NOV 12, 2023

OPEN ACCESS

DOI:
dx.doi.org/10.17504/protocols.io.5jyl8pw86g2w/v1

Protocol Citation: Leonardo A Parra-Rivas 2023. Proteome analysis. **protocols.io** https://dx.doi.org/10.17504/protocols.io.5jyl8pw86g2w/v1

Protocol status: Working
We use this protocol and it's working

Created: Nov 12, 2023

Last Modified: Nov 12, 2023

Proteome analysis

Leonardo A Parra-Rivas[1]

[1]University of California, San Diego

Subhojit Roy Lab

Leonardo A Parra-Rivas
University of California, San Diego

ABSTRACT

Proteome analysis

PROTOCOL integer ID:
90828

1 Mass spectrometry data was analyzed according to a published protocol

CITATION

Wingo TS, Duong DM, Zhou M, Dammer EB, Wu H, Cutler DJ, Lah JJ, Levey AI, Seyfried NT (2017). Integrating Next-Generation Genomic Sequencing and Mass Spectrometry To Estimate Allele-Specific Protein Abundance in Human Brain..

LINK

https://doi.org/10.1021/acs.jproteome.7b00324

2 Spectra were searched using Proteome Discoverer (RRID:SCR_014477) (https://www.thermofisher.com/order/catalog/product/IQLAAEGABSFAKJMAUH) software version 2.1 against 2020 mouse UniProtKB/Swiss-Prot (RRID:SCR_021164)(https://www.expasy.org/resources/uniprotkb-swiss-prot) (17,042 target sequences) along with the human α-synuclein protein sequence.

3 Searching parameters included full tryptic or Asp-N restriction, precursor mass tolerance (± 20 ppm), and fragment mass tolerance (± 0.05 Da). Serine, threonine, and tyrosine phosphorylation (+79.9663 Da), methionine oxidation (+15.99492 Da), asparagine and glutamine deamidation (+0.98402 Da), and protein N-terminal acetylation (+42.03670 Da) were variable modifications (up to 3 allowed per peptide); cysteine was assigned a fixed carbamidomethyl modification (+57.021465 Da).

4 Percolator was used to filter the peptide spectrum matches to a false discovery rate of 1%.

5 Gene ontology was analyzed using The Database for Annotation, Visualization and Integrated Discovery DAVID (RRID:SCR_001881)(https://david.ncifcrf.gov/tools.jsp-DAVID[97].

6 Biological processes involving synaptic function were selected for grouping analysis. Functional grouping was based on Fisher's exact test ($p<0.05$).
Protein-protein interaction networks were then identified using the STRING (RRID:SCR_005223) (https://string-db.org/) version 11.5 , and the protein class was determined using PANTHER (RRID:SCR_004869)(http://www.pantherdb.org/).