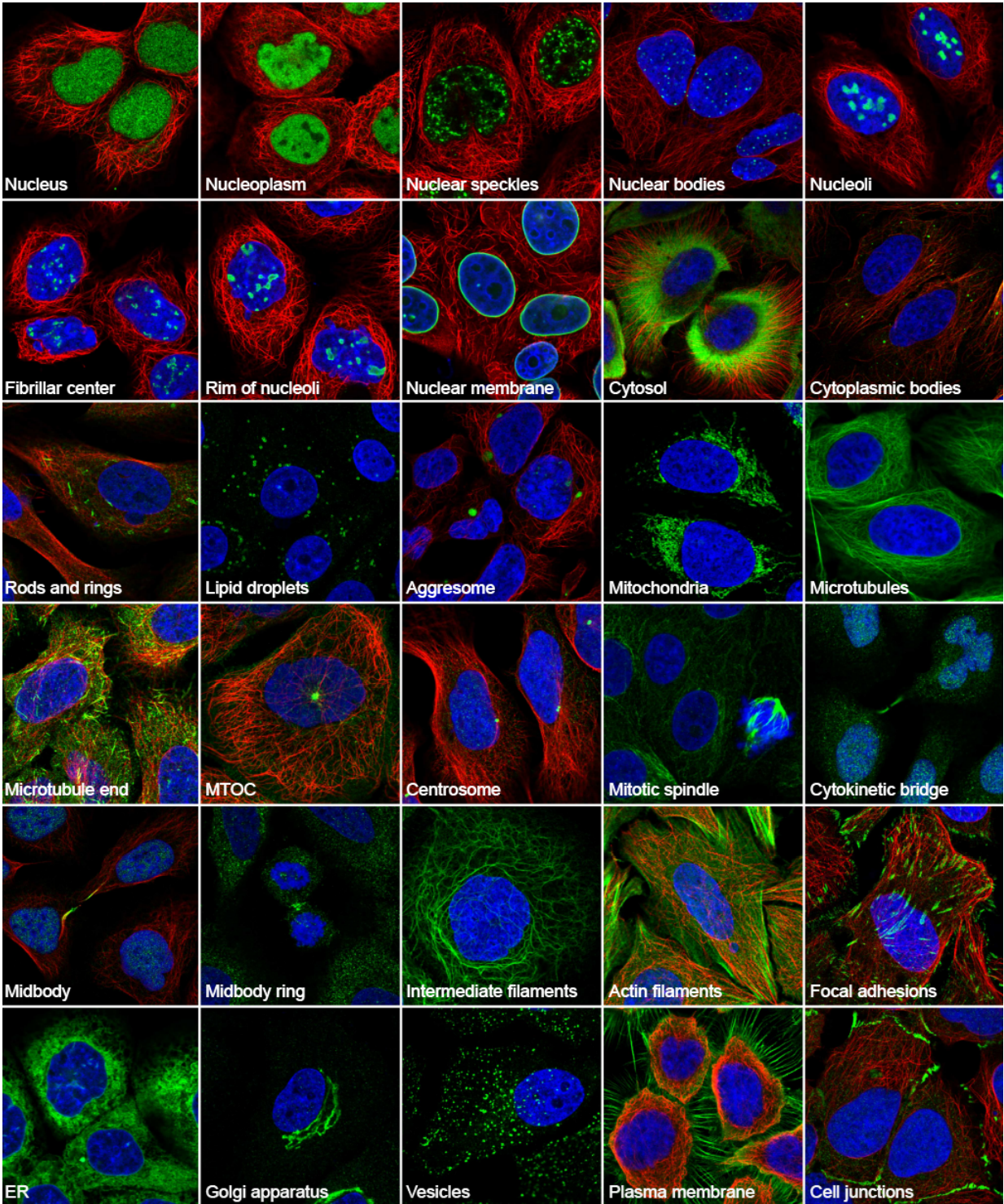


First comprehensive map of subcellular localization of proteins reveals new insights

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Images of cells from the Cell Atlas. Credit: Human Protein Atlas

The first analysis of how proteins are arranged in a cell was published today in *Science*, revealing that a large portion of human proteins can be found in more than one location in a given cell.

Using the Sweden-based Cell Atlas, researchers examined the spatial distribution of the [human proteome](#) that correspond to the majority of [protein](#)-coding genes, and they described in unprecedented detail the distribution of proteins to the various organelles and substructures of the human body's smallest unit, the cell.

Within a cell, the organelles create partitions that form an enclosed environment for chemical reactions tailored to fulfill specific functions in the cell. Since these functions are tightly linked to specific sets of proteins, knowing the subcellular location of the human proteome is key knowledge for understanding the function and underlying mechanisms of the human cell.

The study was led by Emma Lundberg, associate professor at KTH Royal Institute of Technology and responsible for the High Content Microscopy facility at the Science for Life Laboratory (SciLifeLab) in Stockholm, Sweden. The team generated more than 300,000 images to systematically resolve the [spatial distribution](#) of human proteins in cultivated cell lines, and map them to [cellular compartments](#) and substructures with single cell resolution.

The Cell Atlas is the result of more than 10 years of research within the Human Protein Atlas program, and was launched in December 2016. The article in *Science* describes the detailed analysis of hundreds of thousands of images created as part of this international effort, which also involved groups in China, South Korea, India, Denmark, and Germany.

"Only by studying the molecular components of the body's smallest

functional unit - the cell - can we reach a full understanding of human biology," says KTH Professor Mathias Uhlen, director of the Human Protein Atlas. "The Cell Atlas provides researchers with new knowledge that facilitates functional exploration of individual proteins and their role in human biology and disease."

The published article also includes a comparative study performed by Kathryn Lilley, director of the Cambridge Centre for Proteomics, at Cambridge University, UK, which enabled the antibody-based immunofluorescence (IF) microscopy analysis to be validated by an alternative mapping strategy that used mass spectrometry.

A total of 12,003 proteins targeted by 13,993 antibodies were classified into one or several of 30 cellular compartments and substructures, altogether defining the proteome of 13 major organelles. The organelles with the largest proteomes were the nucleus (6,930) and its substructures, such as bodies and speckles, and the cytosol (4,279).

Interestingly, about one-half of the proteins are found in more than one compartment revealing a shared pool of proteins in functionally unrelated parts of the cell. This finding sheds new light on the complexity of [cells](#).

The Cell Atlas is an open access resource that can be used by researchers around the world to study proteins or organelles of interest. Lundberg says. "The Atlas enables systems biology and cell modeling applications, and it is also a highly valuable resource for machine learning applications in image pattern recognition."

More information: "A subcellular map of the human proteome", *Science* (2017). [science.sciencemag.org/lookup/.../1126/science.aal3321](https://www.sciencemag.org/lookup/.../1126/science.aal3321)

Provided by KTH Royal Institute of Technology

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