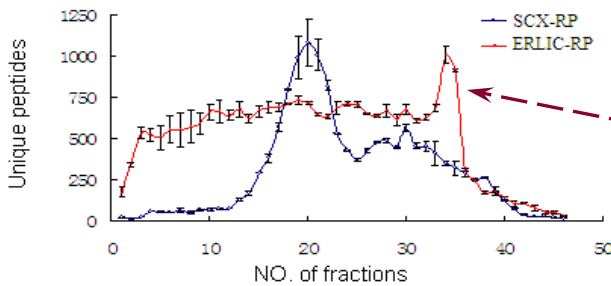


Superior Proteomics Fractionations with **ERLIC***-RPC

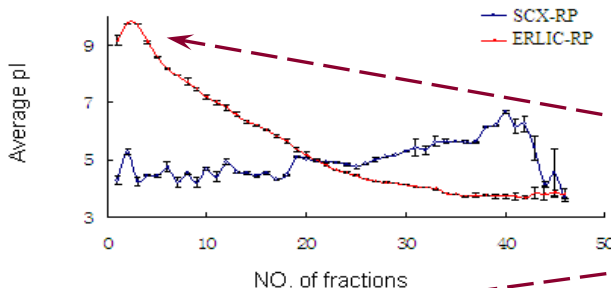
*(Electrostatic Repulsion-Hydrophilic Interaction Chromatography) March 2010

In bottom-up proteomics, more peptides of lower abundance are identified if complex digests are fractionated via two dimensions of chromatography. The most widely used combination at present is SCX-RPC. There are significant advantages to substitution of the new ERLIC mode for SCX. ERLIC of peptides is performed with an anion-exchange column operated in the HILIC mode at low pH. With a decreasing organic solvent gradient, hydrophilic interaction becomes so weak that electrostatic repulsion causes the peptides' elution. Volatile solvents can be used!

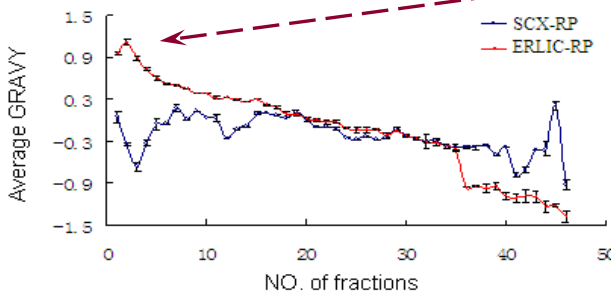
Example: 2 mg. peptides from tryptic digest of rat kidney homogenate



Distribution of peptides:
 Much more uniform in ERLIC than in SCX



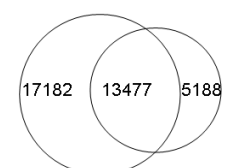
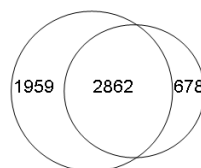
Basis of separation in ERLIC:
 pI of peptide (high to low)
 and
 polarity (low to high)



- both variables are complementary to selectivity in RPC -

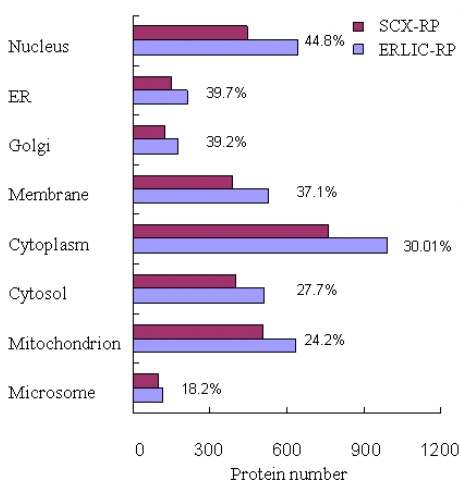
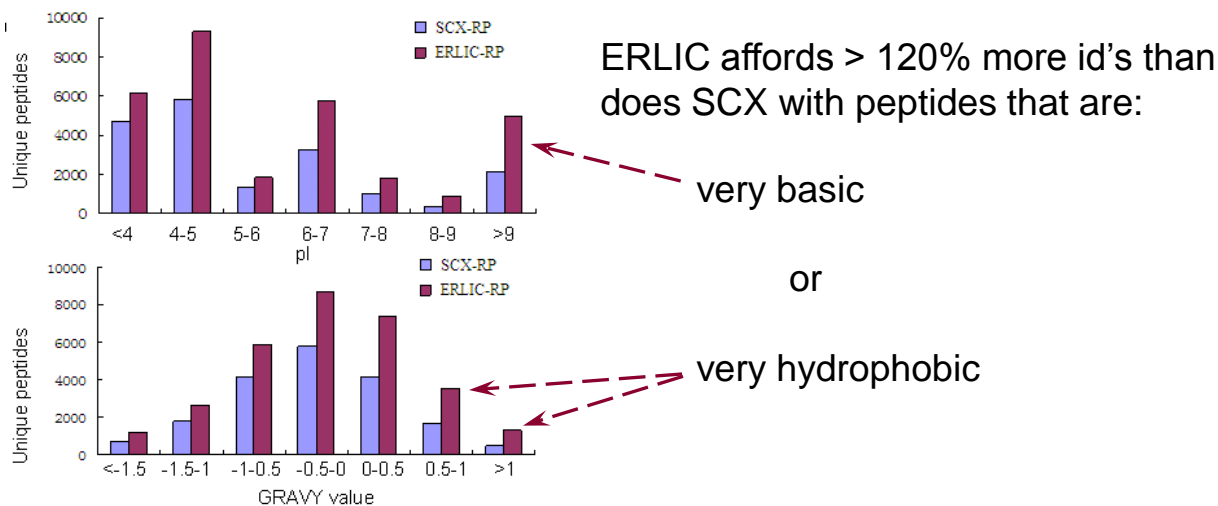
The number of identifications is significantly higher with ERLIC than with SCX

Protein id's Unique Peptide id's



ERLIC-RPC SCX-RPC

ERLIC-RPC SCX-RPC



This makes it more effective at identifying peptides from membrane-rich organelles

- data courtesy of S.K. Sze, Nanyang Technological Univ. -

References on ERLIC:

- 1) A.J. Alpert, *Anal. Chem.* 80 (2008) 62
- 2) C.S. Gan, T. Guo, H. Zhang, S.K. Lim, and S.K. Sze, *J. Proteome Res.* 7 (2008) 4869
- 3) U.L. Lewandrowski, K. Lohrig, R. Zahedi, D. Walter, and A. Sickmann, *Clin. Proteom* 4 (2008) 12
- 4) H. Zhang, T. Guo, X. Li, A. Datta, J.E. Park, J. Yang, S.K. Lim, J.P. Tam, and S.K. Sze, *Mol. Cell Proteomics*, online Jan. 2010
- 5) P. Hao, T. Guo, X. Li, S. Adav, J. Yang, W. Meng, and S.K. Sze, *submitted for publication*

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ERLIC: PolyWAX LP column, 200 x 4.6mm, 5µm, 300Å (item# P204WX0503)

SCX: PolySULFOETHYL A column, 200 x 4.6mm, 5µm, 200Å (item# P204SE0502)

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