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Modeling of E5 human papillomavirus ion channel

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Human papillomavirus (HPV) belongs to the papillomavirus family and is quite common in the world. Currently, there are more than 170 types of this virus, of which about 30 can cause cancer. Despite the availability of a vaccine, the development of methods of medical treatment of diseases caused by HPV is still appropriate.

Human papillomavirus virions contain several targets for possible chemotherapeutic intervention. One of the most promising targets is the ion channel E5, which is involved in the proliferation of human keratinocytes and their transformation into a malignant tumor. It is known that the E5 ion channel has a rather large internal cavity, as well as side pockets located near the bilipid membrane and containing lipophilic and hydrophilic regions.

During the work on the project, the E5 HPV ion channel was modeled and molecular docking was performed. The structures contained adamantane, homo-adamantane and bicyclo [3.3.1] nonane moieties, which facilitate penetration through the membrane to the target and its binding to lipophilic sites, connected with aromatic, and / or non-aromatic carboxy and heterocycles containing hydrogen bond donors and acceptors for interaction with hydrophilic amino acid residues within binding sites. For the structures that showed the highest binding energies, the blocking of the HPV channel was verified using molecular dynamics, and the influence of the structure of the molecule on its binding energy to the HPV ion channel was evaluated. On the basis of the data obtained, the leading structures and the most promising directions for their modification were selected.

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