

Binding free energies of the antiviral peptide ATN-161 with integrin $\alpha_5\beta_1$ and target of SARS CoV-2

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Abstract: ATN-161 is a small anti-integrin peptide that has been extensively studied for fighting cancer [1], and has recently demonstrated activity against SARS-CoV-2 in vitro and in vivo [2][3]. Studies indicate that integrins are alternative routes for virus entry into cells[4], but few studies demonstrate how this molecule binds to $\alpha_5\beta_1$ integrin. This work aimed to study the binding affinities and interactions of the ATN-161 pentapeptide with the $\alpha_5\beta_1$ integrin and potential targets against Sars cov-2. We chose the Integrin $\alpha_5\beta_1$ open and closed conformation, SARS-CoV-2 protein S variant omicron linked to hACE2, and SARS-CoV-2 3CL protease (M^{PRO}) as targets. We used molecular docking and molecular dynamics studies to determine the stability of the system and the umbrella sampling method to obtain the binding energy between ATN-161 and each target. Our results showed that ATN-161 can bind $\alpha_5\beta_1$ integrin in both its active and inactive form, weakly binds to hACE2-complexed omicron variant S protein, and shows a high binding affinity for M^{PRO} .

Key-words: coronavirus, integrin, Umbrella sampling method, energy binding.

Support: CAPES, CNPq, FAPERJ, INCT-FCx.

References:

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