

This work focuses on the modernization of the web plugin MolArt, which is used to illustrate the relationship between the annotated protein sequence and the experimental or predicted 3D structure of the protein. The new MolArt (MolArt 2.0) consists of two components. The first one provides visualization of the protein sequence using the Nightingale library. The second one is responsible for rendering the 3D structure of the protein using the Mol\* library. We connect these two components by using graphical highlighting (even multi-highlighting) of corresponding groups of amino acids in both parts, which makes it easier to generate biological hypotheses. The data is read from several external databases or it is possible to use the data provided by the user. MolArt 2.0 is implemented in TypeScript.