

PROTEOMICS

Supporting Information

for Proteomics

DOI 10.1002/pmic.201000722

Yuexi Wang, Feng Yang, Marina Gritsenko, Yingchun Wang,
Therese Clauss, Tao Liu, Yufeng Shen, Matthew E. Monroe,
Daniel Lopez-Ferrer, Theresa Reno, Ronald J Moore,
Richard L. Klemke, David G. Camp II and Richard D. Smith

**Reversed-phase chromatography with multiple fraction concatenation
strategy for proteome profiling of human MCF10A cells**

Supplementary figures:

Figure 1. Overview of the experimental workflow. Same amount of starting material was applied to each approach in such a manner that each method was comparable. Details of the methods are described in the Materials and Methods part.

Figure 2. Physicochemical Properties of Identified Peptides.

Figure 3. Comparison of cellular component (A) and molecular function (B) of proteins identified using high pH RPLC, SCX LC and low pH RPLC fractionation methods.

Figure 4. LC profile of first dimension fractionation approaches (UV absorbance at 280nm).

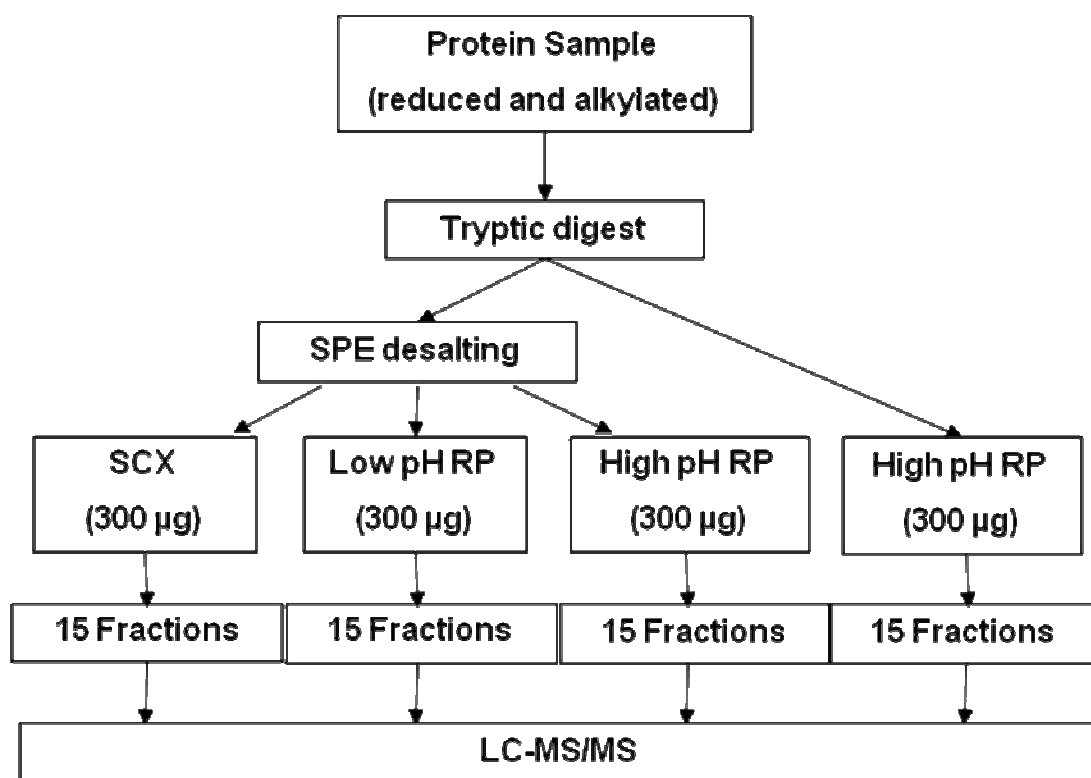


Figure 1.

(A)

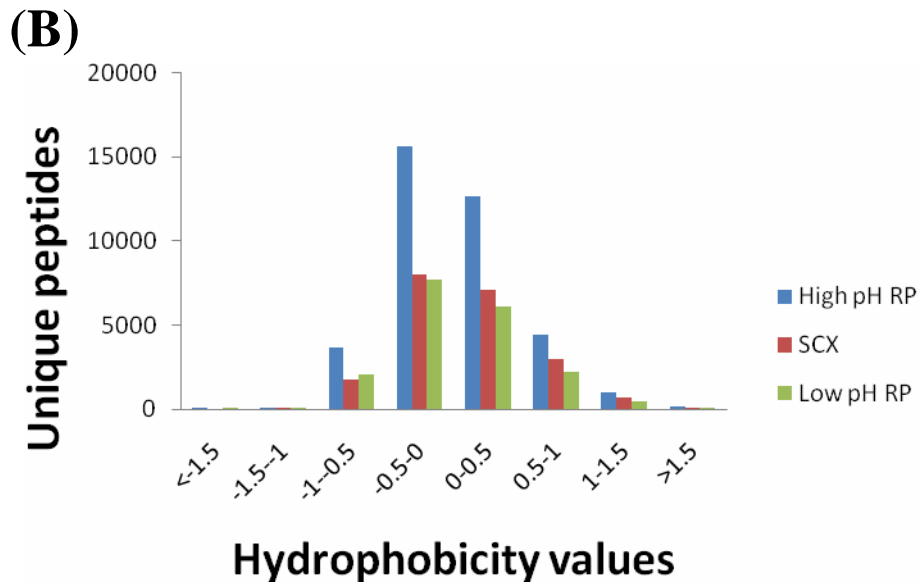
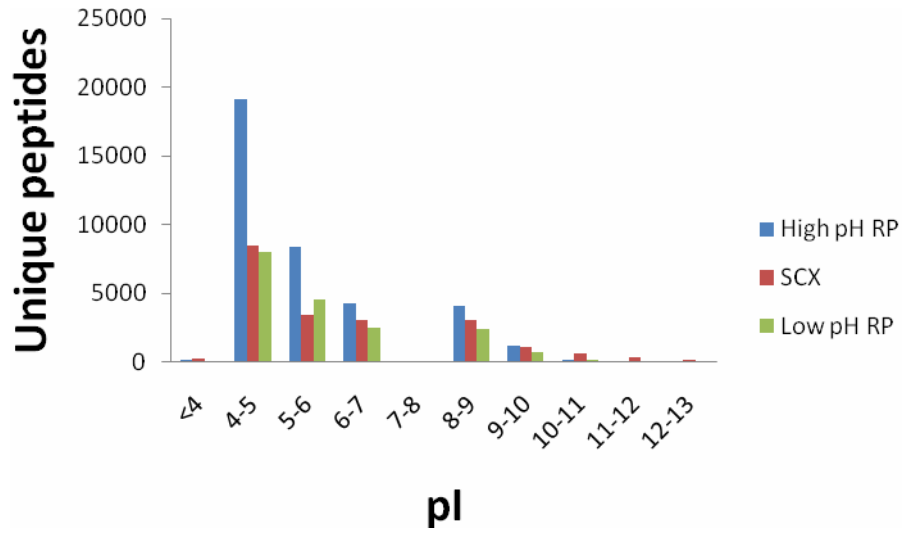


Figure 2.

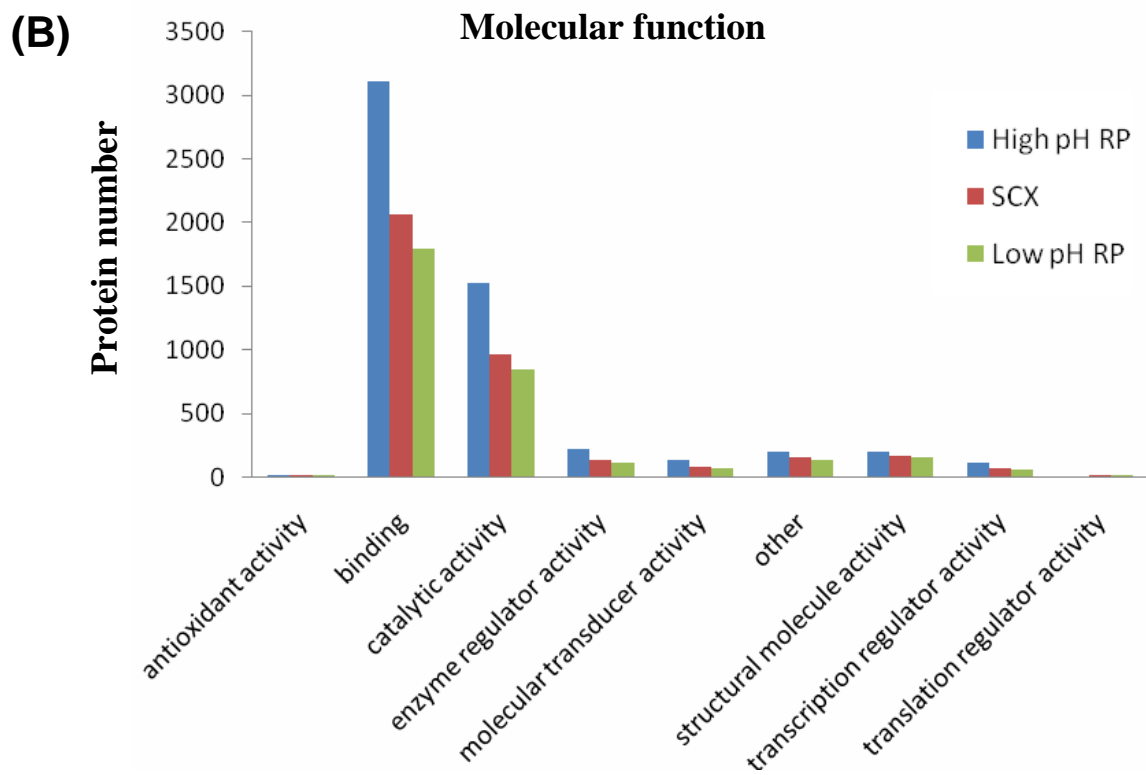
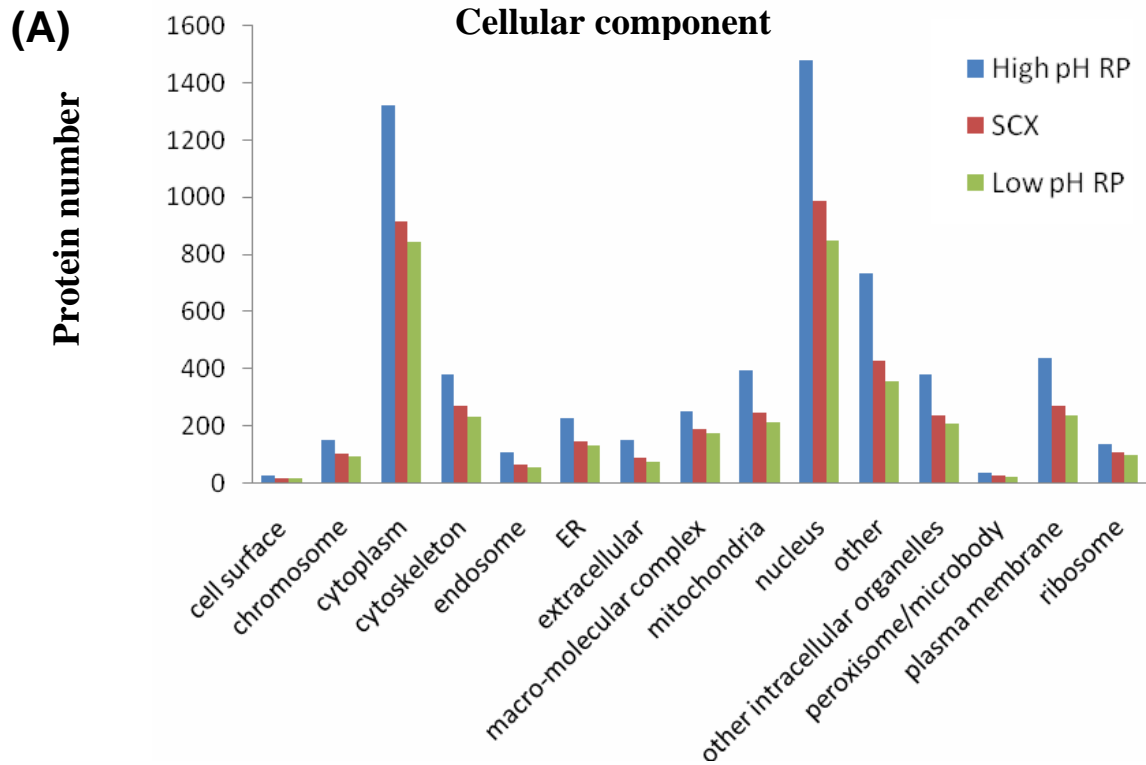


Figure 3.

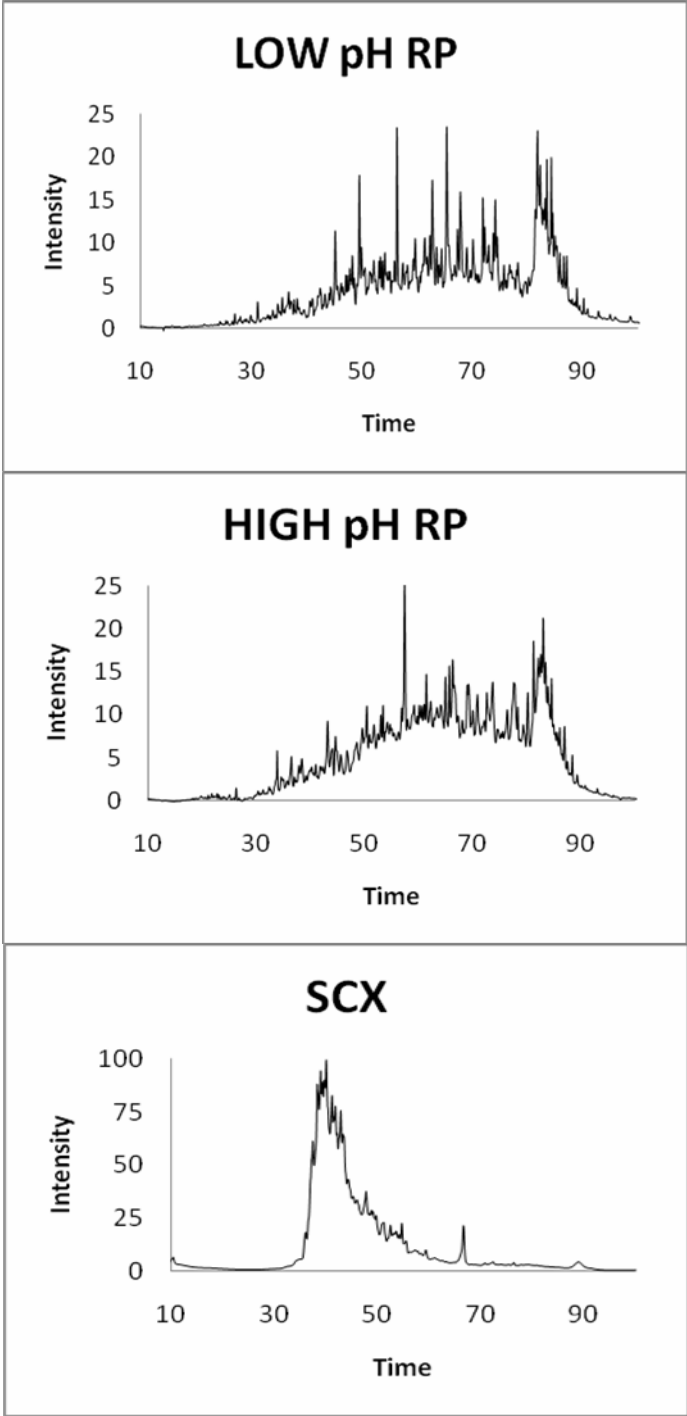


Figure 4.