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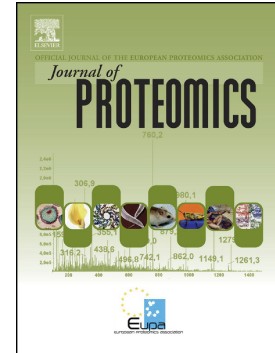
Experimental design and data-analysis in label-free quantitative LC/MS proteomics: A tutorial with MSqRob

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Title:

Experimental design and data-analysis in label-free quantitative LC/MS proteomics: a tutorial with MSqRob

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Abbreviations:

CPTAC, Clinical Proteomic Technology Assessment for Cancer Network; DDA, data-dependent acquisition; DIA, data-independent acquisition; FC, fold change; FDR, false discovery rate; HCD, higher-energy collisional dissociation; IQR, interquartile range; KO, knock-out; MCAR, missingness completely at random; MDS, multidimensional scaling; MNAR, missingness not at random; PSM, peptide-to-spectrum match; SILAC, stable isotope labeling of amino acids in cell culture; TMT, tandem mass tags; UPS1, Universal Proteomics Standard 1; WT, wild type.

Keywords: differential protein abundance; biostatistics; label-free quantification; tandem mass spectrometry; experimental design; peptide-based linear model

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