DEVELOPING A COMPREHENSIVE DATABASE OF CATHEPSIN-GAG IN SILICO INTERACTIONS

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Glycosaminoglycans (GAGs) represent a class of linear anionic periodic polysaccharides known to regulate enzymatic activity in various biological processes. Among the enzymes influenced by GAGs are cysteine cathepsins, a family of proteases primarily involved in protein degradation [1]. While cathepsins have been extensively studied for their proteolytic functions, their interactions with GAGs remain poorly understood due to the limited availability of experimental structures [2, 3].
To address this research gap, we are developing a web-based database designed to provide a comprehensive analysis of GAG-cathepsin interactions. This work is focused on the entire family of 11 cathepsins and 6 classes of GAGs, resulting in over 300 unique complexes. Advanced *in silico* approaches, including all-atom and coarse-grained molecular dynamics simulations, along with Hamiltonian replica exchange molecular dynamics techniques, are employed to investigate these interactions. With a total of over 5000 simulations, this resource aims to generate novel insights into the role of GAGs in modulating cathepsin function, offering a comparative computational framework to support the rational design of GAG-based therapeutic strategies.

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