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Version 2

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LC-MS/MS Label-Free Proteomic Data Analysis Parameters V.2

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1 Works for me dx.doi.org/10.17504/protocols.io.bfshjnb6

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Human BioMolecular Atlas Program (HuBMAP) Method Development Community

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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

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