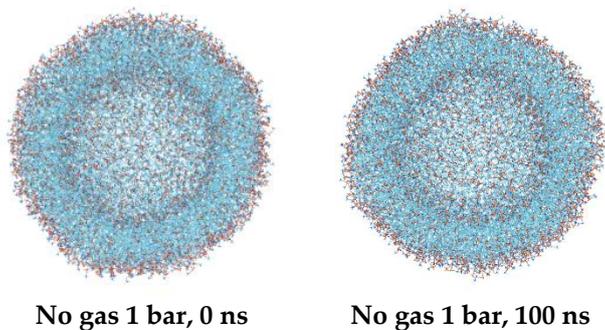


Figure S4. Semi-Isotropic Pressure coupling. Representative MD trajectory frames of DOPC liposome at 1bar; at $t=0, 100$ ns.

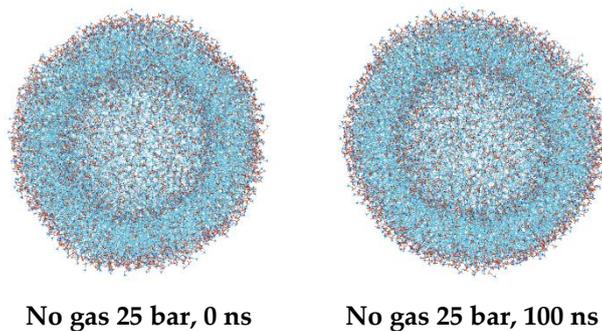


Figure S5. Semi-Isotropic Pressure Coupling. Representative MD trajectory frames of DOPC liposome at 25bar; at $t=0, 100$ ns.

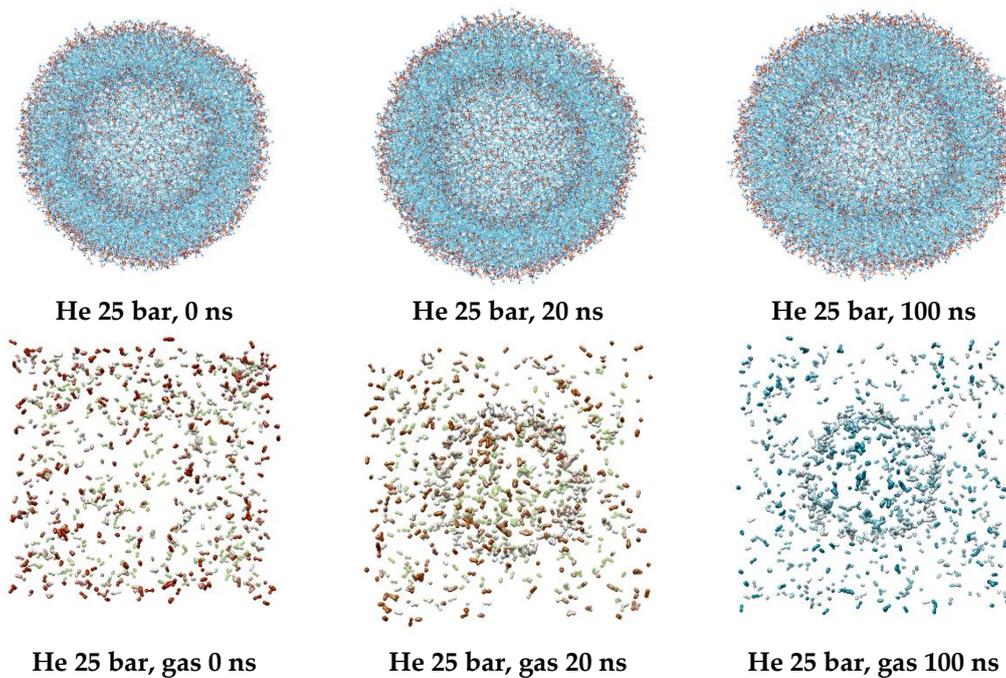


Figure S6. Semi-Isotropic Pressure Coupling. Representative MD trajectory frames of DOPC liposome and dissolved helium at 25bar; MD frames are shown at t= 0, 20, 100 ns.

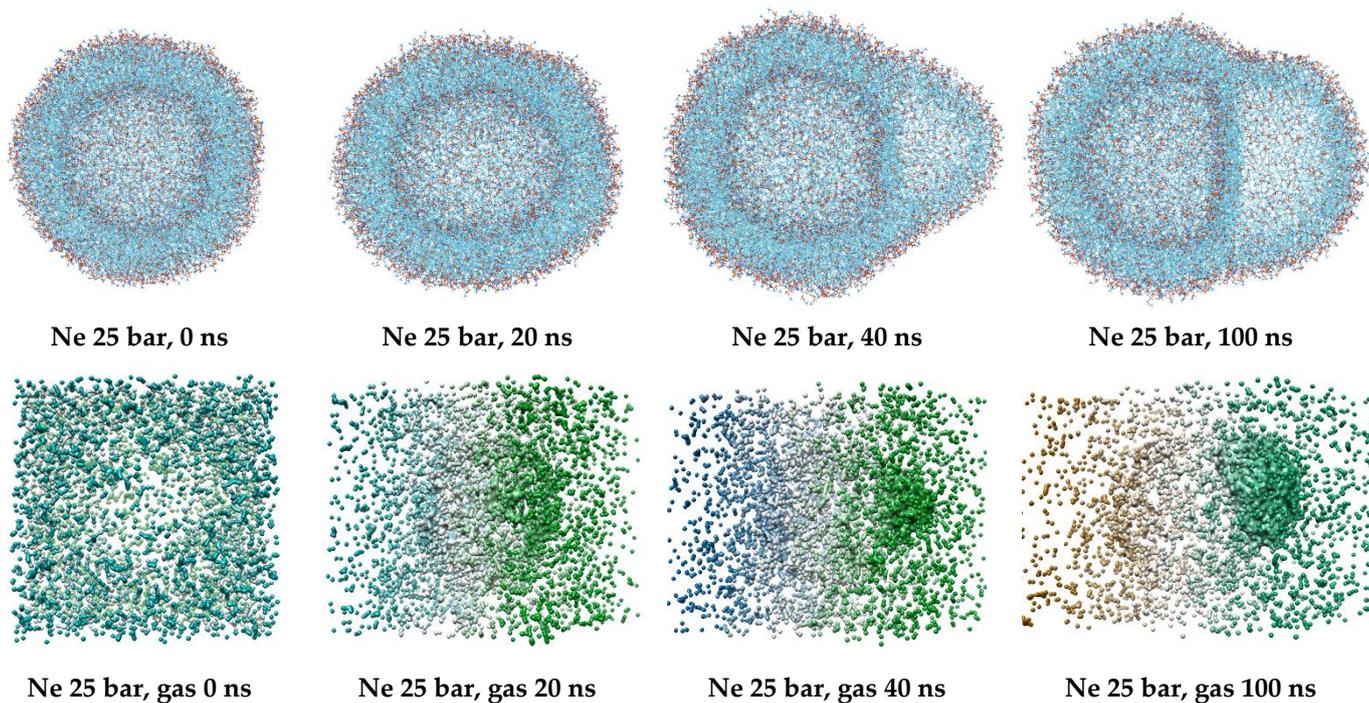


Figure S7. Semi-Isotropic Pressure Coupling. Representative MD trajectory frames of DOPC liposome and dissolved neon at 25bar; MD frames are shown at t = 0, 20, 40, 100 ns.

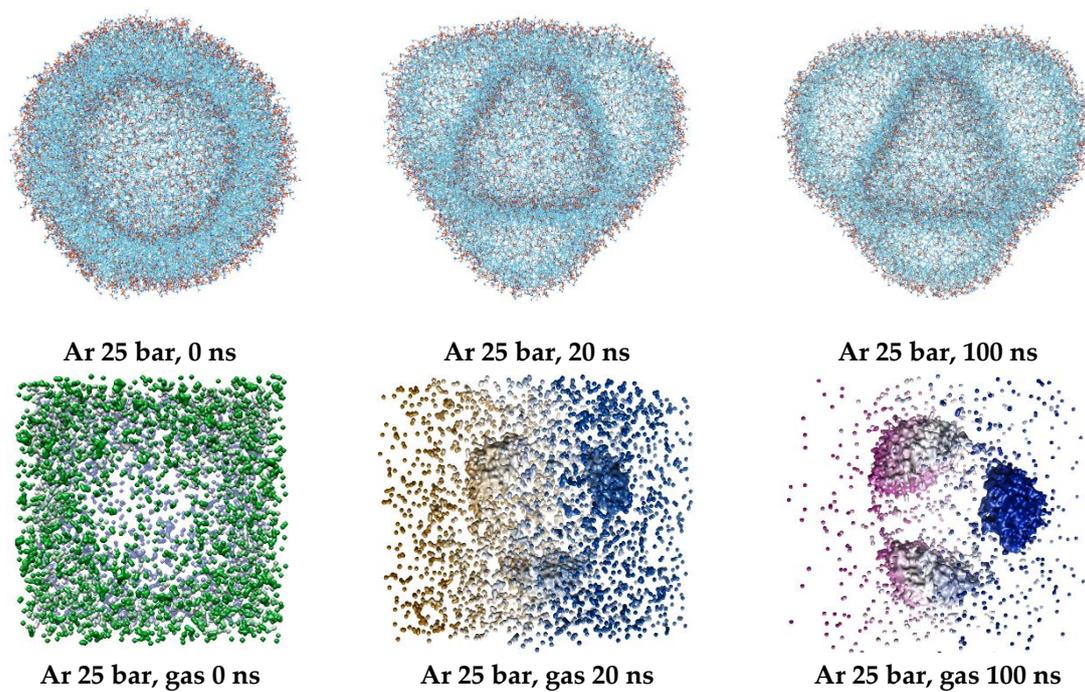


Figure S8. Semi-Isotropic Pressure Coupling. Representative MD trajectory frames of DOPC liposome and dissolved argon at 25bar; MD frames are shown at $t = 0, 20, 100$ ns.

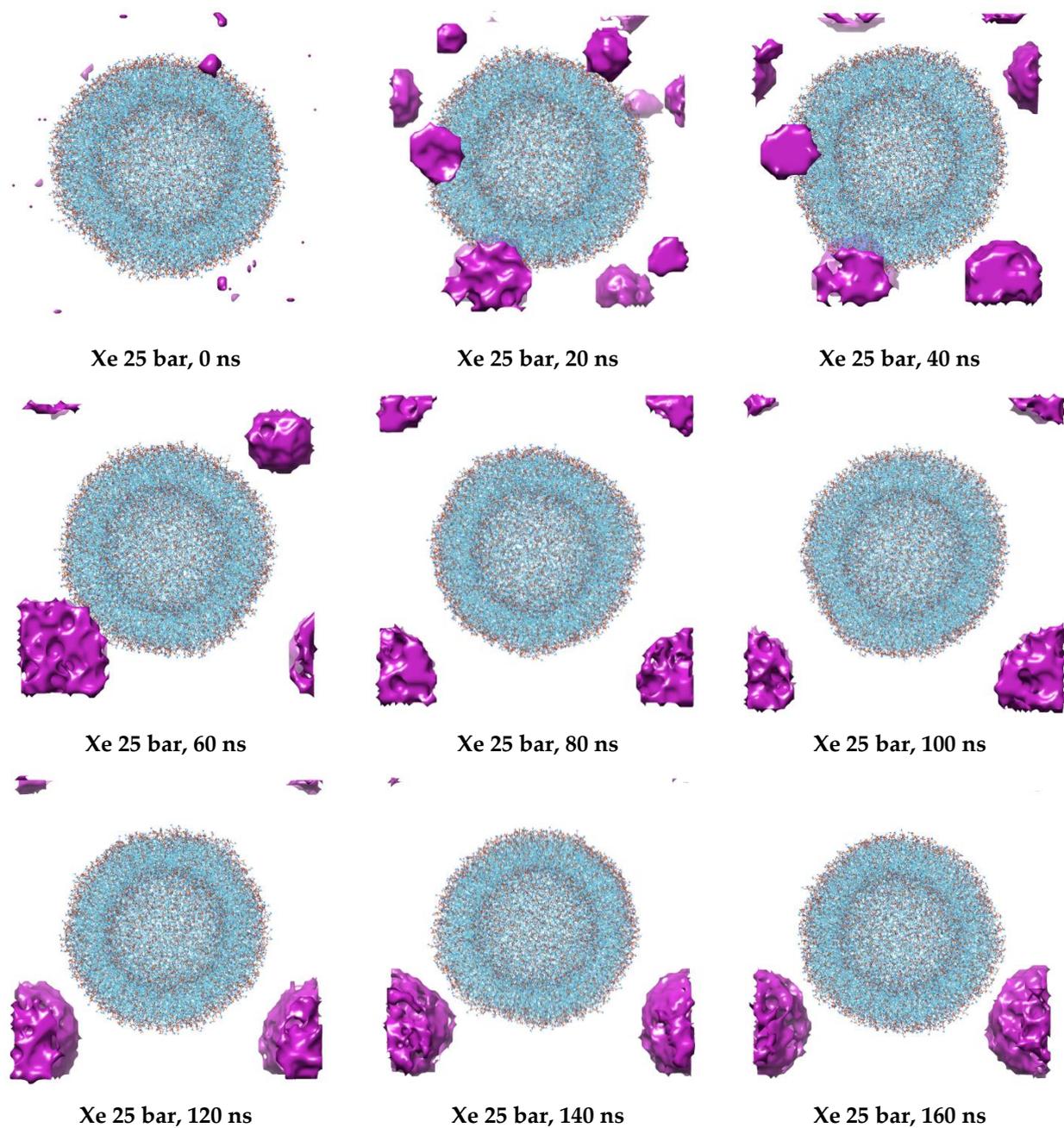


Figure S9. Semi-Isotropic Pressure Coupling. Representative MD trajectory frames of DOPC liposome and dissolved xenon at 25bar; MD frames are shown at $t = 0, 20, 40, 60, 80, 100, 120, 140, 160$ ns.