عنوان مقاله:

A Comparative Molecular Dynamics Simulation Study on The Unfolding of a Bacterial Albumin-Binding Domain

محل انتشار:

نهمین همایش بیوانفورماتیک ایران (سال: 1398)

تعداد صفحات اصل مقاله: 1

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خلاصه مقاله:

Investigating the proteins at the atomic level enables the protein dynamics to be described at the microscopic level. This can lead to obtain the macroscopic parameters of a protein studying in the desired conditions. Here molecular dynamics (MD) simulation has been used as a practical tool to study the characterization and the conformational changes of a protein, especially in the studies of protein unfolding process[1,2].

کلمات کلیدی: