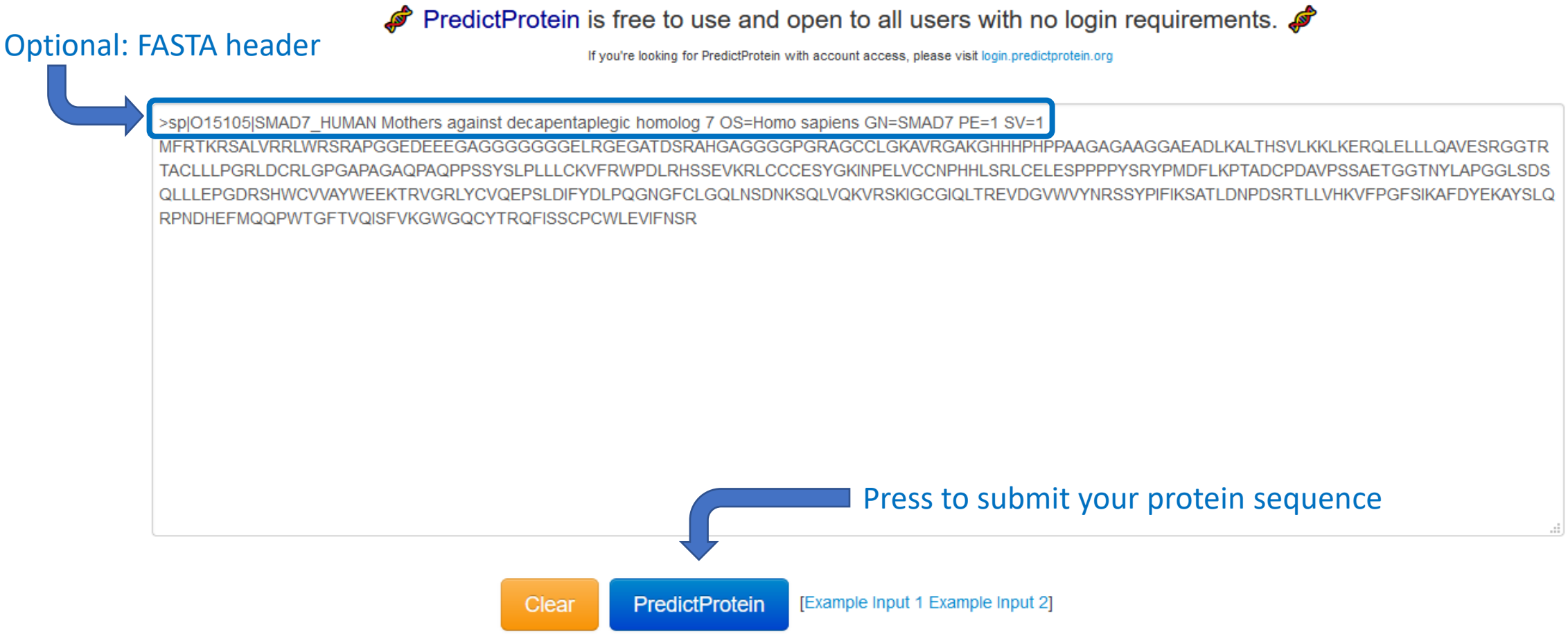
Quick Guide

Submitting Sequences to PredictProtein

- PredictProtein supports only single sequence submission
  - If you want to predict multiple sequences, you can contact us via email

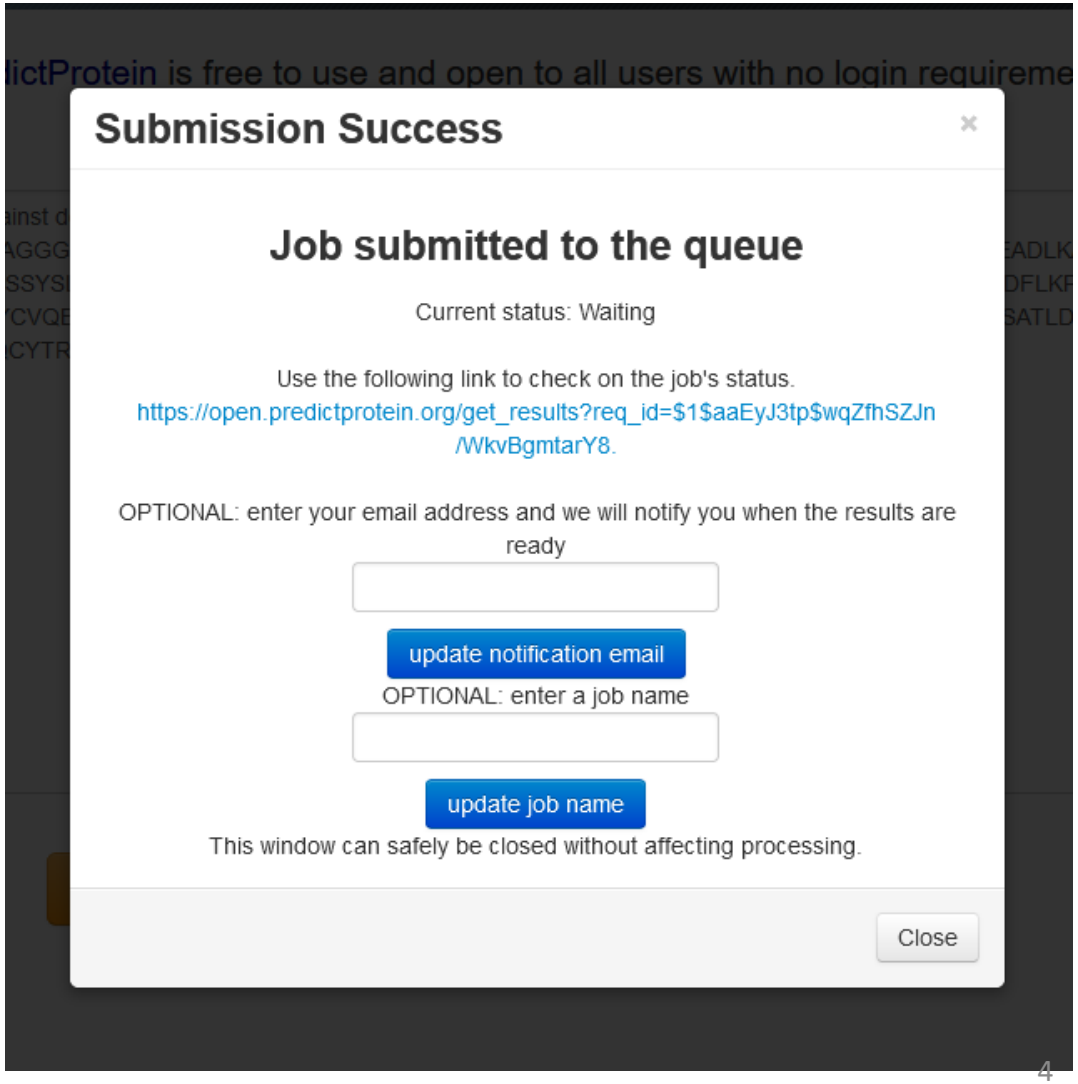
- Sequence format
  - Optional: Sequences can have a FASTA header
  - Sequences must not contain non-standard amino acids
  - Sequences must be at least 17 amino acids long

Submitting Sequences to PredictProtein



Submitting Sequences to PredictProtein

- If the results are already in our PredictProtein cache, you will be automatically directed to the results page. If not, you will get a notification box with the associated job ID and link.
- Optional: You can provide an email address which will be notified once the job has been completed.



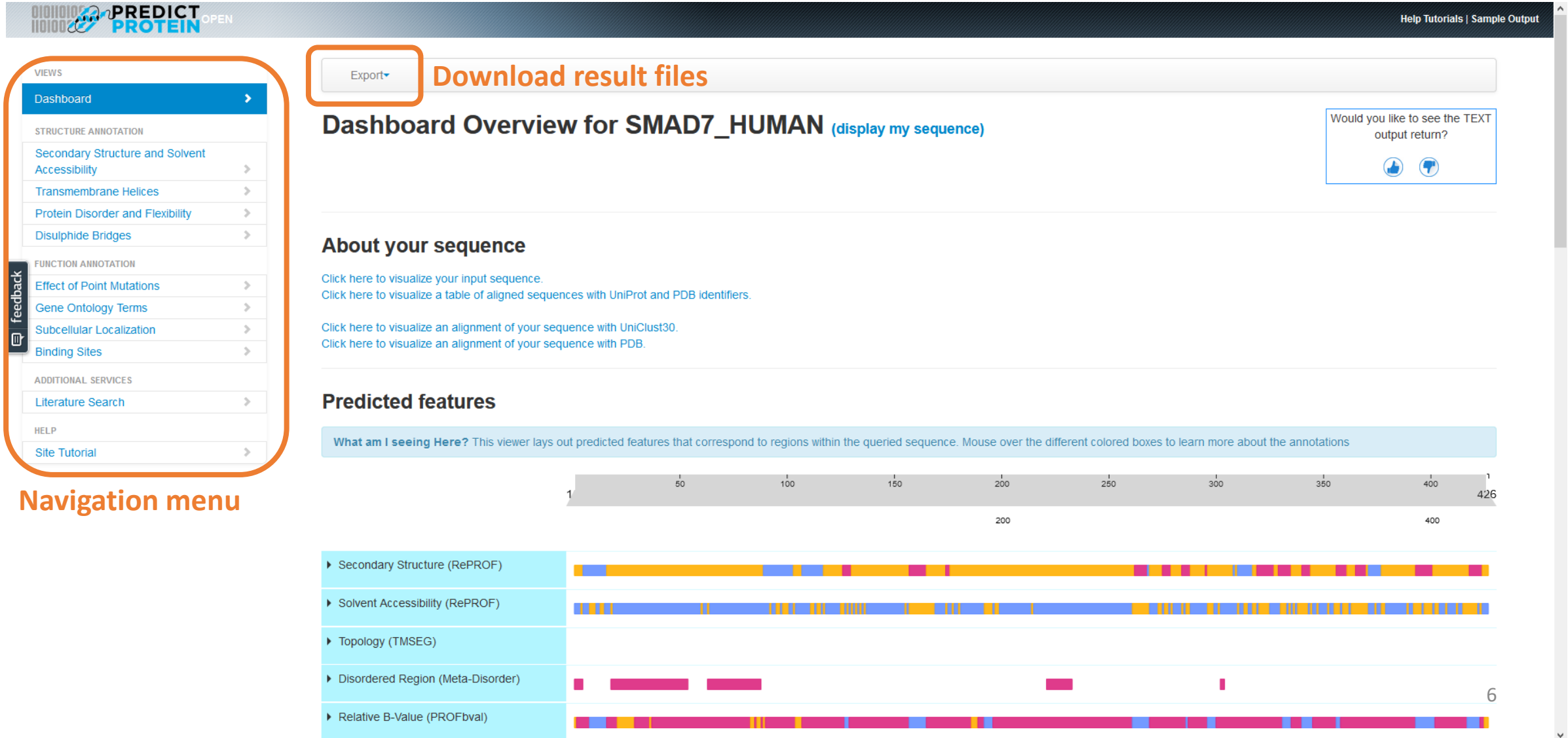
PredictProtein Result: Dashboard

- The main results page (dashboard) contains an overview of all results
  - Sequence alignments
  - Predicted sequence features
  - Length and amino acid composition

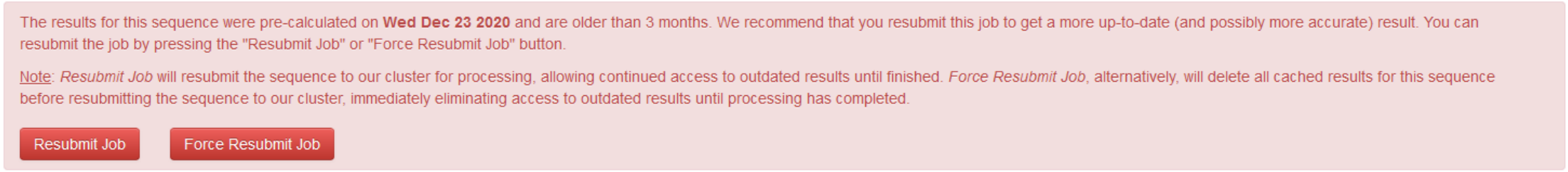
- Navigation menu to more specialized tabs on the left

- Export button to quickly download all result files

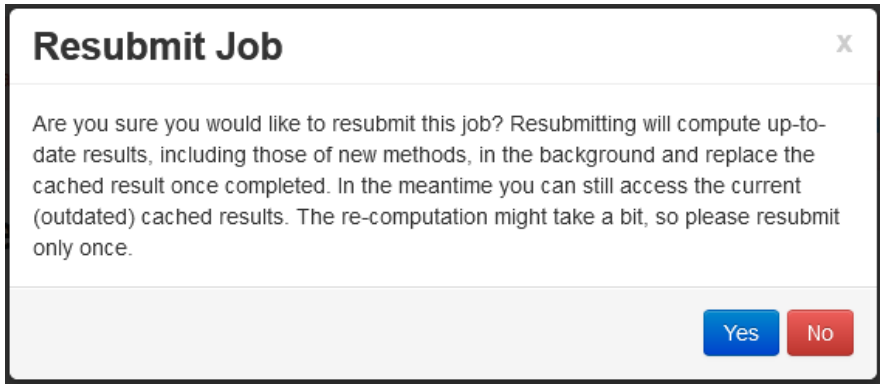
PredictProtein Result: Dashboard

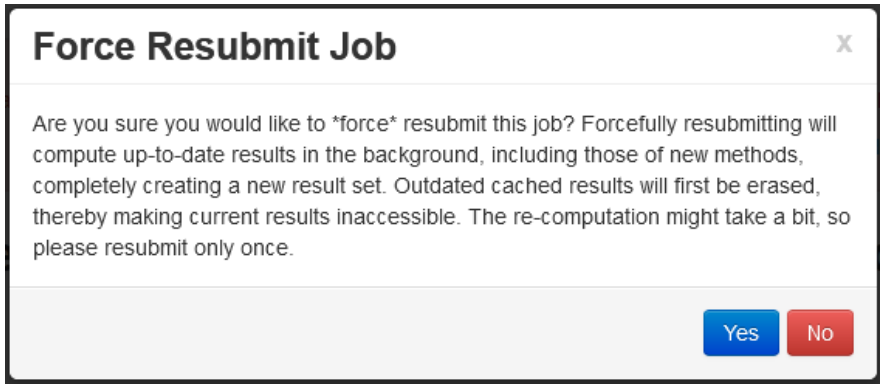


PredictProtein Result: Old Results



- Results older than 3 months are marked, as they may be outdated.
- You can resubmit them by pressing the **“(Force) Resubmit Job”** button on the dashboard



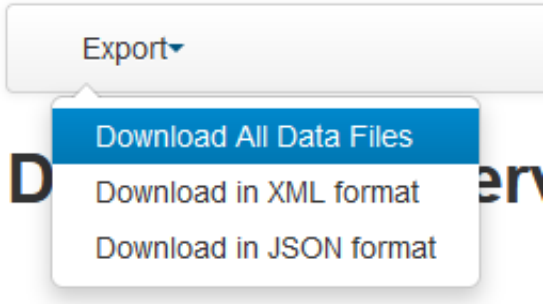


PredictProtein Result: No or Weak Alignments

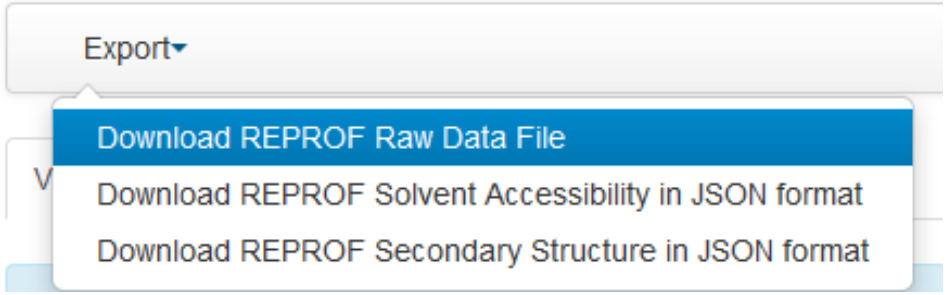
- Many of the methods run by PredictProtein use sequence alignments as part of their input (either PSSMs or MSAs).
- The web server will display a warning if no or only a few sequences have been aligned with the query, as this can affect the reliability of the predictions.

PredictProtein Result: Download Files

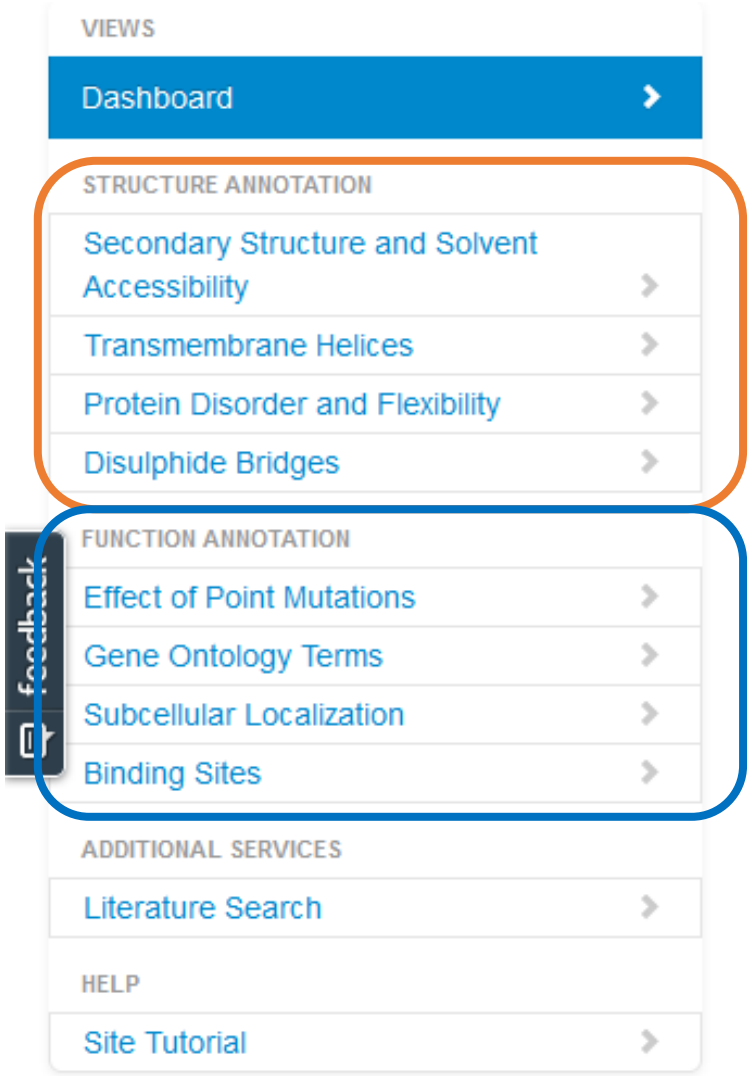
- You can download results via the export button on the dashboard



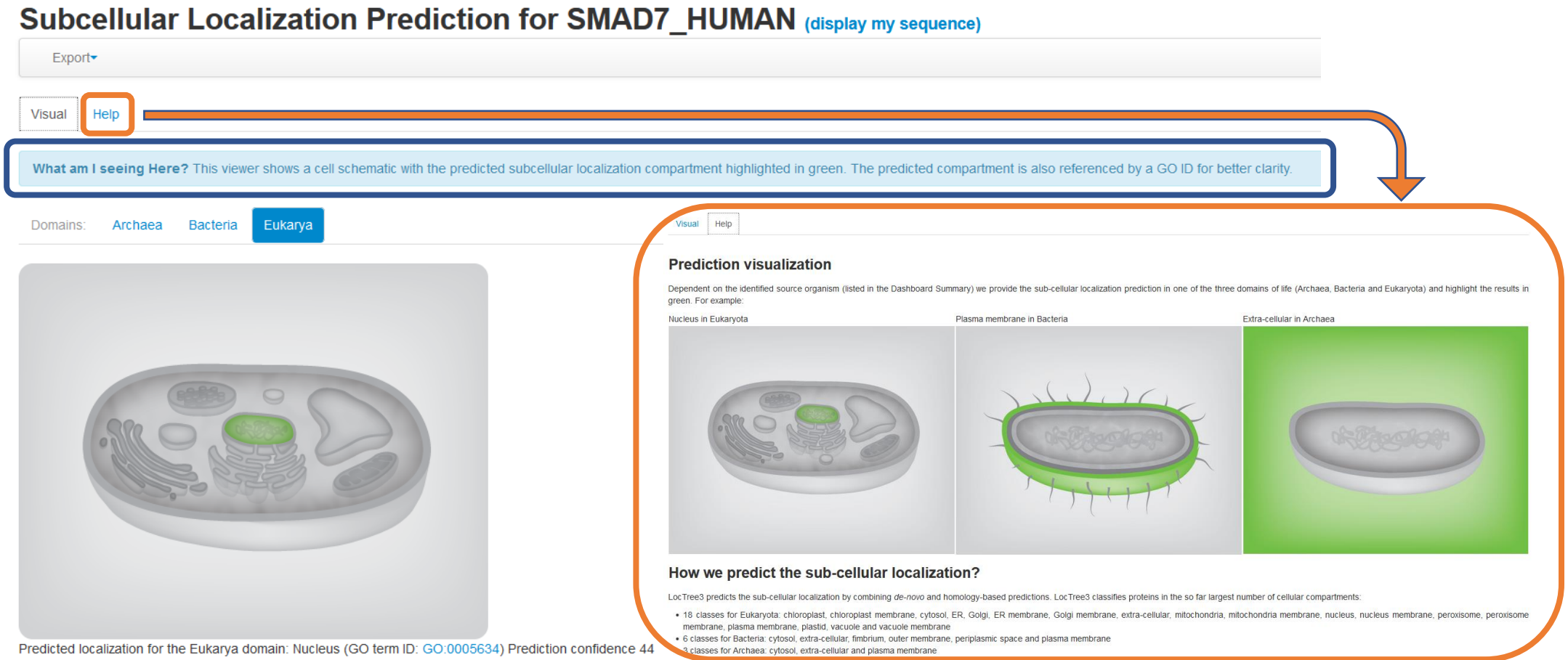
- The specialized tabs provide downloads for individual results



PredictProtein Result: Specialized Tabs



Specialized tabs on the left provide predictions for structural and functional aspects of the submitted protein sequence

PredictProtein Result: Specialized Tabs

Specialized tabs contain a quick summary of the visualized results and a *help* tab with more details about the prediction methods