

THE HUMAN PROTEIN ATLAS

Towards a Cell Cycle Atlas

[February 24th, 2021]. Today researchers within the Human Protein Atlas (HPA) publish a study of single-cell RNA and protein expression in relation to cell cycle progression in the journal of Nature. At the same time, the dataset is made publicly available as an integrated part of the Cell Atlas, providing a new resource for researchers around the globe to explore in the quest to further understand the human cell cycle and proliferative diseases such as cancer.

The human body is made of around 37 trillion cells, all arising from cellular division, starting from the single zygote formed upon fertilization. The division of a parental cell into two daughter cells takes place in a coordinated series of events referred to as the cell cycle. This process engages numerous proteins, both for the execution and for the careful regulation of the cellular events that enables cells to grow and divide. Aberrant control of the cell cycle leads to drastic consequences, such as uncontrolled cell proliferation and cancer. Proteins that regulate the cell cycle are considered important targets for cancer therapies, and the identification of these proteins are of great importance for the continued advances in terms of diagnosis as well as treatment of proliferative diseases.

Recent work in the research group of P Emma Lundberg, professor at KTH Royal Institute of Technology and head of the Cell Atlas part of the Human Protein Atlas (HPA), contributes a comprehensive characterization of the expression of cell-cycle dependent proteins in time and space. The study by Diana Mahdessian, Anthony Cesnik, and colleagues, uses a combination of immunofluorescence microscopy and single-cell RNA sequencing to systematically characterize the temporal expression patterns of RNAs and proteins over the course of the cell cycle. The proteins targeted in this study are selected based on their display of cell-to-cell variations in protein abundance and/or subcellular localization, to which the cell cycle is expected to be an important contributor. The analysis reveals a large number of previously unknown cell cycle dependent proteins, some of which are shown to have oncogenic or anti-oncogenic properties by gene silencing and prognostic association analyses. The authors also demonstrate that most cycling proteins are regulated at the translational or post-translational level, rather than by transcriptomic cycling. These results paint a more complete picture of the human cell cycle, which is crucial for understanding the molecular underpinnings of this fundamental biological process and the emergence of proliferative diseases such as cancer. Moreover, the authors reveal that while a large portion of the human proteome displays cell-to-cell variability in spatiotemporal protein expression, less than half of these variations can be attributed to the cell cycle. This opens intriguing questions regarding other factors that govern cell-to-cell proteome variability.

The research article is published in Nature journal and the underlying data is made available as part of the open access Human Protein Atlas (HPA) database version 20.1. We believe that this work will serve as a valuable resource to provide a greater functional understanding of the orchestration of the human cell cycle, the roles of newly identified cycling proteins in tumorigenesis, and the potential application of these proteins as new clinical targets and/or markers for cellular proliferation.

Additional information:

See the cell cycle dependent transcriptome and proteome on the HPA:

www.proteinatlas.org/humanproteome/cell/cell+cycle+dependent

Read the full article:

<https://www.nature.com/articles/s41586-021-03232-9>

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About:**Human Protein Atlas**

The Human Protein Atlas (HPA), initiated in 2000 and funded from 2003, is a program based at SciLifeLab (Science for Life Laboratory), Stockholm, with the aim to map all of the human proteins in cells, tissues and organs using integration of various omics technologies, including antibody-based imaging, mass spectrometry-based proteomics, transcriptomics and systems biology. All the data in the knowledge resource is open access to allow scientists both in academia and industry to freely access the data for exploration of the human proteome. The Human Protein Atlas program has already contributed to several thousands of publications in the field of human biology and disease and it has been selected by the organization ELIXIR (www.elixir-europe.org) as a European core resource due to its fundamental importance for the wider life science community. The HPA consortium is funded by the Knut and Alice Wallenberg Foundation.

For more information, see: www.proteinatlas.org

Knut and Alice Wallenberg Foundation

The Knut and Alice Wallenberg Foundation is the largest private financier of research in Sweden and also one of Europe's largest. The Foundation's aim is to benefit Sweden by supporting basic research and education, mainly in medicine, technology, and the natural sciences. The Foundation can also initiate grants to strategic projects and scholarship programs.

For more information, see: <https://kaw.wallenberg.org/en>

KTH Royal Institute of Technology

Since its founding in 1827, KTH Royal Institute of Technology in Stockholm has grown to become one of Europe's leading technical and engineering universities, as well as a key center of intellectual talent and innovation. We are Sweden's largest technical research and learning institution and home to students, researchers and faculty from around the world dedicated to advancing knowledge.

For more information, see: www.kth.se

SciLifeLab (Science for Life Laboratory)

SciLifeLab is an institution for the advancement of molecular biosciences in Sweden. SciLifeLab started out in 2010 as a joint effort between four universities: Karolinska Institutet, KTH Royal Institute of Technology, Stockholm University and Uppsala University. The center provides access for advance infrastructure in life science for thousands of researchers creating a unique environment for health and environmental research at the highest level. The Human Protein Atlas is one of the Research Community Programs with funding from the SciLifeLab.

For more information, see: www.scilifelab.se