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Quantitative Proteomic Profiling of Human Sarcoma Using Isobaric Labelling Coupled to LC MS/MS

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Sarcomas are rare forms of cancer that can form in connective tissue, such as muscle, bone, nerves, cartilage, blood vessels and fat. Although rare, the outcome for patients is poor, with surgery and post-operative radiotherapy the standard treatment for patients. A better understanding of the molecular pathology of these diseases may allow for the development of improved strategies for their treatment. Genomics has provided detailed knowledge of genetic abnormalities in sarcomas but provides no information on levels or localisation of targetable proteins expressed by these tumours. To begin to define the proteome of sarcoma and to attempt to identify novel targets and biomarkers expressed in different forms of high grade sarcoma we have carried out an initial study using Tandem Mass Tag (TMT) isobaric labelling coupled to liquid chromatography-tandem mass spectrometry (LC-MS/MS) of a panel of different sarcomas. We identified 1568 proteins that could be quantified and we found that a loose trend in dysregulated proteins exists between the 3 sarcomas studied, with 749 proteins >2 fold up-regulated and 88 <0.5 fold down-regulated in all 3 sarcomas. We further validated 4 proteins deemed to be potential drug targets and demonstrated by qRT-PCR and immunohistochemistry that CD44, CD63, CLIC1 and CLIC4 are all up-regulated in sarcoma.