

# Precolumn Ion Exchange Fractionation for RPC LC/MS Applications

When there are too many proteins to identify fast but you want to do it fast anyway  
...try SCX-RPC-MS

**Problem:** Suppose you know all the proteins in an organism. Which ones are in the ribosome? Digest the complex with trypsin. Mass spec can identify the tryptic peptides if they're presented in manageable numbers. This is accomplished with a capillary packed with a PolySULFOETHYL Aspartamide™ SCX segment and an RPC segment. The complete digest is trapped on the SCX segment. A step gradient of increasing salt pulses is used to release sets of increasingly basic peptides to a RPC column where the salt is shunted to waste. Each set is then resolved by RPC gradients and analyzed by MS. Approximately 400-500 peptides in a sample can be identified this way.

*Courtesy of John Yates (University of Washington)*

