

A computational platform for deciphering complex cancer mutations

Yoram Zarai and Tamir Tuller, Tel Aviv University

We apply a state-of-the-art computational engine, which is based on a multidisciplinary computational approach, to analyse the wealth of clinical and genetic data of patients' tumors.

The engine outputs many novel mutations, several of which are silent or seemingly silent, that are predicted to affect cancer progression, and may be targeted by known or novel treatments.

Advanced molecular tools, such as CRISPR, are then used to validate the role of the mutations in cancer pathology.