Procedure :

**<Section|Preparation and Environment>**

The structure { PDB-ID: 5xm9| structure} was downloaded from the PDB. The chains A-D, G, and H were deleted and the DNA substrate was changed to RNA.

The complex was embedded in a {cubic|box type} water box using {TIP3P|water type} with a minimal shell of {15 Å|shell radius} around the solute. {150 mM NaCl| ions} and {20 mM hexahydrated Mg2+|ions} were added.

All atom {molecular dynamics (MD)|simulation} simulations were performed using the {AMBER14|suite}.

The {OL3| force field} was used for the RNA and the {OL15|force field} was used for the DNA.

The monovalent ions were treated with the {Joung-Chetham parameters for monovalent ions|parameters} and the Mg2+ ions were treated with the {Li-Merz parameters for two-fold positively charged metal ions|parameters}.

The time step for all MD simulations was set to {2 fs|dt} with a direct space, nonbonded cutoff of {9 Å|cut}. During the {production|period}, the time step for all MD simulations was set to {4 fs|dt} as hydrogen mass repartitioning was used with a direct-space, non-bonded cutoff of {8 Å|cut}. <elif|membrane simulation|e|false>, the time step for all MD simulations was set to {4 fs|dt} as hydrogen mass repartitioning was used with a direct-space, non-bonded cutoff of {8 Å|cut}.

To cope with long-range interactions, the Particle Mesh Ewald method was used; the SHAKE algorithm was applied to bonds involving hydrogen atoms.

A picture containing graphical user interface

Description automatically generated

**<Section|Minimization>**

At the beginning, {17,500|maxcyc} steps of steepest descent and conjugate gradient minimization were performed for each of the 10 replicas.

print {2500|maxcyc}, steps of minimization were performed.

During these steps positional harmonic restraints with a force constant of print {25 kcal mol-1 Å-2|restraint\_wt} were applied to solute atoms.

**<Section|Thermalization>**

Thereafter, {50 ps|simulation time} of {NVT|MD} simulations were conducted.

The system was then heated up to {100 K|temp0} varying a fraction of a Kelvin for each replica.

The previous step is followed by {300 ps|simulation time} to adjust the density of the simulation box to a pressure of {1 atm|pres0} and to heat the system to {300 K|temp0}. During these steps, a harmonic potential with a force constant of {10 kcal mol-1 Å-2|restraint\_wt} was applied to the solute atoms.

As the final step in thermalization, {300 ns|simulation time} {NVT|MD} simulations were performed.

During this process, the restraint forces on solute atoms were gradually reduced to {0 kcal mol-1 Å-2|restraint\_wt} within the first {250 ns|simulation time}.

**<Section|Production>**

Afterward, {10|overall repetitions} replicas of independent production {NVT|MD} simulations were performed.

For each production run, simulations of {1 µs|simulation time} were performed.