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Version 1

LC-MS/MS Label-Free Proteomic Data Analysis Parameters V.1

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Protocol status: Working

We use this protocol and it's working

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Abstract

List of parameters and settings for searching label free proteomic data in MaxQuant version 1.6.7.

- 1 Label-free proteomic samples were searched using MaxQuant version 1.6.7.
- 2 *Group Specific Parameter settings included:*
 - Standard
 - Multiplicity = 1
 - Variable modifications: Oxidation (M); Acetylation (Protein N-term), Carbamidomethyl (C)
 - Fixed modifications: Carbamidomethyl (C)
 - Max number of modifications per peptide: 5
 - Instrument settings: Orbitrap (default settings)
 - Digestion: Specific, Trypsin /P
 - Max missed cleavages: 2
 - LFQ: None
- 3 *Global Parameters included:*
 - Database: UniProt Human Proteome (UP000005640, 9606) Reviewed, downloaded July 30, 2019
 - Min peptide length: 7
 - Max peptide mass: 4600 Da
 - MS/MS analyzer: Default settings
 - Identification: Default settings