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FAS-cinating proteomics

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Comprehensive [proteome analysis](#) offers a powerful tool to move beyond the genome. In a study published online ahead of print in the [Journal of Biological Chemistry](#), Gerner *et al.* ([J. Biol. Chem., published online 7 September 2000](#)) describe the use of high-resolution two-dimensional gel electrophoresis analysis to investigate changes to 1000 protein spots following Fas-induced apoptosis in Jurkat T-lymphocyte cells. Gerner *et al.* used a range of techniques including metabolic radiolabelling, subcellular fractionation and mass spectrometry fingerprinting to catalogue diverse post-transcriptional events. Altogether, 57 protein spots changed in some way - including changes in protein synthesis, translation, phosphorylation, dephosphorylation and translocation. Using caspase inhibitors Gerner *et al.* were able to identify caspase targets during apoptosis. Further comparison with other death inducers highlighted similarities and distinctions between apoptosis and necrosis. These results will help focus the spotlight on comparative proteomic studies.

References

1. Proteomics: applications in basic and applied biology.
2. Journal of Biological Chemistry, [<http://www.jbc.org>]
3. The Fas-induced apoptosis analyzed by high-throughput proteome analysis.