

## عنوان مقاله:

Investigating the ability of Lysobacter protease in the formation of nanoparticles using computational methods

## محل انتشار:

سومین همایش بین المللی تحقیقات در علوم و فناوری نانو (سال: 1402)

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## خلاصه مقاله:

The presence of hydrophobic parts and the ability to interact with glutaraldehyde may lead to protein-assembly and nanoparticle formation. The aggregability of an enzyme increases its stability for industrial uses. This article investigates the aggregation potential of the Lysobacter protease enzyme (Alpha- Lytic protease). The genus Lysobacter belongs to the family Xanthomonadaceae within the Gammaproteobacteria and includes at least ۴۶ named species. The first maximal score value of aggregation of Alpha- Lytic protease and also Beta- Clamp, and Amyloid as standard proteins were obtained by the Aggrescan ۳D software. In order to investigate the mode of interactions among Glutaraldehyde and Alpha- Lytic protease, the Glutaraldehyde structure was designed in the ChemDraw program and then energy was minimized in HyperChem. Finally, by using the AutoDock program, Glutaraldehyde docked into the Alpha- Lytic protease, Beta- Clamp, and Amyloid. The maximal score value of Alpha- Lytic protease by Aggrescan ۳D software was ۲.۹۴۲۱ that higher than Beta- Clamp, and Amyloid as standard proteins. Glutaraldehyde successfully docked into Alpha-Lytic and made van der Waals bonds with Arg ۸۲ and Val ۸۴. according to the observed information, Lysobacter's protease enzyme has hydrophobic parts and interacts with Glutaraldehyde. Therefore, this enzyme shows appreciable aggregation property in computational studies

## کلمات کلیدی:

nanoparticles, Lysobacter, aggregation, Glutaraldehyde, bioinformatic study

## لینک ثابت مقاله در پایگاه سیویلیکا:

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