



Version 3

Mar 05, 2021

LC-MS/MS Label-Free Proteomic Data Analysis Parameters V.3

Danielle Gutierrez¹, Jamie Allen¹, Zach Jenkins¹, Jeff Spraggins¹¹Vanderbilt University

1 Works for me dx.doi.org/10.17504/protocols.io.bsu5ney6

VU Biomolecular Multimodal Imaging Center

Human BioMolecular Atlas Program (HuBMAP) Method Development Community

Jamie Allen
Vanderbilt University

SUBMIT TO PLOS ONE

ABSTRACT

List of parameters and settings for searching label free proteomic data in MaxQuant version 1.6.17.

DOI

dx.doi.org/10.17504/protocols.io.bsu5ney6

PROTOCOL CITATION

Danielle Gutierrez, Jamie Allen, Zach Jenkins, Jeff Spraggins 2021. LC-MS/MS Label-Free Proteomic Data Analysis Parameters. **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.bsu5ney6>
Version created by [Danielle Gutierrez](#)

KEYWORDS

HuBMAP, BIOMIC, MSRC, Vanderbilt, Proteomics, MaxQuant, Data Analysis

LICENSE

————— This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Feb 28, 2021

LAST MODIFIED

Mar 05, 2021

OWNERSHIP HISTORY

Mar 05, 2021 Jamie Allen Vanderbilt University

PROTOCOL INTEGER ID

47741

DISCLAIMER:

DISCLAIMER – FOR INFORMATIONAL PURPOSES ONLY; USE AT YOUR OWN RISK

The protocol content here is for informational purposes only and does not constitute legal, medical, clinical, or safety

advice, or otherwise; content added to protocols.io is not peer reviewed and may not have undergone a formal approval of any kind. Information presented in this protocol should not substitute for independent professional judgment, advice, diagnosis, or treatment. Any action you take or refrain from taking using or relying upon the information presented here is strictly at your own risk. You agree that neither the Company nor any of the authors, contributors, administrators, or anyone else associated with protocols.io, can be held responsible for your use of the information contained in or linked to this protocol or any of our Sites/Apps and Services.

- 1 Label-free proteomic samples were searched using MaxQuant version 1.6.17.
- 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