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PRESS RELEASE

THE HUMAN PROTEIN ATLAS

Human Protein Atlas version 26 adds four new resources and novel AI tools to explore human biology

[November 11, 2026]. The Human Protein Atlas (HPA) today launches version 26, combining extensive new data with artificial intelligence (AI) tools to help researchers explore human biology and disease. The update adds four new resources (sub-atlases) to the nine existing resources. The atlas contains almost 10 million manually annotated biological images and data from over 6 billion assay measurements across more than 300,000 biological samples. Protein profiles based on proteomics and transcriptomics data across cells, tissues, organs and blood are presented for all human protein-coding genes.

The new **Metabolic** resource provides genome-wide information on enzymes and other proteins involved in human metabolism. It provides cell type- and cell group-specific views of human metabolism by integrating HPA transcriptomic data with genome-scale metabolic modelling. Over 100 manually curated metabolic subsystem maps facilitate visualization of each protein's participation in different metabolic processes. Each subsystem map is accompanied by heatmaps for all proteins involved in the subsystem.

The new **Isoform** resource presents RNA expression data for all individual isoforms of all human protein-coding genes. Based on data from HPA and GTEx, the resource covers almost 90,000 isoforms across a large number of tissues. For each gene, the resource shows tissue-specificity categories for individual isoforms, alongside gene-level expression and specificity categories. The gene-level overview plot allows users to explore the transcriptomics data and the predicted localization of expressed isoforms.

A new **Evolutionary** resource enables researchers to explore and compare gene expression across different mammalian species, including macaque, pig, mouse and rat. By combining RNA expression data from major organs and tissues throughout the body, the resource provides information on how gene expression has been conserved or changed during mammalian evolution. Comparative mammalian brain data, previously included in the Brain resource, is now available in this resource.

The new standalone **Immune Cell** resource, previously included in the Single Cell resource, provides detailed RNA expression profiles across 18 different immune cell types, including B cells, T cells, monocytes, granulocytes and dendritic cells.

The revised **Brain** resource has been expanded with spatial transcriptomics data from three additional brain regions, bringing the total to five. The extensive single-nucleus RNA sequencing data from the

human brain has now been integrated into this resource, bringing together information on brain regions, neuronal and non-neuronal cell types, and spatial gene expression. This resource thus provides a detailed view of how genes are expressed across different anatomical structures and cellular environments in the human brain.

Additional data and features have been added to the existing resources. Data on post-translational modifications (PTMs) have been added to the **Structure** resource, enabling visualization of six common types of PTMs (phosphorylation, N-glycosylation, methylation, acetylation, sumoylation and ubiquitination) in 3D structures and in the Protein Browser. Both predictions generated in-house based on the structure-aware prediction framework MTPrompt_PTM and experimental data from dbPTM and UniProt are shown.

In the **Interaction** resource, high-confidence predictions based on the deep-learning model Rosettafold2-PPI have been integrated, alongside an updated method for selecting consensus interactions and a new aggregated network view. A feature highlighting known heterodimers has also been added. The resource now presents protein-protein interaction networks for 16335 genes, of which 7298 have consensus interactions.

In the **Blood** resource, disease summaries now cover 71 disease types across seven disease classes (cardiovascular, metabolic, cancer, psychiatric, autoimmune, infectious and pediatric diseases), correlations between Olink HT and SomaScan measurements are now available, and targeted mass spectrometry data for 176 proteins (DiscoveryEdge175 panel) from more than 2896 samples have been added.

The **Tissue** resource has undergone a major data quality update, aligning antibody-based protein data with expression levels using transcriptomics and mass spectrometry-based proteomics data. This has resulted in the removal of antibody data for 2050 genes and change in reliability score for 665 genes. Extended protein profiling on specialized tissue samples, aiming to provide important biological context where the standard tissue dataset is not sufficient, has been added for 100 proteins. The new data includes 79 proteins profiled in premenopausal women with known menstrual phases – proliferative or secretory phase.

A major effort has been made to expand the integration of mass spectrometry-based proteomics data across the Human Protein Atlas. Following the integration of data from the Matthias Mann Lab at the Max Planck Institute of Biochemistry earlier this year, additional datasets from the laboratory of Tiannan Guo at Westlake University are now being incorporated. These large-scale proteomics datasets provide complementary information on protein abundance across normal tissues and 25 different cancer types. By bringing together independently generated datasets, the atlas continues to expand its coverage of the human proteome and enables researchers to explore protein expression across tissues and diseases using multiple complementary sources.

To facilitate the exploration of human biology and disease, new features include **AtlasAI**, a multi-agent AI system. This system is designed to help users navigate and explore the Human Protein Atlas by

finding, summarizing, explaining and visualizing data based on user queries. Users can also generate custom reports directly from the search box, with data visualizations such as boxplots, UMAPs, heatmaps and bar plots of Human Protein Atlas transcriptomics and proteomics data for their selected gene sets. In addition, the gene summary pages now feature a **visual summary** for each of the approximately 20,000 human protein-coding genes: an AI-generated infographic built with Google's Gemini models that draws on Human Protein Atlas data to present the gene's function, expression, localization and disease relevance.

"The HPA team is proud to launch this new version of the open-access Human Protein Atlas, with extensive new data generated both internally and externally and four additional resources (sub-atlases). We are also pleased to introduce AI tools that help researchers explore human biology and disease," says Mathias Uhlen, director of the Human Protein Atlas consortium.

Looking ahead, the HPA's protein maps and annotated images will provide a foundation for Alpha Cell, a research program at SciLifeLab and KTH that aims to build predictive models of human cells. By combining this knowledge with new molecular measurements and AI, Alpha Cell seeks to move from mapping the cell's components to predicting how they work together in health and disease.

The work was funded by the Knut and Alice Wallenberg Foundation.

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Data availability

Link to the new version of the Human Protein Atlas: www.proteinatlas.org

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 began in 2003 with the aim of mapping all human proteins in cells, tissues and organs by integrating various omics technologies, including antibody-based imaging, mass spectrometry-based proteomics, transcriptomics and systems biology. All data in the resource are

open access, allowing scientists in academia and industry to explore the human proteome freely. The Human Protein Atlas program has contributed to several thousand publications on human biology and disease. It has been selected by ELIXIR (www.elixir-europe.org) as a European core resource due to its fundamental importance to 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.

Knut and Alice Wallenberg Foundation. The Knut and Alice Wallenberg Foundation is the largest private funder of research in Sweden and one of the largest in Europe. The Foundation aims to benefit Sweden by supporting basic research and education, mainly in medicine, technology and the natural sciences. The Foundation can also provide funding for strategic projects and scholarship programs. For more information, see: https://kaw.wallenberg.org/en

Alpha Cell program. Alpha Cell is a scientific program at SciLifeLab and KTH Royal Institute of Technology, coordinated by Jan Ellenberg and Mathias Uhlén. Building on the Human Protein Atlas (HPA), the program will combine HPA protein maps and annotations, new molecular measurements in space and time, and advanced artificial intelligence to develop dynamic, predictive models of human cell biology. By integrating life science technologies with advanced computation, it aims to explain how human cells function and adapt, and how cellular processes change in disease. The program brings together research groups across disciplines to develop and experimentally validate these models, with the long-term ambition of supporting drug discovery and precision medicine. The Alpha Cell program is funded by the Knut and Alice Wallenberg Foundation.

Science for Life Laboratory (SciLifeLab). As a national hub for molecular biosciences in Sweden, SciLifeLab develops and maintains unique research infrastructure, services and data resources for life science. SciLifeLab coordinates research communities in health and environmental sciences, supports the recruitment and training of young scientists, and fosters collaboration with industry, healthcare, public research organizations and international partners. The overall aim of SciLifeLab is to facilitate cutting-edge, multidisciplinary life science research and promote its translation for the benefit of society. SciLifeLab was founded in 2010 by KTH Royal Institute of Technology, Karolinska Institutet, Stockholm University and Uppsala University. Today, SciLifeLab operates also at a large number of additional universities in Sweden.