



Proteomics at AgResearch

# Redox Proteomics

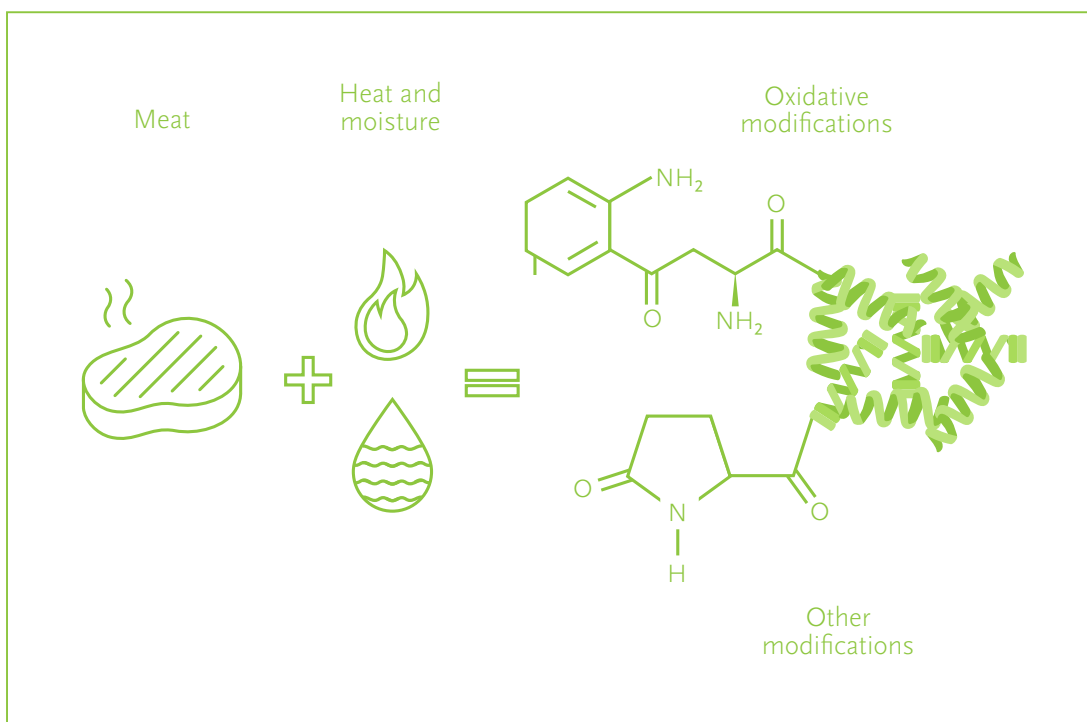
# Linking protein modifications with oxidative events.

At AgResearch, we have developed a simple scoring system that enables comparison of the extent of peptide modifications due to redox reactions between different samples.

This facilitates the investigation of biological systems undergoing oxidative stress, or the influence of processing methods on oxidative damage in food and other products.

The prevalence of modified amino acids in sample peptides is calculated using in-house-developed software and scoring is performed on the hierarchy of chemical modifications.

The redox scoring system is based on the oxidative cascade which occurs in redox-sensitive amino acid residues (e.g., W, Y, C, F) with a higher score assigned to modifications that are formed further down the cascade. For example, a di-oxidation modification contributes more to the final redox score for the sample than a single oxidation.



Above: Characterisation of oxidation and other redox-related modifications at the amino acid level allows us to estimate what the impact of a treatment is on proteins.