



Proteomics at AgResearch

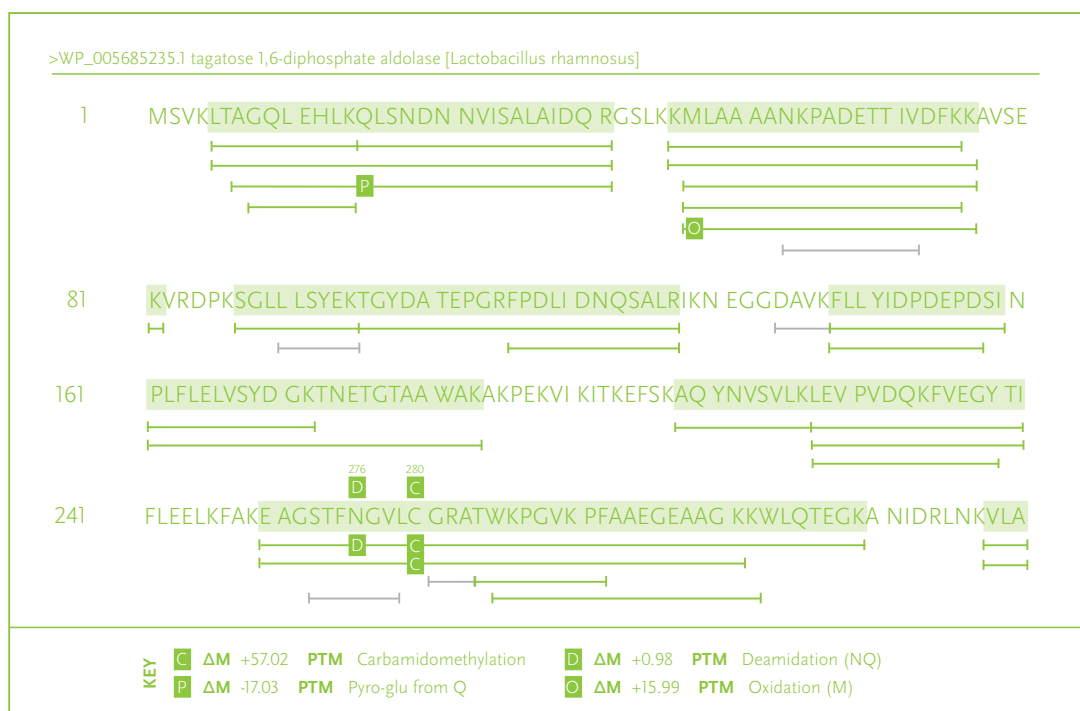
Protein identification and PTM characterisation

Discover modifications the proteins carry.

Linking acquired mass spectra with protein databases to identify the proteins present in your samples and discover the post-translational modifications the proteins carry.

With our high-resolution mass spectrometry instruments and state of the art data analysis software, we can map the peptides identified per protein in a large variety of samples, as long as either protein or genomic sequence data are available to build an identification database.

Further investigations into the post-translational modifications (PTMs) that are present at the protein primary structural level enable us to also map the site-specificity of these modifications.



Above: Example of a protein sequence where post-translational modifications detected in samples are mapped to an identified protein.