

## **ABSTRACT 2**

# **Comparative Proteomic Analysis of the HSF Cells Exposed to IR at Different Doses: Identification of Unique Proteins Sensitive to Low-dose IR**

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By using a newly developed proteomics approach, multiple amino acid-coded mass tagging, we systematically investigated the differential expression patterns associated with the IR-exposed HSF cells at different dose levels. In contrast to non-irradiated HSF cells, two other HSF populations were irradiated at 1.6 Gy and 0.08 Gy respectively. Interestingly, using high throughput MS quantitative analysis we have identified over 100 proteins uniquely responsive to IR at low dose level.