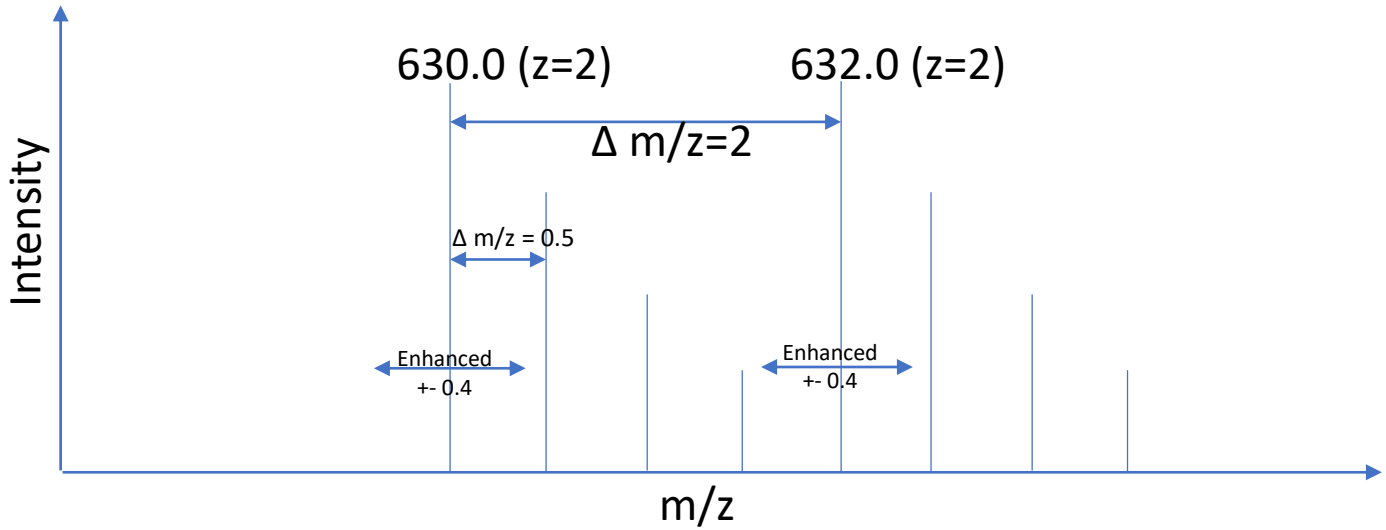
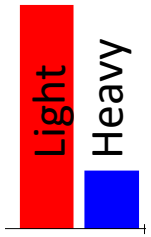
Our aim: Quantify endogenous peptides in a complex sample with stable isotope labeled standards (SIS).
Our SIS: Labeled with Ala (+4) close to the N-terminus.
Our precursor ions are dual and triple charged, therefore the delta m/z is 2 for dual charged and 1.3 for triple charged.

Can we reliably distinguish with Agilent 6490 iFunnel between endogenous peptides and SIS?



The Agilent 6490 with MassHunter software allows an enhanced MRM MS1 Resolution with +- 0.4 m/z. Is this a hard cut-off?

We did MRM measurements with very pure SIS-only but Agilent 6490 registered big portions of it as unlabeled peptides.



We did an MS2 scan to see if the machine was out of tune but it was exact to +- 0.1 m/z.

Why is the machine classifying so much SIS as unlabeled peptide?