

[P29] ProTox: A web server for the *in silico* prediction of rodent oral toxicity

Malgorzata N. Drwal¹, Priyanka Banerjee^{1,2}, Mathias Dunkel¹, Martin R. Wettig¹, Robert Preissner^{1,3}

¹ *Structural Bioinformatics Group, Institute for Physiology, Charité – University Medicine Berlin, Lindenberger Weg 80, 13125 Berlin, Germany*

² *Graduate School of Computational Systems Biology, Humboldt-Universität zu Berlin, Invalidenstr. 42, 10115 Berlin, Germany*

³ *German Cancer Consortium (DKTK), Im Neuenheimer Feld 280, 69120 Heidelberg, Germany*

Animal trials are currently the major method for determining the possible toxic effects of drug candidates and cosmetics. *In silico* prediction methods represent an alternative approach and aim to rationalize the preclinical drug development, thus enabling the reduction of the associated time, costs and animal experiments. Here, we present ProTox, a web server for the prediction of rodent oral toxicity. The prediction method is based on the analysis of the similarity of compounds with known median lethal doses (LD50) and incorporates the identification of toxic fragments, therefore representing a novel approach in toxicity prediction. In addition, the web server includes an indication of possible toxicity targets which is based on an in-house collection of protein-ligand-based pharmacophore models (“toxicophores”) for targets associated with adverse drug reactions. The only requirement for the prediction is the two-dimensional structure of the input compounds. All ProTox methods have been evaluated based on a diverse external validation set and displayed strong performance (sensitivity, specificity and precision of 76, 95 and 75 %, respectively) and superiority over other toxicity prediction tools, indicating their possible applicability for other compound classes. The data set used for ProTox prediction were extracted from SuperToxic database[1].

[1] Schmidt, U., Struck, S., Gruening, B., Hossbach, J., Jaeger, I.S., Parol, R., Lindequist, U., Teuscher, E. and Preissner, R. *Nucleic Acids Res.*, 37 (2009), D295–9.