

**P044** Translational recruitment of pro-apoptotic genes via IRES elements during the induction of apoptosis  
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It is estimated that up to 10% of all mRNAs contain IRESes, subpopulations of these are used under particular patho-physiological conditions, when global translation is impaired, e.g. apoptosis. During apoptosis there is a release of a number of mitochondrial components into the cytosol, which plays an important role in both caspase-dependent and independent apoptosis. Using cDNA micro-array technology, we have found that there are dramatic changes in the identity of mRNA species translated during the induction of apoptosis. Interestingly, a number of the genes that are selected for translation play major roles in the apoptotic process, including caspase-3, and two factors which are released from the mitochondria during apoptosis, apoptosis-inducing factor and a novel protein, endonuclease G-like 1, which has high homology to endonuclease G. Using Northern blot analyses, we have confirmed that these mRNAs are still present in polysomes during apoptosis and contain IRESes in the 5'UTR regions that are responsible for maintaining the translation initiation during the induction of apoptosis. We are now examining the requirement for IRES trans-acting factors in the activation of these IRESes and the role of their gene products in the apoptotic pathway. Data from these studies will be discussed.