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Approaches to Defining Mitochondrial Protein Function Using Systems Biochemistry

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In the post-genomic era, defining functions for the whole complement of proteins is a major task, but it is critical for our understanding of basic biology and disease causation. In recent years, a mix of current large-scale and classical reductionist approaches—a process we call "systems biochemistry"—has aided in the characterization of poorly understood proteins, overcoming previous hurdles. This method is proven particularly successful for mitochondria, whose well-defined proteome has allowed for extensive analysis of the entire mitochondrial system, allowing understudied proteins to be positioned for beneficial mechanistic investigations. Recent advances in systems biochemistry have aided in the discovery of new disease-related mitochondrial proteins as well as long-sought "missing" proteins that perform critical activities. These researches, taken together, are leading to a better knowledge of mitochondrial functions and a molecular foundation for investigating mitochondrial disease [1].

Mitochondrial Dark Matter Revolutions in imaging and structural biology allow us to observe subcellular components at stunning resolution, and gene editing technologies allow us to manipulate DNA seemingly without restriction. Our ability to measure, observe, and modify biological systems, on the other hand, has perhaps overtaken our basic knowledge of the gene activities that underpin them. There are a variety of reasons why so many proteins are still poorly understood. Many are just difficult to research because they may have redundant roles, fail to perform important functions under typical laboratory conditions, or affect many cellular processes. Others are hampered by a scarcity of tools and reagents (such as antibodies and mice lines) for more "popular" proteins. Furthermore, the continued focus on a small number of proteins may be based on the incorrect belief that they are more important for human health and disease [2].

Biography

Justyna M. Płotka-Wasylka (born 1986) graduated from the Gdańsk University of Technology with a Ph.D. in Chemical Science in 2014, after which she started work at the Gdańsk University of Technology (Department of Analytical Chemistry). In 2019, she ranked up to Professor at GUT, Poland. She was called as Member of Young Scientists Council of Minister of Science and Higher Education in 2018.

Her research interests include the quality determination of wine and characterization of wine origin from different part of Poland. She is also interested in green aspects of chemistry, especially analytical chemistry; thus, her researches are always performed in accordance with principles of green analytical chemistry. In order to assess developed procedures, she developed a tool for assessing analytical protocols relative to green analytical chemistry attributes, called GAPI (Green Analytical Procedure Index). This tool can be applied for evaluation of the green character of whole analytical methodology, from sample collection to final determination.

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