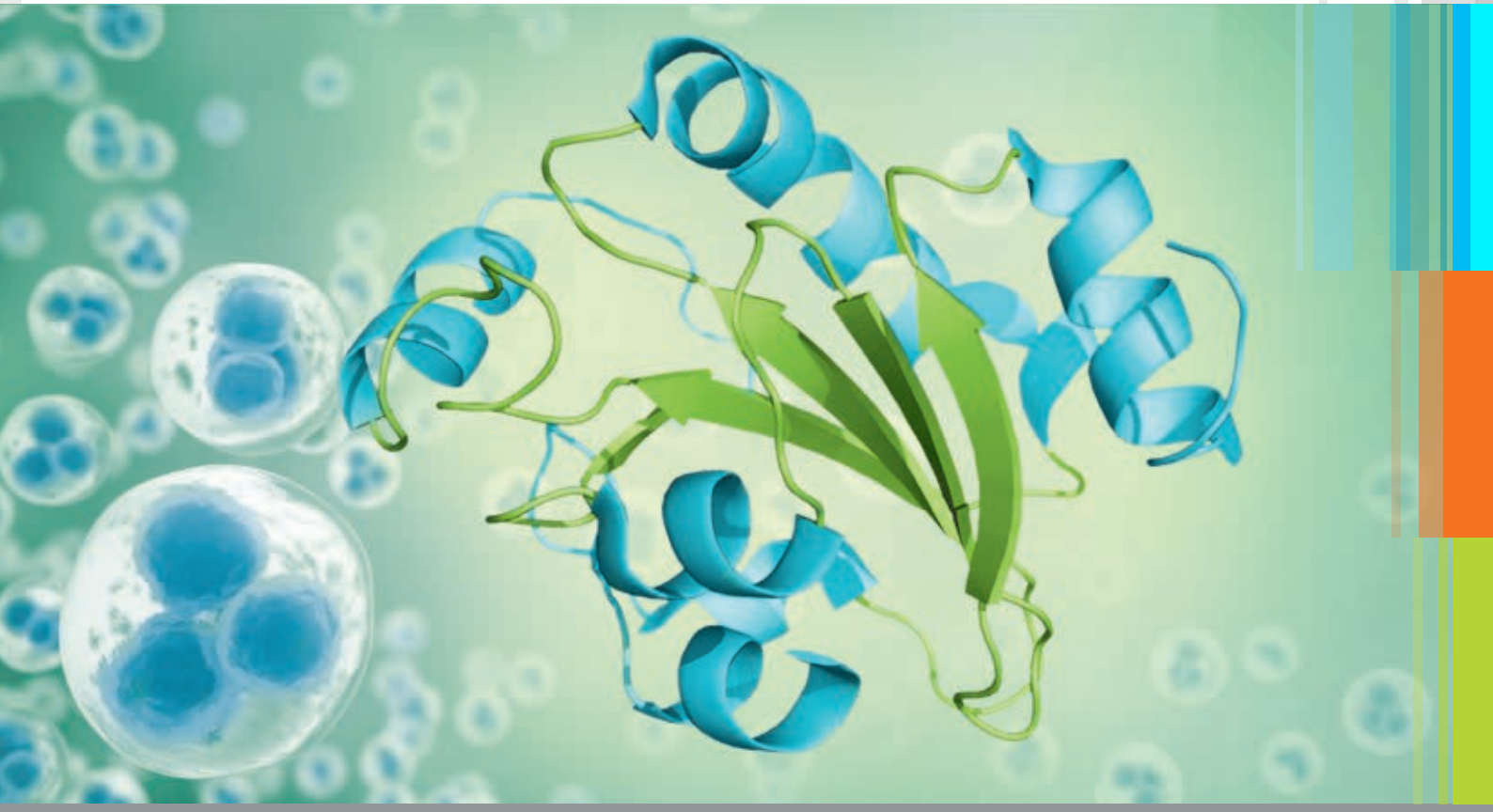
Innovative Peptide Solutions



# Proteomics Resources

## Reference Peptides & Kits for

- **Discovery Proteomics**
- **Targeted / Quantitative Proteomics**
- **Clinical Proteomics**
- **Immunopeptidomics**
- **Functional Proteomics**

Contact us for further information: peptide@jpt.com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jpt
Innovative Peptide Solutions

# Largest Selection of Peptides …

## SpikeTides™ & SpikeMix™

- Individual reference peptides
- For protein detection and quantification by mass spectrometry
- Proteotypic or other selected peptides
- Inexpensive and fast
- Light or stable isotope-labeled
- Large variety of optional modifications such as PTMs and Cys-carbamidomethylation
- SpikeMixes™ are reference peptide pools with similar features as SpikeTides™

## SpikeTides™_TQL & SpikeTides™_TQL PLUS

- Absolute quantification approach for reference peptides
- Unique and highly efficient
- Quantification tag (QTag) added to each peptide
- UV active QTag is released by trypsin
- Fast and inexpensive
- Very accurate quantification
- SpikeTides™_TQL PLUS for clinical applications enables end-user to reconfirm peptide quantity

## Catalog Peptides & Kits

- Largest variety of ready-to-use reference peptides
- The Human Proteome Peptide Catalog (> 400k peptides)
- SpikeMix™ and SpikeTides™ Kits, e.g. cytokines, TAAs or peptide hormones
- Quantified SpikeTides™ Kits, e.g. metabolic enzymes or histones
- SpikeTides™ PTM Reference Kits
- Standardization Kits, e.g. Retention Time Standardization Kit (PROCAL)

### Our Service is the Best!

We offer quick and personal consultation with experienced scientists and help you with the selection of peptide specifications, provide tips for storage, solvents and more. Take advantage of our rush order service for urgent projects.

# … from JPT!

## Mass Spectrometry-Based Proteomics

Proteomics is the study of a cell's protein inventory by protein identification and quantification. In mass spectrometry-based proteomics, samples containing relevant proteins are typically digested into peptides and analyzed by LC-MS/MS as surrogates of the original proteins. To increase accuracy of detection and to enable protein quantification, chemically synthesized stable isotope-labeled (SIL) peptides are added.

## Why Work with JPT?

- Largest resource of proteomics reference peptides
- Our proprietary technologies facilitate projects world-wide
- Over 1000 peer-reviewed papers with our products
- Comprehensive know-how and dedicated staff make us the peptide experts
- ISO 9001:2015 regulated quality management system
- We provide strong bioinformatics support

## Mass Spectrometry-Based Assays

**The Human Proteome Peptide Catalog**

**SpikeTides™, SpikeMix™ & SpikeMix™ Kits**

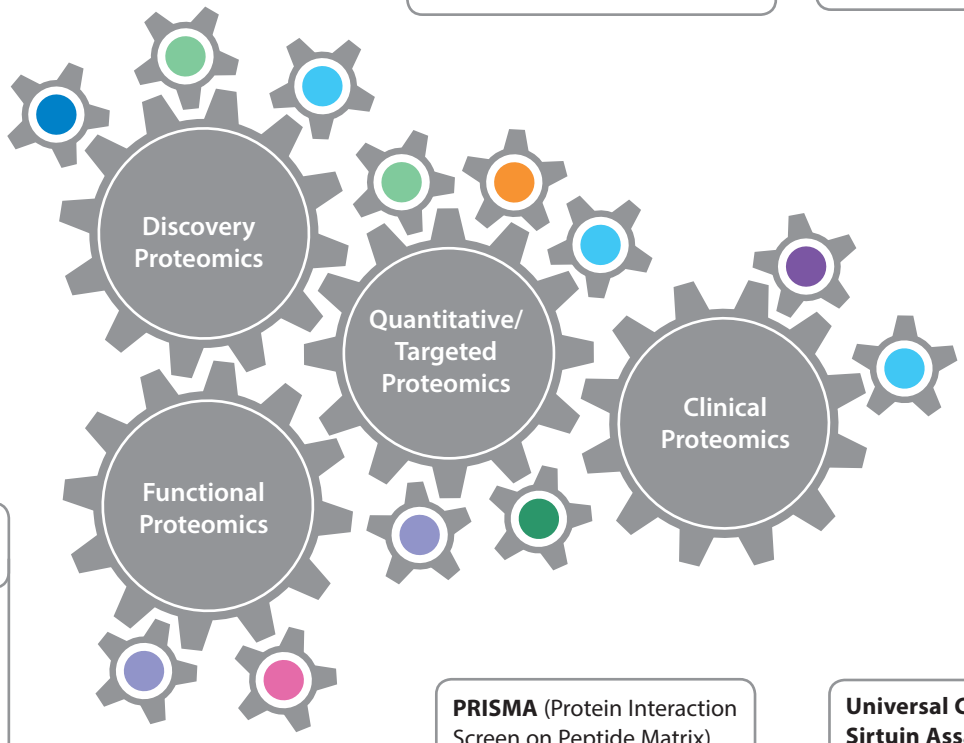
**Assay Standards & Controls**

**Quantified SpikeTides™_TQL & Quantified SpikeTides™ Kits**

**PTM Reference Kits**

**Quantified SpikeTides™_TQL PLUS**

**NeoSpikeMix™**




**Histone Code Analysis Tools & Services**

**Enzyme Profiling Tools & Services**
Phosphatases, Kinases, Proteases, Acetyltransferase, Deacetylase

**PRISMA** (Protein Interaction Screen on Peptide Matrix)

**Universal Continuous Sirtuin Assay Kit**

## Functional Assays

*JPT's products and services for proteomics*

# Proteomics Resources

## Selected References

- *"ProteomeTools: Systematic Characterization of 21 Post-Translational Protein Modifications by LC-MS/MS Using Synthetic Peptides"*
  Zolg et al., Molecular and Cellular Proteomics (2018)
- *"Quantification of Urinary Protein Biomarkers of Autosomal Dominant Polycystic Kidney Disease by Parallel Reaction Monitoring"*
  Chien-Yun Lee et al., Molecular and Cellular Proteomics (2018)
- *"PROCAL: A Set of 40 Peptide Standards for Retention Time Indexing, Column Performance Monitoring, and Collision Energy Calibration"*
  Zolg et al., Proteomics (2017)
- *"Building ProteomeTools Based on a Complete Synthetic Human Proteome"*
  Zolg et al., Nature Methods (2017)
- *"Targeted Proteomics for Multiplexed Verification of Markers of Colorectal Tumorigenesis"*
  Uzozie et al., Mol Cell Proteomics (2017)
- *"Quantification of 87 Proteins by nLC-MRM/MS in Human Plasma: Workflow for Large-scale Analysis of Biobank Samples"*
  Rezeli et al., J Proteome Res. (2017)
- *"Quantitative Multiple Reaction Monitoring Proteomic Analysis of Gβ and Gγ Subunits in C57Bl6/J Brain Synaptosomes"*
  Yim et al., Biochemistry (2017)

**Find more at:**
**www.jpt.com/literature/**

## Application Notes

- *"SpikeTides™ for Subcellular Marker Proteins offer Improved Analysis of Complex Plant Samples"*
  Hooper et al., Application Note (2017)
- *"Fast and Accurate Determination of Cysteine Reduction and Alkylation Efficacy in Proteomics Workflows"*
  Schnatbaum et al., Application Note (2016)
- *"Absolute Quantification of Metabolic Enzymes via Targeted Proteomics Using a New Kit of SpikeTides™ Peptides"*
  Bindel et al., Application Note (2015)
- *"Development of a Multiplexed Targeted SRM Assay for NCI's Top Tumor Associated Antigens"*
  Soderblom et al., Application Note (2015)
- *"Histone PTM Profiling Reveals Global and Specific Responses to Systematic Enzyme Ablations"*
  Feller et al., Application Note (2015)
- *"Development & Characterization of SpikeMix™ ABRF (cross-species standard) Consisting of 1000 Stable Isotope-Labeled Peptides"*
  Colangelo, Application Note (2014)

**Full text at:**
**www.jpt.com/application-notes/**

*"At Cambridge University we have significantly benefited from a suite of SpikeTides™ from JPT which have been developed for use as organelle markers in Arabidopsis. Using these we have developed faster and more accurate methods, using SRM and PRM, for estimating organelle enrichment along linear density gradients. Results have been very instrumental in optimizing downstream methodologies, a process which has delivered improved resolution in ensuing datasets for lower costs than our original methods."*

*Harriet Parsons, PhD, Department of Biochemistry, University of Cambridge, UK*

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