

## THURSDAY

### KN9 Advantages and applications of radical probe mass spectrometry (RP-MS) – a decade on

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Review of development and application of RP-MS to study protein structures and interactions

Radical probe mass spectrometry (RP-MS) was introduced in the late 1990's [1,2] as a new method for the structural characterisation of proteins and their interactions. The basis of RP-MS approach [3,4] is that oxygen-containing radicals generated in high fluxes within microseconds by photochemical, discharge or other sources are reacted with proteins in solution on millisecond timescales to effect the limited oxidation at specific amino acid side chains. The extent and site of oxidation as measured by mass spectrometry are highly influenced by the solvent accessibility of the residues. This enables a three-dimensional model of a protein, either in its folded or unfolded state, or a protein complex [5] to be assembled based on degree of oxidation at the reactive residues.

The RP-MS approach was initially validated and exploited to investigate the structure of lysozyme, the unfolding of apomyoglobin, the binding of cytoskeletal protein actin with gelsolin and ribonuclease S-peptide and protein [1-4]. The application of RP-MS was later expanded to study protein assemblies such as the amyloid fibrils [6] and the onset of oxidative damage of tissue proteins important to disease and aging [4]. This presentation will review the approach a decade on from its invention and present the increasingly wide range of applications of RP-MS.

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