

**ANALYSIS OF THE DIFFERENCES IN MITOCHONDRIAL PROTEIN EXPRESSION  
IN RAT PANCREATIC INSULINOMA CELLS CULTURED IN HIGH OR LOW  
GLUCOSE USING ISOBARIC MASS TAGGING**

Martin J Middledich,<sup>1,2</sup> Tony A Hickey,<sup>1</sup> and Joshua Bradley<sup>1</sup>

<sup>1</sup>*School of Biological Sciences, University of Auckland, Auckland, New Zealand.*

<sup>2</sup>*Maurice Wilkins Centre for Molecular Biodiscovery, University of Auckland, Auckland, New Zealand*

Pancreatic beta cell secretion of insulin granules is dependent on cytosolic ATP/ADP ratios, which in turn are dependent on glucose concentration and oxidation by mitochondria. In diabetes mellitus, glucose levels are significantly elevated resulting in an increase in free radical production and impaired mitochondrial function. To investigate the effects of high glucose on mitochondrial protein expression we compared the protein profile of mitochondria isolated from rat insulinoma cells cultured under normoglycaemic and hyperglycaemic conditions. A multidimensional chromatography approach was used, which incorporated ITRAQ isobaric mass tags to generate relative quantitation data for each protein identified. At the 95% confidence level, a total of 228 non-redundant proteins were identified, of which 36 were up-regulated and 35 down-regulated under hyperglycaemic conditions. A number of proteins from granules were also detected, indicating a close association with the mitochondria. Most of the heat shock proteins identified were found to be up-regulated, along with both insulins 1 and 2 as expected. Additionally, a comparison was made of two different software platforms for the data analysis, namely ProQuant and ProteinPilot, both from Applied Biosystems.