Supplementary Table S1.

Table S1 lists information regarding the 1253 proteins identified from the post-synaptic density preparation, including the Protein name; Protein Accession number; Protein Function; the number of peptides used to identify the protein as well as the Mascot Score and Expectation Values for the most confident peptide identification for each protein, and finally the percent sequence coverage for each protein. Protein functions were grouped as follows: A=Adaptor/Sorting; D=DNA/nucleus/histone; E=Enzyme/G protein; F = Folding/Chaperone/Heatshock; G=Glia; K=Kinase/Phosphatase; M=Mitochondria/Metabolism/Energy; O = Other; P=Presynaptic; R=Receptor/Channel/Transporter; S=Structural/Scaffold/Adhesion/Cytoskeleton; T=Translation/Ribosomal

Supplementary Table S2.

Table S2 lists information regarding the 1008 unique phosphopeptides identified from the postsynaptic density, including the peptide m/z; peptide charge; Mascot Score and Expectation values; as well as the number of phosphorylation sites on a given peptide. When the MS/MS spectra did not contain sufficient information to limit the site of phosphorylation to a single amino acid, the potentially phosphorylated sites are listed in parenthesis. Lower case “m” in the peptide sequence corresponds to oxidized methionine, lower case “q” corresponds to peptide amino terminal pyroglutamine; and “acetyl” corresponds to protein amino terminal acetylation.

Supplementary Table S3

Table S3 lists all the interpreted peaks for individual phosphopeptide MS/MS spectra. The peptide sequence is listed along with the m/z ratio, precursor charge, elution time, and MASCOT
expectation value. Column H lists the possible amino acids within the peptide that might be phosphorylated. Column I lists the total number of phosphorylations for that given peptide. Columns J through Q list b-ion and b-18 ion information. Columns S through Z list y-ion and y-18 ion information. Column AA through AD list b+phosphate ion information. Column AE through AH list y+phosphate ion information.

**Supplementary Table S4**

Table S4 lists information for all proteins identified by a single peptide. The protein name, accession number, peptide sequence, precursor mass, precursor charge, Mascot score and Mascot Expectation value (searched against Uniprot Rodent) are listed.