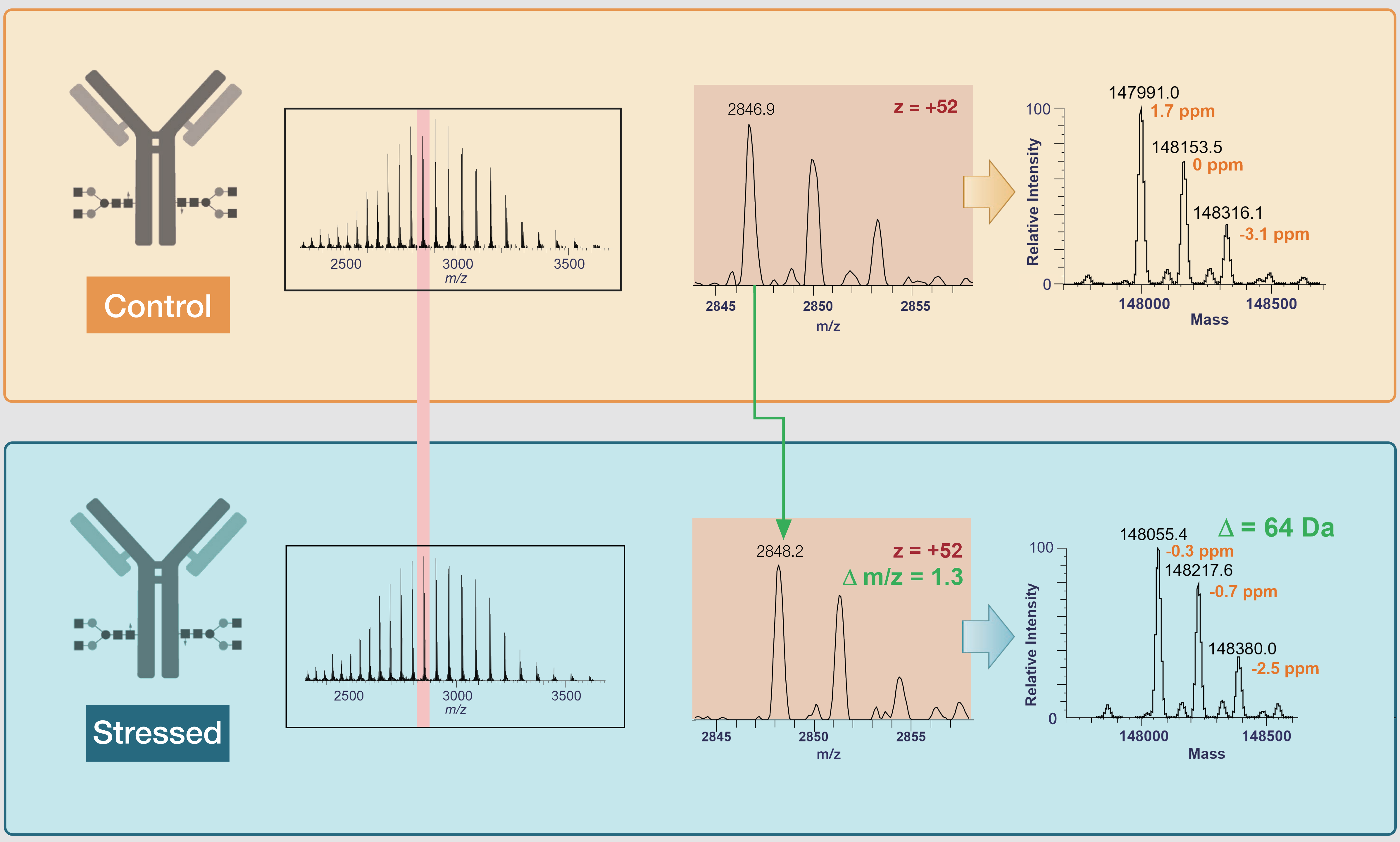
ThermoFisher SCIENTIFIC

# Intact Protein Characterization Workflows

Comparing Ipilimumab and stressed Ipilimumab to understand the impact of oxidative stress on the antibody

## 1 Intact Mass

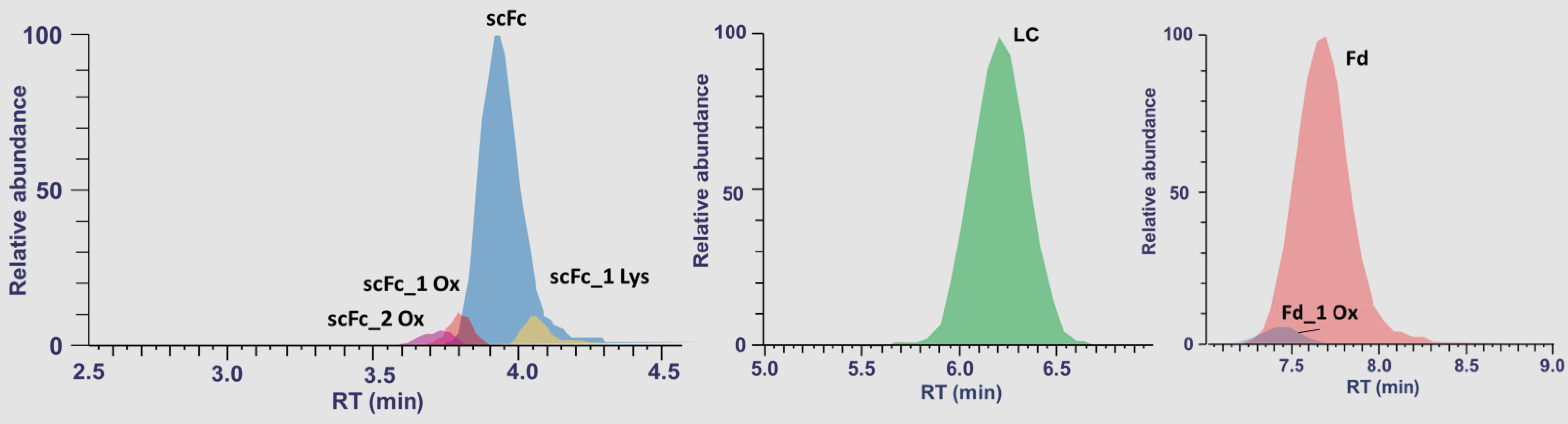
Monitor the identity, purity, post-translational modification (PTM)s
Distinguish between different proteoforms of an antibody



**Mass shift of 64 Da indicating potential oxidation at four methionine residues.**

## 2 Subunit Analysis

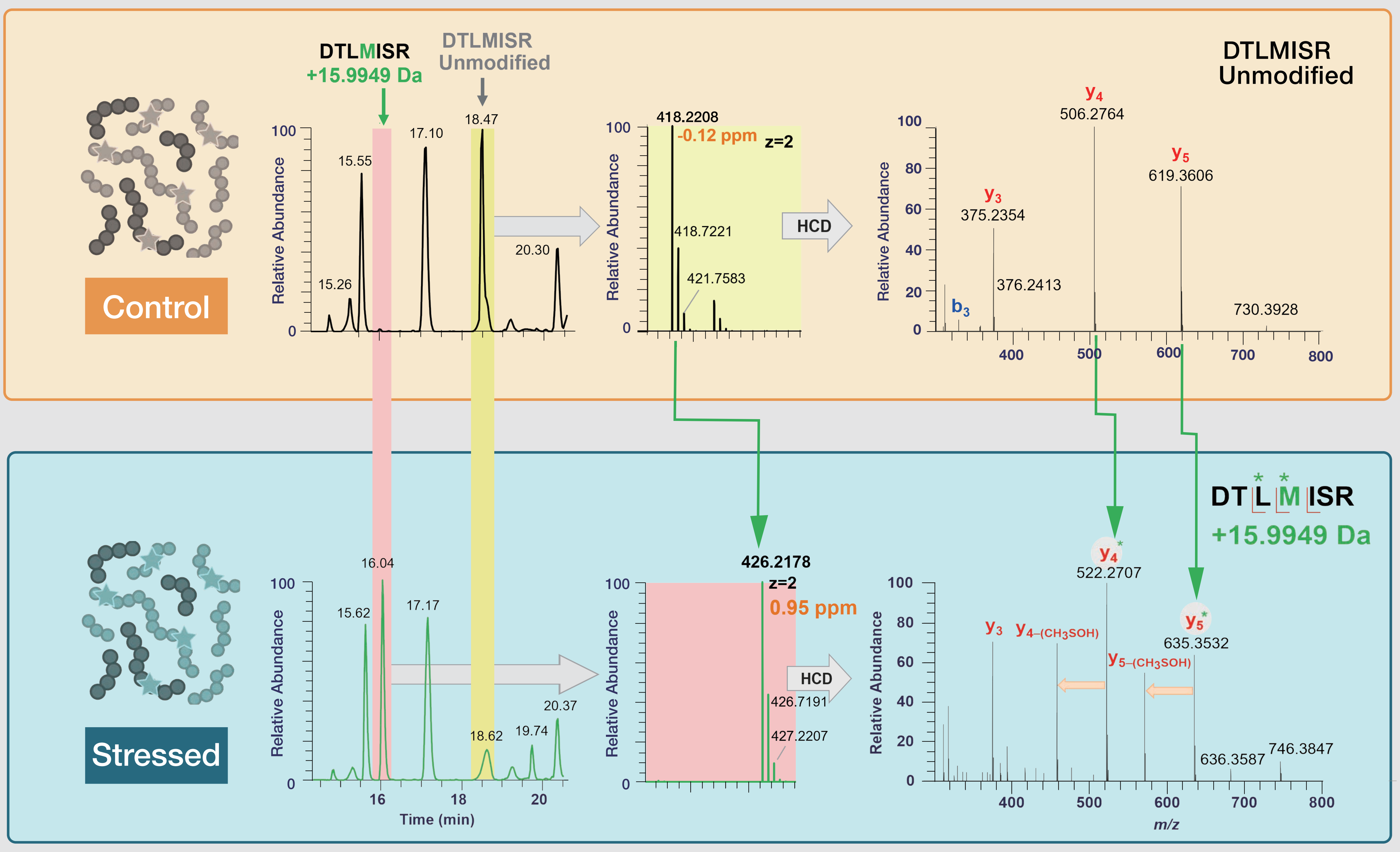
Determine regional location of modification / sequence
Differentiate & characterize Fc, Fab glycosylation



**Modifications found on heavy chain, in Fd and scFc regions.**

## 3 Peptide Mapping

Perform detailed comparisons between samples
Confirm amino acid sequence and locate modifications



**+15.9949 Da shifts for $y_4$ and $y_5$ fragment ions and diagnostic loss of methane sulfenic acid ($CH_3SOH$) in oxidized peptide.**

Click or visit ***thermofisher.com/biopharmaprotein*** to watch Dr Jonathan Bones as he delves into the world of protein characterization.

Learn more at thermofisher.com/biopharmaanalyticaltesting

thermo scientific