



FIGURE 1. Overview of the AP-MS procedure. In Scheme A, SDS-PAGE separates a purified protein complex, the gel slice is excised, the proteins are digested, and the peptides are extracted from the gel. Peptides arising from a single protein are either separated by HPLC and analyzed by ESI/MS or MS/MS, or they are analyzed by MALDI/TOF. In Scheme B, the entire protein complex is digested. Peptides arising from the digestion of multiple proteins are separated by HPLC and analyzed by ESI MS/MS. Database searching reveals the identity of the proteins in the complex. RP is reverse phase and SCX is a strong cation exchange.