

# Electronic Supporting Information

## Effects of the Structure of Lipid-based Agents in their Complexation with a Single Stranded mRNA fragment: a Computational Study

Anastassia N. Rissanou<sup>a,b,\*</sup> and Kostas Karatasos<sup>a,\*</sup>

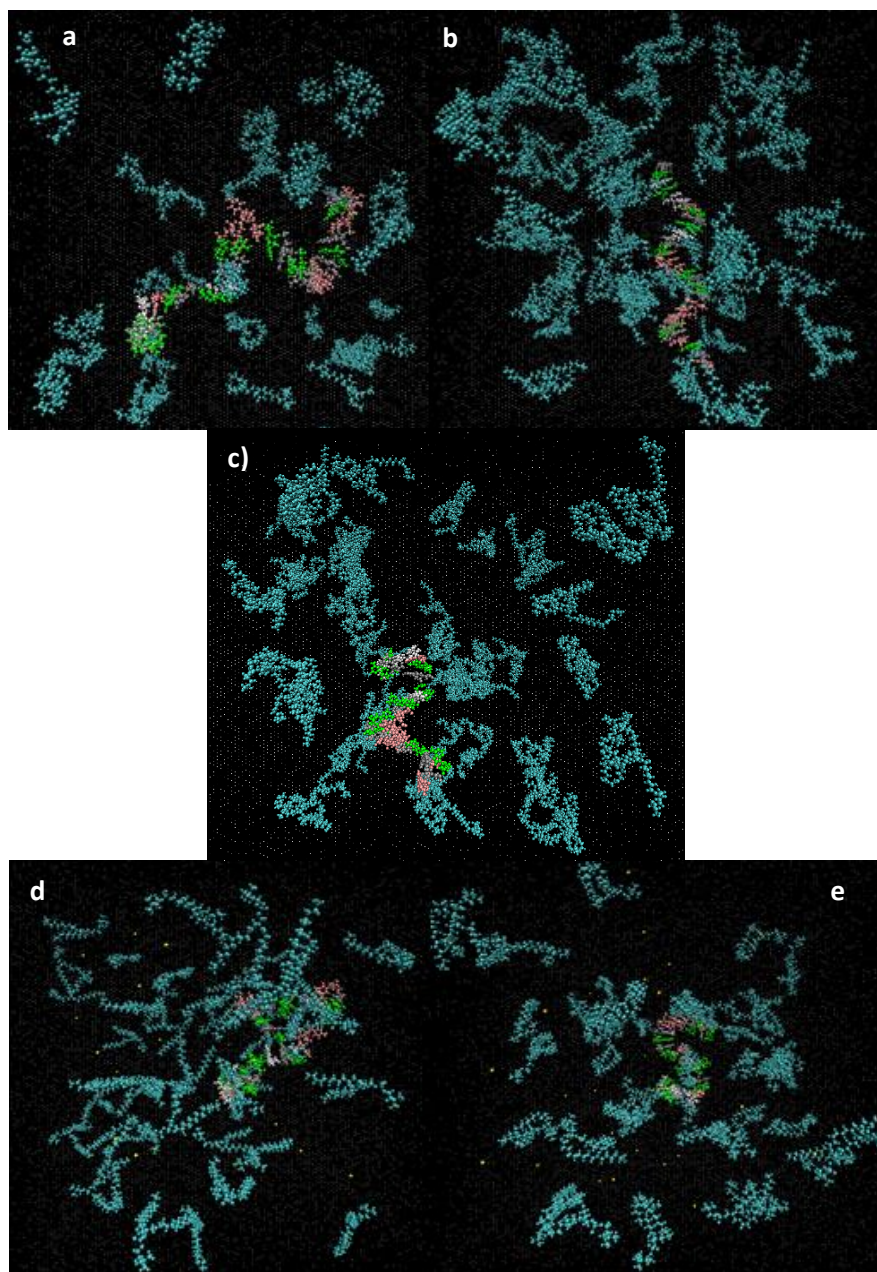
- a. Department of Chemical Engineering, University of Thessaloniki, P.O. BOX 420, 54124 Thessaloniki, Greece.
- b. Department of Mathematics and Applied Mathematics, University of Crete, GR-71409, Heraklion, Crete, Greece.

**Keywords:** RNA; cationic lipids; phospholipids; complexation; kinetics; Molecular Dynamics Simulations

---

\* Author to whom correspondence should be addressed:  
[risanou@uoc.gr](mailto:risanou@uoc.gr) +30 2810393746 fax: +30 2810393701  
[karatas@eng.auth.gr](mailto:karatas@eng.auth.gr) +30-2310995850 fax: +30-2310996222

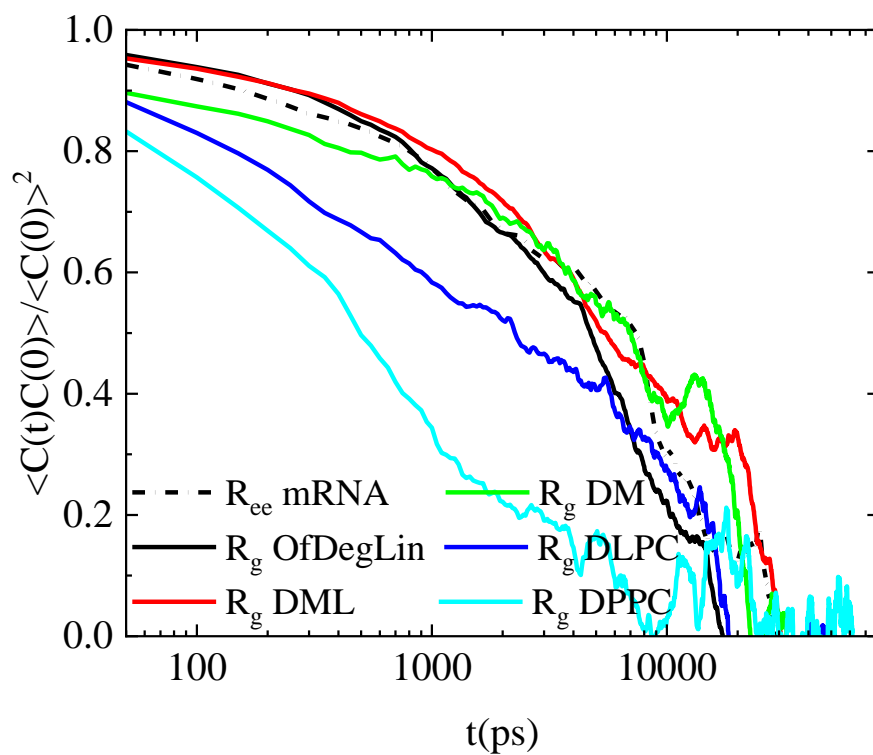
## Initial Configurations



**Figure S1:** Typical initial configurations of lipid molecules complexed with the oligonucleotide mRNA for a) DM; b) DML; c) OfDegLin; d) DPPC and e) DLPC systems. Water molecules are shown as ghost for clarity.

### Nucleotide sequence for the mRNA fragment

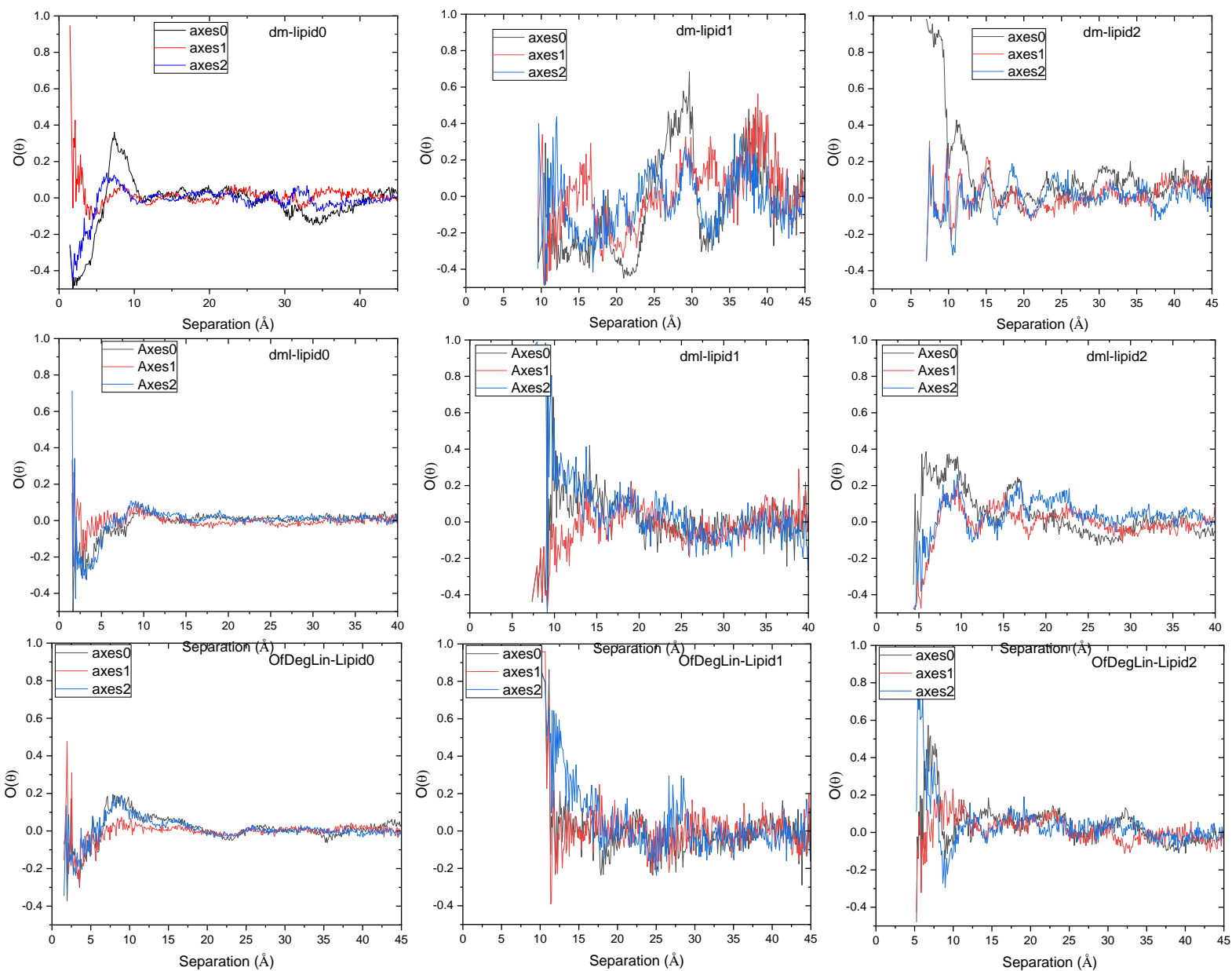
GAUAUUCAGAUGACCCAGAGCCCGACAGC

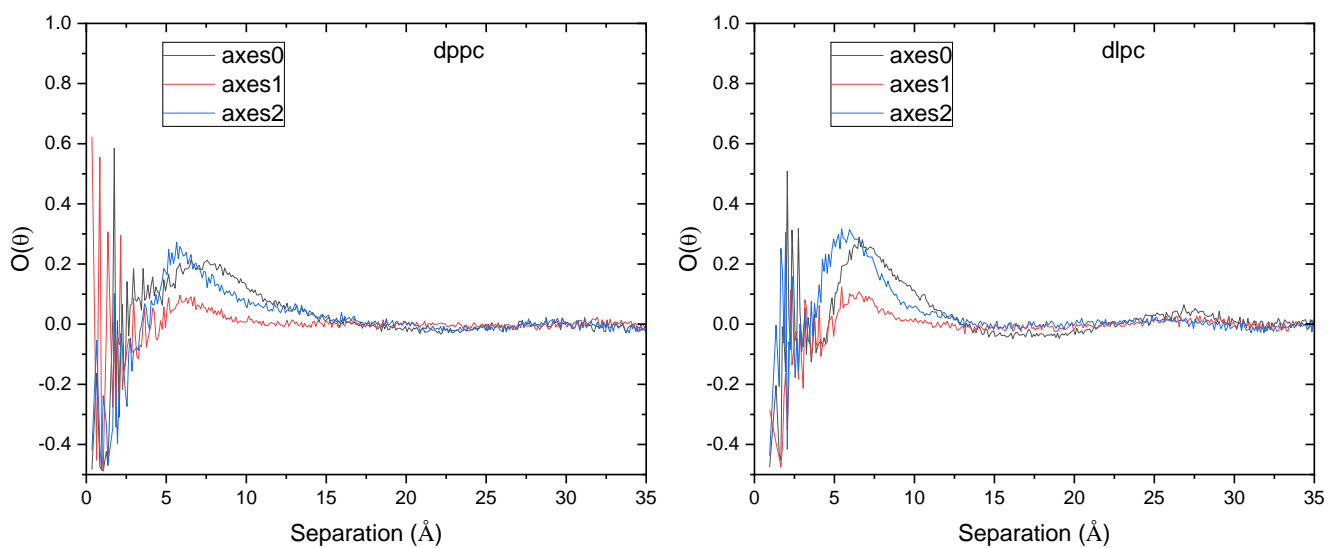


**Figure S2:** Autocorrelation functions of the e-e distance of the RNA chain ( $C(t)=R_{e-e}(t)$ ) and the radius of gyration ( $C(t)=R_g(t)$ ) of the complexation agents.

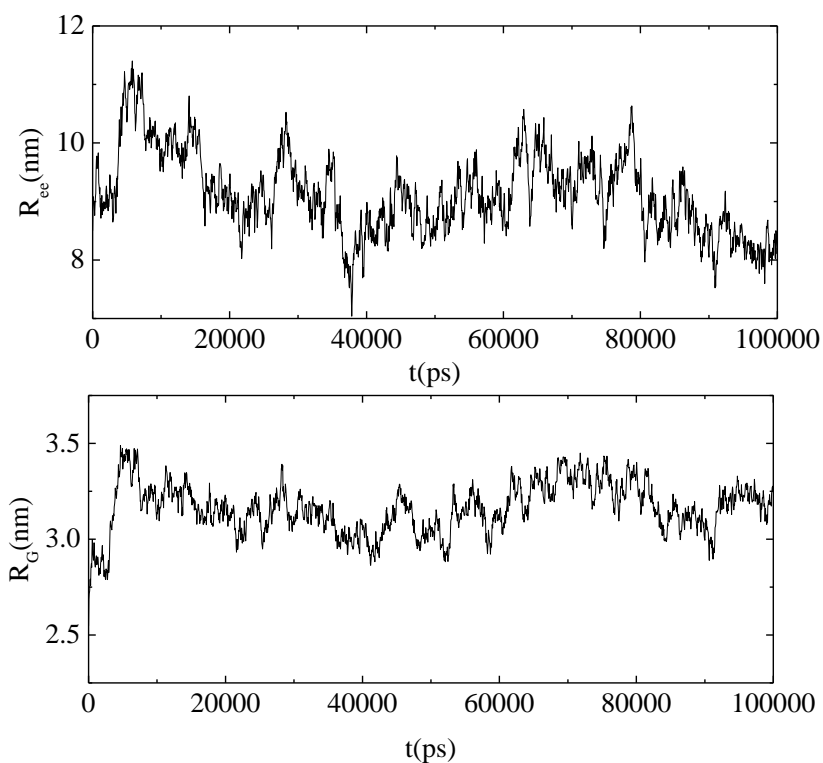
## Orientalional order parameter between the complexation agents in formed clusters.

The orientational order parameter between individual complexation agents within the formed clusters, were calculated through the expression  $O(\theta) = \frac{1}{2}(3\langle \cos^2 \theta \rangle - 1)$ . Here  $\theta$  is the angle between the direction of an eigenvector of the inertia tensor of a lipid, and the corresponding eigenvector of a different lipid of the same kind. This was calculated as a function of the separation between the centers of mass of the lipids.  $O(\theta)$  assumes values of 1 if the orientation of the lipids is parallel, -0.5 when there is a mutually perpendicular arrangement along the examined direction and 0 if there is no preferred orientation with respect to the examined direction. The figures below depict the orientational parameter along the 3 eigenvectors of the inertia tensor for each lipid.

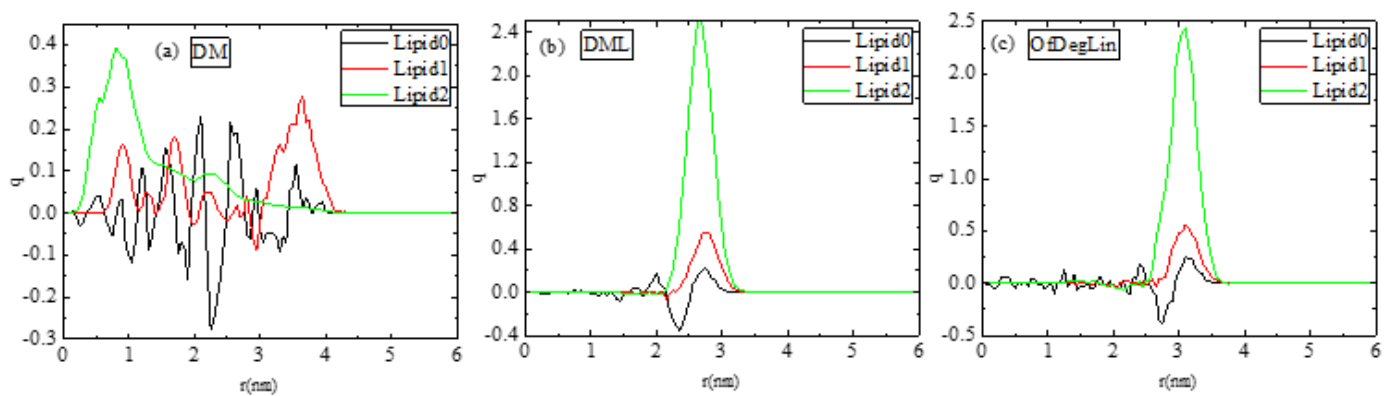




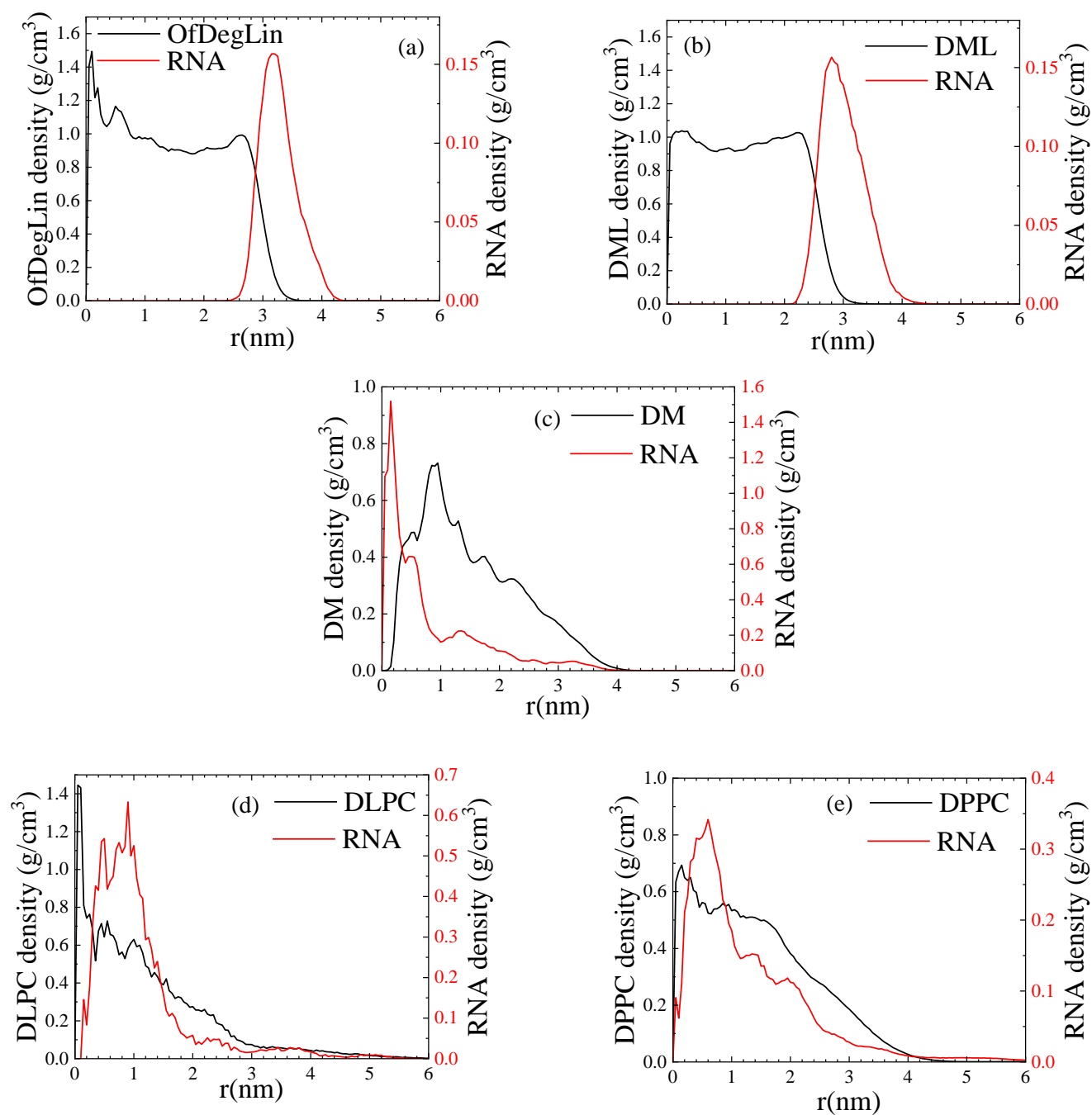
**Figure S3:** Orientational parameter along the directions of the 3 eigenvectors of the inertia tensor for each lipid.



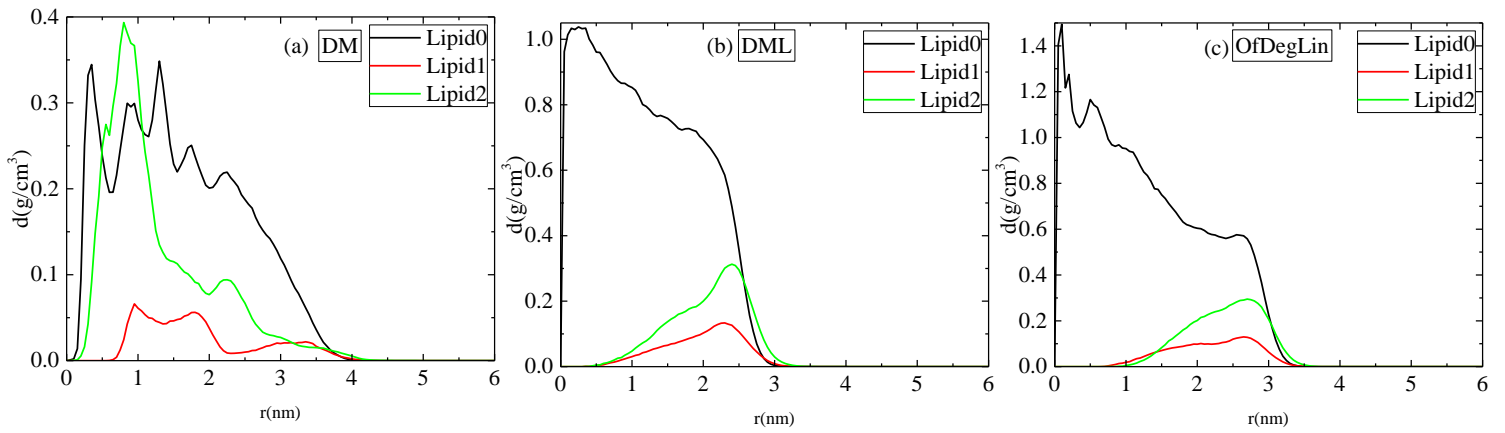
**Figure S4:** Time variation of the radius of gyration and the end-to-end distance of the RNA fragment in water, in the absence of the complexation agents.



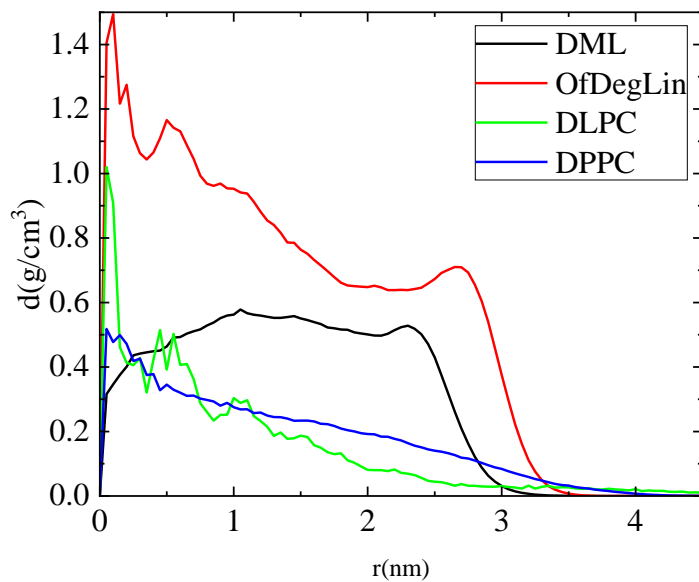
**Figure S5:** Charge distributions of the ionizable complexation agents which bear different overall charge. a) DML b) DM c) OfDegLin. The charge is expressed in electron charge units.



**Figure S6:** Density profiles of the complexation agents and the RNA with respect to the center of mass of the formed cluster.

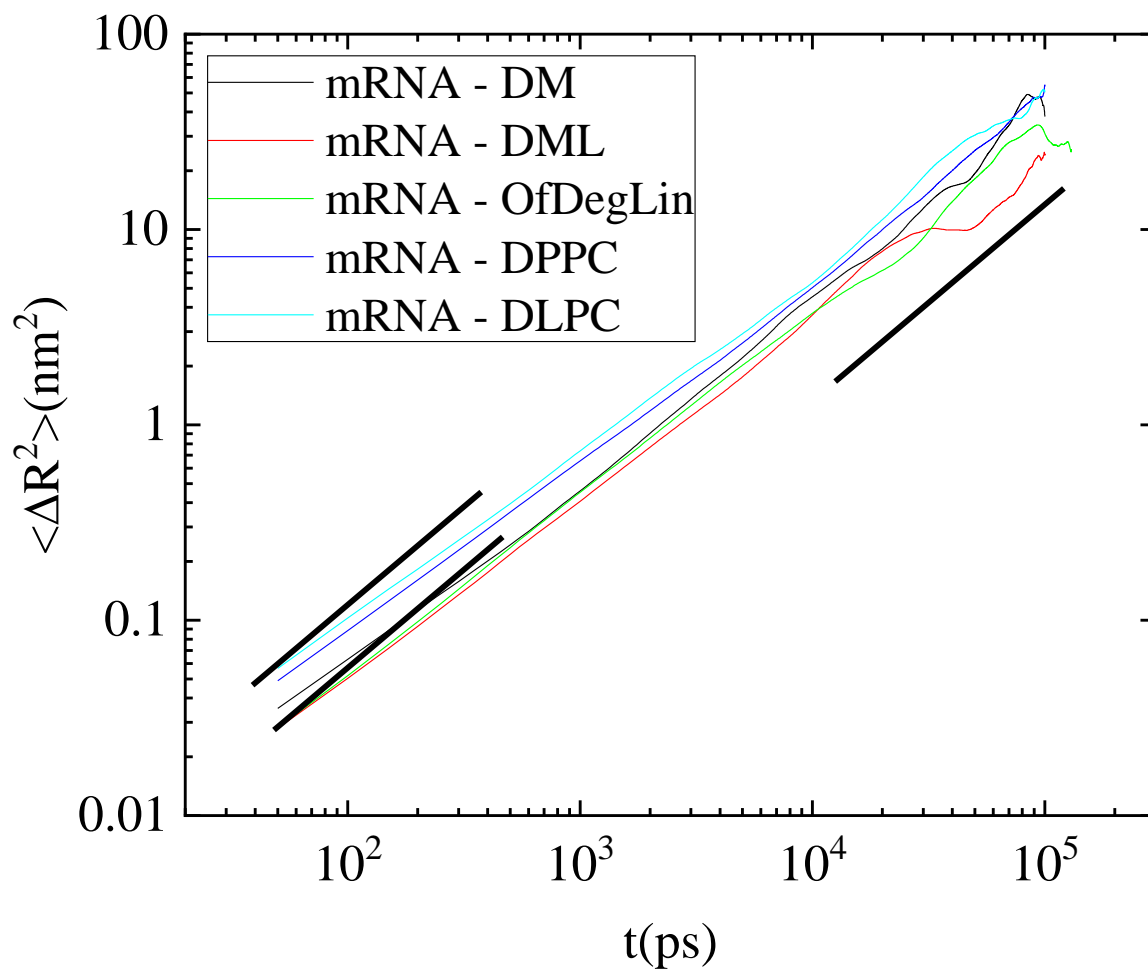


**Figure S7:** Density distributions of the ionizable complexation agents which bear different overall charge: a) DM b) DML c) OfDegLin.

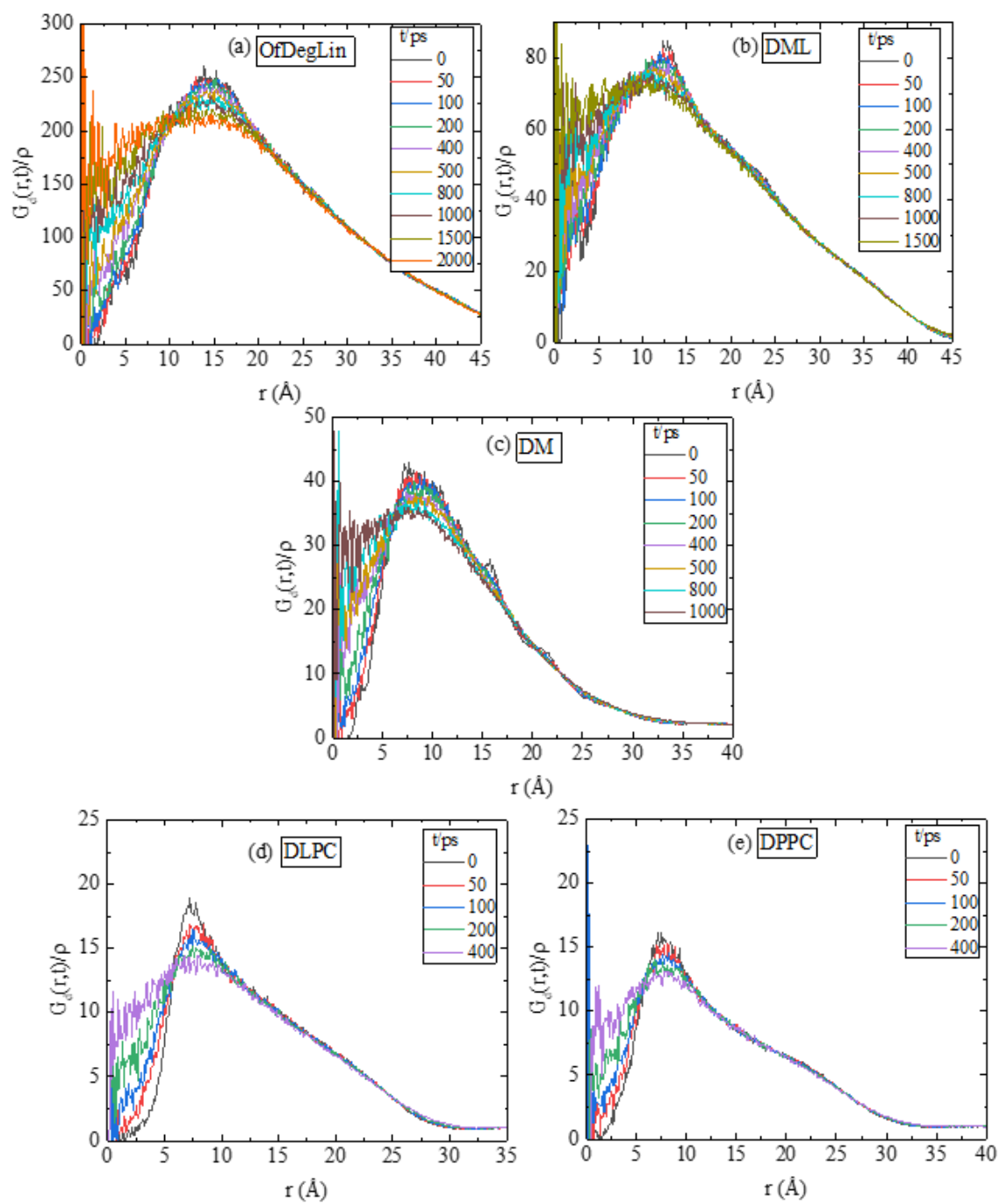


**Figure S8:** Mass density profiles of the tails in clusters formed by the complexation agents DML, OfDegLin, DLPC, DPPC (single cluster formation). Distance 0 corresponds to the geometric center of the cluster.





**Figure S9.** MSDs arising from the center of mass of the complexation agents, for the part of the trajectory beyond 100ns from the start of the production run, when self-assembled groups of lipids have already been associated with mRNA. The thick short straight lines denote a slope of 1.



**Figure S10:** Distinct van Hove correlation functions arising from the centers of mass of the complexation agents, for different time intervals.