

Embargo until November 11. 2025, 16.00 CET

PRESS RELEASE

# THE HUMAN PROTEIN ATLAS

**A new version 25 of the open access Human Protein Atlas resource has been released at the HUPO meeting in Toronto, Canada**

**[November 11, 2025].** A new version of the Human Protein Atlas has been launched (version 25) containing lots of additional data and new features. The open access resource harbors more than 10 million manually annotated bioimages and data for over 6 billion assay measurements from 300,000 separate biological samples. Data corresponding to all human protein-coding genes is presented with protein profiles in cells, tissues, organs and blood.

The Human Protein Atlas consortium today launched the version 25 of the open access resource ([www.proteinatlas.org](http://www.proteinatlas.org)) that contains nine major resources aiming to profile and explore different aspects of all human proteins.

In the new extended Blood resource, new data from Olink Explore HT and SomaScan have been included across 32 cohorts, including different diseases as well as longitudinal analysis of health and childhood. The resource now displays pan-disease blood profiling for in total 71 diseases including patients with cancers, autoimmune, infectious, neurobiology and cardiovascular diseases and in addition reports blood protein profiles in healthy cohorts reflecting childhood development, aging and pregnancy.

A new feature is that the Interaction resource which contain protein-protein interaction networks for more than 15,000 proteins, now includes 23000 “in-house” generated predicted protein interaction structures (based on AlphaFold3). Predicted alignment error (PAE) plots are displayed together with template modelling scores and the location of HPA antigens can be highlighted in the structures.

The Single cell resource now presents data from 34 different tissue types with the new additions from adrenal gland, pituitary gland, epididymis and urinary bladder. To improve data quality and cell type representation, the single cell data for adipose tissue, heart muscle, skeletal muscle and kidney have been replaced with single nuclei data. The Single cell resource now includes 154 different cell types, thus representing the majority of all cell types in the human body.

The Tissue resource includes eight new tissues, including choroid plexus, efferent ducts, ovary and different phases of placental development. In addition, a new pancreas antibody panel has been used for multiplex tissue profiling. Furthermore, the subcellular localization of proteins in human induced pluripotent stem cells (hiPSCs) has been added to the Subcellular resource.

“The HPA team is proud to launch this new version of the open access Human Protein Atlas with a vast amount of new data generated both internally and externally. In particular, the new Human Disease

Blood resource should be valuable for all researchers interested in translational medicine and the efforts to move from discovery into precision medicine”, says Mathias Uhlen, Director of the Human Protein Atlas consortium.

The work was funded by the Knut and Alice Wallenberg Foundation

Link to the new version of the Human Protein Atlas: [www.proteinatlas.org](http://www.proteinatlas.org)

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### Data availability

All data in the Human Protein Atlas is publicly available and to further increase and simplify access downloadable files with related meta data are included for each resource. The complete data is available in XML format and in collaboration with [BioImage Archive](#) also >10M raw images, corresponding to about 300TB of data, are available and can be used as a resource for bioimage analysis.

### About

**Human Protein Atlas.** The Human Protein Atlas (HPA) is a program based at SciLifeLab (Science for Life Laboratory), Stockholm, that started in 2003 with the aim to map of all 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 are 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](http://www.elixir-europe.org)) as a European core resource due to its fundamental importance for the wider life science community and by the GCBR as a Global Core Biodata Resource. The HPA consortium is funded by the Knut and Alice Wallenberg Foundation. For more information, see: [www.proteinatlas.org](http://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>

Figure 1. Olink HT and SomaScan pan-disease blood profiling data for the protein tyrosine kinase FGR across disease, health and childhood related cohorts.

