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Quantitative analysis of medulloblastoma using tandem mass spectrometry

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Medulloblastoma is the most common malignant pediatric brain tumour that is distinguished in four major subgroups. Therefore, there is an important need to identify clinically reliable protein markers for these subgroups which would be useful for the choice of appropriate treatment. Here, we present a novel proteomic approach for the quantification of proteins obtained from medulloblastoma tissue samples using tandem mass tags (TMT). We analysed medulloblastoma samples of all four known molecular subgroups in clinically standard risk patients. The tissue was lysed using urea buffer, stored at -80°C overnight and centrifuged for 30 minutes. The protein concentration was determined using BCA protein assay kit. Flowingly 100 μg of proteins was digested using filter aided sample preparation (FASP). Observed peptides were labelled using TMT10plex isobaric mass tags and mixed together. Finally, the samples were analysed using Orbitrap Elite coupled with UltiMate 3000 RSLCnano chromatograph and the acquired data processed with Proteome Discoverer 1.4. We obtained a list of quantified proteins from tumour proteome of medulloblastoma. Results has been subjected to statistical and bioinformatic evaluation. This new approach allowed to distinguish proteomic signatures linked to different clinical characterisation within medulloblastoma molecular subgroups.

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