

ST. ANNE'S UNIVERSITY HOSPITAL BRNO INTERNATIONAL CLINICAL RESEARCH CENTER



RESEARCH GROUP



PRINCIPAL INVESTIGATOR

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KEY WORDS

Alzheimer Disease, Biocatalysis, Bioinformatics, Computer Modelling, Lab-on-chip, Microfluidics, Protein Engineering, Metabolic Engineering, Mechanistic Enzymology

RESEARCH FOCUS

The research group focuses on **protein and metabolic engineering for biomedicine**. The group develops new theoretical concepts, software tools and lab-on-chip technologies for protein engineering. It uses these newly developed tools for the design of proteins with improved properties for biocatalysis, biodegradation, biosensing, cell culturing and differentiation. The group has published more than 200 original articles, 20 book chapters and filed 7 international patents and founded the biotechnology spin-off Enantis Ltd.

Bioinformatics – identification of interesting genes in genomic databases for molecular cloning and experimental characterization

Lab-on-Chip Technologies – development of microfluidic lab-on-chip technologies for biochemical and biomedical research

Pathway Engineering – design and construction of bacterial strains expressing newly assembled biochemical pathways

Protein Stabilization - computational design of stabilization mutations

International Collaborations: ETH Zurich, Switzerland; Tohoku University, Katahira, Japan; University of Cambridge, Cambridge, UK; Novo Nordisk Foundation Center for Biosustainability (CFB), Copenhagen, Denmark; Spanish National Research Council (CSIC), Madrid, Spain

RESEARCH OBJECTIVES

Computational design and engineering of hyperstable proteins Application of novel theoretical concepts for proteins engineering Development of user-friendly software tools and microfluidic chips













TECHNOLOGICAL EQUIPMENT

Computer cluster Circular dichroism Colony picking robot Hardware and software for computer modeling Microfluidics Pipetting robot Rapid quench-flow system Stopped flow-kinetic system

OFFERED SERVICES AND EXPERTISE

- **Bioinformatics** identification of interesting genes in genomic databases for molecular cloning and experimental characterization.
- Lab-on-Chip Technologies development of microfluidic lab-on-chip technologies for biochemical and biomedical research.
- Pathway Engineering design and construction of bacterial strains expressing newly assembled biochemical pathways.
- **Protein Stabilization**

TOP PUBLICATIONS

- GORA, A., BREZOVSKÝ, J., DAMBORSKÝ, J. Gates of Enzymes. Chemical Reviews. 2013, 113(8), 5871-5923.
- ŠTOURAČ, J., VÁVRA, O., KOKKONEN, P., FILIPOVIČ, J., PINTO, G., BREZOVSKÝ, J., DAMBORSKÝ, J., BEDNÁŘ, D. Caver Web 1.0: Identification of tunnels and channels in proteins and analysis of ligand transport. 2019. Nucleic Acid Research gkz378.
- KOKKONEN, P., SYKORA, I., PROKOP, Z., GHOSE, A., BEDNÁŘ, D., AMARO, M., BEERENS, K., BIDMANOVÁ, S., SLÁNSKÁ, M., BREZOVSKÝ, J., DAMBORSKÝ, J., HOF, M. Molecular gating of an engineered enzyme captured in real time. 2018. Journal of the American Chemical Society 140: 17999-18008.
- MUSIL, M., ŠTOURAČ, J., BENDL, J., BREZOVSKÝ, J., PROKOP, Z., ZENDULKA, J., MARTÍNEK, T., BEDNÁŘ, D., DAMBORSKÝ, J. FireProt: Web server for automated design of thermostable proteins. 2017. Nucleic Acids Research 45: W393-W399.
- LIŠKOVÁ, V., SŤEPÁNKOVÁ, V., BEDNÁŘ, D., BREZOVSKÝ, J., PROKOP, Z., CHALOUPKOVÁ, R., DAMBORSKÝ, J. Different structural origins of the enantioselectivity of haloalkane dehalogenases toward linear β-haloalkanes: Open-solvated versus occluded-desolvated active sites. 2017. Angewandte Chemie International Edition 56: 4719-4723
- SÝKORA, J., BREZOVSKÝ, J., KOUDELÁKOVÁ, T., LAHODA, M., FORTOVÁ, A., CHERNOVETS, T., CHALOUPKOVÁ, R., ŠTĚPÁNKOVÁ, V., PROKOP, Z., KUTÁ SMATANOVÁ, I., HOF, M., DAMBORSKÝ, J. Dynamics and hydration explain failed functional transformation in dehalogenase design. Nature Chemical Biology. 2014, 10(6), 428-430.

OTHER SELECTED RESULTS

Stabilization of growth factors to study the stem cells

Patented technology for stabilization of proteins

Software CAVER, CAVER WEB, CAVERDOCK, CALFITTER, HOTSPOT WIZARD, and PREDICTSNP for protein design and prediction of mutation effects on human health

TOUL, M., NIKITIN, D., MAREK, M., DAMBORSKY, J., PROKOP, Z. Extended mechanism of the plasminogen activator staphylokinase revealed by global kinetic analysis: 1000-fold higher catalytic activity than that of clinically used alteplase. 2022. ACS Catalysis 12: 3807-3814.

ŠTOURAČ, J., VÁVRA, O., KOKKONEN, P., FILIPOVIČ, J., PINTO, G., BREZOVSKÝ, J., DAMBORSKÝ, J., BEDNÁŘ, D. Caver Web 1.0: Identification of tunnels and channels in proteins and analysis of ligand transport. 2019. Nucleic Acid Research: gkz378.

KOKKONEN, P., SÝKORA, J., PROKOP, Z., GHOSE, A., BEDNÁŘ, D., AMARO, M., BEERENS, K., BIDMANOVÁ, S., SLÁNSKÁ, M., BREZOVSKÝ, J., DAMBORSKÝ, J., HOF, M. Molecular gating of an engineered enzyme captured in real time. 2018. Journal of the American Chemical Society 140: 17999-18008.

MUSIL, M., ŠTOURAČ, J., BENDL, J., BREZOVSKÝ, J., PROKOP, Z., ZENDULKA, J., MARTÍNEK, T., BEDNÁŘ, D., DAMBORSKÝ, J. FireProt: Web server for automated design of thermostable proteins. 2017. Nucleic Acids Research 45: W393-W399.

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BENDL, I., ŠTOURAČ, I., ŠEBESTOVÁ, E., VÁVRA, O., MUSIL, M., BREZOVSKÝ, I., DAMBORSKÝ, I. HotSpot Wizard 2.0: automated design of site-specific mutations and smart libraries in protein engineering. Nucleic Acids Research 2016, 44(W1): W479-487.

SÝKORA, J., BREZOVSKÝ, J., KOUDELÁKOVÁ, T., LAHODA, M., FORTOVÁ, A., CHERNOVETS, T.,



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