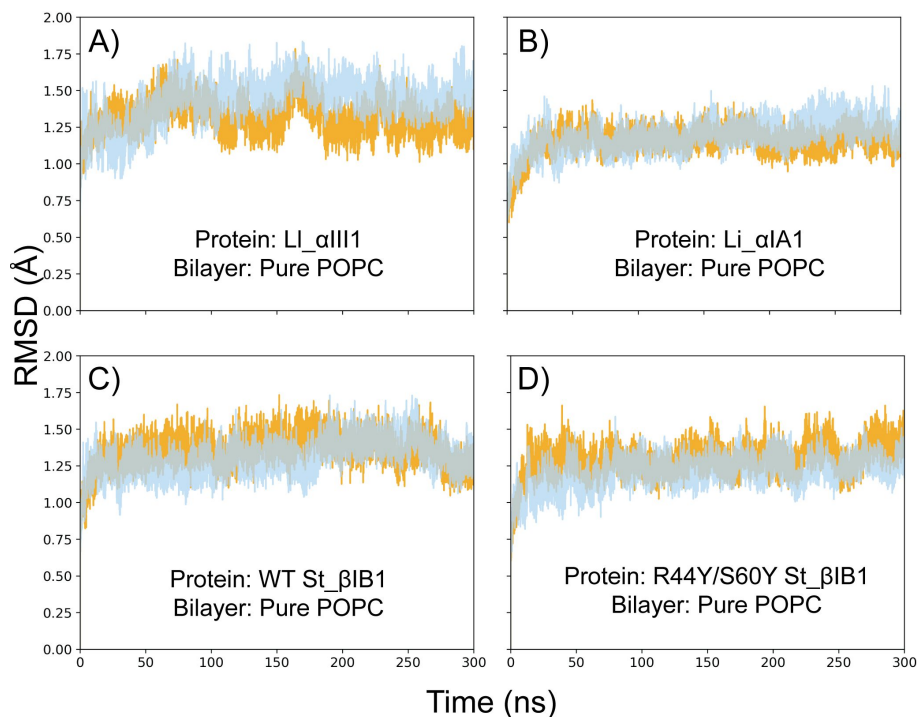
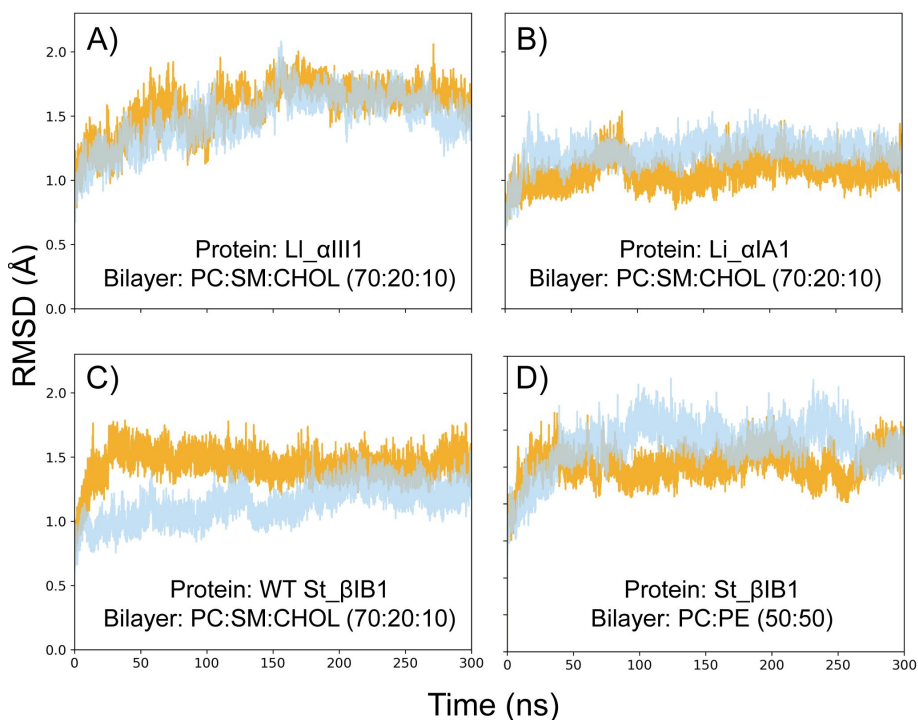


## Stability of the Molecular Dynamics simulations

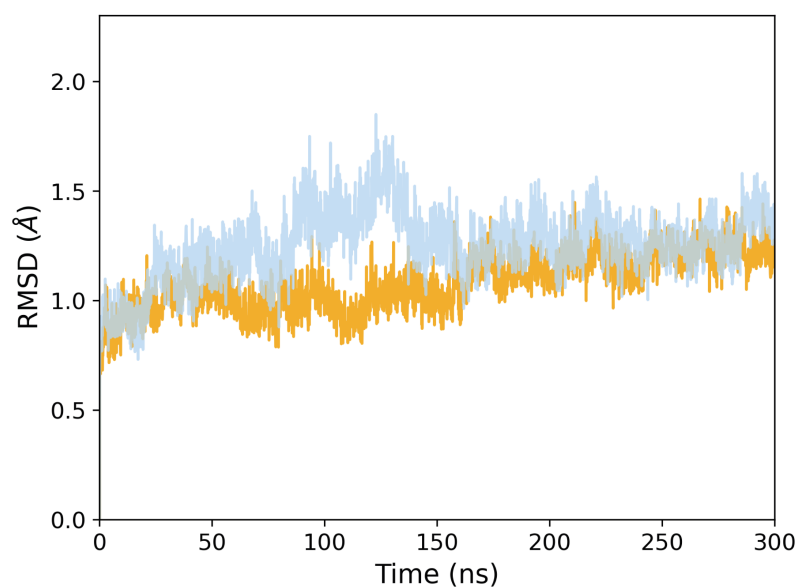
**Figure A.** Evolution of the protein backbone Root Mean Square Deviation (RMSD) during all simulations involving a pure POPC bilayer. Replica 1 is represented in orange and replica 2 in cyan.



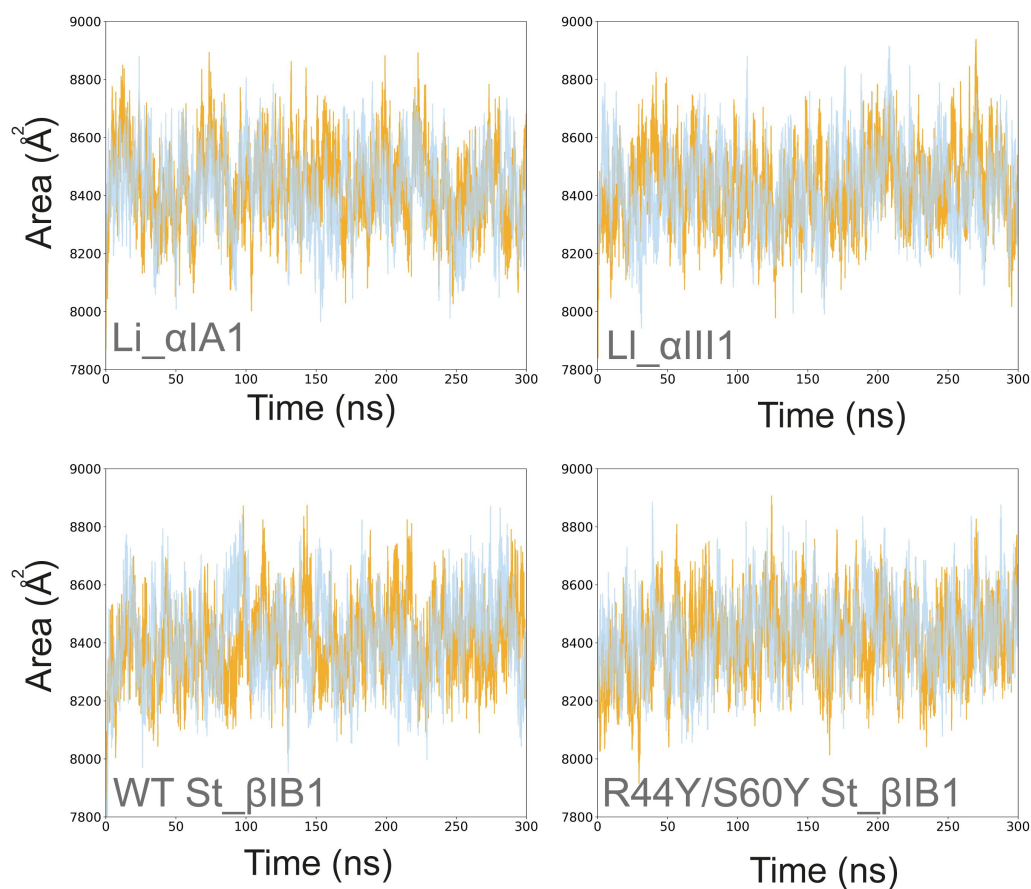
**Figure B.** Evolution of the protein backbone Root Mean Square Deviation (RMSD) during all simulations involving a PC:SM:CHOL (70:20:10) or a POPC:POPE (50:50). Replica 1 is represented in orange and replica 2 in cyan.



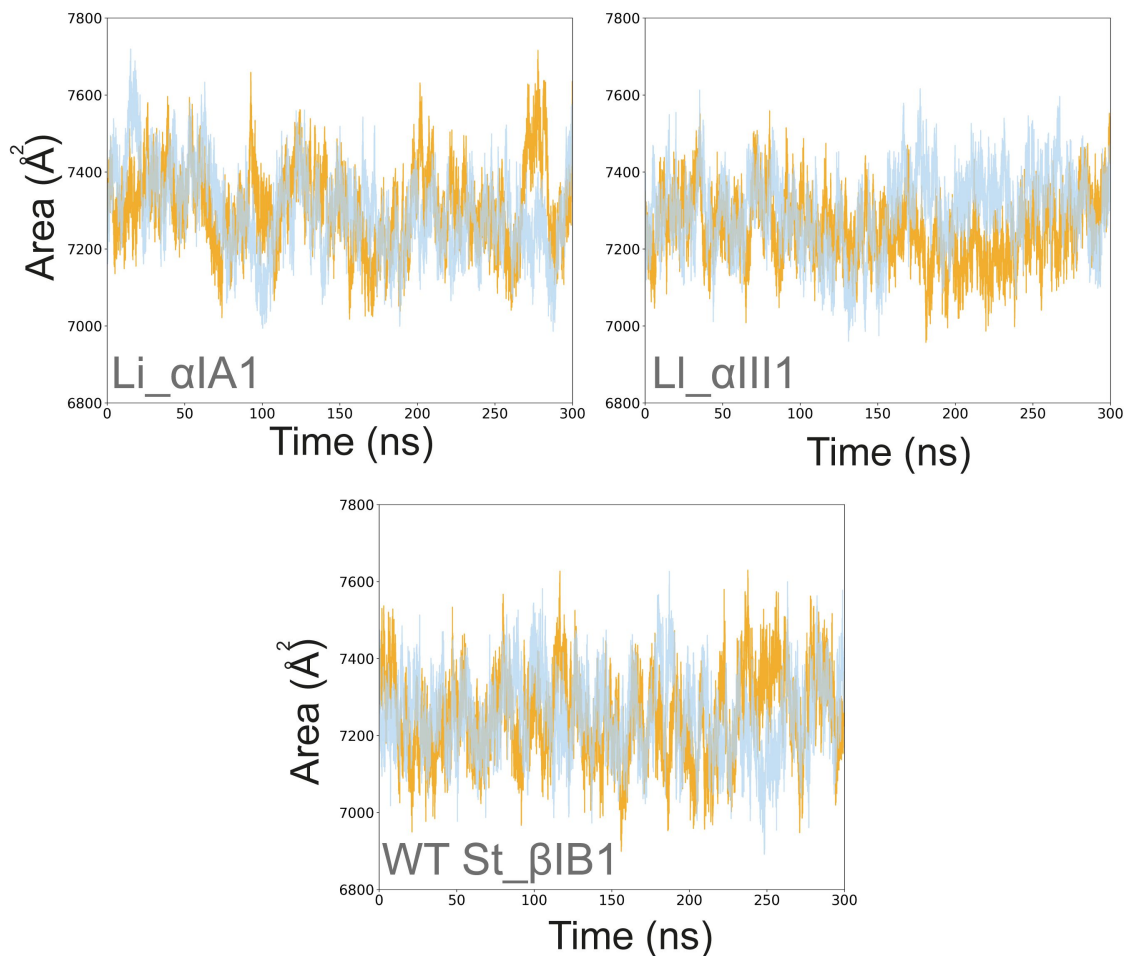
**Figure C. Evolution of the protein backbone Root Mean Square Deviation (RMSD) during the simulations of Li\_αIA1 on a POPC:POPE (50:50) bilayer.** Replica 1 is represented in orange and replica 2 in cyan.



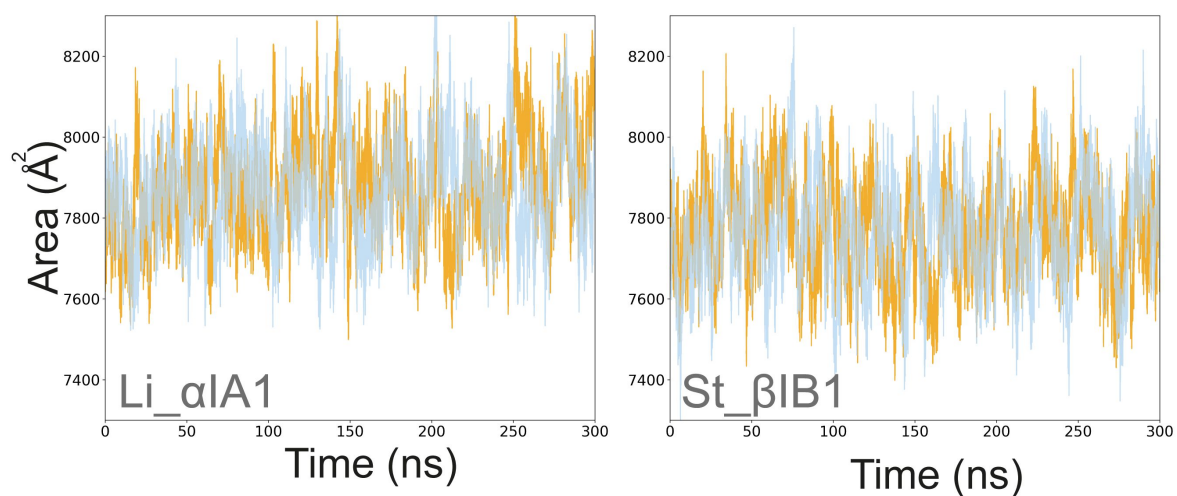
**Figure D. Simulations with POPC bilayers: simulation box area in the bilayer plane.** Replica 1 is represented in orange and replica 2 in cyan.



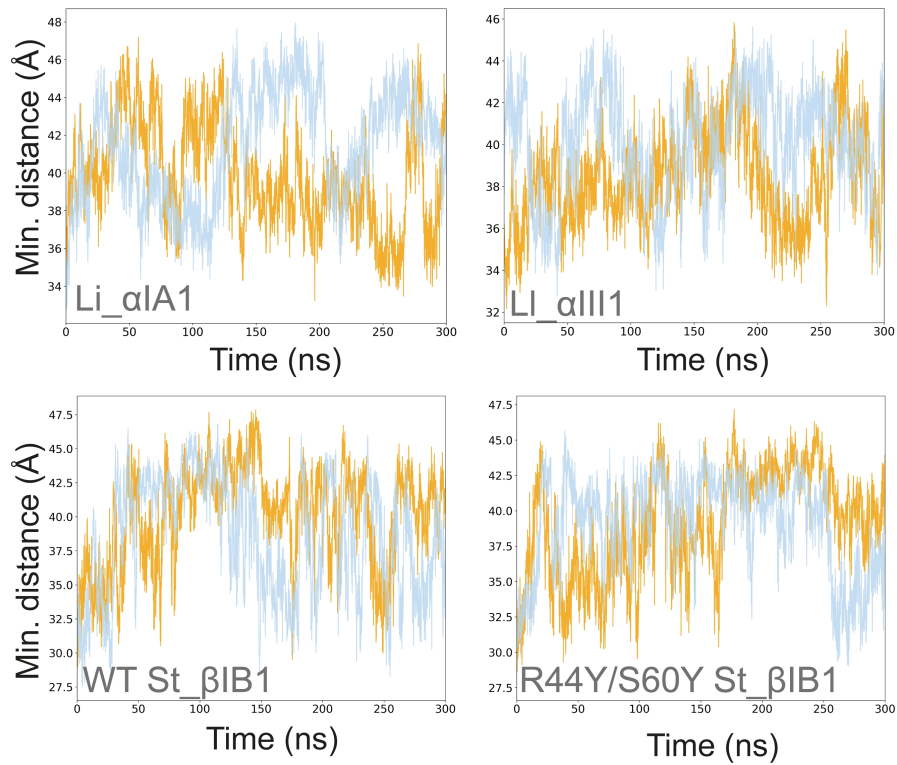
**Figure E. Simulations with PC:SM:CHOL (70:20:10) bilayers: simulation box area in the bilayer plane.** Replica 1 is represented in orange and replica 2 in cyan.



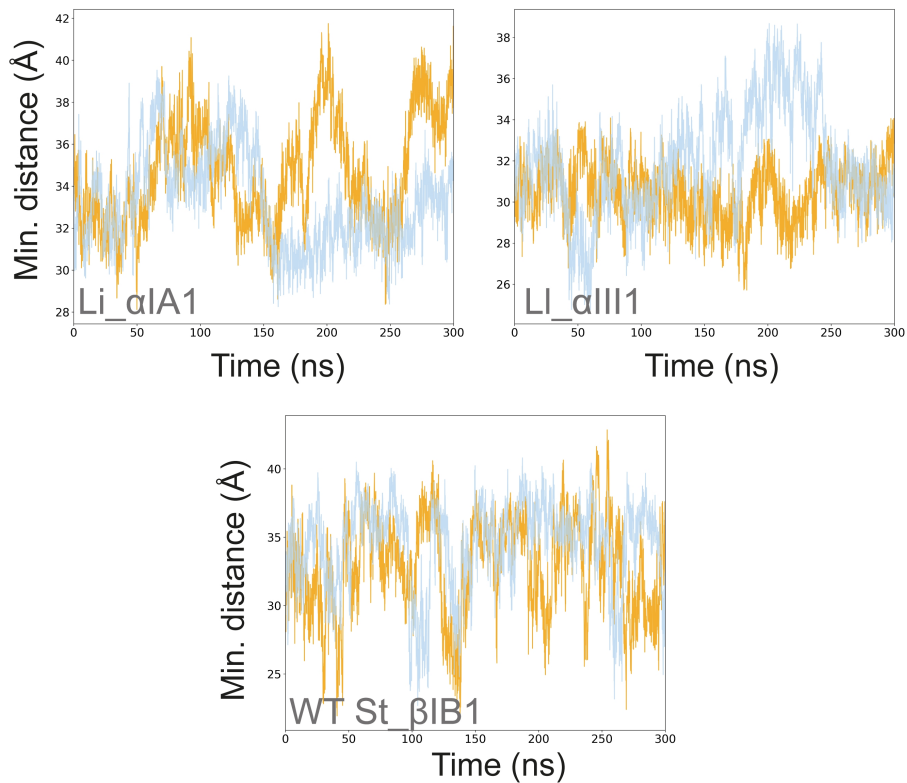
**Figure F. Simulations with POPC:POPE (50:50) bilayers: simulation box area in the bilayer plane.** Replica 1 is represented in orange and replica 2 in cyan.



**Figure G. Minimum distance between PLDs and their nearest image in simulations with POPC bilayers.** Replica 1 is represented in orange and replica 2 in cyan.



**Figure H. Minimum distance between PLDs and their nearest image in simulations with PC:SM:CHOL (70:20:10) bilayers.** Replica 1 is represented in orange and replica 2 in cyan.



**Figure I. Minimum distance between PLDs and their nearest image in simulations with PC:PE (50:50) bilayers.** Replica 1 is represented in orange and replica 2 in cyan.

