Acetylase & Deacetylase Peptide Microarrays

Use JPT’s microarrays to investigate PTMs on a proteome level. You can:
- Detect epigenetic targets for lysine-acetyltransferases
- lysine-deacetylases and other lysine modifying enzymes
- Profile antibodies
- Study cross-talk of different enzyme modifications

→ Acetylome Peptide Microarrays
Acetylation is a post-translational modification that plays a major role in regulating transcription and other metabolic processes. Recent mass spectrometric investigations have identified more than 5500 acetylation sites in human proteins. We created two high-density peptide microarrays, each displaying 5599 peptides derived from reported human lysine acetylation sites (plus 384 control peptides).

Selected References
→ “Exploring the Human Acetylome Using High Density Peptide Microarrays”
Masch et al., Application Note (2012)
Download at: http://www.jpt.com/fileadmin/user_upload/pdf/AppNote_Acetylome_1206.pdf

Assay principle of deacetylase microarrays

1. Microarray…
   (control) is incubated with fluorescently labeled acetyl-lysine specific antibody only.

2. Microarray…
   is incubated with the enzyme of interest (e.g. deacetylase) followed by fluorescently labeled acetyl-lysine specific antibody. By comparison of both microarrays a signal decrease will be detected (differential measurement).
Histone Code Peptide Tools

As histones are a major focus of epigenetics, we compiled a unique library of synthetic histone peptides. The extensive library covers all reported sequence variants of histones carrying PTMs in various combinations. Featured modifications are: Lys [ac, (mono-, di-, tri-) met, but, prop, succ, mal]; Arg [(mono-, di-) met (symmetries an asymmetrics)], Cit, and Ser, Thr, Tyr [phospho].

Individual Histone Code Peptides
Several hundred peptides from our histone code library are now available as purified, high quality biotinylated or non-biotinylated peptides. Among other applications they can be used for fast and efficient confirmation of microarray results. All peptides are purified and qualified by HPLC-MS and arrive as freeze-dried aliquots for increased shelf stability.

For a full up-to-date list please visit our webshop at http://shop.jpt.com/4-Single-Peptides/

Histone Code Peptide Microarrays
Histone Code Microarrays are made up of 3668 peptides derived from our histone code peptide library with and without PTMs. Most potential post-translational modification sites are represent-ed. JPT’s comprehensive Histone Code Microarrays enable mapping of protein-histone interactions with unprecedented resolution due to its high coverage of natural sequence variants.

Please ask for our comprehensive microarray incubation and analysis service!

“JPT’s new extremely high-density histone peptide arrays is a dramatic leap forward for analysis of the histone code hypothesis. The complete sequence coverage across core histones and histone variants as well as the presence of common and rare histone post-translational modifications – alone and in combination – makes this an unparalleled tool for studying the “writers” and “readers” of the histone code. My laboratory has used these arrays to ask the sequence and PTM dependence of a histone writer enzyme and we have discovered an activity specifying code that will keep us busy for years to come.”

David Shechter, PhD, Department of Biochemistry, Albert Einstein College of Medicine, Yeshiva University, New York, NY (USA)