

# A Mechanistic Insight into Doxorubicin Adsorption on N-isopropyl Acrylamide Grafted Nanotube: Optimization Study of Loading Temperature

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## Research

**Keywords:** Temperature-responsive, Doxorubicin, Molecular Dynamics, N-isopropyl acrylamide, Hydrogel

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1 **A Mechanistic Insight into Doxorubicin Adsorption on N-isopropyl Acrylamide Grafted**  
2 **Nanotube: Optimization Study of Loading Temperature**

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24 **Abstract**

25 **Background:** The drug development process is costly and time-consuming; hence, nowadays,  
26 enormous efforts have been established through computational studies for finding appropriate  
27 strategies, methods and solutions for enhancing the drug production and administration  
28 procedures. Hydrogels that undertake deformation upon pertinent changes in temperature have  
29 significant aptitude as drug delivery systems. These biomaterials have made a substantial impact  
30 on the development of drugs for critical diseases, especially cancer therapy. Drug loading and  
31 uptake are primary and fundamental steps of the drug development and discovery process. N-  
32 isopropyl acrylamide is a common and well-known thermo-sensitive and injectable hydrogel for  
33 the drug uptake under the lower critical solution temperature (LCST). In the current study,  
34 carbon nanotube (CNT) as a nanocarrier was modified via N-isopropyl acrylamide. On the other  
35 hand, Doxorubicin as an anti-cancer drug applied on mentioned systems to develop drug  
36 packing at three different temperatures.

37 **Results:** After computational parametrization of the system via bioinformatics software and  
38 databases, Molecular dynamics (MD) simulation was run. To this end, the detailed simulations  
39 were carried out to reveal the interaction energy, numbers of hydrogen bonds, the gyration  
40 radius, mean square displacement, and radial distribution function as well as Gibbs free energy.  
41 Besides, the optimal loading temperature for doxorubicin was determined. The results achieved  
42 from simulating the polymer demonstrated a decrease in the gyration radius at a higher  
43 temperature. A decrease of gyration radius resulted in more concentrated aggregation with  
44 stronger bonds.

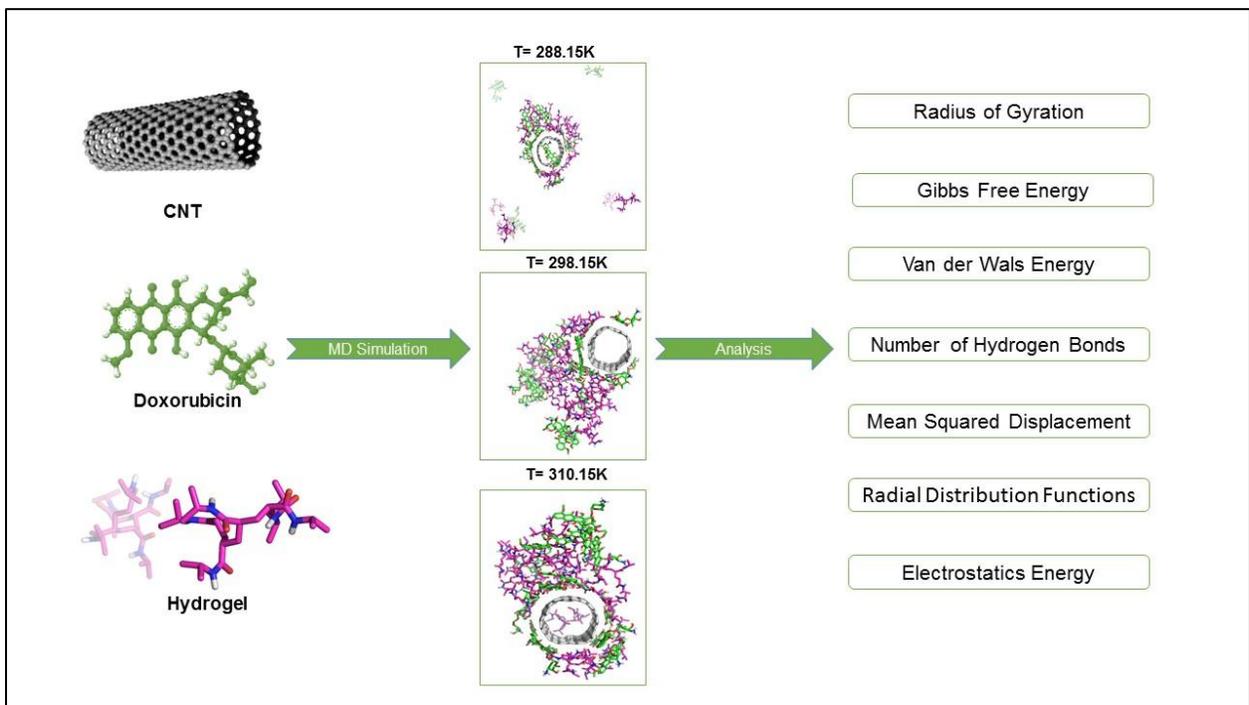
45 **Conclusions:** Therefore, at the higher temperature, the more stable polymer interaction and  
46 better doxorubicin loading were acquired. The smart absorption of doxorubicin onto the CNT

47 modified via N-isopropyl acrylamide (NIPA) give a significant and valuable view on the future  
48 studies regarding the drug development and novel, biocompatible, and biodegradable stimuli-  
49 sensitive drug delivery system.

50 **Keywords:** Temperature-responsive; Doxorubicin; Molecular Dynamics; N-isopropyl  
51 acrylamide; Hydrogel

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62 **Background**

63 Cancer is one of the global, critical and life-threatening diseases which was the third leading  
64 causal factor of death in 1990, while it rose to be the second leading cause of mortality in 2013.  
65 In 2013, around 15 million cancerous patients were identified, and cancer led to around 8.2  
66 million deaths. In that year, statistical analysis showed that the cancer resulted in 196.3 million  
67 cancer cases (1).

68 Many drugs and modalities have been introduced to battle the cancerous cells. Doxorubicin  
69 (DOX) is one of the essential and common anti-cancer drugs which fights against the  
70 proliferation and metastasis of cancerous cells. DOX binds to the DNA and inhibits the nucleic  
71 acid production (2). As such, it disrupts the molecular structure as well as the spatial blockage.  
72 DOX is used to treat various cancers such as gastric, lung, breast, bladder, ovary, thyroid, bone,  
73 nerve tissue, muscles, joints, and soft tissue malignancies (3). It is also used to heal Hodgkin's  
74 lymphoma and multiple types of leukemia (4). On the contrary, the drawback of the DOX which  
75 has an adverse effect, is the fact that it can also damage healthy human cells and prevent their  
76 growth as well (5). This requires implementing novel techniques to minimize these drug-related  
77 systemic toxic effects. There are multiple methods to achieve such a goal; one of them is  
78 nanostructures which provide the targeted drug delivery. Targeted and smart drug delivery via  
79 the nanoparticles not only minimize the doxorubicin adverse and unwanted effects on the non-  
80 cancerous and healthy cells but also maximizes the efficiency of the drug on tumor cells (6).

81 Novel nanostructured drug delivery systems have dramatically improved drug therapies (7).  
82 Various polymeric (8), carbon-based (9), and ceramic nanostructures (10) have been studied for  
83 this purpose. These structures have specific features including targeted drug delivery (11), high

84 biocompatibility (12), enhancing drug viability in the bloodstream (12), controlling and  
85 decelerating the drug release (13), protecting drug molecules (14), having a smaller size than the  
86 cells (15), and the ability to cross biological barriers to deliver a drug to the targeted site (16).  
87 Therefore, nanostructures can be a suitable carrier for doxorubicin delivery. Because of the high  
88 therapeutic utility of doxorubicin in oncology and clinical fields, the DOX drug development can  
89 decrease the manufacturing cost and increase the efficacy and minimize the drawbacks (17).  
90 Carbon nanotubes have recently received massive attention in the delivery of various drugs (18).  
91 Carbon nanotubes have an amazing ability to detect and damage cancer cells in vivo. Many  
92 researchers have focused on the potential capabilities of carbon nanotube as a carrier for anti-  
93 cancer agents that may have unique physical and chemical characteristics such as size, geometric  
94 shape, surface charge, surface chemistry, hydrophobicity, and more importantly, the ability to  
95 cross biological barriers in vivo (17, 19-22). These particles are small enough to cross the  
96 membranes and biological barriers and carry the drug into the malignant cells (23). These  
97 structures possess a high surface area which enables us to accomplish the surface engineering  
98 and change the surface properties. The carbon nanotubes can be functionalized according to the  
99 intended use with various functional groups and compounds to enhance their solubility and  
100 biocompatibility (24, 25). Drug compounds are loaded onto the surface or into the carbon  
101 nanotubes. The surface engineered nanotubes are widely used in the drug delivery (26). The  
102 nanotubes can move comfortably inside the biological membranes, skin, blood vessels, and  
103 penetrate into the biological tissues. These features have made nanotubes a useful carrier for  
104 drugs, genes, proteins, and vaccines (27, 28). For such reasons, the chemical and physical  
105 functionalizations of the nanotubes have been investigated to stabilize the functional groups in  
106 the water environment (29).

107 Hydrophilic polymers can stabilize nanotubes in the aquatic environment. The pH-sensitive  
108 polymers such as polyacrylic acid have been used as a carbon nanotube functional group, in  
109 which the nanotubes are dispersed in water based on the degree of polymer ionization and pH.  
110 For nanotubes, the use of temperature-sensitive polymers instead of the pH-sensitive polymers is  
111 a more suitable option in the aqueous environment. The pores in the hydrogels facilitate the  
112 loading of the drug on/into the carriers and may serve as a drug delivery system (30). The  
113 hydrogels used for drug delivery systems are used in the form of slabs, microparticles, nano  
114 particles, coatings, or films. Hydrogels are used to release both hydrophilic and hydrophobic  
115 drugs (31). Both hydrophilic and hydrophobic drugs can be simultaneously incorporated into  
116 hydrogels because hydrogels have both hydrophilic and hydrophobic groups. Hydrophobic  
117 groups interact with doxorubicin, which is hydrophobic, and hydrophilic groups interact with  
118 water. Thus, hydrogels can inhibit the accumulation of doxorubicin molecules and are attractive  
119 carriers for doxorubicin (32).

120 N-isopropyl acrylamide (NIPA) is one of the thermal-sensitive hydrogels and hydrogels. These  
121 polymers have a critical solution temperature in aqueous solution. The volume and shape of the  
122 NIPA are changed reversibly in the vicinity of solution temperature. There is a polymer phase  
123 transition in the water at the low critical solution temperature (LCST), whereby the polymer is  
124 transformed from a distended hydrophilic structure below the critical solution temperature to a  
125 condensed hydrophobic structure above this temperature (33).

126 The polymer of our current study, NIPA, is one of the conventionals, biocompatible,  
127 biodegradable and thermo-sensitive injectable hydrogels which are physiologically and  
128 chemically compatible to load and delivery Therapeutic agents. Anticancer agents are naturally

129 entrapped in the thermo-sensitive hydrogel by mixing with precursor solution and then after by  
130 sterilization procedure the hydrogel is capable to inject to the body biofluids (34, 35).

131 Other studies showed that the essential solution temperature of the NIPA could be increased by  
132 combining with carbon nanotubes (28). Other properties of the NIPA, such as the release time,  
133 can also be improved in combination with carbon nanotubes. Hydrophilicity and hydrophobicity  
134 of the NIPA can also be varied according to their composition. Multiple functional groups have  
135 been used to modify the properties of the NIPA. One of the attractive compounds for drug  
136 delivery and features of the NIPA can be the NIPA@CNT nanocomposite composite (36).

137 Molecular dynamics (MD) is a powerful tool that can provide qualitative and quantitative  
138 information on the Physico-chemical interactions and mechanisms of chemical and biological  
139 systems that provide more conceptual results in comparison to machine learning methods (37-  
140 39). Considering the difficulties and high-cost of empirical experiments, many studies have been  
141 done by MD to simulate the drug delivery systems in cancer therapy (40, 41). In previous  
142 studies, MD has been carried out for the release of the doxorubicin by carriers such as graphene  
143 and graphene oxide (42). In these studies, the effects of pH, molecular bonds, carrier size, and  
144 functional groups have been investigated (43). Previous works have not studied the drug  
145 development process during temperature changes, such as the uptake and loading mechanism of  
146 the doxorubicin by carbon nanotubes using MD (44).

147 Utilizing the molecular cloning, this work investigates the N-isopropyl acrylamide@CNT  
148 nanocomposite as a suitable carrier for the loading of the doxorubicin. To analyze the  
149 characteristics of this attractive carrier, the interactions between the carrier and drug, gyration  
150 radius, hydrogen bonds, and radial distribution function have been investigated. In order to  
151 peruse the effect of the polymer nano-particle synthesis temperature on the loading and drug

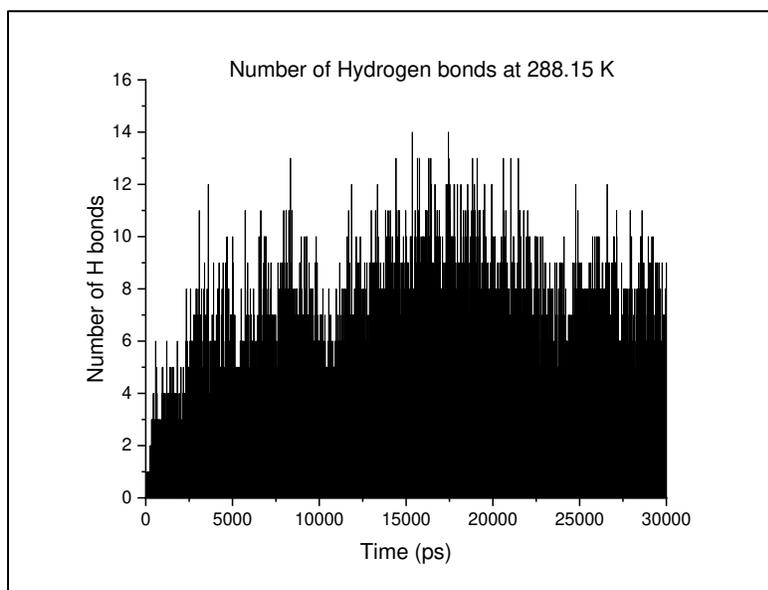
152 delivery properties, three different temperatures have been considered for isopropyl acrylamide,  
153 and three simulations have been performed for isopropyl acrylamide polymers. The comparison  
154 of results determines the optimal temperature for the drug loading.

## 155 **Result and discussion**

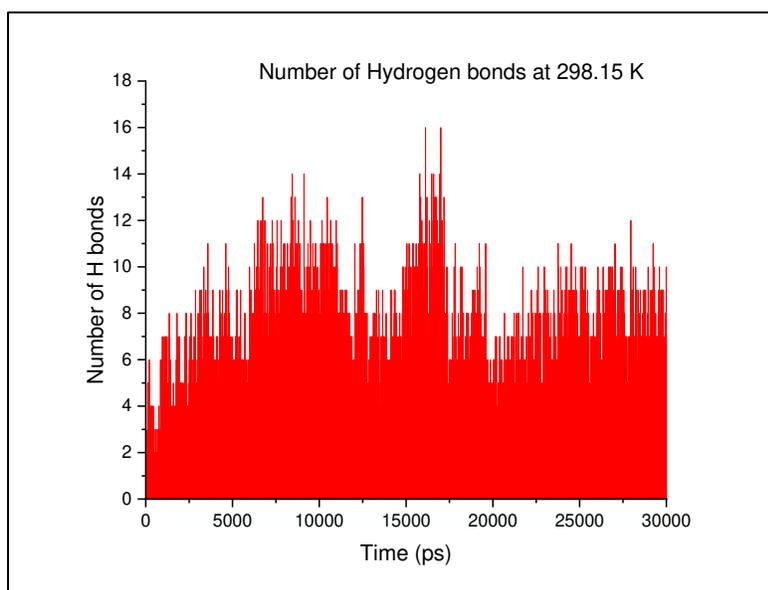
### 156 **1.1. Hydrogen bond analysis**

157 Hydrogen bonds can be formed between hydrogen atoms and high electronegative atoms (such  
158 as oxygen, nitrogen, or fluorine) as well as between various electronegative biomolecules. The  
159 H-bond analysis is one of the most well-organized indicators for comparing the ability of several  
160 structures in capturing various adsorbates. The higher number of hydrogen bonds reveal the more  
161 interactions between the biomolecules as well as the propensity for the two different or same  
162 particles to be highly attracted to each other. Hence, the number of hydrogen bonds formed  
163 between the DOX, N-isopropyl acrylamide, and CNT is an index to evaluate the drug uptake and  
164 stability of drug delivery systems at three various temperatures. The amine and carboxylic acid  
165 functional group can form hydrogen bonds; under proper conditions, the hydrogen attached to  
166 the amine or carboxylic group can create Hydrogen bonds. The N-isopropyl acrylamide  
167 possesses an N containing group, in which, the N atoms can create H-bonds. According to the  
168 presence of a Hydroxyl group in the DOX molecular structure, H-bonding is possible between  
169 the OH group and the other molecules. Regarding Figure 2, the average number of H-bonds  
170 created during the MD simulation at 288.15 K, 298.15 K, and 310.15 K temperatures were  
171 6.01966113, 5.937687438, and 1.325558147, respectively. The higher numbers of H-bond at  
172 288.15 K indicate the more appropriate drug loading and uptake in comparison with two other  
173 temperatures. However, this analysis alone is not sufficient to evaluate the interactions between

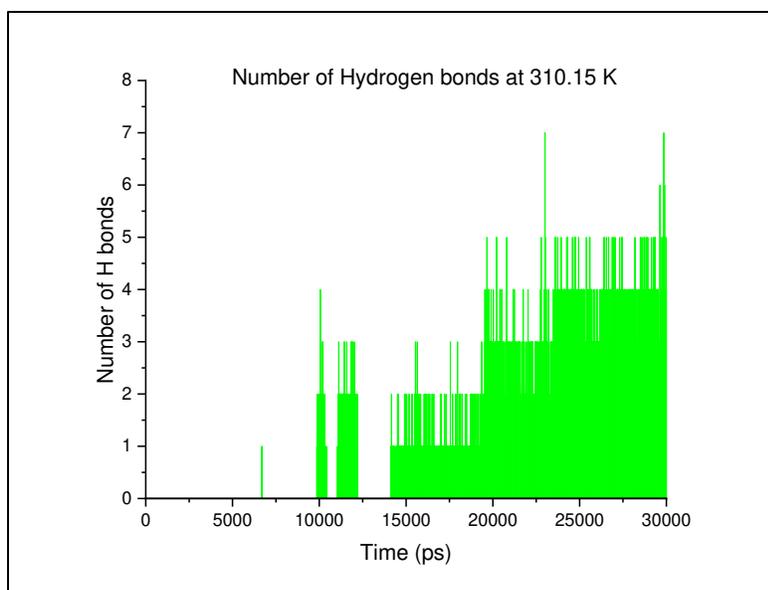
174 molecules, so we studied the other bond interactions between the drug, hydrogel, and  
175 nanocarrier.



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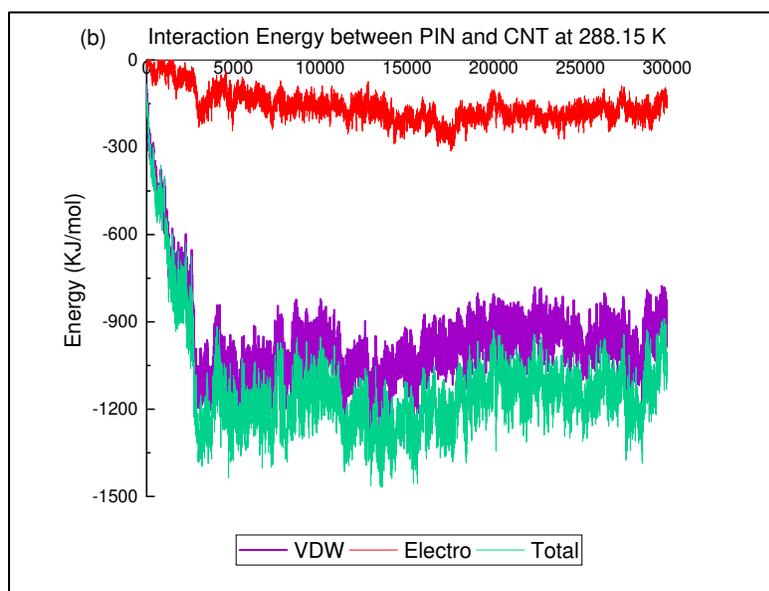
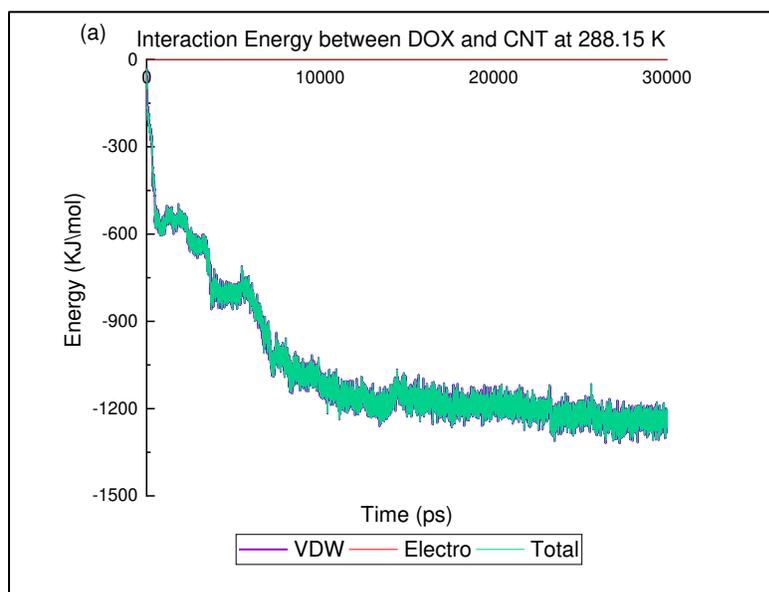
178  
 179 **Figure 2.** The numbers of hydrogen bonds between DOX and NIPA at three different  
 180 temperatures

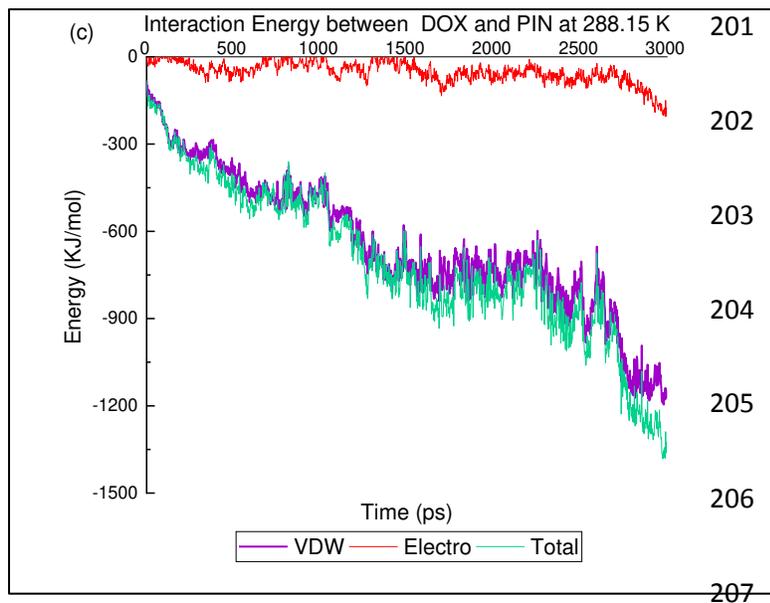
181 **1.2. Interactions of energy analysis at three different temperature**

182 Figures 3, 4, and 5 demonstrate the DOX@CNT / DOX@NIPA / NIPA@CNT interactions at  
 183 three different temperatures including 288.15 K, 298.15 K, and 310.15 K. The diagrams (a), (b)  
 184 and (c) illustrate the van der Waals and Electrostatic interaction energies. According to these  
 185 curves, the total interaction energies at 310.15 K are higher than others. This fact would assist in  
 186 the adsorption of the DOX. It can be inferred that the temperature of 310.15K is an optimal  
 187 temperature for the DOX loading onto the surface of the CNT.

188 In both interaction diagrams, the electrostatic energy is lower and near to zero. This can be  
 189 attributed to the absence of the charge for the drug, polymer, and nanocarrier. While the van der  
 190 Waals interaction is noticeable, so dominant interaction energy of total is related to recent  
 191 energy. The total interaction energy between the DOX and PIN at 310.15 K and 298.15 K were  
 192 almost the same while the energy at 288.10 K was the lowest. These curves also indicate that the

193 electrostatic energy has no role in the DOX@CNT and NIPA@CNT interactions at different  
194 temperatures, in which the total energy was almost equal to the van der Waals energy. This can  
195 be ascribed to the Aromatic groups of the DOX molecules, which can establish significant van  
196 der Waals interactions with the non-polar functional groups of the CNT and NIPA molecules at  
197 different temperatures.



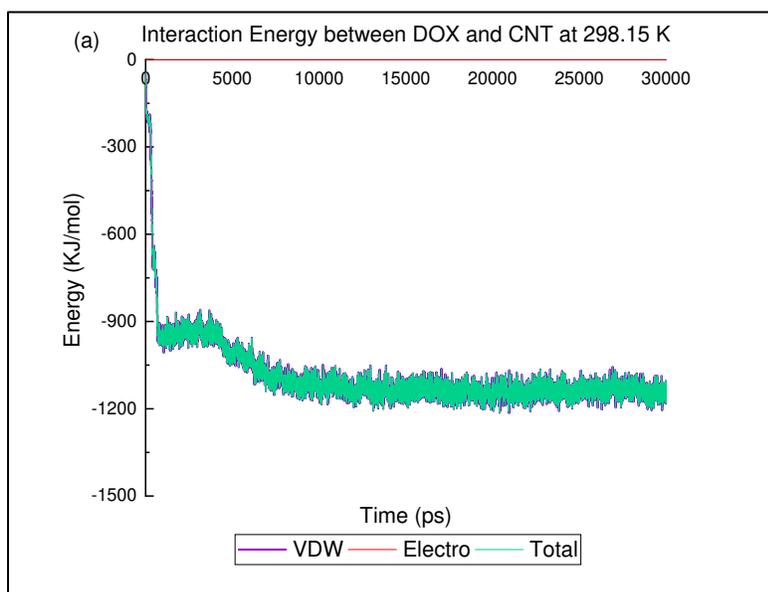


208 **Figure 3.** Interaction energies diagrams at 288.15 K

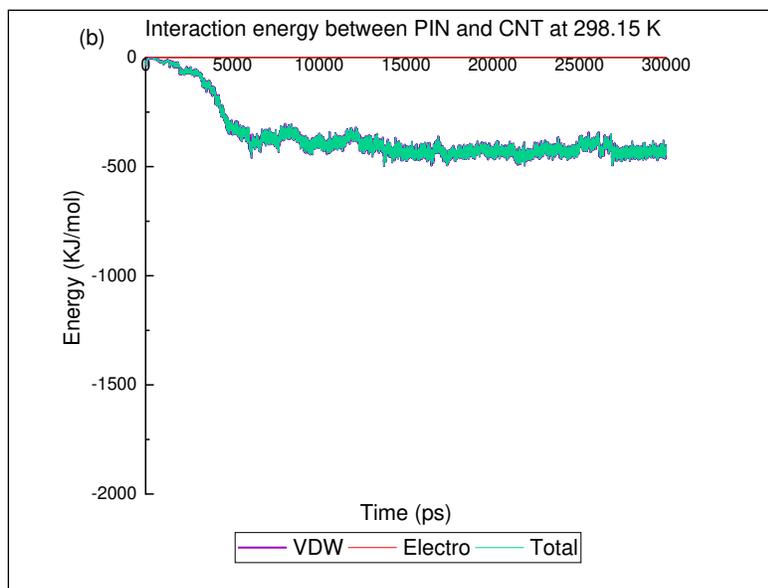
209 (a) Electrostatic and van der Waals energies of DOX@CNT interaction versus time at 288.15 K;

210 (b) Electrostatic and van der Waals energies of NIPA@CNT interaction versus time at 288.15 K;

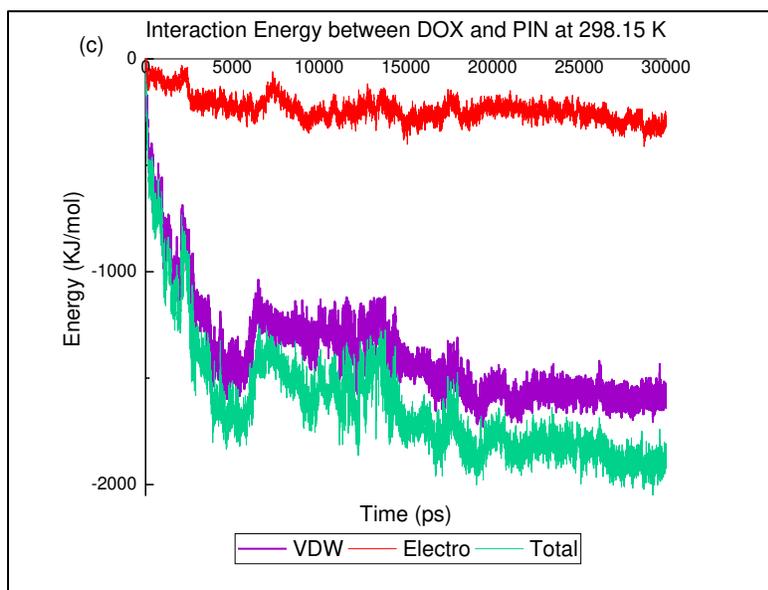
211 (c) Electrostatic and van der Waals energies of DOX@NIPA interaction versus time in 288.15 K



212



213



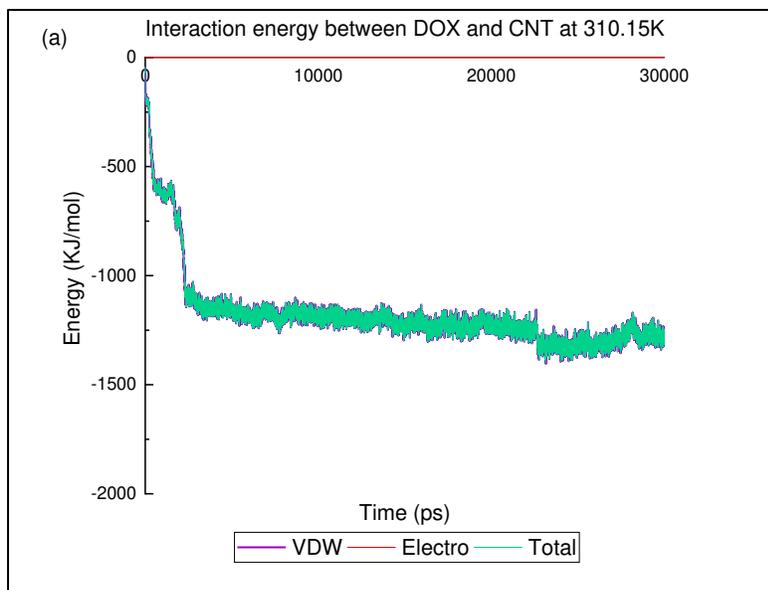
214

215 **Figure 4.** Interaction energies diagrams at 298.15 K

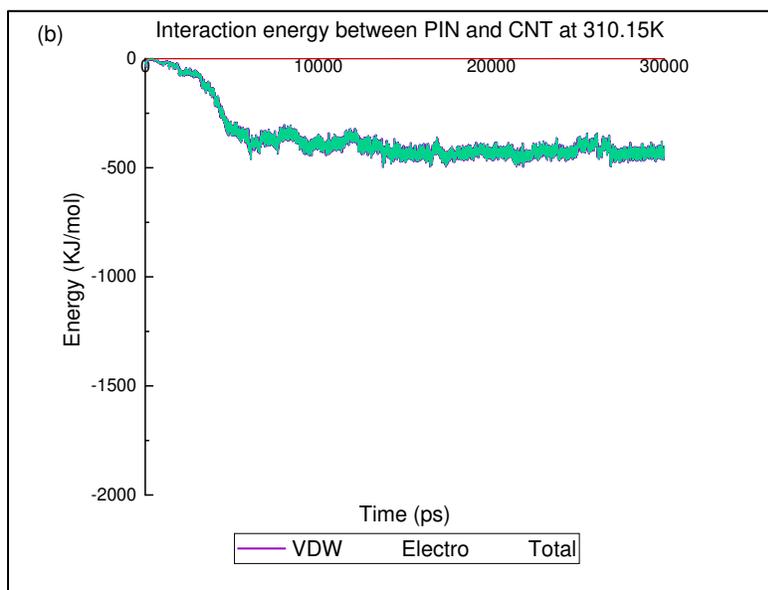
216 (a) Electrostatic and van der Waals energies of DOX@CNT interaction versus time at 298.15 K;

217 (b) Electrostatic and van der Waals energies of NIPA@CNT interaction versus time at 298.15 K;

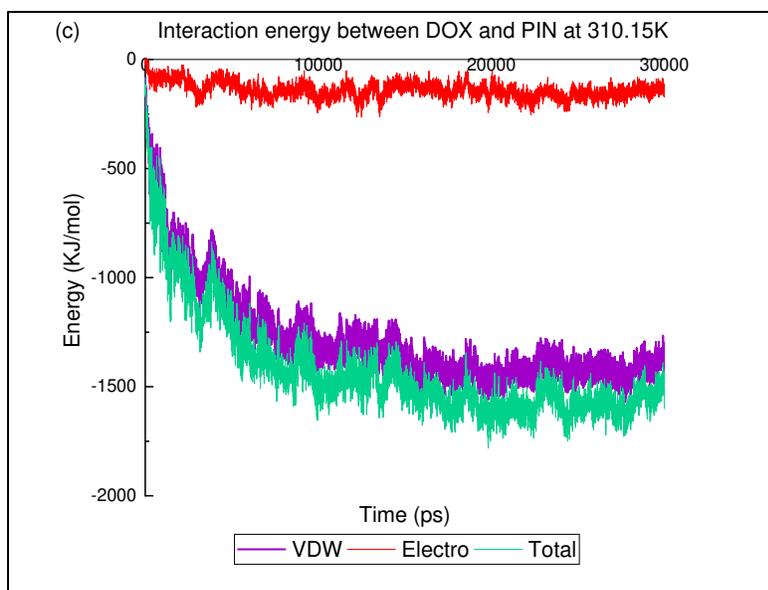
218 (c) Electrostatic and van der Waals energies of DOX@NIPA interaction versus time in 298.15 K.



219



220



221

222 **Figure 5.** Interaction energies diagrams at 310.15 K

223 (a) Electrostatic and van der Waals energies of DOX@CNT interaction versus time at 310.15 K;

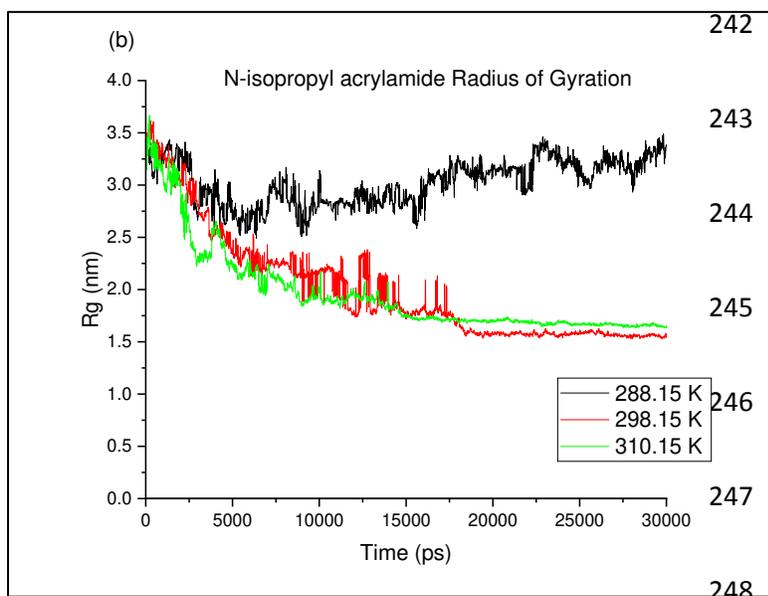
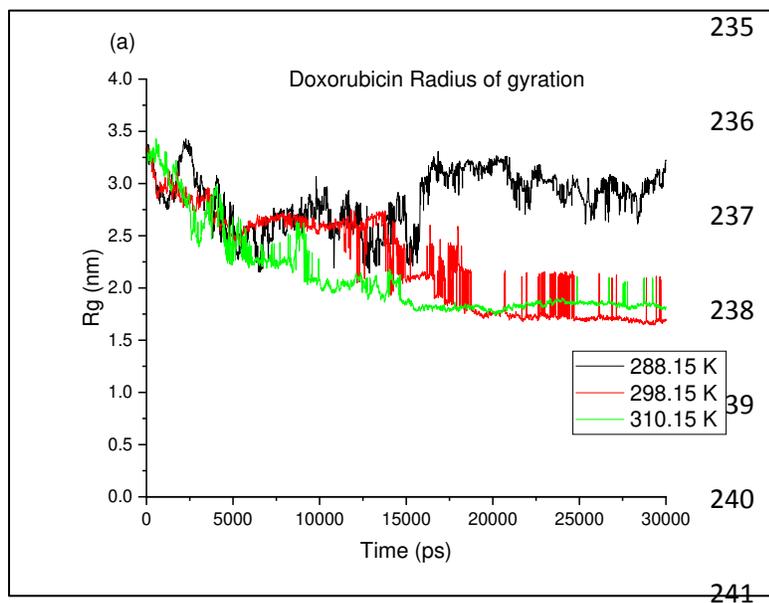
224 (b) Electrostatic and van der Waals energies of NIPA@CNT interaction versus time at 310.15 K

225 (c) Electrostatic and van der Waals energies of DOX@NIPA interaction versus time in 310.15 K.

### 226 1.3. Radius of Gyration

227 Gyration radius ( $R_g$ ) is a factor by which the accumulation of molecules (such as hydrogels)  
 228 and alteration of bio-macromolecule size (nucleic acids) can be computed and evaluated. The  
 229 higher the gyration radius, the stronger the aggregation of the DOX@NIPA, and thus the  
 230 conjugation would be of a more stability. Figure 6 shows the gyration radius of the DOX and  
 231 NIPA for the CNT carriers. At different temperatures, the gyration radius of the interacting  
 232 particles for NIPA and DOX was in a similar order, while at 310.15 K the lower  $R_g$  indicated the  
 233 better stability.

234



249 **Figure 6.** Gyration Radius of Molecules versus time in different temperatures for CNT carrier:

250 (a) DOX Rg at three temperatures (b) NIPA Rg at three temperatures

251 **1.4. Mean Square Displacement Analysis**

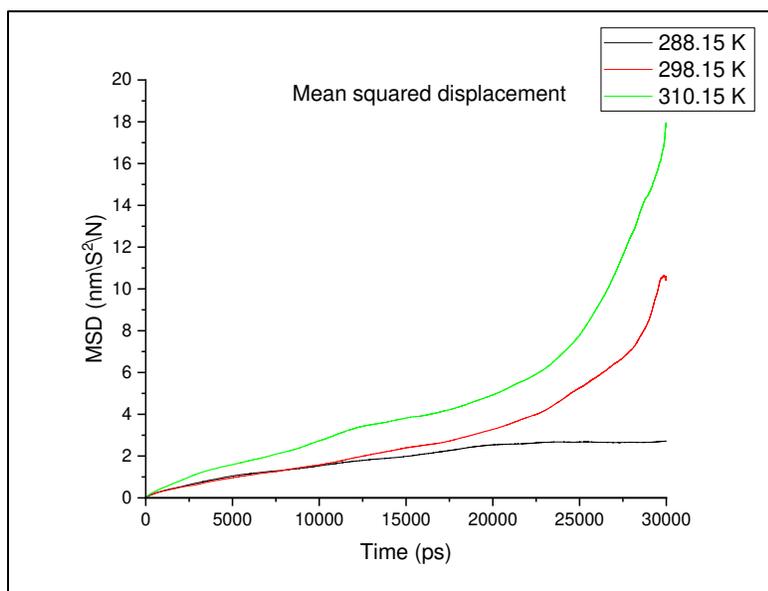
252 The mean displacement square (MSD) is a computational factor to estimate the drug diffusion  
 253 coefficient. The situation of all atoms is denoted by 'r', while 't' signifies the time. The

254 following formula indicates how the mean square displacement is obtained:

255 
$$MSD = \langle [r(t) - r(0)]^2 \rangle = \frac{1}{t} \sum_{t=t_0}^t [r(t) - r(0)]^2 \quad (3)$$

256 Einstein's relation reveals how the diffusion coefficient for the three-dimensional system can be  
257 calculated.

258 
$$D = \frac{1}{6} \frac{MSD}{t} \quad (4)$$



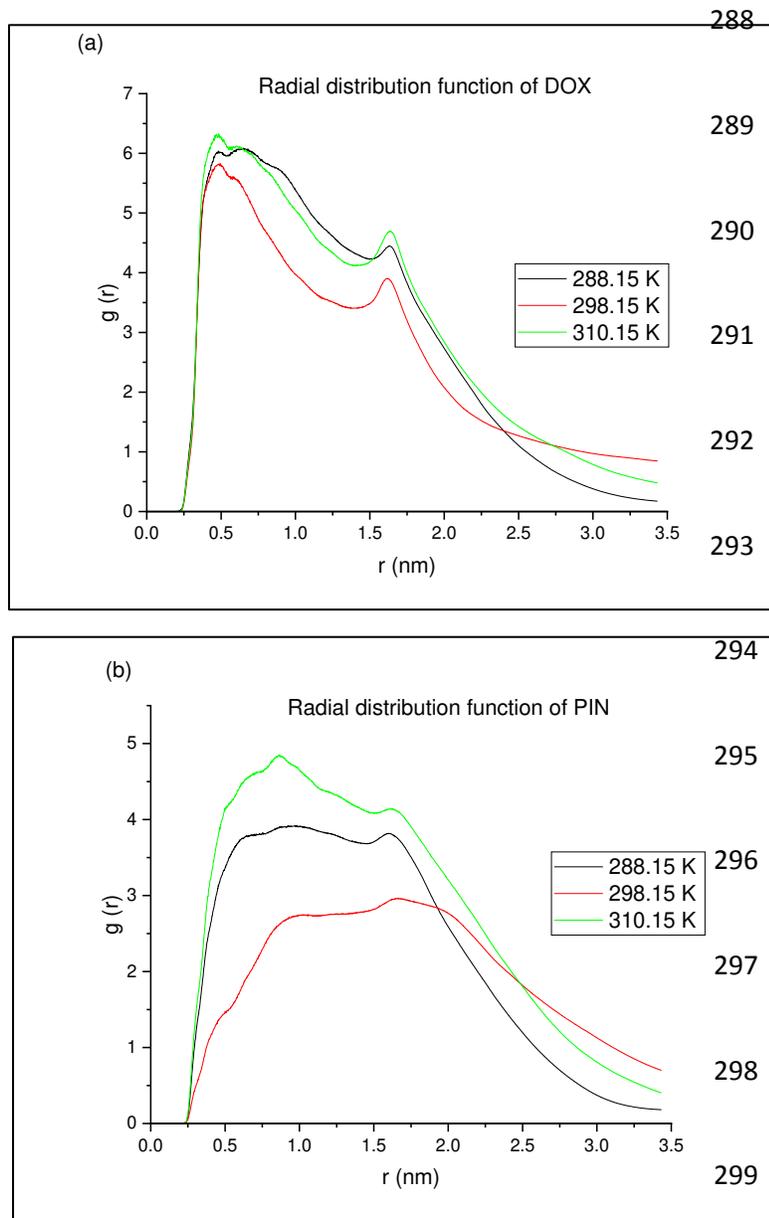
259  
260 **Figure 7.** Mean square displacement of the system versus time at different temperature

261 In Figure 7, the vertical axis represents the MSD and the horizontal axis indicates the time in  
262 picoseconds. According to the mentioned equation, the slope of the MSD curve demonstrates the  
263 diffusion coefficient, and the higher the slope of the graph, the higher the diffusion coefficient.  
264 The comparison of the figures reveals that at 310.15 K, the chart has a higher slope. Therefore, at  
265 310.15 K, the diffusion coefficient was more significant. The higher diffusion coefficient means  
266 that the drug is absorbed more rapidly over the surface of the CNT and the hydrogel; accordingly,  
267 the efficiency and rate of the drug absorption will be higher. So, the drug loading takes place

268 excellently at 310.15 K, and this temperature is better for loading the doxorubicin onto the  
269 nanotube-polymer carrier.

### 270 **1.5. Radial Distribution Function analysis**

271 Figure 8 (a) shows the radial distribution function (RDF) of the DOX's in interaction with  
272 the CNT. The vertical axis represents the RDF value, and the horizontal axis indicates the  
273 location of the molecules. As mentioned earlier, at any point where the RDF is higher, the  
274 molecule accumulates at that point. It is clear from the figure that all curves have a  
275 maximum point where the RDF value is maximum, and at that point, there is a more  
276 significant accumulation of molecules. The temperature of 310.15 K has a higher peak point  
277 than other temperatures. As a result, the optimal temperature for both the accumulation of  
278 doxorubicin on the CNT and its absorption is 310.15 K. (Figure 8 a). Moreover, the RDF of  
279 the polymer in connection with the CNT is demonstrated in Figure 8 b. Three curves are  
280 visible in the graph corresponding to three temperatures of 288.15 K, 298.15 K, and 310.15  
281 K. The RDF curve for each temperature has a maximum point. At the maximum point, the  
282 accumulation of molecules is more significant than elsewhere in the simulation box. The  
283 RDF curve at 310.15 K had a higher peak point than other temperatures, so there is more  
284 molecular accumulation at this temperature than other temperatures. The polymers are better  
285 assembled around a point at 310.15 K and form a more stable structure. Therefore, it can be  
286 concluded that 310.15 K is a temperature better for the accumulation of polymers around the  
287 carbon nanotube in comparison to the 288.15 and 298.15 K temperatures.



300 **Figure 8.** The radial distribution function of the DOX@CNT and NIPA@CNT versus  
 301 location at different temperatures: (a) The RDF of the DOX at three temperatures; and (b)  
 302 the RDF of the NIPA at three temperatures.

303 **Conclusion**

304 In recent decades, development of biomaterials, especially drug delivery and tissue  
305 engineering systems, has increased the quality and selectivity of the medical products in  
306 patients. Poly (n-isopropyl acrylamide) as a thermo-responsive polymeric nanoparticle has a  
307 significant role in smart drug delivery systems. In this work, the loading of doxorubicin on  
308 the carbon nanotube and Poly (n-isopropyl acrylamide) as a thermo-sensitive polymer, was  
309 simulated at three variouse temperatures, and the effect of the temperature on drug loading  
310 and packaging was investigated. Utilizing Gromacs software the molecular dynamics factors  
311 including. the gyration radius, hydrogen bonding, mean square displacement as well as  
312 radial distribution functions was calculated. This study, provided a molecular and atomistic  
313 insight into the doxorubicin, Poly (n-isopropyl acrylamide), and carbon nanotube interaction  
314 which is a prerequisite of developing novel nanomedicine systems for pre experimental drug  
315 development studies. Particularly, simulation results indicated that the drug loading at  
316 298.15K and 310.15K have stronger interaction in comparsion with 288.15K. This result is  
317 related to percence of injectable and thermo-sensitive hydrogel in delivery systems.  
318 Furthermore, According to Gibss energy calculation,.....so the .....temprature is  
319 appropriate value for loading of dox. For the subsequent studies, researchers could  
320 investigate the condition of the Physico-chemical properties of DOX/NIPA@CNT.

## 321 **Materials and Methods**

### 322 **1- Molecular dynamics**

323 Gromacs version 5.1.2 software was used to perform the simulation. Ambertools software  
324 was used to obtain the polymer optimum parameters. The OPLS-aa force field was used and  
325 the TIP3P water model was adopted as the solvent. Parameters of Ambertools were  
326 converted to Gromacs using the ACPYPE script.

327 The parameters analyzed in these simulations are:

- 328 1- The gyration radius or aggregation of polymer molecules at one point
- 329 2- The number of hydrogen bonds between the polymer/polymer, polymer/drug,  
330 polymer/nanotube, and drug/nanotube
- 331 3- The van der Waals energy between the polymer-polymer, polymer-drug, polymer-  
332 nanotube, and drug-nanotube
- 333 4- The mean displacement square at three various temperatures
- 334 5- The radial distribution function of the polymer, drug, and nanocarrier

335 In this simulation, we will label the polymer as NIPA, the drug as DOX, and the nanotube as  
336 CNT. Calculations and simulations were performed using the Gromacs software, and all  
337 images and charts were provided using the VMD® 1.9.3 and OriginLab® software.

338 The gyration radius can indicate the interactions between the polymer chains and solvent  
339 molecules. Gyration radius is a parameter that can be used to analyze the accumulation or  
340 aggregation of the molecules such as polymers and resize biological macromolecules such as  
341 proteins and nucleic acids over time. The gyration radius is obtained from the following  
342 formula:

343

$$344 \quad R_g^2 = \frac{1}{2N^2} \sum_{i,j} (r_i - r_j)^2 \quad (1)$$

345 where, 'N' is the number of monomers, and 'r' is the location vector of each monomer.

346 Radial distribution function (RDF) was used to compare the drug molecules distribution  
347 around the polymer and to calculate the aggregation of drug molecules and drug-polymer  
348 diffusion. The drug-polymer radial distribution function is the probability of finding an atom  
349 of the drug molecule at a radial distance 'r' from an atom of the polymer molecule.

350 Moreover, the RDF of the drug-drug is the probability of finding one atom of the drug  
351 molecule at a radial distance from an atom of the drug molecule. The general formula for the  
352 radial distribution function is as follows:

353

$$354 \quad g_{AB}(r) = \frac{\rho_{B(r)}}{\rho_{B(local)}} \quad (2)$$

355

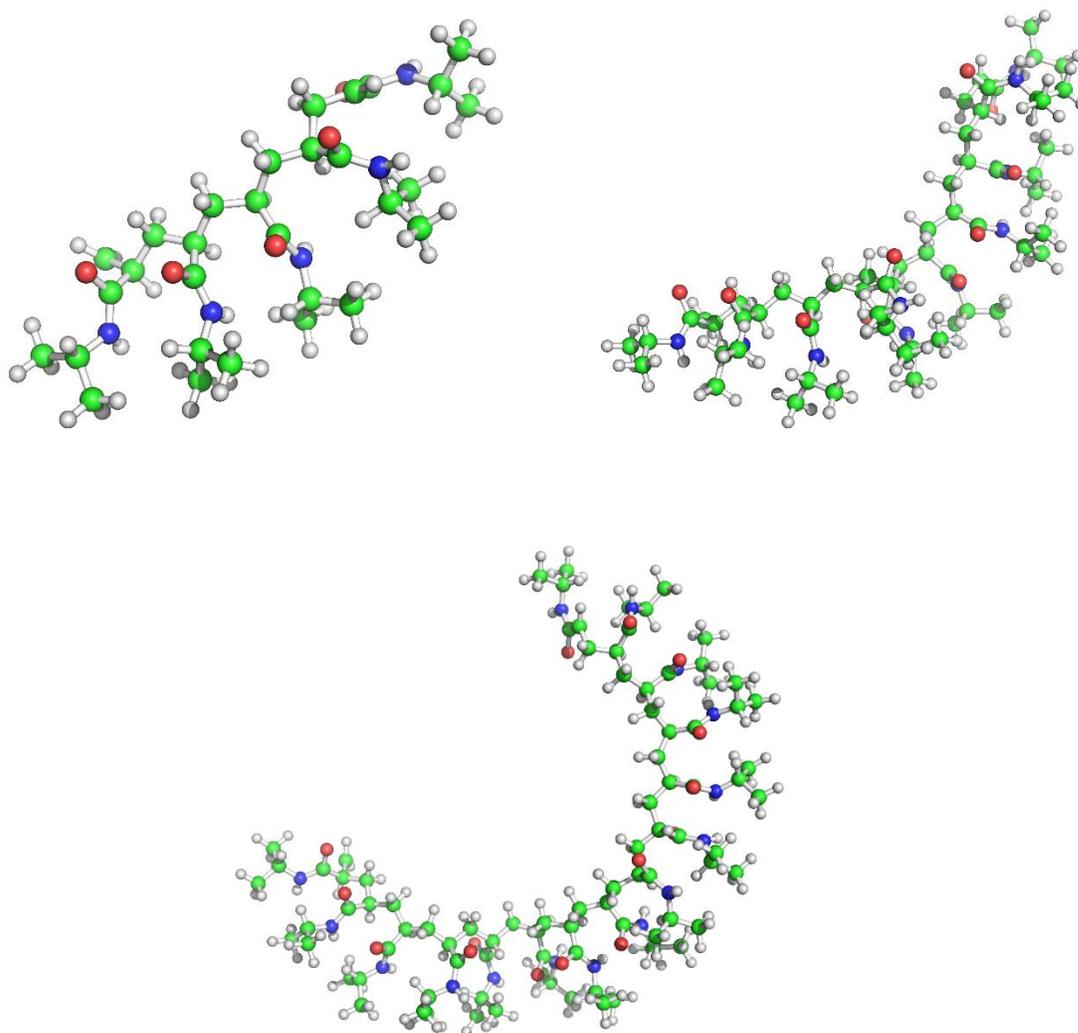
356 In this equation, 'ρ' is the density of the particle at 'r' distance.

357 Figure 1 shows a three-dimensional schematic of the 5-mer, 10-mer, and 15-mer polymer  
358 molecules of the N-isopropyl acrylamide.

359

360

361



362

363 **Figure 1.** The 3D image of the 5-mer, 10-mer, and 15-mer polymer

364

365 **Table 1:** Surface charge of polymer atoms with single mer

Atom	BCC	$\Sigma$
C1	-0.23	0.34
H8	0.08	0.265

H9	0.08	<del>0.365</del> 0.265
H10	0.08	<del>0.367</del> 0.265
C	0.021	0.34
C2	-0.23	<del>0.368</del> 0.34
H5	0.08	<del>0.365</del> 0.265
H6	0.08	<del>0.370</del> 0.265
H7	0.08	0.265
H1	0.13	<del>0.371</del> 0.247
N	-0.381	<del>0.325</del> 0.225
H	0.219	<del>0.373</del> 0.107
C3	0.335	0.34
O	-0.379	<del>0.374</del> 0.296
C4	-0.22	<del>0.375</del> 0.34
H2	0.128	<del>0.376</del> 0.26
C5	-0.133	<del>0.377</del> 0.34
H3	0.129	0.26
H4	0.129	<del>0.378</del> 0.26

379

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382

383 There are noticeable Hydrogen bonds and electrostatic interactions between the drug and N-  
384 isopropyl acrylamide. Therefore, measuring the surface charges of the system is very important.  
385 One popular and appropriate mathematical method to precisely calculate the surface charge in  
386 quantum mechanics (QM) is the Bond Charge Correction (BCC) method. Table 1 shows the  
387 monomer parameters in the polymer according to the surface charge correction method.

## 388 **2- Structure preparation**

389 The crystal structures of the DOX were obtained from the DrugBank database (Accession  
390 Number: DB00997). By employing the Avogadro and Gaussian software, the NIP structural  
391 topology and structure were determined and optimized. The CNT structure was designed with  
392 Nanotube Modeler 1.7.9 software.

## 393 **3- Molecular dynamics simulation**

394 In this study, N-isopropyl acrylamide polymer (NIPA) was used in the presence of CNT to  
395 investigate the uptake and loading of the doxorubicin as an anticancer agent. According to our  
396 previous study (41), polymer sizes were selected for simulation in three modes:

397 1- A polymer with five subunits length (15 polymers of 5-unit polymers were used in this  
398 simulation, and the total number in the simulation box was 75).

399 2- A Polymer with 10 mer lengths (8 number of 10-unit polymers were used in this  
400 simulation)

401 3- A Polymer with 15 mer length (5 polymers of 15-unit polymers were used in this  
402 simulation)

403 The number of simulations was three and the duration was 30 nanoseconds. In the first  
404 simulation, 15 5-unit polymers with five drugs and one nanotube were used. In the second

405 simulation, eight polymers of 10 units with five drugs and one nanotube were used and in the  
 406 third simulation, five polymers of 15 units with five drugs and one nanotube were used. As  
 407 reported in our last study, the optimum length of the NIPA chains was obtained to be 5-mer  
 408 hydrogel; hence, we developed this polymer for our current study to investigate the DOX  
 409 loading. In particular, three different temperatures including 288.15 K, 298.15 K, and 310.15 K  
 410 were assumed as the critical points and the loading of drugs was developed at these three  
 411 temperatures. Furthermore, by applying the Umbrella Sampling simulation method, we  
 412 calculated the Gibbs free energy of the system during our MD simulations.

413 **List of abbreviations**

<b>Abbreviations</b>	<b>Full form</b>
CNT	Carbon nanotube
NIPA	N-isopropyl Acrylamide
DOX	Doxorubicin
Fig	Figure
GROMACS	Groningen machine for chemical simulations
<i>OPLS-aa</i>	Optimized Potentials for Liquid Simulations-all atom
MD	Molecular dynamics
Rg	Radius of Gyration
BCC	Bond Charge Correction
QM	quantum mechanics
RDF	radial distribution function
ACPYPE	AnteChamber Python Parser interface
MSD	Mean square displacement

LCST	low critical solution temperature
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414

415 **Declarations**

416 **Ethics approval and consent to participate**

417 Not applicable

418 **Consent for publication**

419 Not applicable

420 **Availability of data and materials**

421 The datasets used and/or analysed during the current study are available from the corresponding  
422 author on reasonable request.

423 **Competing interests**

424 The authors declare that they have no competing interests

425 **Funding**

426 This research received no external funding

427 **Author Contributions**

428 Reza Maleki and Mohammad Dahri: conceptualization, methodology, software, analysis,  
429 visualization, data curation .Hossein Akbarialiabad: conceptualization and writing the original  
430 draft. Amirhossein Hasanpoor & Ebrahim Gasemi: supervision, writing, review, and editing

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# Figures

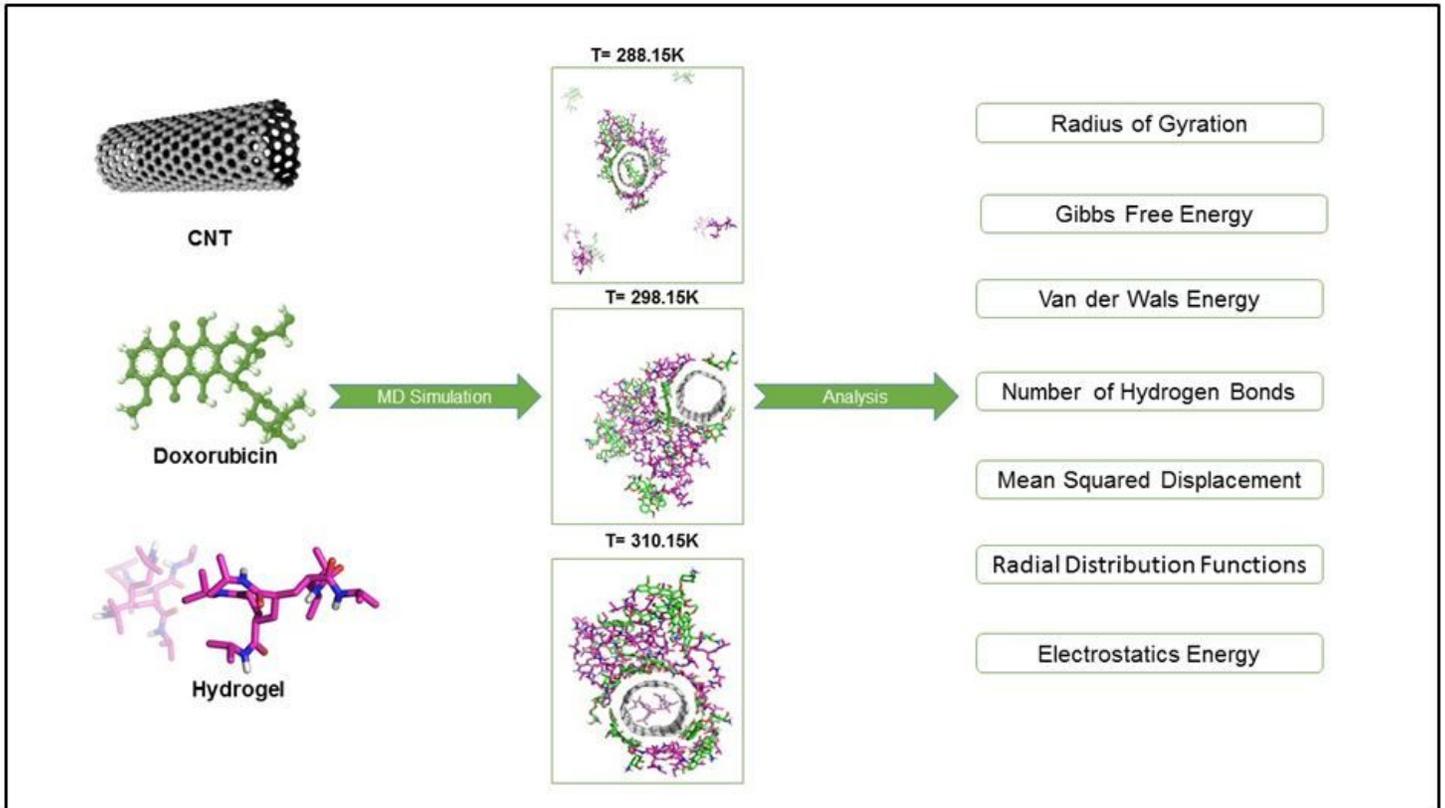


Figure 1

Flow Chart

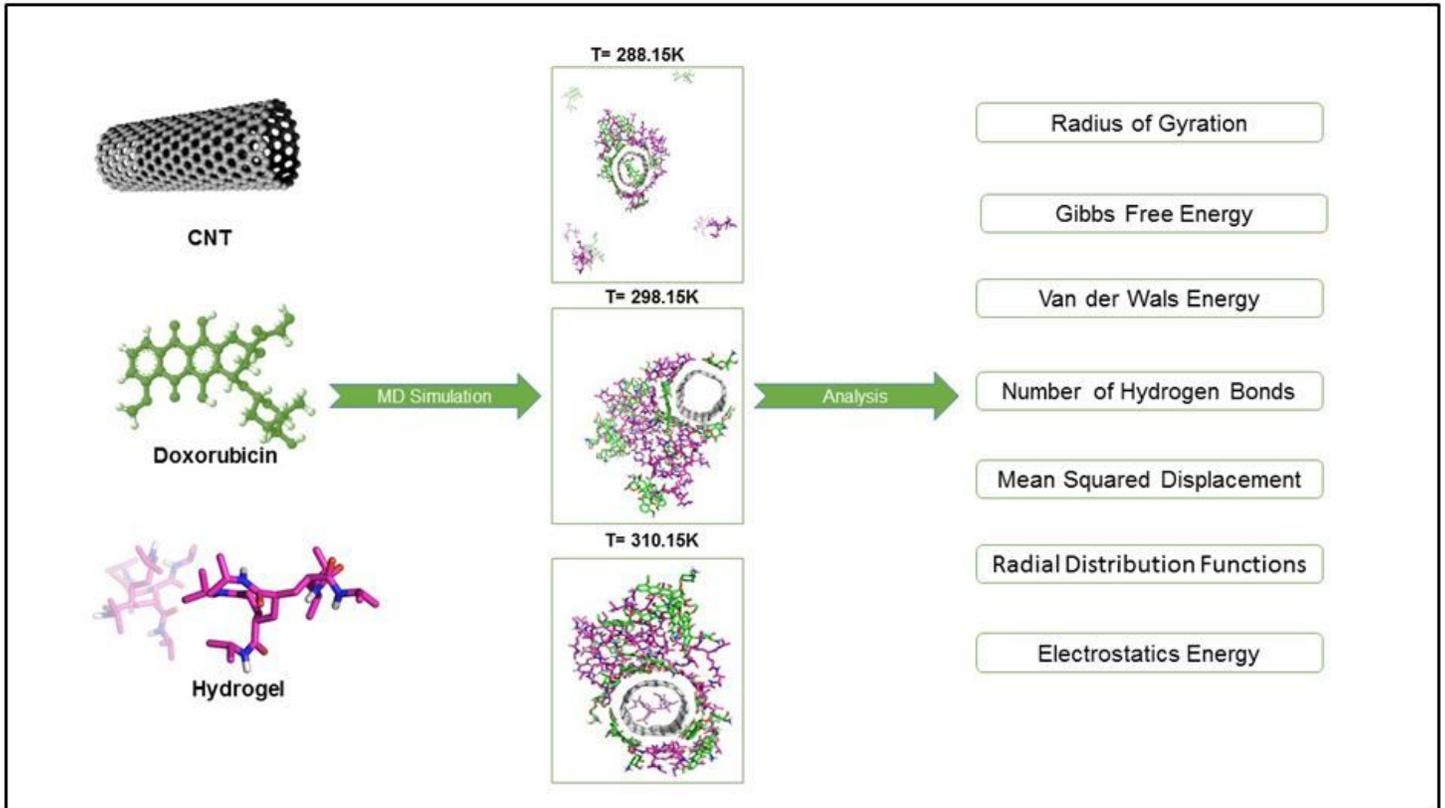
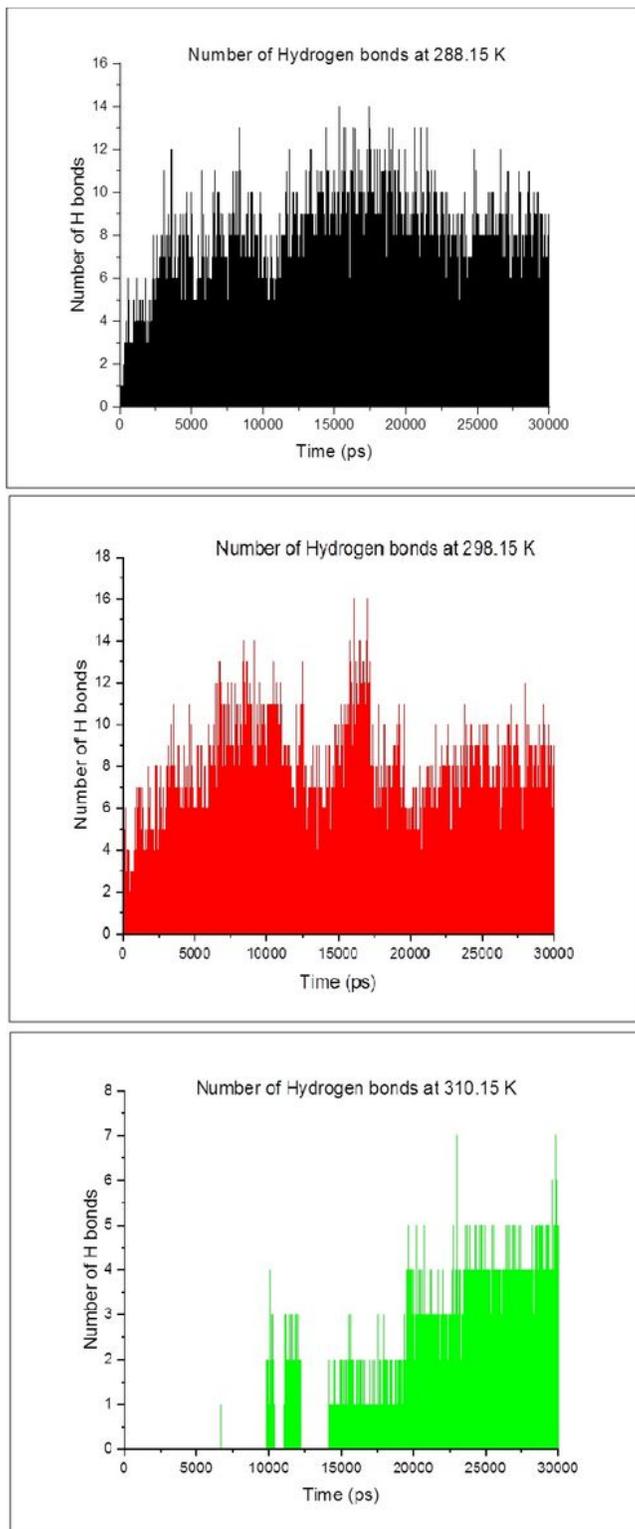


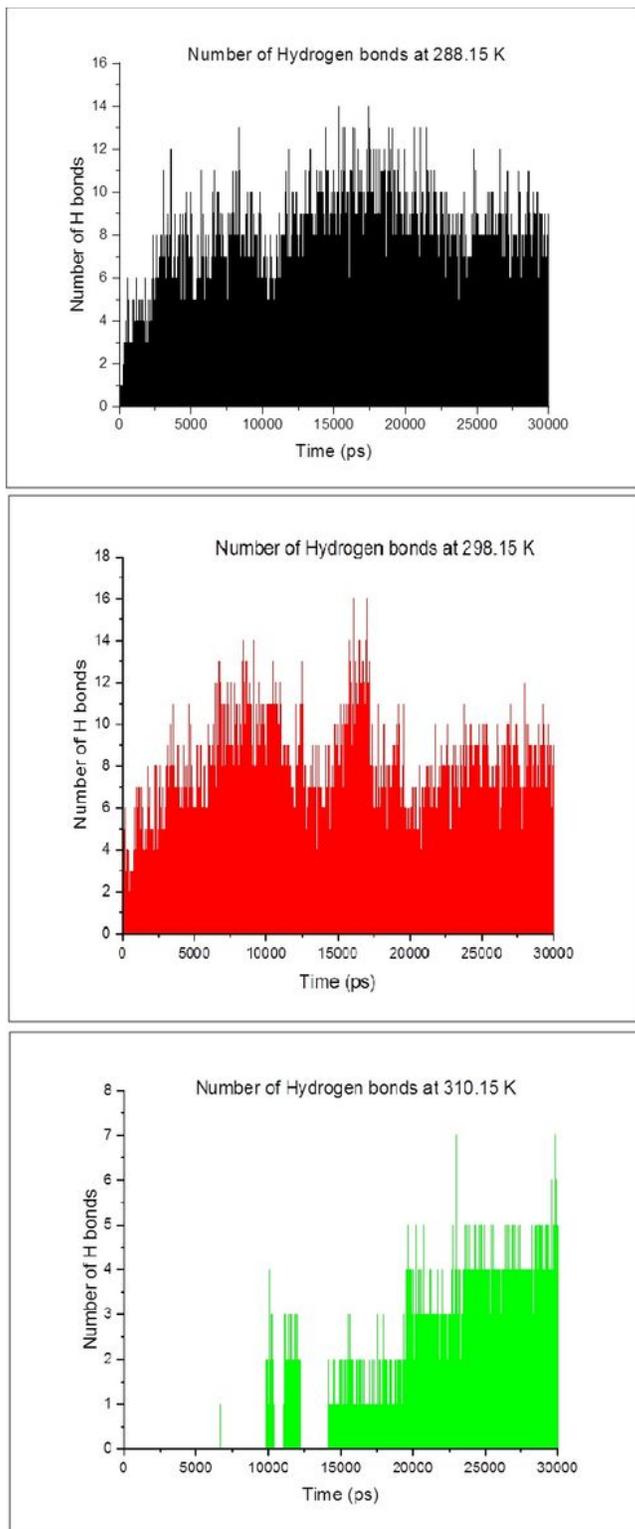
Figure 1

Flow Chart



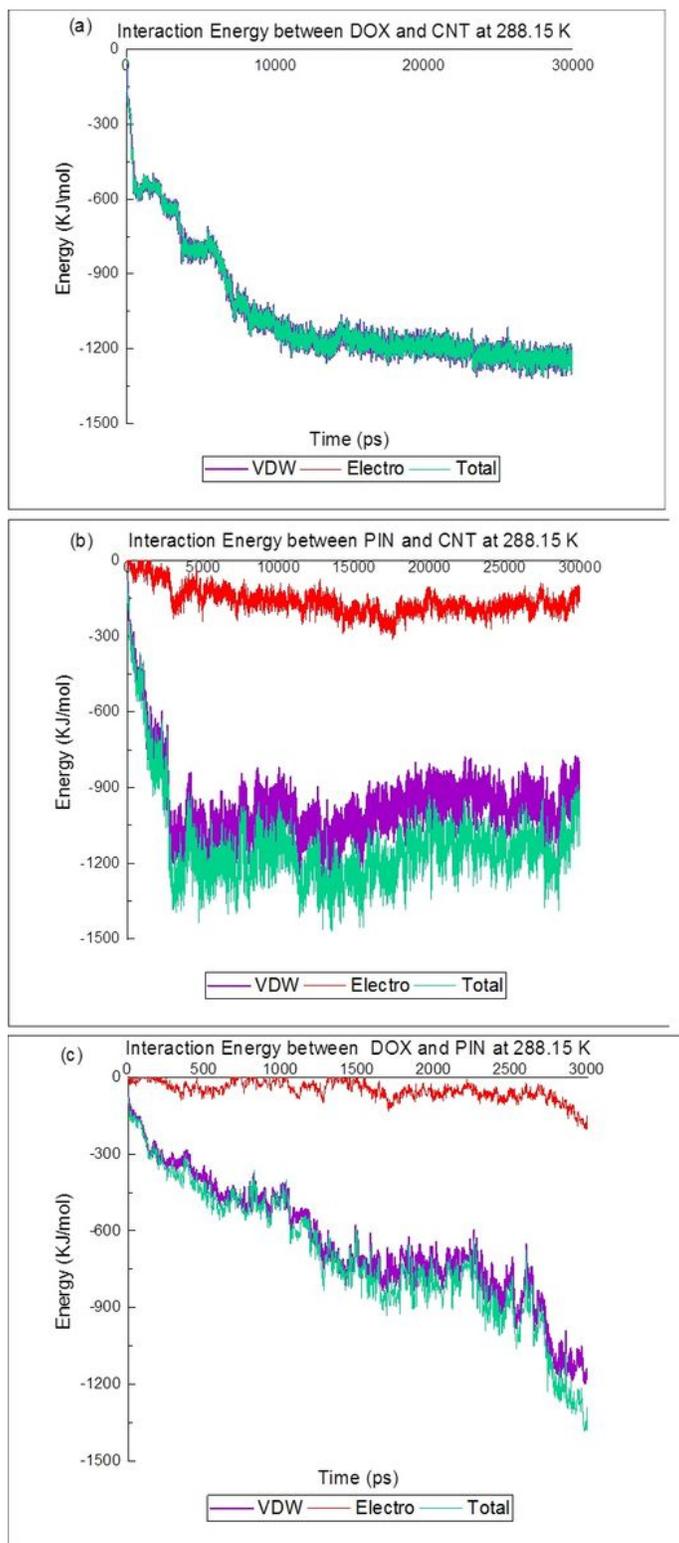
**Figure 2**

The numbers of hydrogen bonds between DOX and NIPA at three different temperatures



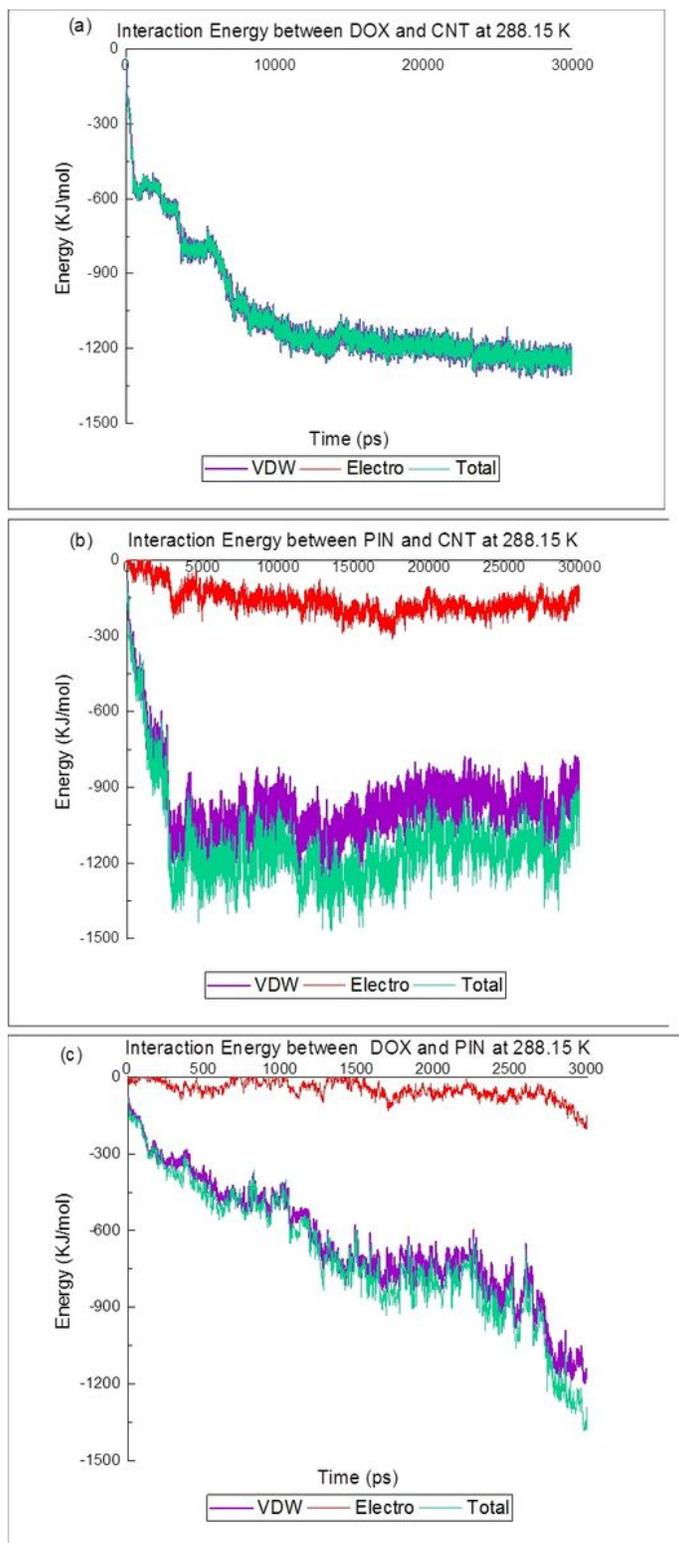
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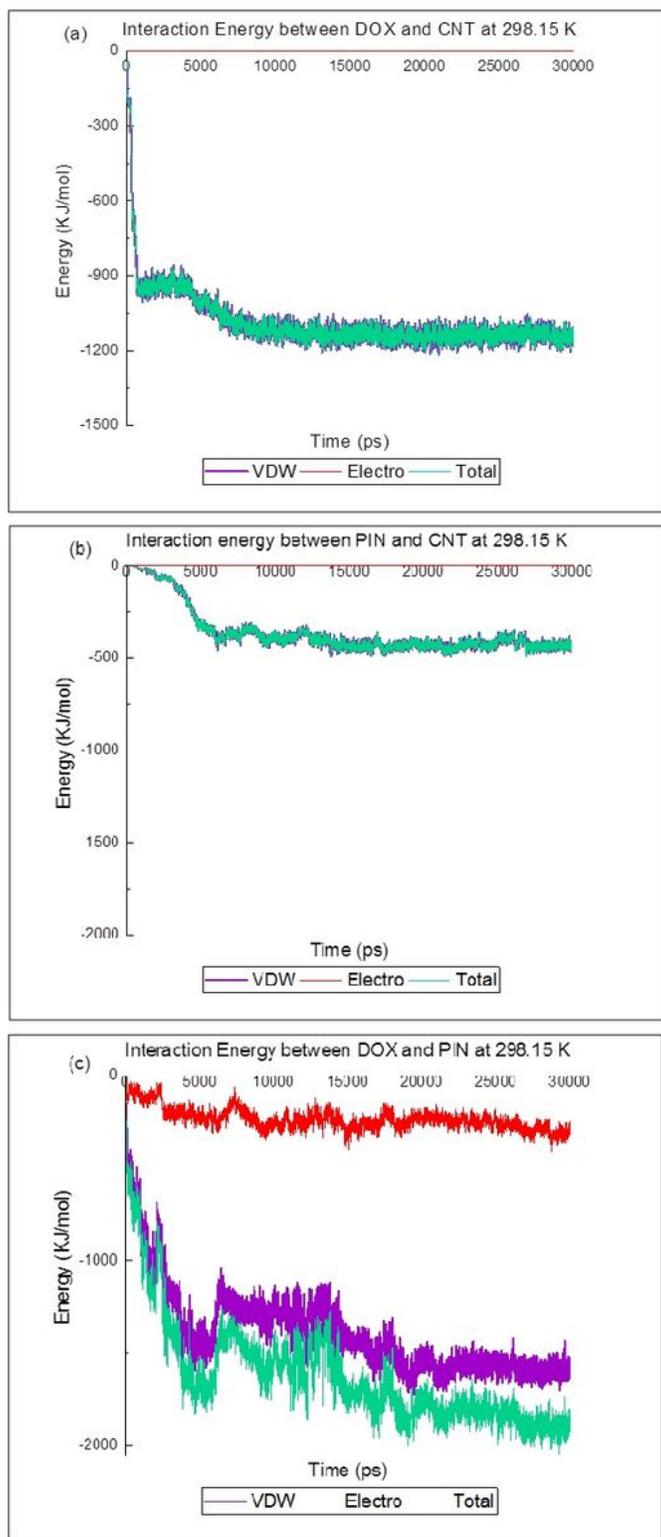
**Figure 3**

Interaction energies diagrams at 288.15 K (a) Electrostatic and van der Waals energies of DOX@CNT interaction versus time at 288.15 K; (b) Electrostatic and van der Waals energies of NIPA@CNT interaction versus time at 288.15 K; (c) Electrostatic and van der Waals energies of DOX@NIPA interaction versus time in 288.15 K



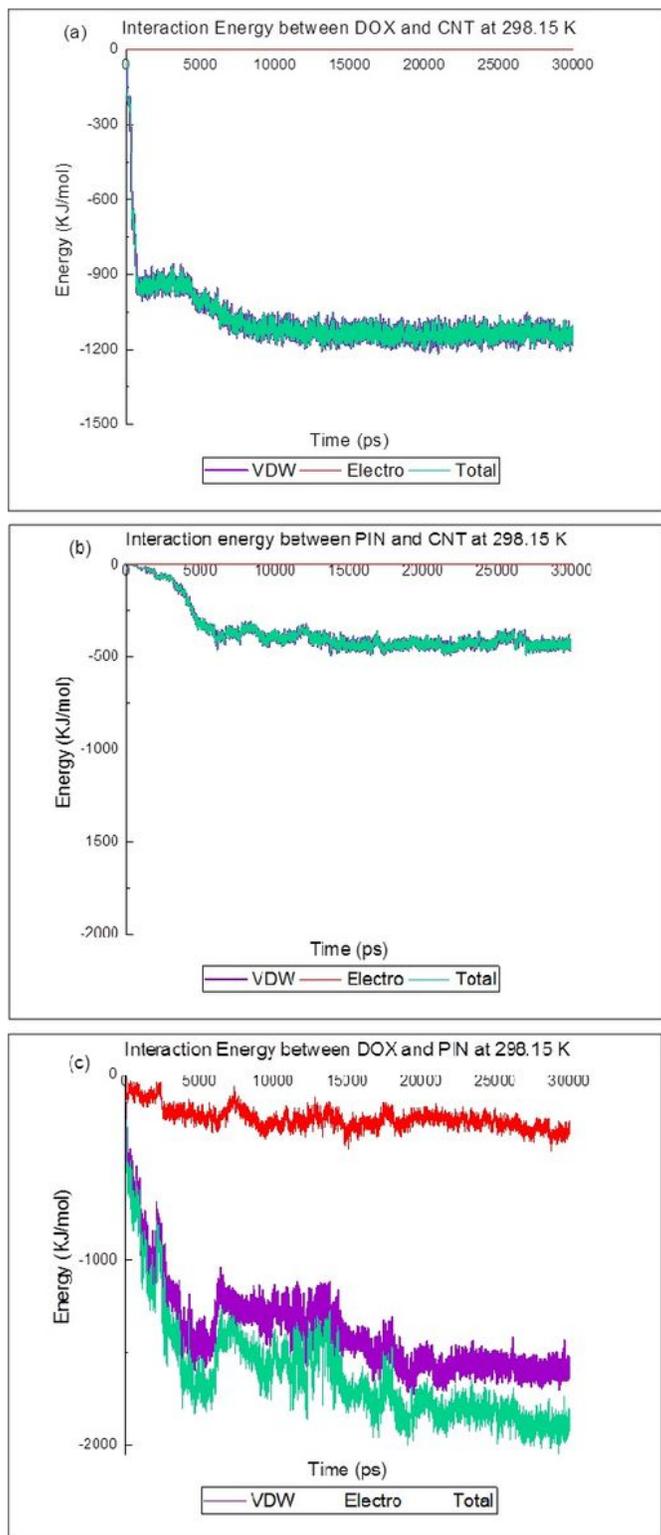
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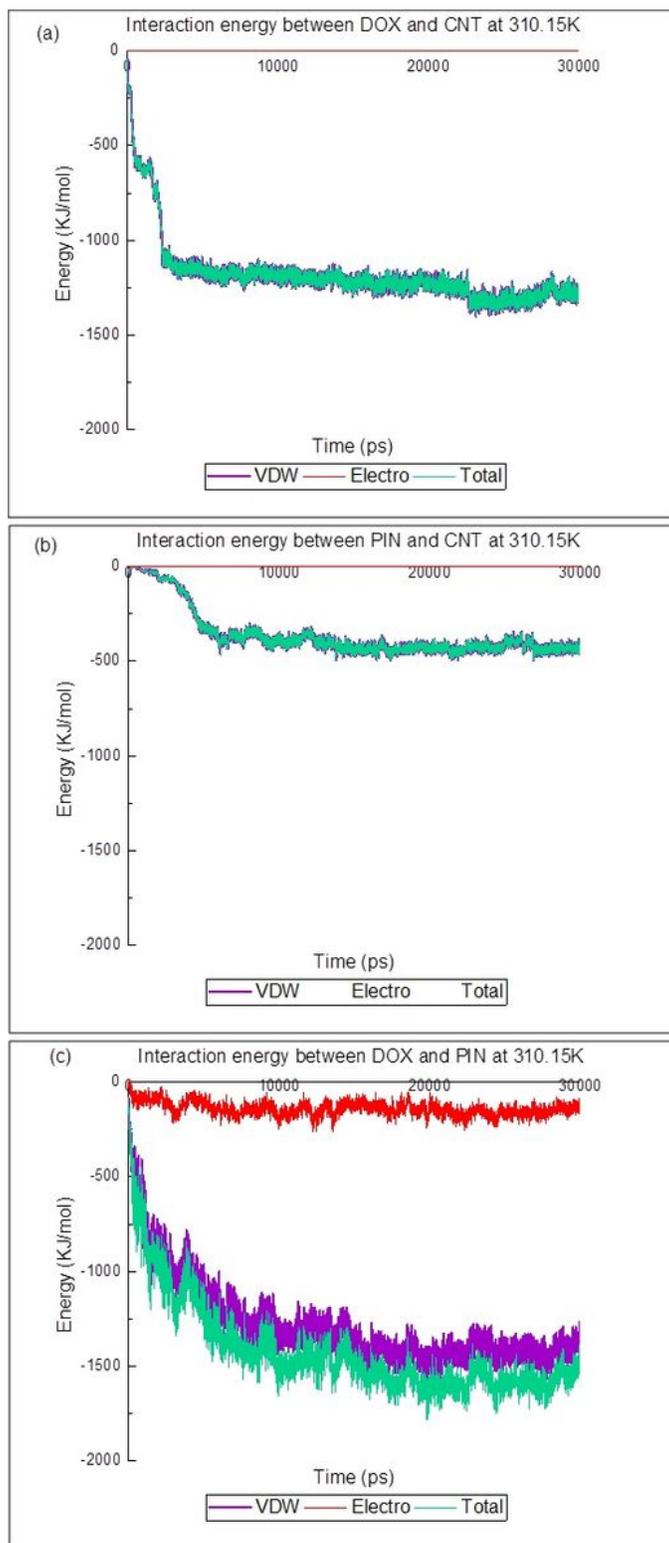
**Figure 4**

Interaction energies diagrams at 298.15 K (a) Electrostatic and van der Waals energies of DOX@CNT interaction versus time at 298.15 K; (b) Electrostatic and van der Waals energies of NIPA@CNT interaction versus time at 298.15 K; (c) Electrostatic and van der Waals energies of DOX@NIPA interaction versus time in 298.15 K.



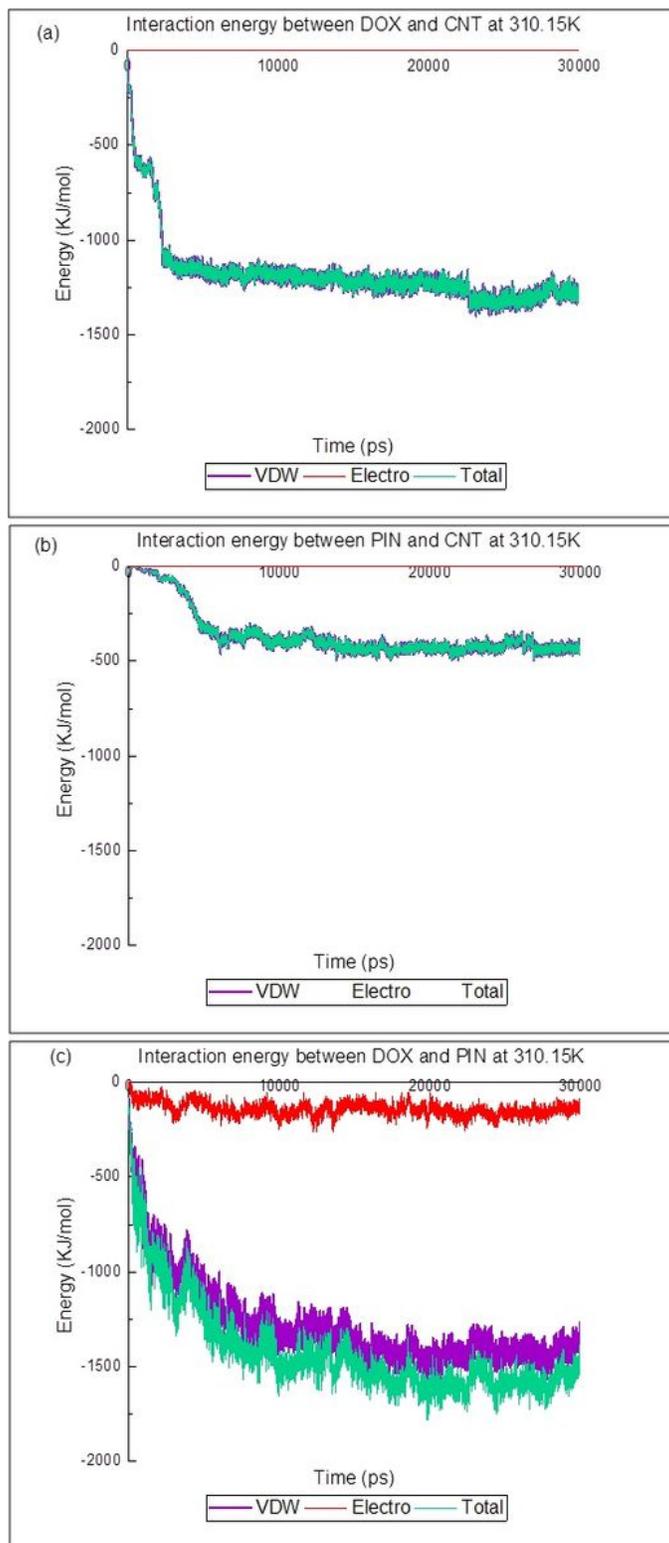
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Interaction energies diagrams at 298.15 K (a) Electrostatic and van der Waals energies of DOX@CNT interaction versus time at 298.15 K; (b) Electrostatic and van der Waals energies of NIPA@CNT interaction versus time at 298.15 K; (c) Electrostatic and van der Waals energies of DOX@NIPA interaction versus time in 298.15 K.



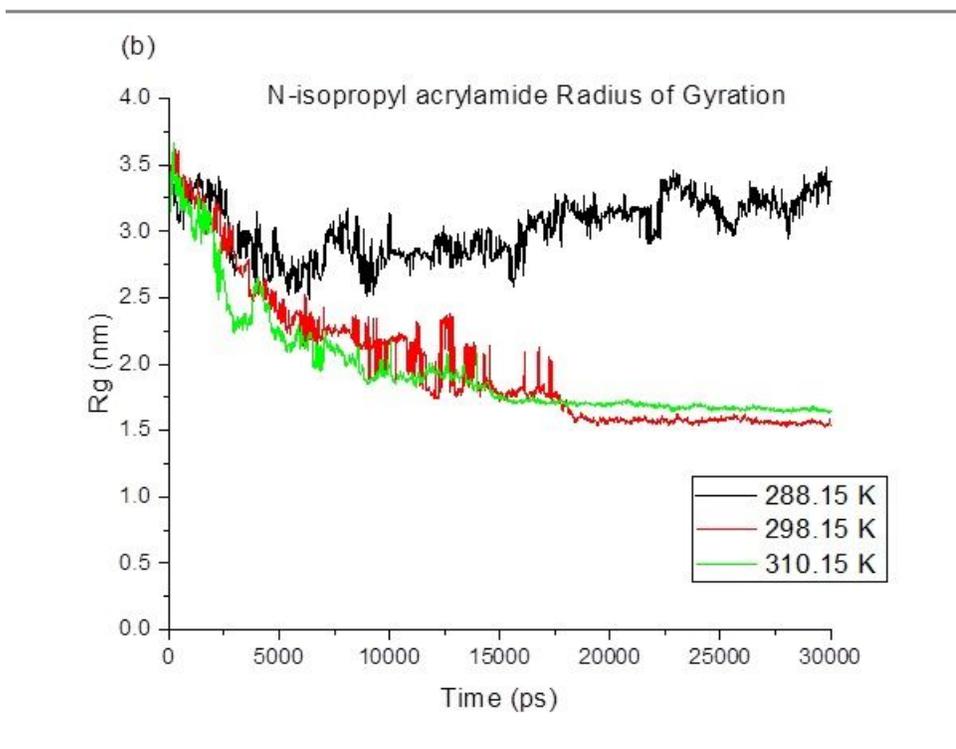
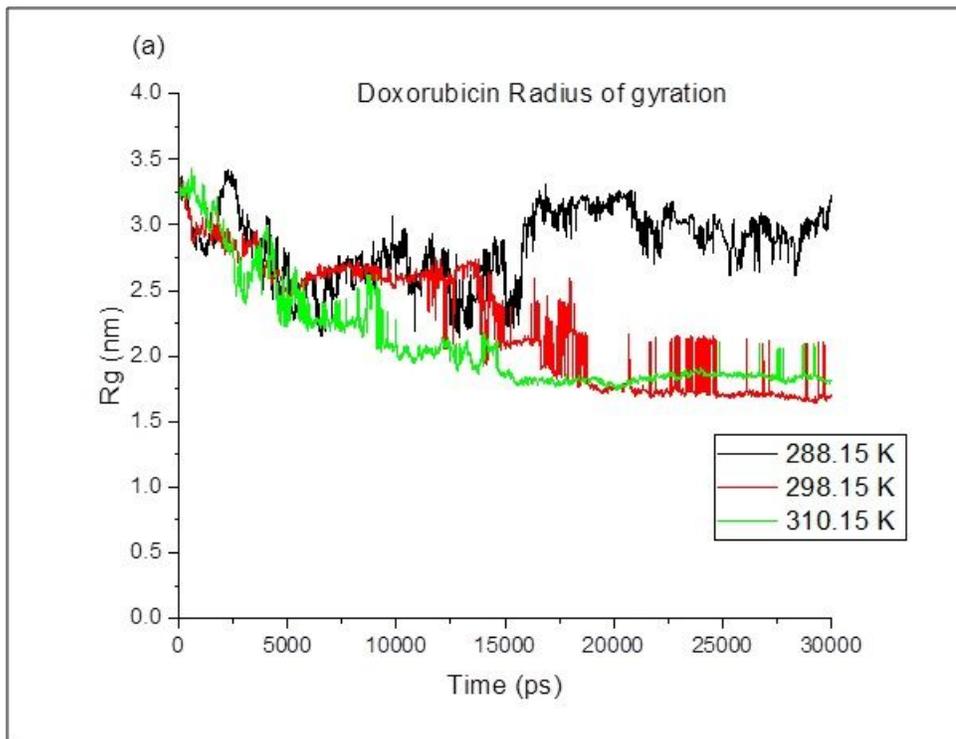
**Figure 5**

Interaction energies diagrams at 310.15 K (a) Electrostatic and van der Waals energies of DOX@CNT interaction versus time at 310.15 K; (b) Electrostatic and van der Waals energies of NIPA@CNT interaction versus time at 310.15 K (c) Electrostatic and van der Waals energies of DOX@NIPA interaction versus time in 310.15 K.



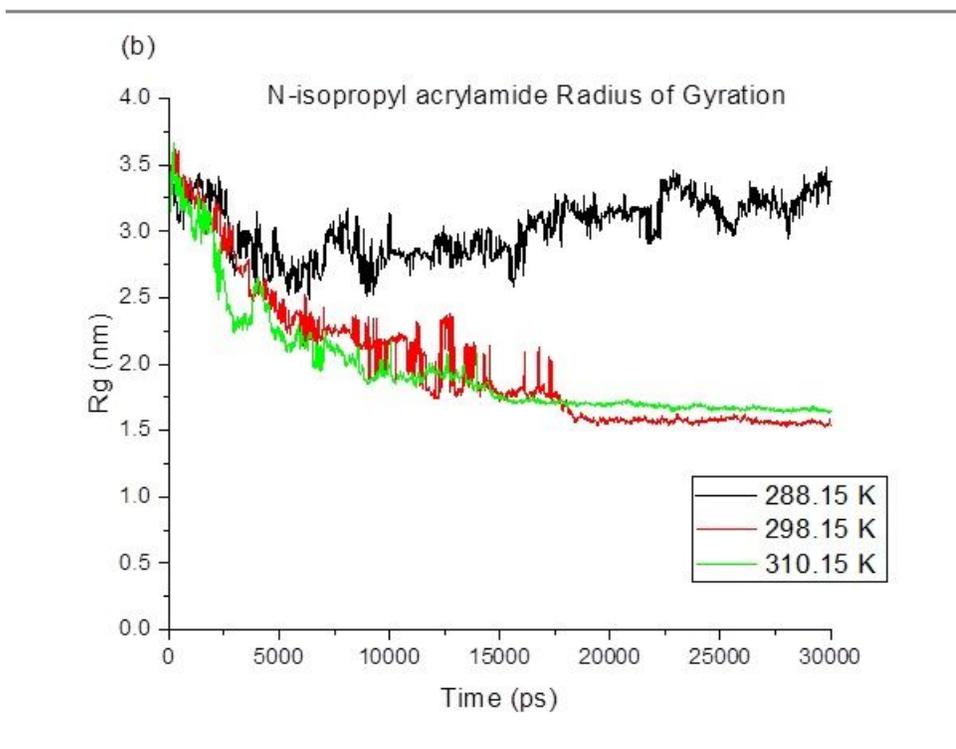
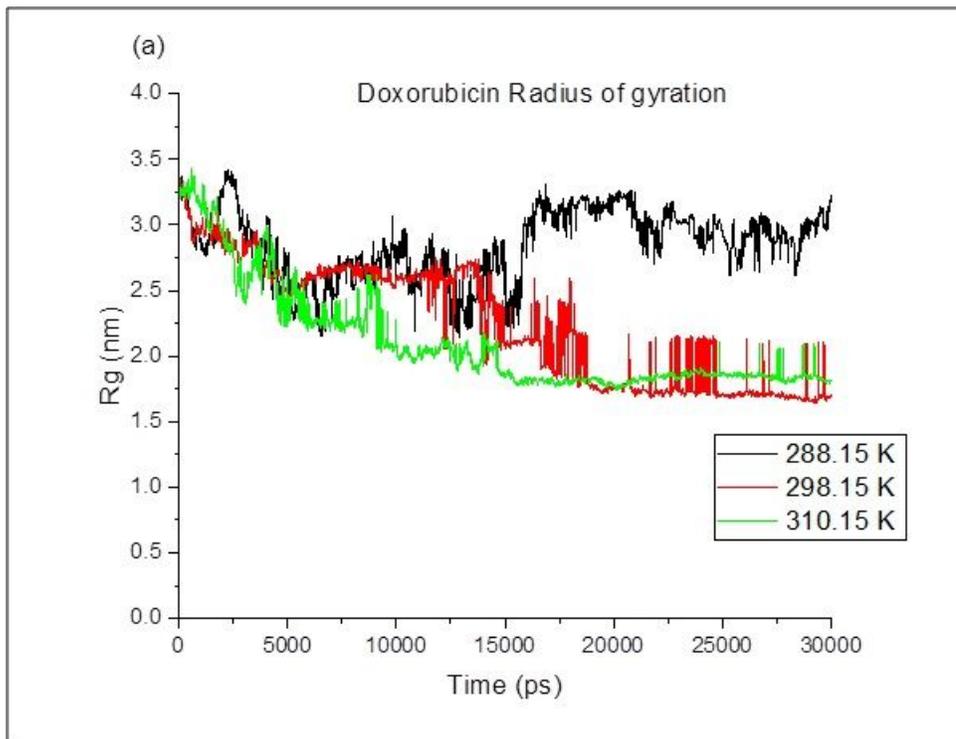
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Interaction energies diagrams at 310.15 K (a) Electrostatic and van der Waals energies of DOX@CNT interaction versus time at 310.15 K; (b) Electrostatic and van der Waals energies of NIPA@CNT interaction versus time at 310.15 K (c) Electrostatic and van der Waals energies of DOX@NIPA interaction versus time in 310.15 K.



**Figure 6**

Gyration Radius of Molecules versus time in different temperatures for CNT carrier: (a) DOX Rg at three temperatures (b) NIPA Rg at three temperatures



**Figure 6**

Gyration Radius of Molecules versus time in different temperatures for CNT carrier: (a) DOX Rg at three temperatures (b) NIPA Rg at three temperatures

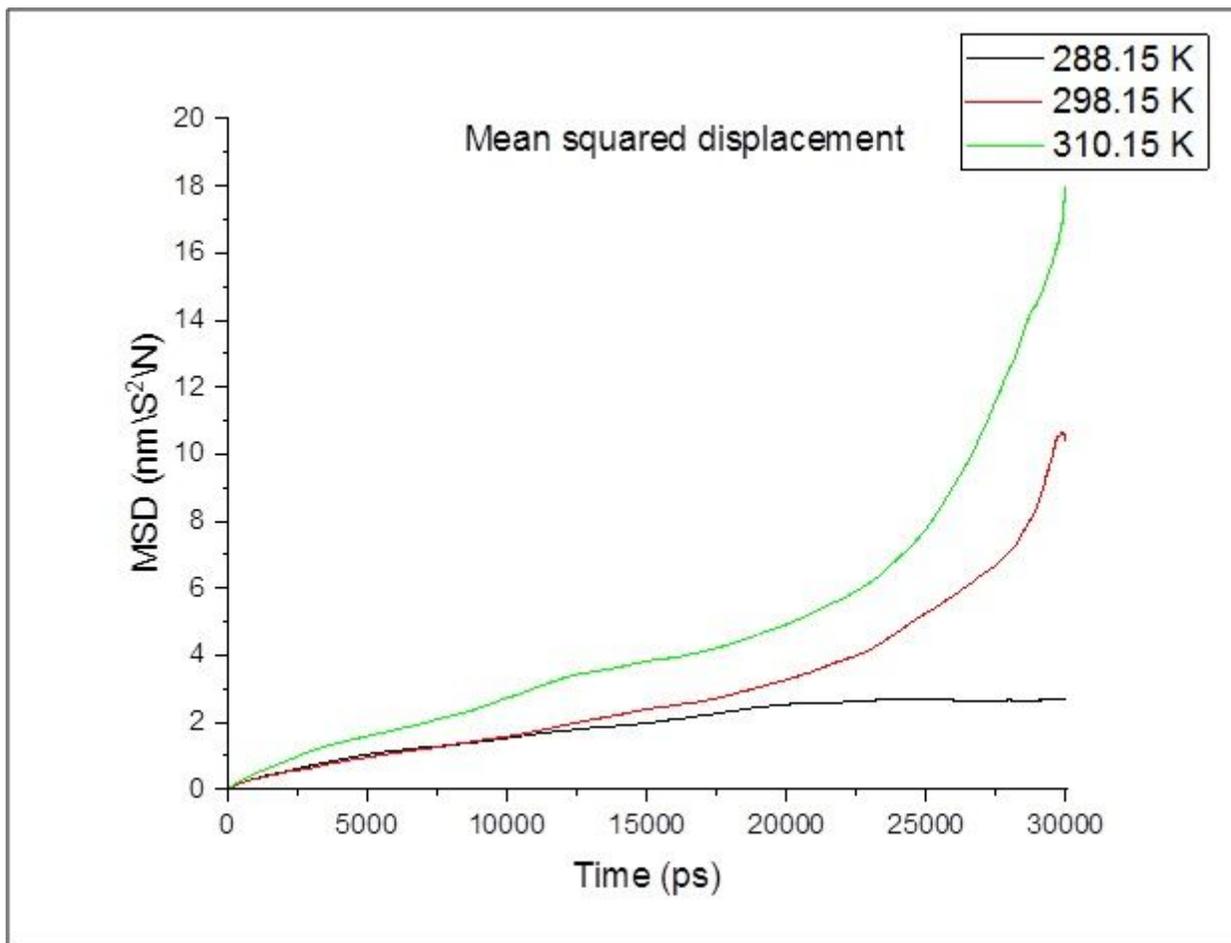


Figure 7

Mean square displacement of the system versus time at different temperature

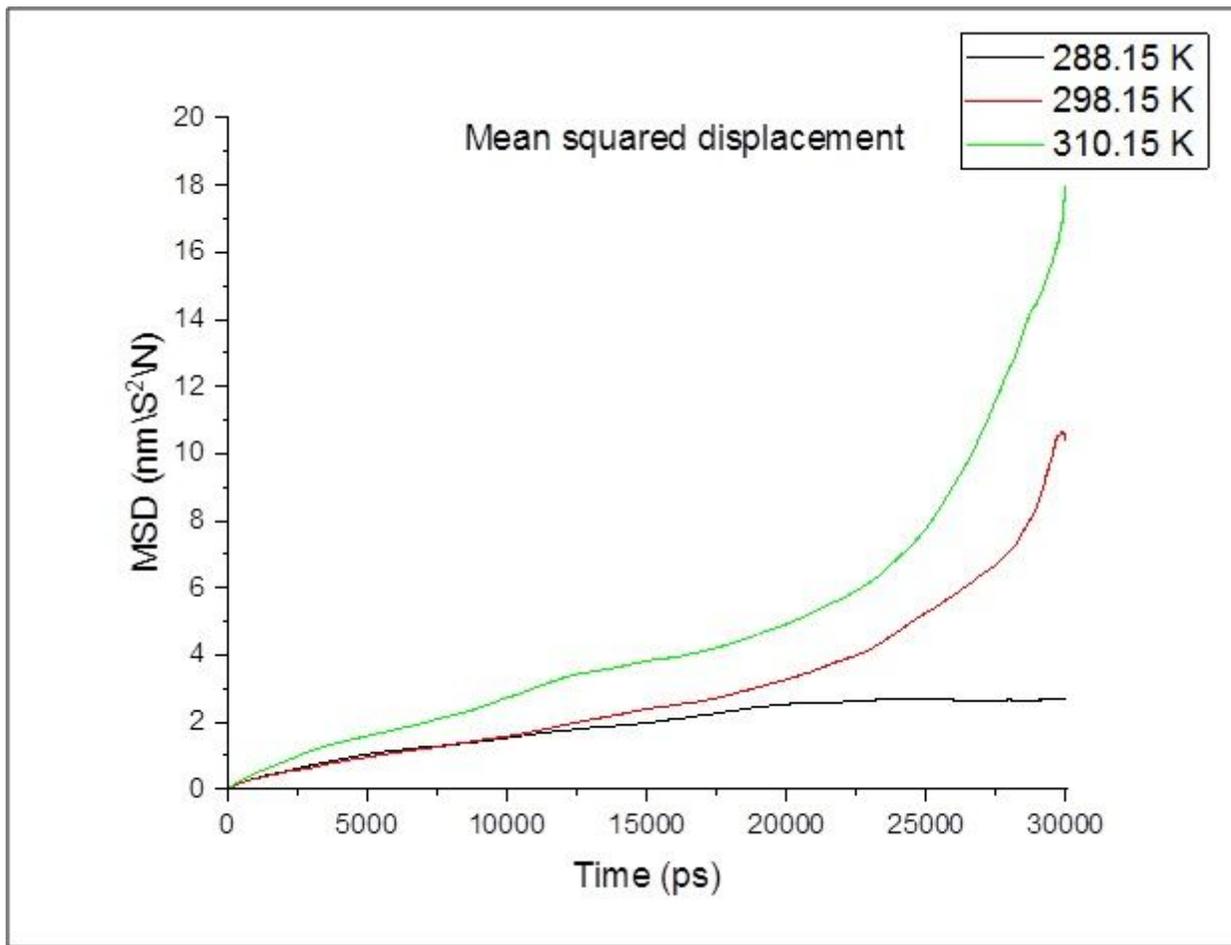
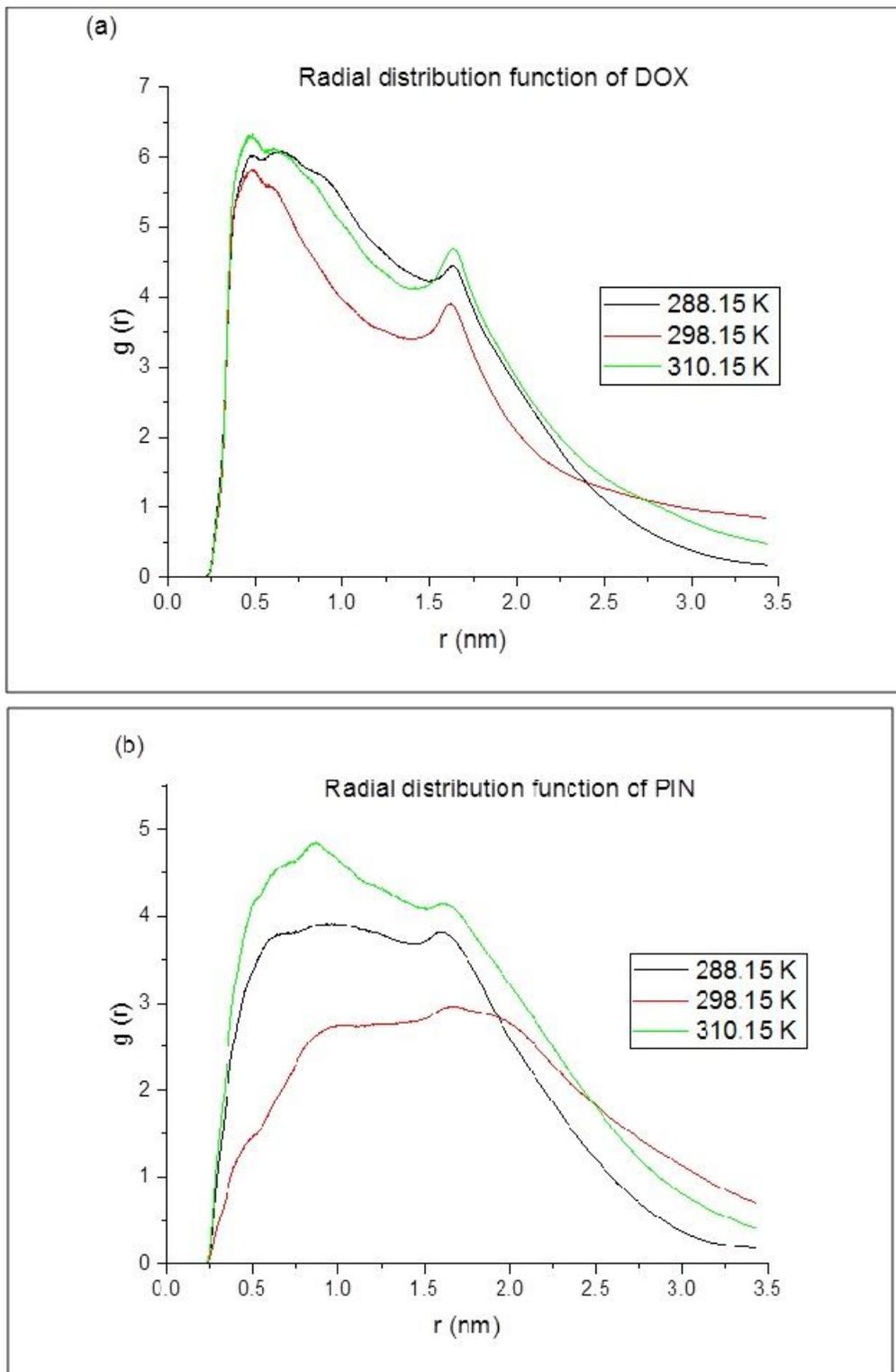


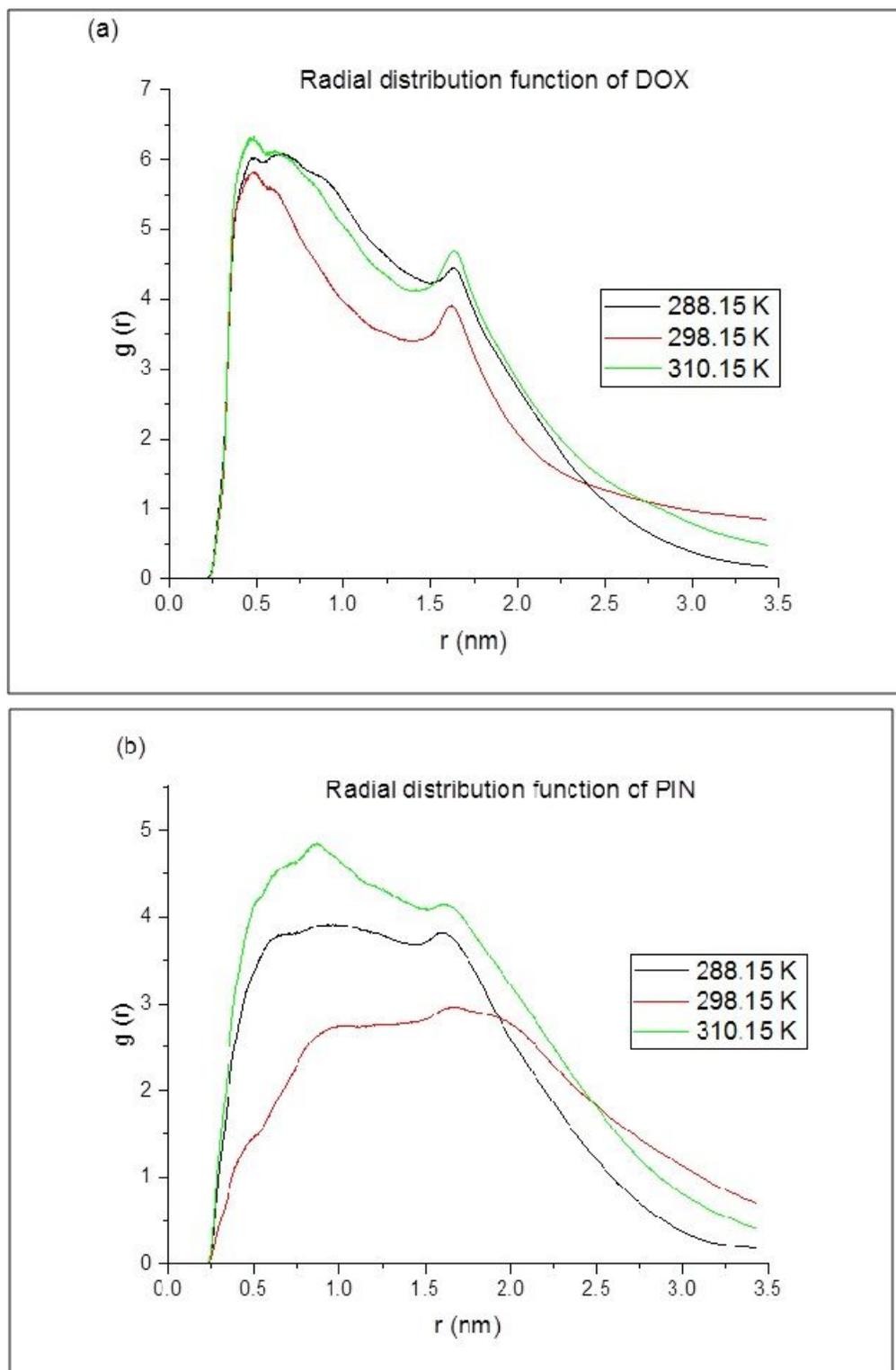
Figure 7

Mean square displacement of the system versus time at different temperature



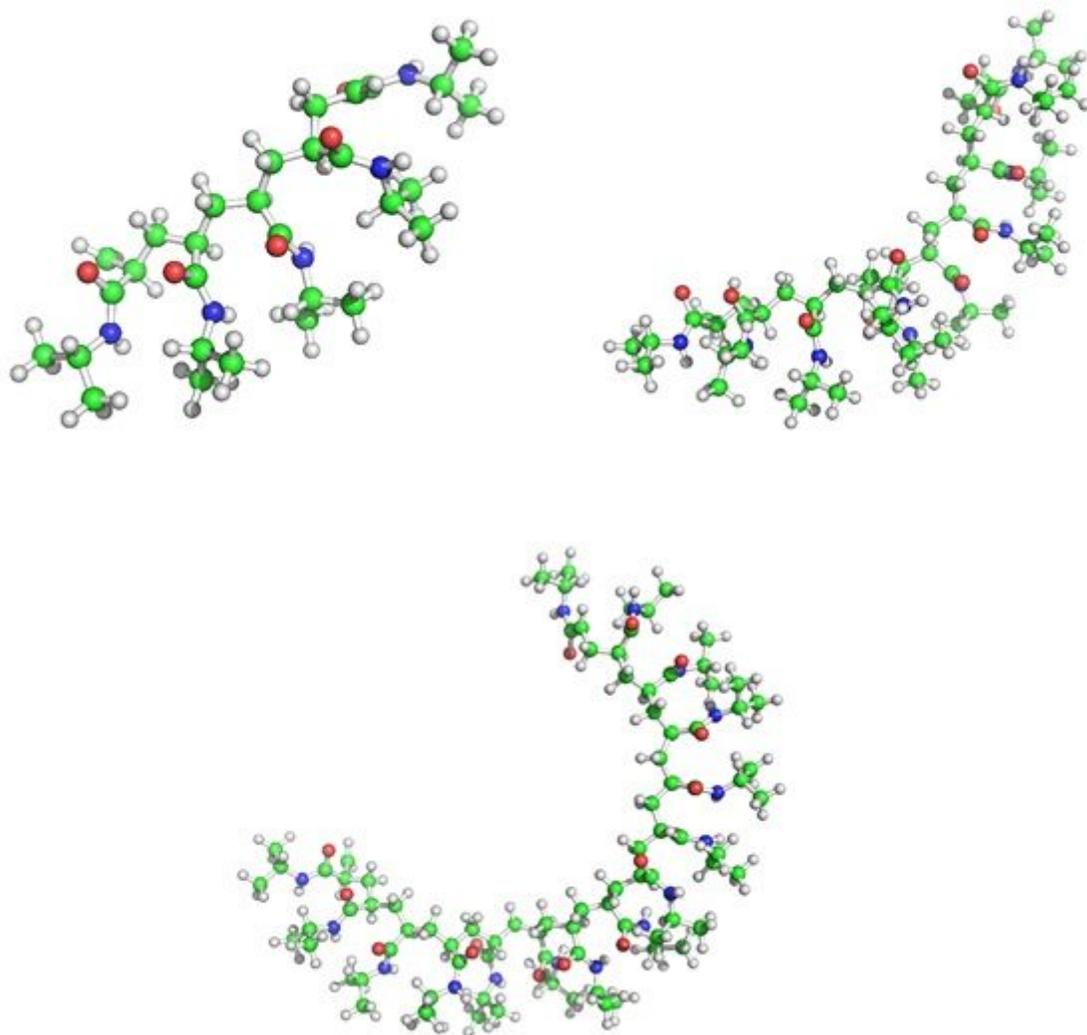
**Figure 8**

The radial distribution function of the DOX@CNT and NIPA@CNT versus location at different temperatures: (a) The RDF of the DOX at three temperatures; and (b) the RDF of the NIPA at three temperatures.



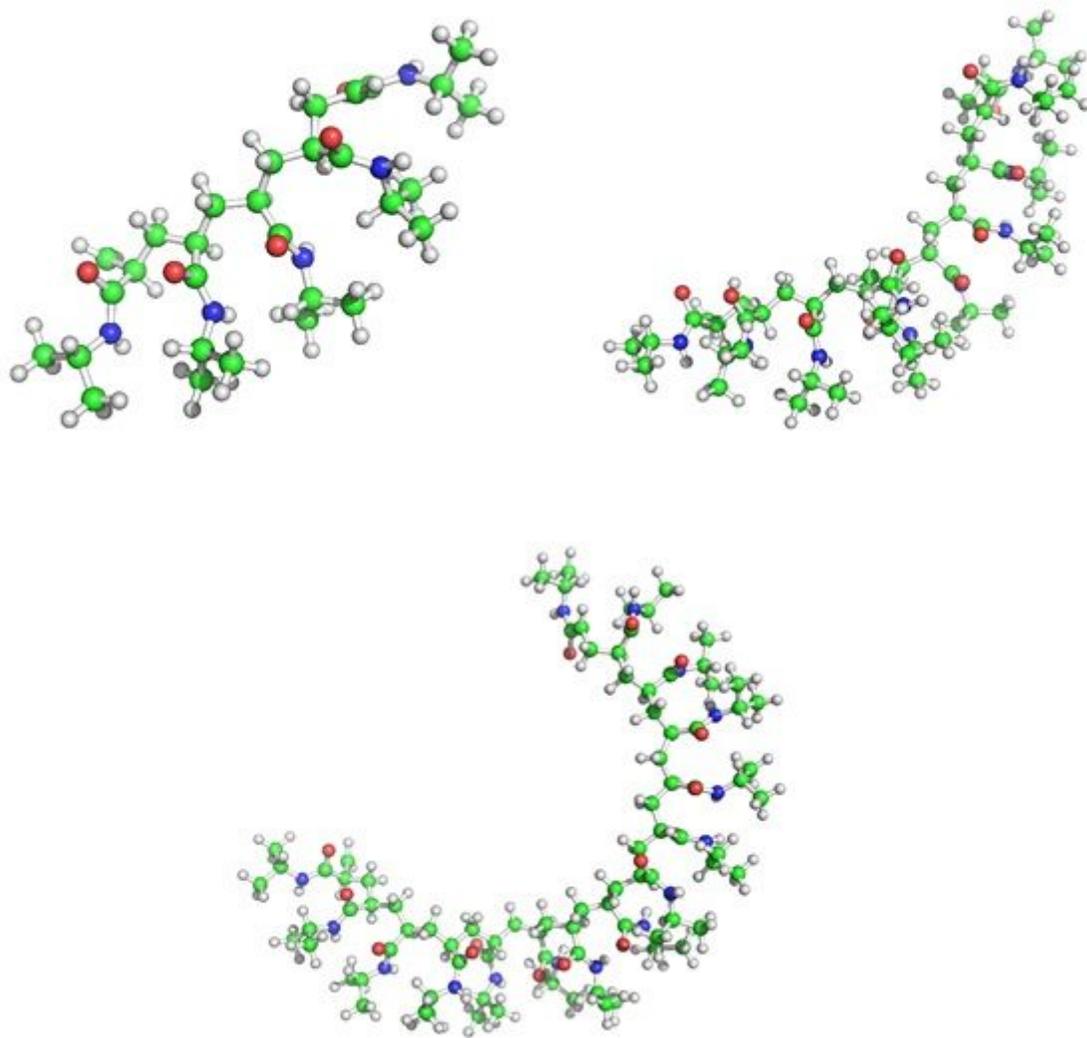
**Figure 8**

The radial distribution function of the DOX@CNT and NIPA@CNT versus location at different temperatures: (a) The RDF of the DOX at three temperatures; and (b) the RDF of the NIPA at three temperatures.



**Figure 9**

The 3D image of the 5-mer, 10-mer, and 15-mer polymer



**Figure 9**

The 3D image of the 5-mer, 10-mer, and 15-mer polymer