## Solution behaviour of poly( N -isopropylacrylamide) stereoisomers: a molecular dynamics simulation study

G. Paradossi and E. Chiessi*

Department of Chemical Sciences and Technologies, University of Rome Tor Vergata, Via della Ricerca Scientifica I, 00133 Rome, Italy
*Corresponding author. E-mail: ester.chiessi@uniroma2.it

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Figure 1. Radial distribution functions between atoms belonging to different PNIPAM chains, calculated for m45_2 at 323 K in a time interval of 30 ns within the production run. (a) $\operatorname{CE}$ _ $C F(A)-C E \_C F(B)$ and $\mathrm{CI}(A)-\mathrm{CI}(B)$, red and blue curve, respectively. (b) $C E=C F(A)-C I(B)$. (c) $N(A)-O C(B)$.
The letters $A$ and $B$ indicate the chain, CE and CF are the carbon atoms of the methyl groups of the isopropyl moiety and Cl is the tertiary carbon atom of the isopropyl moiety. N and OC are nitrogen and oxygen atom of the amide group.
2. Polymer-Polymer Hydrogen Bonding

Table 1. Features of Polymer-Polymer Hydrogen Bonding

| Temperature <br> (K) | System | Chain | Number | Fraction of HB's between selected pairs of residues |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | of HB's per residue ${ }^{a}$ | $\mathrm{n}-(\mathrm{n}+1)^{\text {b }}$ | $\mathrm{n}-(\mathrm{n}+2)^{\text {c }}$ | $\mathrm{n}-(\mathrm{n}+3)^{\text {d }}$ | $\mathrm{n}-(\mathrm{n}+4)^{\text {e }}$ | $\mathrm{n}-(\mathrm{n}+5)^{\dagger}$ | $\begin{aligned} & \mathrm{n}-(\mathrm{n}+\mathrm{k})^{\mathrm{g}} \\ & \mathrm{k}>5 \end{aligned}$ |
| 283 | m45_2 | A | 0.07(1) | 0.54 | 0.39 | 0.00 | 0.06 | 0.00 | 0.01 |
|  |  | B | 0.07(1) | 0.51 | 0.41 | 0.00 | 0 | 0 | 0.08 |
|  | m59_2 | A | 0.09(1) | 0.71 | 0.19 | 0.05 | 0.01 | 0 | 0.04 |
|  |  | B | 0.06(1) | 0.34 | 0.63 | 0.00 | 0 | 0 | 0.03 |
| 323 | m45_2 | A | 0.12(2) | 0.64 | 0.29 | 0.01 | 0 | 0.02 | 0.04 |
|  |  | B | 0.12(2) | 0.41 | 0.42 | 0.08 | 0.08 | 0.00 | 0.00 |
|  | m59_2 | A | 0.14(2) | 0.69 | 0.12 | 0.03 | 0.15 | 0 | 0.01 |
|  |  | B | 0.14(2) | 0.50 | 0.36 | 0.03 | 0.02 | 0 | 0.09 |

${ }^{\text {a }}$. Time average and standard deviation over the production run.
${ }^{\mathrm{b}}$. Fraction of HB's formed between adjacent residues.
${ }^{\text {c }}$. Fraction of $\mathrm{HB}^{\prime}$ 's formed between residues separated by 1 repeating unit.
${ }^{\text {d }}$. Fraction of HB's formed between residues separated by 2 repeating units.
${ }^{e}$. Fraction of HB's formed between residues separated by 3 repeating units.
${ }^{f}$. Fraction of HB's formed between residues separated by 4 repeating units.
${ }^{g}$. Fraction of HB's formed between residues separated by more than 4 repeating units.


Figure 2. (a) Time behaviour of the radius of gyration of $A$ and $B$ chains (purple and brown curves, respectively) of m45_2 at 323 K . (b) Time behaviour of the radius of gyration of A and B chains (green and violet curves, respectively) of m59_2 at 323 K .

## 4. Time Evolution of Inter-residue Contacts

The matrix of the mean smallest distances between atoms of pairs of residues was calculated with a time average of 2 ns along the whole trajectory. Residues numbered from 1 to 30 form the first 30 -mer, residues numbered from 31 to 60 form the second 30 -mer. The 105 images of the map were collected in a movie, displaying the time behaviour of both intra and interchain contacts between residues. The residues located within isotactic sequences were labelled with a dot on the diagonal of the matrix, at the aim to highlight a preferential connectivity of such chain regions. The label PR in the movie indicates the time interval of production run.

Below the LCST:
files movie_m45_2_283K.avi, movie_m59_2_283K.avi

Above the LCST:
files movie_m45_2_323K.avi, movie_m59_2_323K.avi.

