**PredictSNPONCO: A Web Server for Rapid Structural Bioinformatics Analysis of the Effect of Cancer-associated Mutations**

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Cancer is one of the top leading causes of death in the world. Due to its complex nature, there is not a single general-purpose treatment, and the existing ones have varying success rates for different types of cancer. Thus, there is a massive demand for alternative approaches capable of delivering the proper treatment at the right time. One of the most promising approaches is precision medicine which breaks the traditional “one size fits all” paradigm by considering each patient as a unique individual and designing their treatment plan according to their needs. Precision medicine exploits data collected from the patients, such as mutations detected in the affected tissues and their anamnesis. Most of the pipelines used in clinical practice are based on analysing the mutation impact on the DNA level. As many mutations can also occur in the exonic regions of the DNA, this analysis can lack essential data about their effect on the protein level. To fill this gap, we developed a novel web server PredictSNPONCO capable of rapid *in silico* assessment of the mutation effect on multiple essential properties of proteins such as function and stability. The server provides various structure-based analyses such as stability evaluation, virtual screening of potential inhibitors using the dataset of FDA/EMA approved drugs, as well as sequence-based analyses like conservation analysis and prediction of mutational effect on protein function. Important annotations extracted from state-of-the-art databases complement calculated values. The service offers an easy-to-use interactive web interface that allows users to start the analysis and evaluate the results efficiently. The server is available freely to the scientific and medical community at <https://loschmidt.chemi.muni.cz/predictsnp-onco>.