

Research

- 1479 **Glycoproteogenomics: A Frequent Gene Polymorphism Affects the Glycosylation Pattern of the Human Serum Fetuin/ α -2-HS-Glycoprotein**
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- 1491 **Redundancy and Complementarity between ERAP1 and ERAP2 Revealed by their Effects on the Behcet's Disease-associated HLA-B*51 Peptidome**
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- 1511 **Proteomic Analysis of Vocal Fold Fibroblasts Exposed to Cigarette Smoke Extract: Exploring the Pathophysiology of Reinke's Edema**
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- 1607 **Phosphoproteome Analysis Reveals Estrogen-ER Pathway as a Modulator of mTOR Activity Via DEPTOR**
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- 1619 **Cancer Cell Derived Small Extracellular Vesicles Contribute to Recipient Cell Metastasis Through Promoting HGF/c-Met Pathway**
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On the Cover: Based on the premise that subunits of stable protein complexes co-elute, the composition of protein complexes isolated from Arabidopsis leaves was predicted based on mass spectrometry data alone. Label-free protein correlation profiling, combined with orthogonal chromatographic separations of cell extracts, was used to predict hundreds of known and novel protein complexes. For details see the article by Chen *et al.*, pages 1588-1606.

- 1630 **Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability**
 [S] *Kuan-lin Huang, Yige Wu, Tina Primeau, Yi-Ting Wang, Yuqian Gao, Joshua F. McMichael, Adam D. Scott, Song Cao, Michael C. Wendl, Kimberly J. Johnson, Kelly Ruggles, Jason Held, Samuel H. Payne, Sherri Davies, Arvin Dar, Christopher R. Kinsinger, Mehdi Mesri, Henry Rodriguez, Matthew J. Ellis, R. Reid Townsend, Feng Chen, David Fenyö, Shunqiang Li, Tao Liu, Steven A. Carr, and Li Ding*
- 1651 **FusionPro, a Versatile Proteogenomic Tool for Identification of Novel Fusion Transcripts and Their Potential Translation Products in Cancer Cells**
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- 1669 **Mapping Spatiotemporal Microproteomics Landscape in Experimental Model of Traumatic Brain Injury Unveils a link to Parkinson's Disease**
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- 1683 **Simultaneous Improvement in the Precision, Accuracy, and Robustness of Label-free Proteome Quantification by Optimizing Data Manipulation Chains**
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