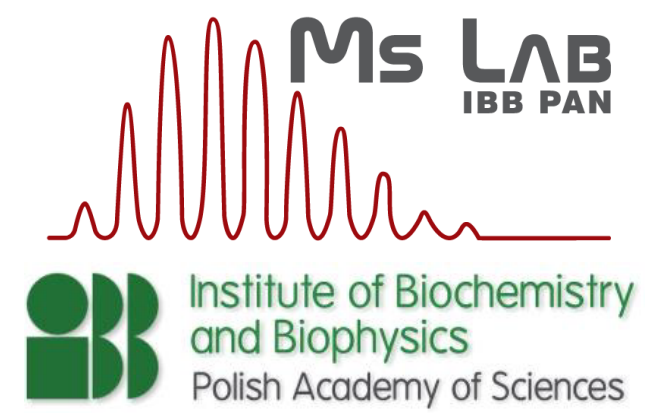




# HaDeX: analysis of the hydrogen-deuterium exchange mass spectrometry experiments data

Dominik Cysewski<sup>1,\*</sup>, Weronika Puchała<sup>1</sup>, Michał Burdukiewicz<sup>2</sup>, Michał Kistowski<sup>1</sup>, Katarzyna A. Dabrowska<sup>1</sup>, Aleksandra E. Badaczewska-Dawid<sup>3</sup>, Michał Dadlez<sup>1</sup>  
\*dominikcysewski@gmail.com



<sup>1</sup>Institute of Biochemistry and Biophysics Polish Academy of Sciences, Poland, <sup>2</sup>Faculty of Mathematics and Information Science, Warsaw University of Technology, Poland, <sup>3</sup>Faculty of Chemistry, Biological and Chemical Research Center, University of Warsaw, Poland.

## Introduction

Hydrogen-deuterium mass spectrometry (HDX-MS) is a staple tool for monitoring dynamics and interactions of proteins. Due to the sheer size of the HDX-MS results, the data analysis require a dedicated software suite. However, the majority of existing tools provides only point-and-click interfaces to black-box models or does not offer a complete analytic workflow. We propose **HaDeX**, a novel tool for processing, analysis and visualisation of HDX-MS experiments. **HaDeX** covers the whole analytic process, including quality control, ISO-based uncertainty and publication-quality figures. The reproducibility of the whole procedure is ensured with advanced reporting functions. It is important to us that our analytic methodology is transparent and understandable for the users so it is consulted with international experts and discussed in-depth in the package vignette.

## Main functionality

The main audience for **HaDeX** is HDX-MS practitioners whose area of expertise doesn't include programming and advanced data analysis skills. To help them with their work, **HaDeX** is also available as a Shiny web server with a wide range of clickable customizable options. To ensure publication-quality figures all the plots are fully editable by the user and processed data is easily downloadable in every step.

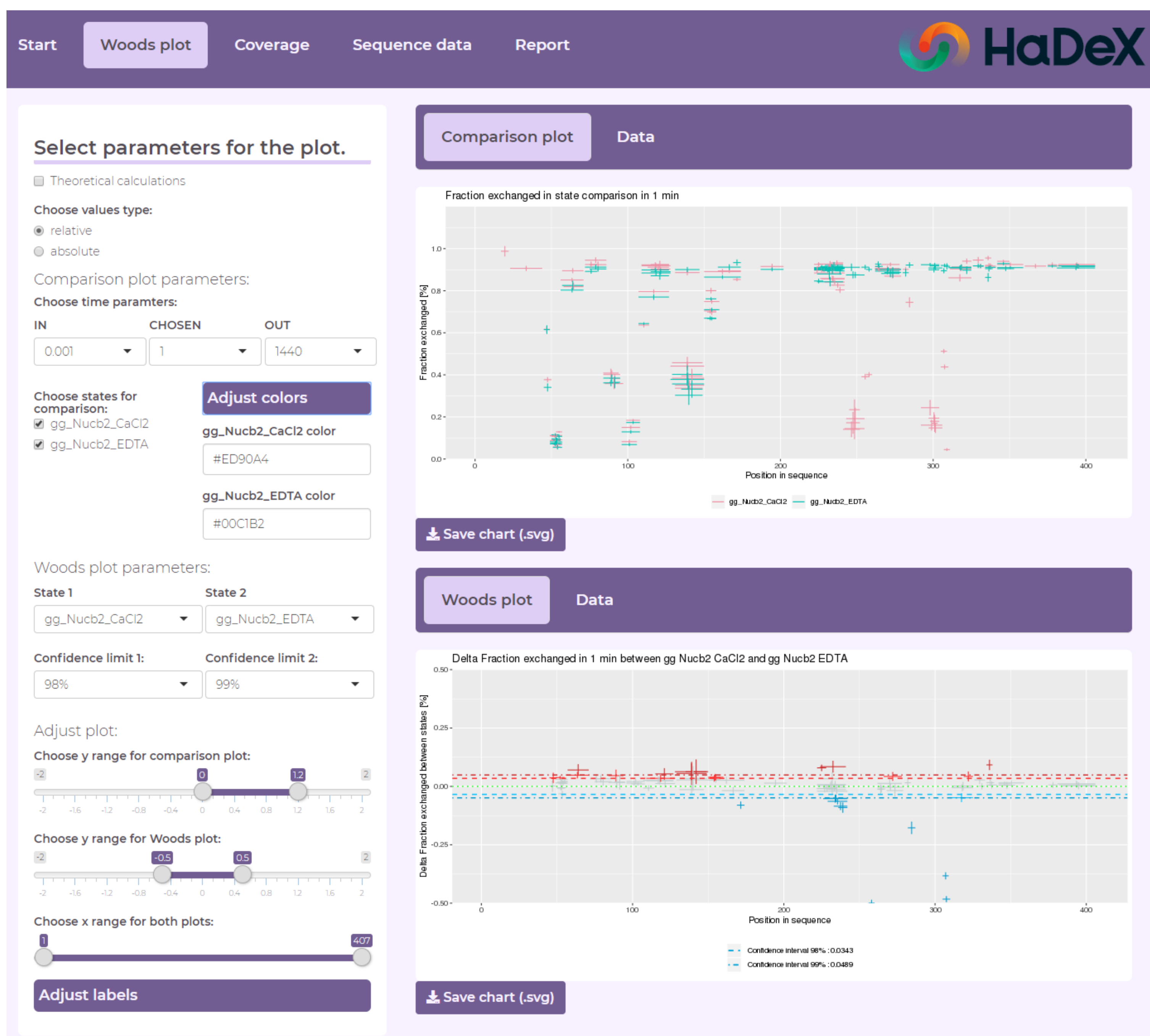


Figure 1: Overview of **HaDeX** app

## Kinetics of the peptides

**HaDeX** has a module for analyzing deuteration uptake change in time for given peptide in given time. For comparison, choosing multiple combinations of peptides and their states is possible for the plot.

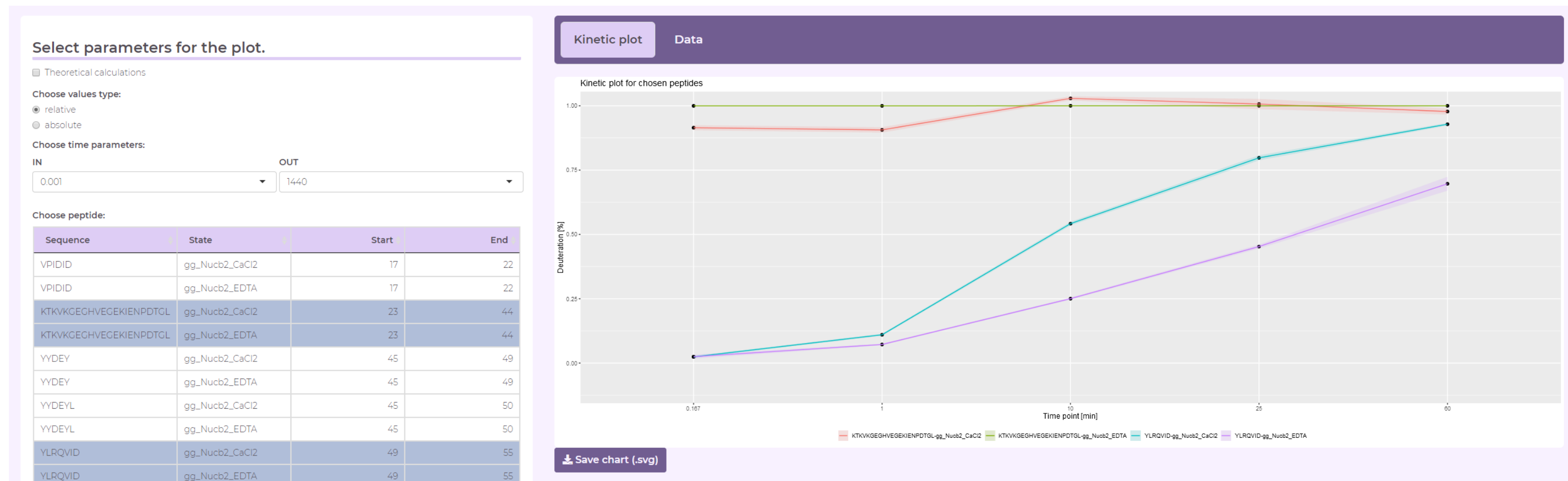


Figure 2: Kinetics plot for chosen peptides

## Availability

**HaDeX** is available as a web server: <http://mslab-ibb.pl/shiny/HaDeX/>



as the R package: <https://cran.r-project.org/web/packages/HaDeX/index.html>



and as a standalone software: <https://sourceforge.net/projects/hadex/>

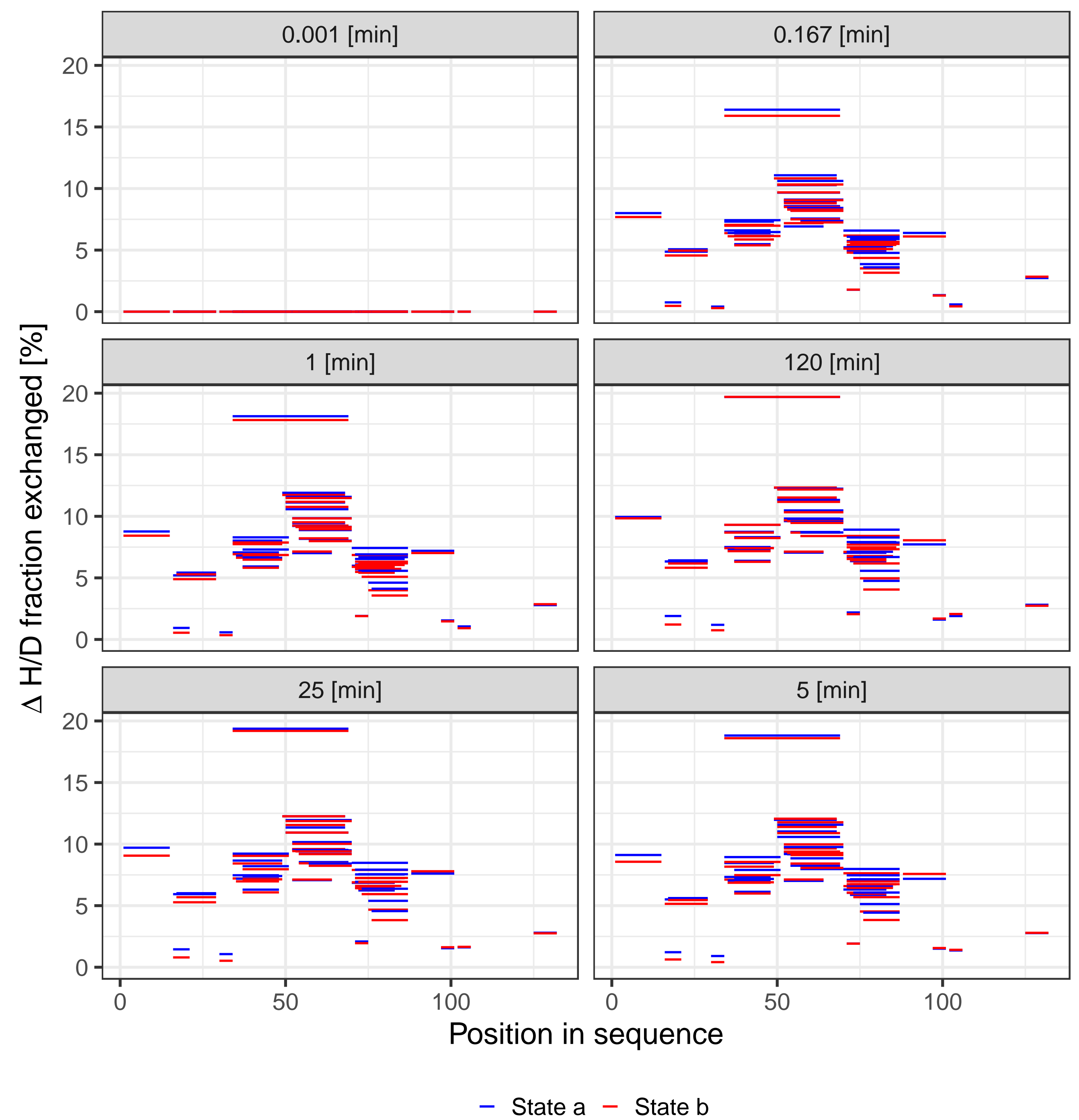


## Acknowledgements

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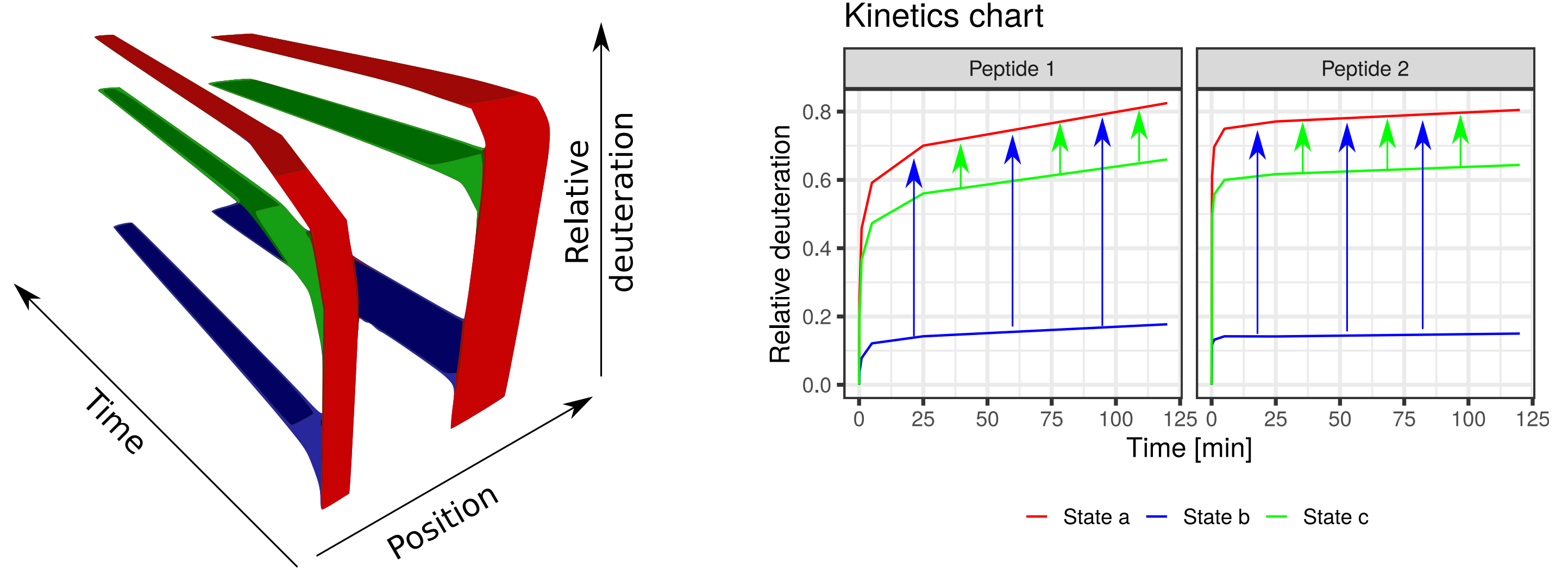


## Woods plot



## Multi-state variability test (MSVT)

A multi-state variability test offers a statistical assessment of regional variability. An user can compare relative deuteration between multiple states in specific regions of the interest (ROI).



MSVT relies on information coming from all peptides which at least partially cover the specified ROI. It means that instead of per-peptide results, we take into account a whole regional variability, which leads to the increase of sensitivity.

Aside from these benefits, MSVT is calibrated to the area between kinetic curves. Thanks to that it offers a straightforward interpretation for experimentalists, while preserving full statistical validity.

As MSVT is not yet a part of the **HaDeX** software suite and is available only upon request.

## Report function

**HaDeX** provides report generation - with parameters chosen by user so is fully personalizable. Additionally, calculated data for plots can be downloaded not only in report form but also in csv/pdf file in panel next to every plot. On figure 3 are shown available elements of the report - that can be chosen by user and limited strictly for user needs.

The customizable report generation makes every analysis made with **HaDeX** highly reproducible.

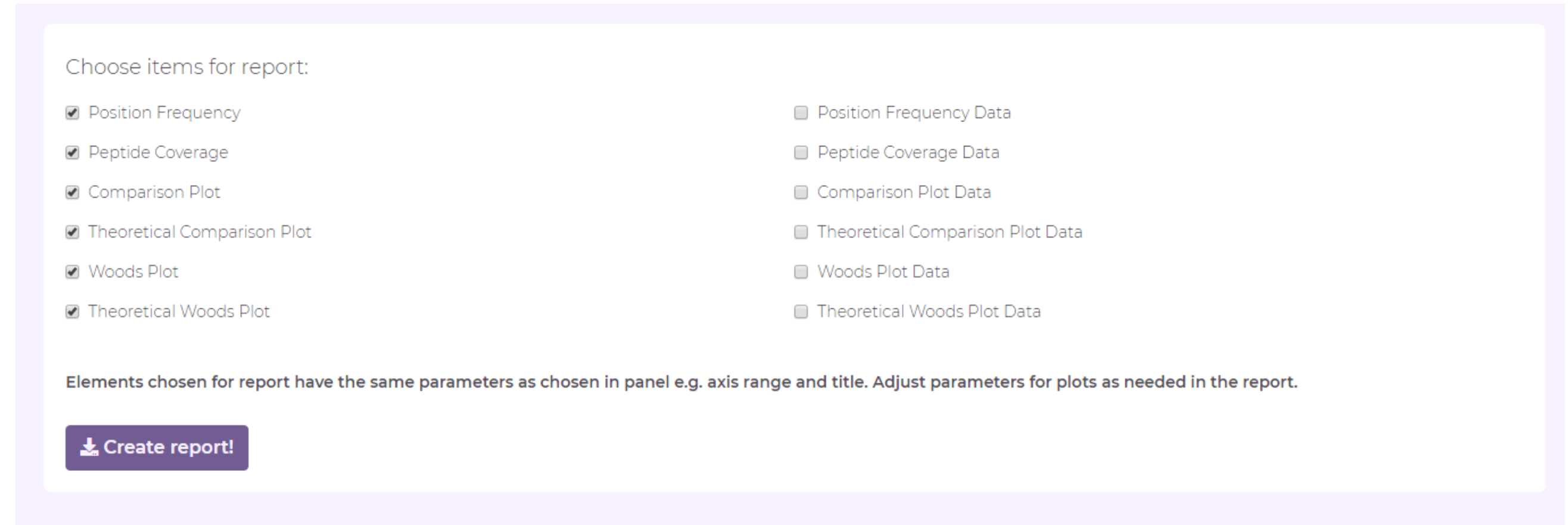


Figure 3: Screenshot of **HaDeX** - reporting page

## Bibliography

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