

**P004** A proteomics approach to studying stress responses in *Saccharomyces cerevisiae*  
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A proteomics approach was employed to identify changes in temporal protein expression profiles in *S. cerevisiae* under controlled environmental stress conditions. Of particular interest to our studies are proteins which effect translation initiation. We are also investigating the proteome of mutants affecting ribosome recruitment, in particular mutations that disrupt eIF4E/eIF4G interactions, e.g., Eap1 disruption strain. Eap1 is a candidate protein for eIF4E binding/modulation. We further investigate yeast strains with sensitivity to butanol and oxidative stress. Our initial experiments combined [<sup>35</sup>S]-methionine/cysteine labelling, 2D-electrophoresis, and MALDI, and suggest differences in translation initiation factor eIF5A2 expression profiles in the presence and absence of butanol. More recently we have optimised procedures for *in vivo* labelling with heavy isotopically labelled leucine [<sup>15</sup>N<sup>13</sup>C] in combination with MudPIT (Multidimensional Protein Identification Technology). We use a capillary Liquid Chromatography system coupled to an online mass spectrometer to separate digested lysates. We routinely obtain sequence information for ~5000-6000 peptides from each 'soluble' (cytoplasmic) fraction and 'insoluble' (membrane) fractions from mixtures of unlabelled and labelled samples. The data is used to search Mascot database. We also analyse the raw data from 2D-LCMSMS runs in a quantitative manner, and are generating bioinformatics tools to assist in this process.