Profiling Metalloproteomes by Chemical and Computational Proteomics

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Metal binding proteins (MBPs) are widely distributed in living systems. They play key roles in diverse biological processes, including but not limited to catalysis, stabilization of proteins' structure, and signal transduction. So far, there are few methods to identify MBPs on the proteome level. In this talk, I will describe our recent and ongoing efforts to profile MBPs in a global scale by chemical and computational proteomics methods[1]. Our approach identified a large number of previously unannotated MBPs, some of which can be experimentally and structurally validated. Our chemoproteomic and computational methods will provide an enabling tool for discovering more MBPs systematically and the data will generate more hypothesis for the community of studying metal biology.
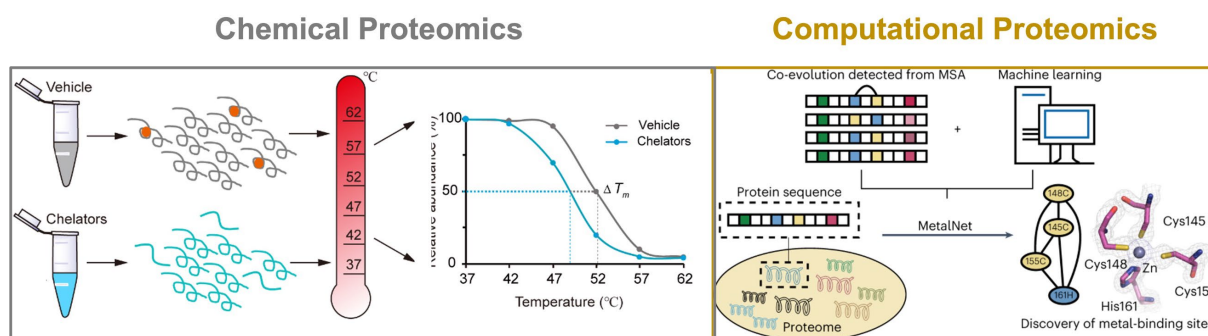

Figure 1. Profiling of metal-binding proteins by TPP-based chemical proteomics and AI-based computational proteomics.

References
[1] Cheng, Y. et al. *Nat. Chem. Biol.* **2023**, doi: 10.1038/s41589-022-01223-z.