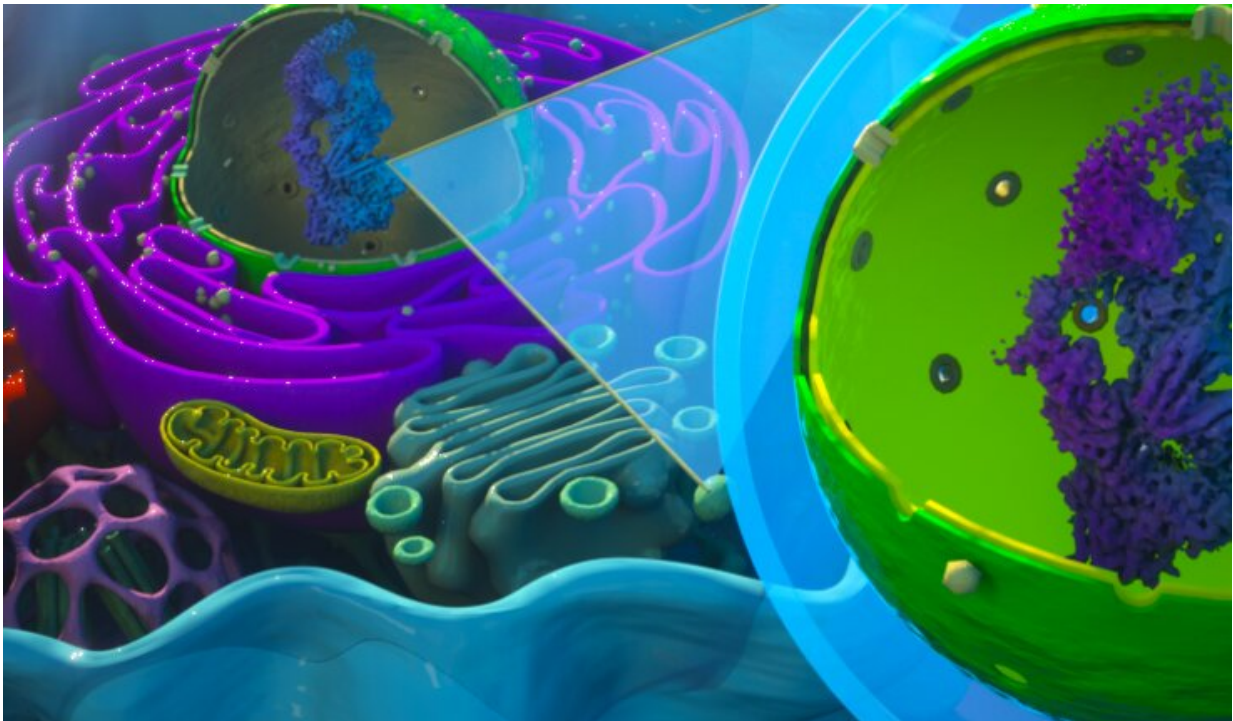


# Recipe for success: Interaction proteomics become a household item

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The MAC-tag workflow allows molecular microscopy of proteins. Credit: Ella Maru Studio

Proteins in human cells do not function in isolation and their interactions with other proteins define their cellular functions. Therefore, detailed understanding of protein-protein interactions (PPIs) is the key for deciphering regulation of cellular networks and pathways, in both health

and disease.

In a study published in the of September issue (advanced online 10th of August) of *Nature Protocols*, a research team led by Research Director Markku Varjosalo from the Institute of biotechnology & HiLIFE, University of Helsinki, introduces an optimized and integrated interaction proteomics protocol (named MAC-tag technology). The protocol combines two state-of-the art methods affinity purification—mass spectrometry (AP-MS) and proximity-dependent biotin identification (BioID to allow rapid identification of protein-protein interactions and more.

The MAC-tag technology allows an easy way to probe the molecular level localisation of protein of interest (an accompanying online resource of MS microscopy is available at [www.proteomics.fi](http://www.proteomics.fi)). The developed MAC-tag and the integrated approach will empower not only the interaction proteomics community, but also cell/molecular/structural biologists, with an experimentally proven integrated workflow for mapping in detail the physical and functional interactions and the molecular context of proteins.

"The MAC-tag technology stems from long-term efforts on developing new systems biology tools for systematically studying the molecular interactions of proteins. The identification of protein-[protein](#) interactions and their changes in disease settings, such as cancer, has proven in our hands a powerful tool and has allowed us to find exact molecular mechanisms underlying these diseases. In principle, our [protocol](#) can be used in so many different ways that we probably have not even envisioned half of them." Dr. Varjosalo states.

The MAC-tag technology is currently in use by Dr. Varjosalo and his consortia of virologists, medicinal chemists and other 'omics' researchers in search for novel druggable host proteins as therapeutic targets to

inhibit the SARS-CoV-2 infection and therefore to fight Covid-19.

**More information:** Xiaonan Liu et al, Combined proximity labeling and affinity purification–mass spectrometry workflow for mapping and visualizing protein interaction networks, *Nature Protocols* (2020). [DOI: 10.1038/s41596-020-0365-x](https://doi.org/10.1038/s41596-020-0365-x)

Provided by University of Helsinki

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