

Minireview

- 706 **Protein Footprinting Comes of Age: Mass Spectrometry for Biophysical Structure Assessment**
[S] *Liwen Wang and Mark R. Chance*

Research

- 717 **Proteome-wide Mapping of Endogenous SUMOylation Sites in Mouse Testis**
[S] ✎ *Lili Cai, Jun Tu, Lei Song, Zihua Gao, Kai Li, Yunzhi Wang, Yang Liu, Fan Zhong, Rui Ge, Jun Qin, Chen Ding, and Fuchu He*
- 728 **Quantitative Proteomic Approach Identifies Vpr Binding Protein as Novel Host Factor Supporting Influenza A Virus Infections in Human Cells**
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- 799 **Development of a Multiplexed Liquid Chromatography Multiple-Reaction-Monitoring Mass Spectrometry (LC-MRM/MS) Method for Evaluation of Salivary Proteins as Oral Cancer Biomarkers**
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On the cover: DSSO-based *in vivo* and *in vitro* cross-linking mass spectrometry (XL-MS) strategies represent new analytical workflows to study protein-protein interactions of large protein assemblies in cells. In combination with EM maps and computational modeling, the architecture of the human 26S proteasome was determined to infer its structural dynamics and regulation. For details, see the article by Xiaorong Wang, *et al.*, pages 840–854.

- 812 **Global Analysis of SUMO-Binding Proteins Identifies SUMOylation as a Key Regulator of the INO80 Chromatin Remodeling Complex**
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- 840 **Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome**
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