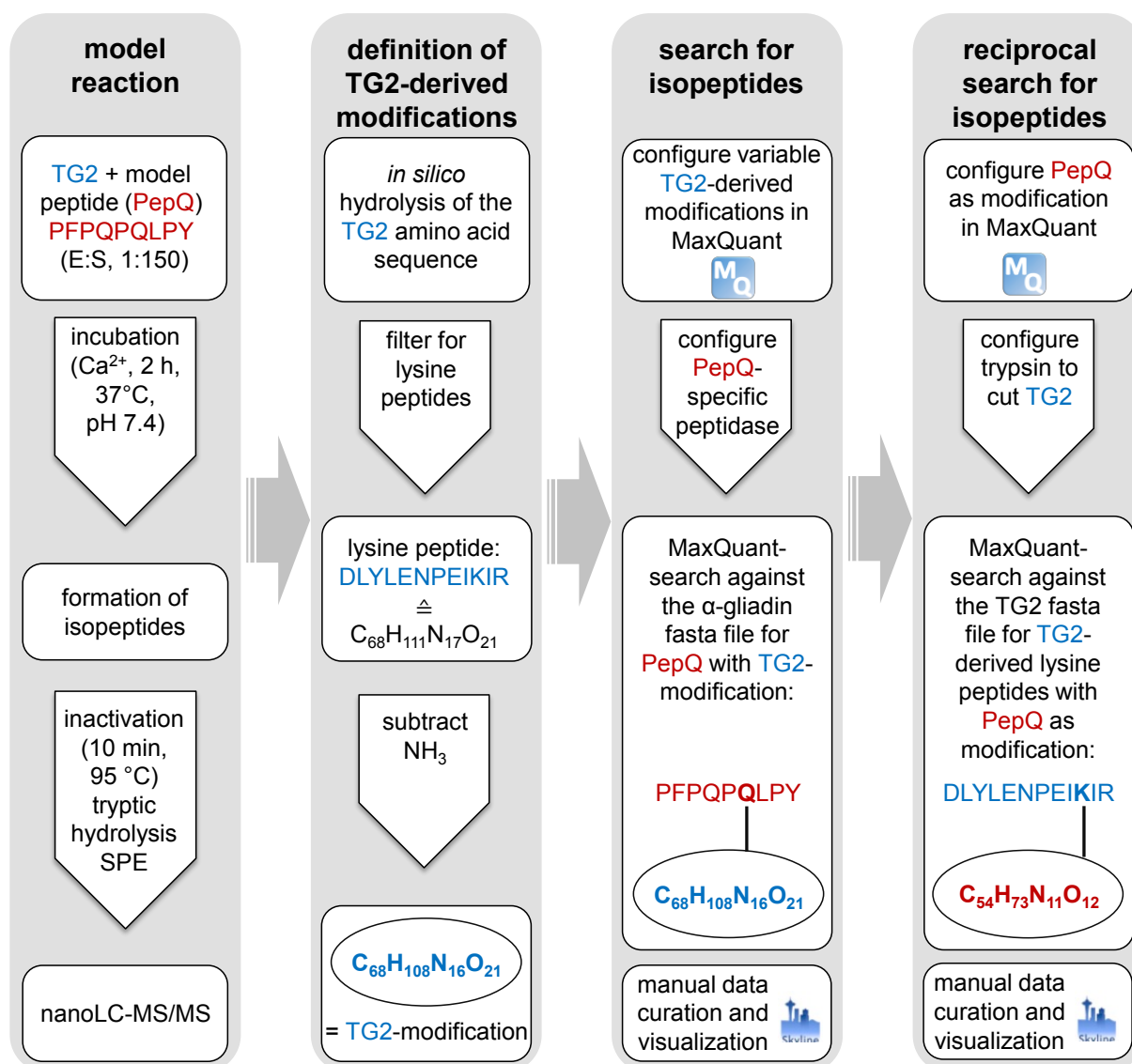


Supplementary Figure S1



Reciprocal search workflow to identify isopeptides with MaxQuant and Skyline.

The workflow consists of four steps: (1) model reaction between TG2 and gluten peptide(s) followed by tryptic hydrolysis, clean-up and untargeted nLC-MS/MS analysis, (2) definition of tryptic TG2-derived lysine peptides as potential isopeptide modification sites, (3) the search for isopeptides by configuring the TG2-modifications in MaxQuant and search against the α -gliadin fasta file and (4) the reciprocal search for isopeptides by configuring the gluten peptide(s) as modification in MaxQuant and search against the TG2 fasta file.