

Web Server for Automated Excel@FIT 2020 MINER Mining of Soluble Enzymes







Author: Simeon Borko^{1,2}, supervisor: Jiří Hon^{1,2}

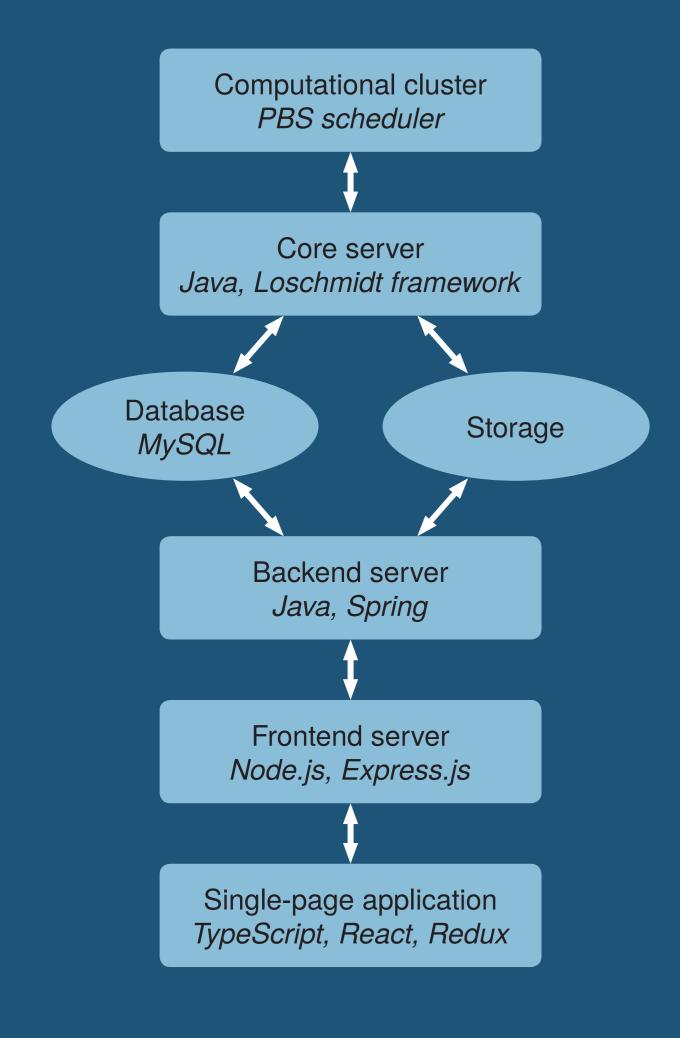
¹Department of Information Systems, Faculty of Information Technology, Brno University of Technology ²Loschmidt Laboratories, RECETOX, Department of Experimental Biology, Faculty of Science, Masaryk University

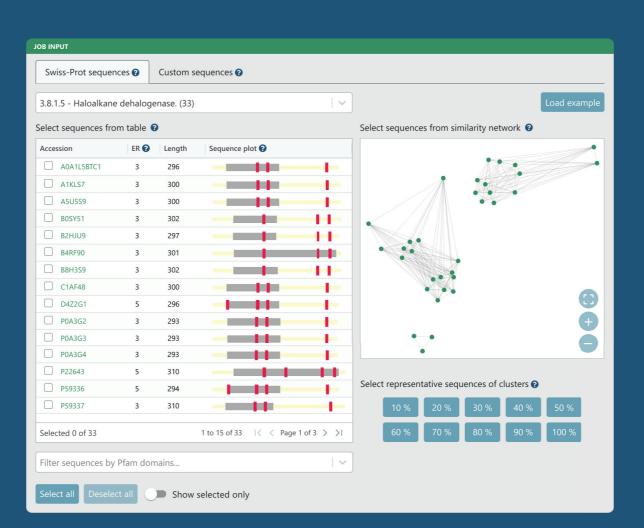
https://loschmidt.chemi.muni.cz/enzymeminer/

Motivation

- Enzymes are proteins catalysing chemical reactions with great applications in the ecological production of chemical compounds
- Millions of protein sequences are being discovered and uploaded to protein databases every year
- Impossible to test all new sequences in laboratory for specific enzymatic function
- EnzymeMiner finds novel enzymes from protein databases and facilitates selection of promising targets for laboratory tests

Web server architecture





Interactive input form using EC number and SwissProt database



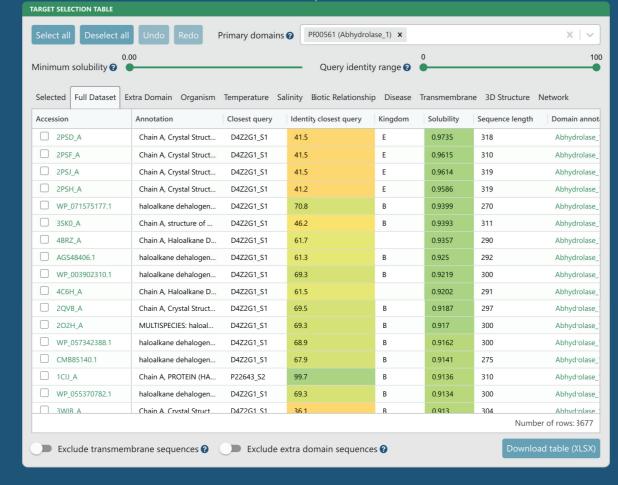
Sequence similarity search

Pairwise essential residue filter

Multiple sequence alignment

Organism annotations and identified domains

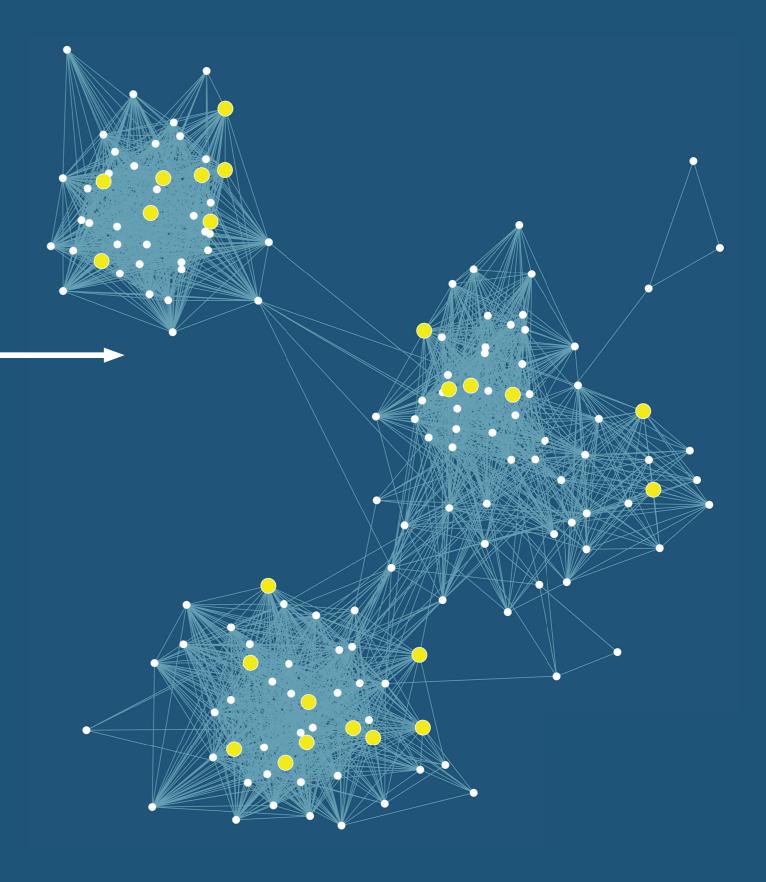
Solubility prediction [2]



Interactive selection table with multiple views and filtering options

Conclusions

- EnzymeMiner identifies novel putative enzymes and facilitates their prioritization and selection for experimental characterization
- Previously published methodology [1] validated on 20 putative haloalkane dehalogenase genes
- Robust web server architecture using high-performance computational cluster of ELIXIR CZ
- Easy-to-use web interface with interactive components implemented using Typescript and React
- Accepted to Nucleic Acids Research journal (JIF 11.15)



Interactive sequence similarity networks in input form and results page

First version of EnzymeMiner pipeline specialized for haloalkane dehalogenase (HLD) enzyme family.

2013

2017

First 20 putative HLDs selected for experimental characterization using conventional methods.

Publication of EnzymeMimer pipeline for HLDs and results of experimental characterization of first 20 selected HLDs.

2020

server and results of experimental characterization of next 47 selected HLDs.

Publication of EnzymeMiner web

2021

Support for homology modelling and analysis of pockets and tunnels. Validation using other enzyme families.

References & acknowledgements

- 1. Vanacek et al. 2018, Exploration of Enzyme Diversity by Integrating Bioinformatics with Expression Analysis and Biochemical
- Characterization. ACS Catalysis 8: 2402–2412 2. Hon et al. 2019, SoluProt: Tool for Prediction of Protein Solubility. Bioinformatics (in preparation)







2018

Next 47 putative HLDs for

experimental characterization

using high-throughput methods.