Charles University

Faculty of Science

DEPARTMENT OF BIOCHEMISTRY

INVITES YOU FOR A LECTURE

THERMAL PROTEOME PROFILING FOR INVESTIGATION OF PROTEIN-DRUG INTERACTIONS IN MALARIA PARASITES

Mgr. Samuel Pažický, Ph.D.

(Nanyang Technological University, Singapore)

MONDAY 25. 5. 2026 at 15:00

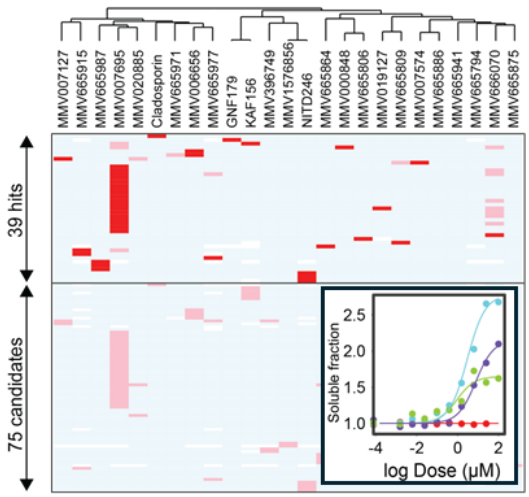
Lecture Hall CH2, the School of Chemistry Building, Hlavova 2030/8, Prague

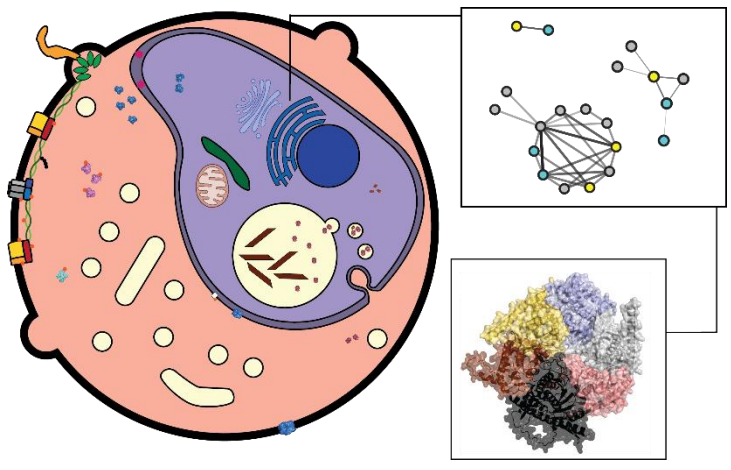
Guests are cordially invited!

Abstract:

Malaria is a devastating disease affecting 300 million people globally. Several classes of compounds have been successfully developed into **antimalarial drugs** over last century, however, their **mechanisms of action** remain **mostly unknown** and the resistance against them is on the rise. **Thermal proteome profiling** (TPP) recently emerged as a proteome-wide method to identify protein-drug interactions in the cells. We used this tool to screen a library **antimalarial compounds** and identified several protein targets, including acetyl-CoA synthetase 10 and parasite-specific proteases.

Expanding the method to track cellular responses, we **screened 45 antimalarials** and found specific responses to clinically important artemisinin derivates and cipargamin. Finally, we repurposed TPP and developed **meltome-assisted profiling of protein complexes (MAP-X)**. This **new tool** uses TPP data **to map protein complexes in live cells**. Applied to malaria parasite *Plasmodium falciparum*, we identified and experimentally verified new protein complexes and mapped their dynamics.





Pazicky, S. *et al.* MAP-X reveals distinct protein complex dynamics across *Plasmodium falciparum* blood stages. **Nature Microbiology** 10, 3229–3244 (2025).