Supplemental Figure 1: Comparison of ProteoPrep® 20 and MARS 6® immunodepletion techniques.

(A) Native CSF or CSF samples immunodepleted of either 20 (ProteoPrep® 20) or 6 (MARS 6®) major plasma proteins (100 µg proteins per lane) were separated by SDS-PAGE. The data illustrated are representative of three experiments performed independently. Six gel pieces were excised in each gel lane corresponding to immunodepleted fractions (as depicted in A) and digested by trypsin. (B) and (C) The data, expressed as mean ± SEM of values obtained in the three independent immunodepletions, represent the number of proteins and peptides identified by LC-MS/MS in the corresponding bands, respectively. Only peptides with *p* values lower than 0.01 were taken into consideration.

Supplemental Figure 2: 2-D gel analysis of immunodepleted fractions obtained in six independent immunodepletions of the same CSF pool.

Proteins not retained on ProteoPrep® 20 columns in each experiment were resolved on 2-D gels (pH 3-11, 11-17% gradient) and gels were stained with silver.

Supplemental Figure 3: List of annotated MS/MS spectra obtained for CSF proteins identified from a single peptide. For each spectrum, a mass list of matching and non-matching peptides is provided.

Supplemental Figure 4: Annotated MALDI-TOF MS spectra of proteins identified in conditioned medium of cortical neurons in primary culture. As all matching peptide masses are not depicted on the spectra by the Flex Analysis software, a comprehensive mass list of matching and non-matching peptides is provided for each identified protein.