|  |  |
| --- | --- |
|  |  |
| Parameter ValueVersion 1.6.1.0User name mpcadminMachine name ADMIN-PCDate of writing 05/22/2021 10:07:11Fixed modifications Carbamidomethyl (C)Include contaminants TruePSM FDR 0.01Protein FDR 0.01Site FDR 0.01Use Normalized Ratios For Occupancy TrueMin. peptide Length 7Min. score for unmodified peptides 0Min. score for modified peptides 40Min. delta score for unmodified peptides 0Min. delta score for modified peptides 6Min. unique peptides 0Min. razor peptides 1Min. peptides 1Use only unmodified peptides and FalsePeptides used for protein quantification RazorDiscard unmodified counterpart peptides TrueLabel min. ratio count 2Use delta score FalseiBAQ FalseiBAQ log fit FalseMatch between runs TrueMatching time window [min] 0.7Alignment time window [min] 20Find dependent peptides FalseFasta file C:\Databases\Swissprot human 201911.fastaDecoy mode revertInclude contaminants TrueAdvanced ratios TrueFixed andromeda index folder Temporary folder Combined folder location Second peptides TrueStabilize large LFQ ratios TrueSeparate LFQ in parameter groups FalseRequire MS/MS for LFQ comparisons FalseCalculate peak properties FalseMain search max. combinations 200Advanced site intensities TrueLFQ norm for sites and peptides FalseWrite msScans table TrueWrite msmsScans table TrueWrite ms3Scans table TrueWrite allPeptides table TrueWrite mzRange table TrueWrite pasefMsmsScans table TrueWrite accumulatedPasefMsmsScans table TRUE | Max. peptide mass [Da] 4600Min. peptide length for unspecific search 8Max. peptide length for unspecific search 25Razor protein FDR TrueDisable MD5 FalseMax mods in site table 3Match unidentified features TrueMS/MS tol. (FTMS) 20 ppmTop MS/MS peaks per Da interval. (FTMS) 12Da interval. (FTMS) 100MS/MS deisotoping (FTMS) TrueMS/MS deisotoping tolerance (FTMS) 7MS/MS deisotoping tolerance unit (FTMS) ppmMS/MS higher charges (FTMS) TrueMS/MS water loss (FTMS) TrueMS/MS ammonia loss (FTMS) TrueMS/MS dependent losses (FTMS) TrueMS/MS recalibration (FTMS) FalseMS/MS tol. (ITMS) 0.5 DaTop MS/MS peaks per Da interval. (ITMS) 8Da interval. (ITMS) 100MS/MS deisotoping (ITMS) FalseMS/MS deisotoping tolerance (ITMS) 0.15MS/MS deisotoping tolerance unit (ITMS) DaMS/MS higher charges (ITMS) TrueMS/MS water loss (ITMS) TrueMS/MS ammonia loss (ITMS) TrueMS/MS dependent losses (ITMS) TrueMS/MS recalibration (ITMS) FalseMS/MS tol. (TOF) 40 ppmTop MS/MS peaks per Da interval. (TOF) 10Da interval. (TOF) 100MS/MS deisotoping (TOF) TrueMS/MS deisotoping tolerance (TOF) 0.01MS/MS deisotoping tolerance unit (TOF) DaMS/MS higher charges (TOF) TrueMS/MS water loss (TOF) TrueMS/MS ammonia loss (TOF) TrueMS/MS dependent losses (TOF) TrueMS/MS recalibration (TOF) FalseMS/MS tol. (Unknown) 0.5 DaTop MS/MS peaks per Da interval. (Unknown) 8Da interval. (Unknown) 100MS/MS deisotoping (Unknown) FalseMS/MS deisotoping tolerance (Unknown) 0.15MS/MS deisotoping tolerance unit (Unknown) DaMS/MS higher charges (Unknown) TrueMS/MS water loss (Unknown) TrueMS/MS ammonia loss (Unknown) TrueMS/MS dependent losses (Unknown) TrueMS/MS recalibration (Unknown) FalseSite tables Oxidation (M)Sites.txt |

**Supplement Table 1** – *MaxQuant Settings for proteomic analysis – An overview of the MaxQuant settings used for quantitative analysis of acquired mass spectrometry data sets.*