

## Milestone for the analysis of human proteomes

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Mathias Wilhelm, Professor Bernhard Kuster and Daniel Paul Zolg (from left to right). Credit: Andreas Heddergott / TUM

Researchers led by the Technical University of Munich (TUM) report on



the synthesis of a library of more than 330,000 reference peptides representing essentially all canonical proteins of the human proteome. It is a major milestone in the ProteomeTools project which aims at translating human proteome information into new molecular and digital tools with the potential for use in drug discovery, personalized medicine and life science research.

In a manuscript published online in *Nature Methods*, ProteomeTools scientists report on the synthesis of a library of more than 330,000 reference peptides (termed PROPEL for ProteomeTools Peptide Library) representing essentially all canonical proteins of the <u>human</u> proteome. All peptides were analysed by multi-modal liquid chromatography-tandem <u>mass spectrometry</u> (LC-MS/MS), creating a compendium of millions of very high quality reference spectra (termed PROSPECT for ProteomeTools Spectrum Compendium). The study illustrates the utility of these reagents and data to verify protein identifications from sparse observations and to predict the behaviour of peptides during liquid chromatography and tandem mass spectrometry.

## Data is freely available to the global scientific community

The consortium of TUM, JPT Peptide Technologies (JPT), SAP and Thermo Fisher Scientific has made the vast quantity of data freely available to the scientific community via the data analytics platform <u>ProteomicsDB</u> and the data repository <u>PRIDE</u> to enable scientists and to foster collaboration around the globe.

Going forward, the <u>ProteomeTools project</u> will generate a further one million peptides and corresponding spectra with a focus on splice variants, cancer mutations and post-translational modifications such as phosphorylation, acetylation and ubiquitinylation.



Using the new resources, ProteomeTools scientists will study human proteomes with the aim of turning the vast amount of molecular information on the human proteome into new reagents, equipment, workflows, assays and software to enhance the application of proteomics in both science and medicine.

"ProteomeTools was started as a collaborative effort bringing together academic and industrial partners to make important contributions to the field of proteomics. It is gratifying to see that this work is now producing a wealth of significant results", says Professor Bernhard Kuster, Chair of Proteomics and Bioanalytics at TUM, and coordinator of the project.

## Develop new and improve upon existing hardware, software and workflows

"Representing the human proteome by tandem mass spectra of synthetic peptides alleviates some of the current issues with protein identification and quantification. The libraries of peptides and spectra now allow us to develop new and improve upon existing hardware, software, workflows and reagents for proteomics. Making all the data available to the public provides a wonderful opportunity to exploit this resource beyond what a single laboratory can do. We are now reaching out to the community to suggest interesting sets of peptides to make and measure as well as to create LC-MS/MS data on platforms not available to the ProteomeTools consortium."

**More information:** Building ProteomeTools based on a complete synthetic human proteome, *Nature Methods*, <u>nature.com/articles/doi:10.1038/nmeth.4153</u>



## Provided by Technical University Munich

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