# Proteomic analysis in food function: Characterization of molecular targets for (–)-epigallocatechin-3-gallate and *α*-lipoic acid

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Much attention has recently been focused on the beneficial health effects of food chemicals such as green tea catechins and sulfur-containing compounds. A variety of possible mechanisms underlying these health effects has been proposed. A promising mechanism is the interaction of food chemicals with proteins. However, the target proteins, which are involved in the mechanism through the binding of the chemicals, are still unclear. In this study, we established new methods for detection and purification of (–)-epigallocatechin-3-gallate (EGCg)- or *α*-lipoic acid (LA)-target proteins. Using redox cycling staining and affinity purification by boronate beads, we identified glyceraldehyde-3-phosphate dehydrogenase (GAPDH) as a target protein of EGCg in cancer cell lines. In addition, we determined that EGCg binds to a cysteine residue on GAPDH, by mass spectrometry. We also confirmed that EGCg modulates the enzyme activity of GAPDH through this binding. The results suggest that the modulation of GAPDH activity by EGCg is due to selective modification of the cysteine residues on the GAPDH molecule. We developed a new probe to directly detect LA-bound proteins, using a biotinylated-LA. Serum albumin was identified as a major target of LA in human serum. This result indicates that serum albumin is a crucial target protein in human serum. Thus, these methodologies permit us to characterize the molecular targets of food chemicals in cell lines and human serum. In conclusion, our approaches identifying the target proteins might help to elucidate how to modulate protein action through the interaction of the chemicals with proteins.