SUPPLEMENTARY FIGURE CAPTIONS

Figure S1: Deconvoluted tandem MS data of two kappa casein glycopeptide isomers corresponding in mass to [S**T**VAT+GalNAc$_1$+Gal$_1$+NeuAc$_1$+2H]$^{+2}$ (**A**) eluting at 19.5 min with the NeuAc residue connected to the Gal residue and (**B**) eluting at 22.0 min with the NeuAc residue connected to the GalNAc residue. Rectangles ( ), circles ( ) and diamond symbols ( ) represent GalNAc, Gal and NeuAc residues, respectively.

Figure S2: Deconvoluted tandem MS data of two ribonuclease B glycopeptides corresponding in mass to the glycopeptides (**A**) [**N**LTK+GlcNAc$_2$+Man$_5$+2H]$^{+2}$ and (**B**) [**N**LTK+GlcNAc$_2$+Man$_9$+2H]$^{+2}$. Circles ( ) and squares ( ) represent mannose and GlcNAc residues, respectively.

Figure S3: Extracted compound chromatograms (ECCs) of ribonuclease B glycopeptides generated following pronase digestion of (**A**) 1 µg of the protein and (**B**) 100 ng of the protein.

Figure S4: Extracted compound chromatogram (ECC) of ribonuclease B glycopeptides generated following subtilisin digestion of 10 µg of the protein.

Figure S5: Deconvoluted tandem MS data of two bovine lactoferrin glycopeptides corresponding in mass to the glycopeptides (**A**) [**N**DT+GlcNAc$_2$+Man$_8$+2H]$^{+2}$ and (**B**) [**N**DT+GlcNAc$_2$+Man$_9$+2H]$^{+2}$. Circles ( ) and squares ( ) represent mannose and GlcNAc residues, respectively.

Figure S6: Detailed site-heterogeneity and detected glycoform abundance of human immunoglobulin M obtained via INPEG analysis on human serum.

Figure S1A and **S1B**

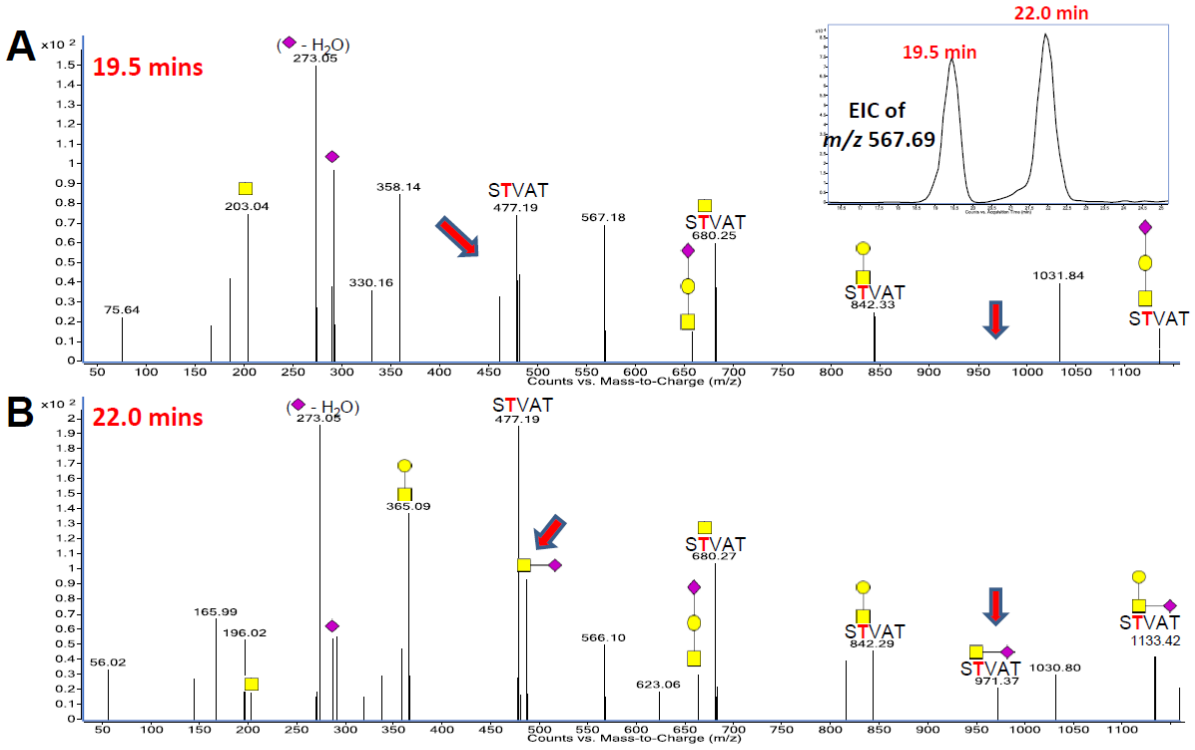

Figure S2A and **S2B**

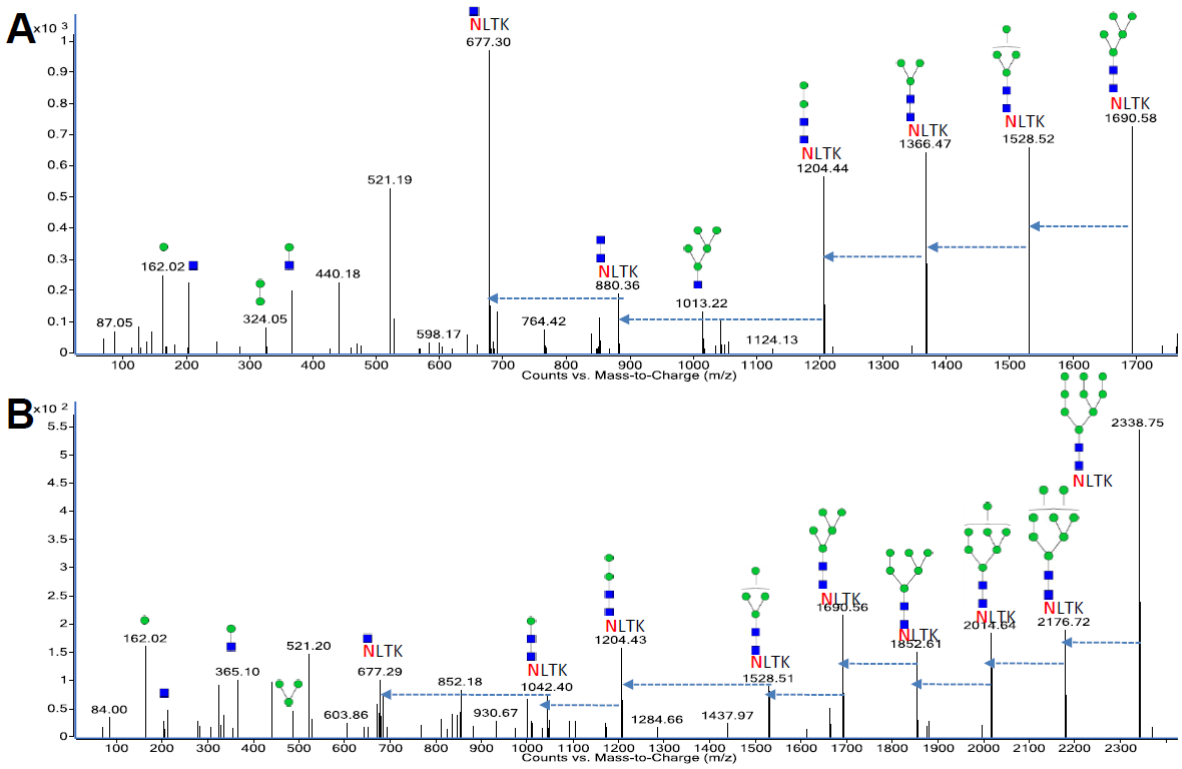

Figure S3A and **S3B**

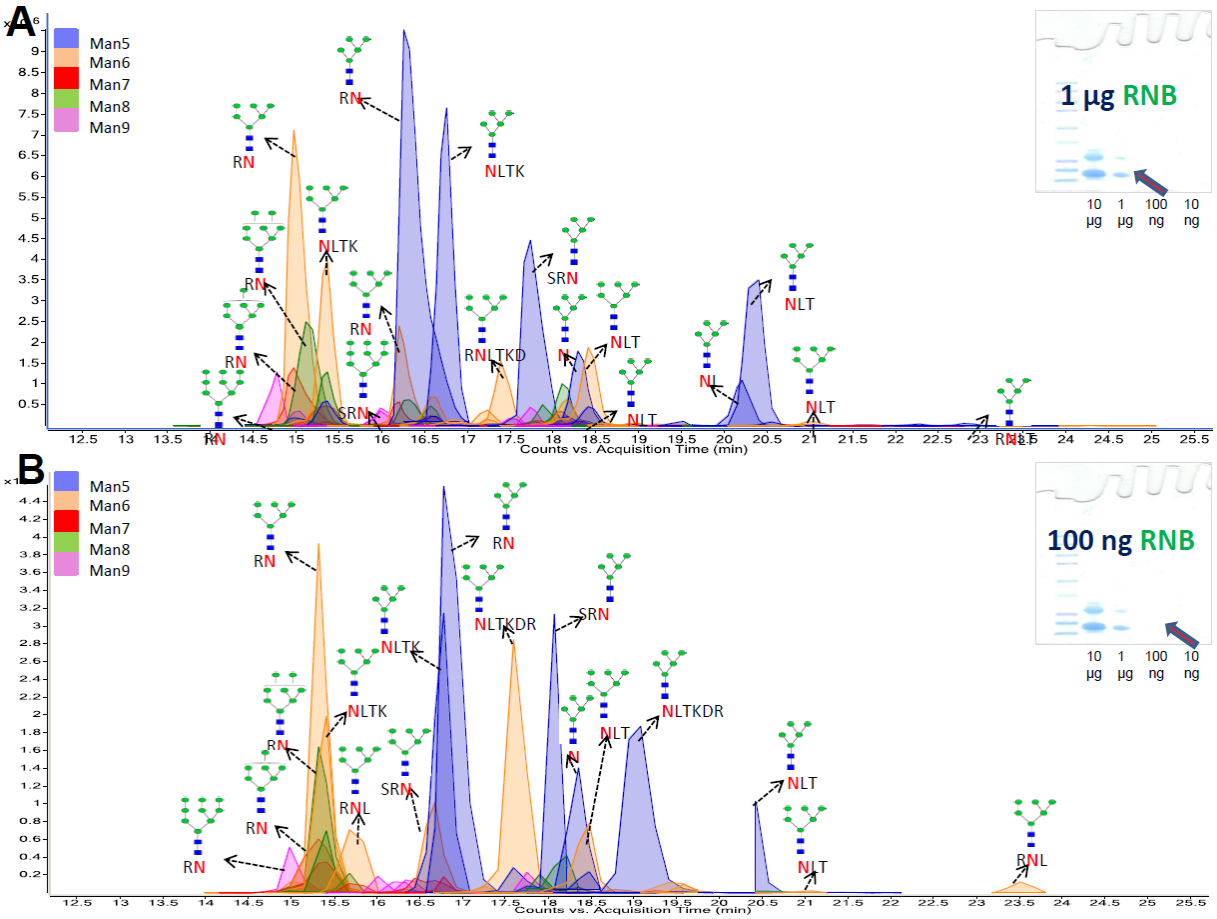

Figure S4

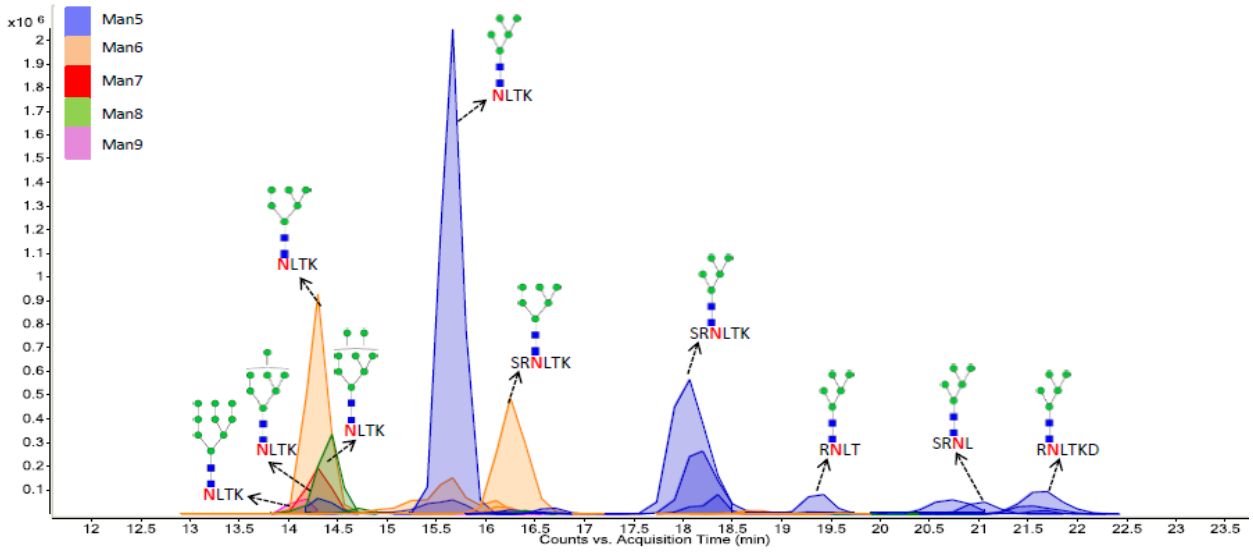
x10 6
Man5
Man6
Man7
Man8
Man9
NLTK
NLTK
NLTK
NLTK
NLTK
SRNLTK
SRNLTK
RNLT
SRNL
RNLTKD
Counts vs. Acquisition Time (min)

Figure S5A and **S5B**

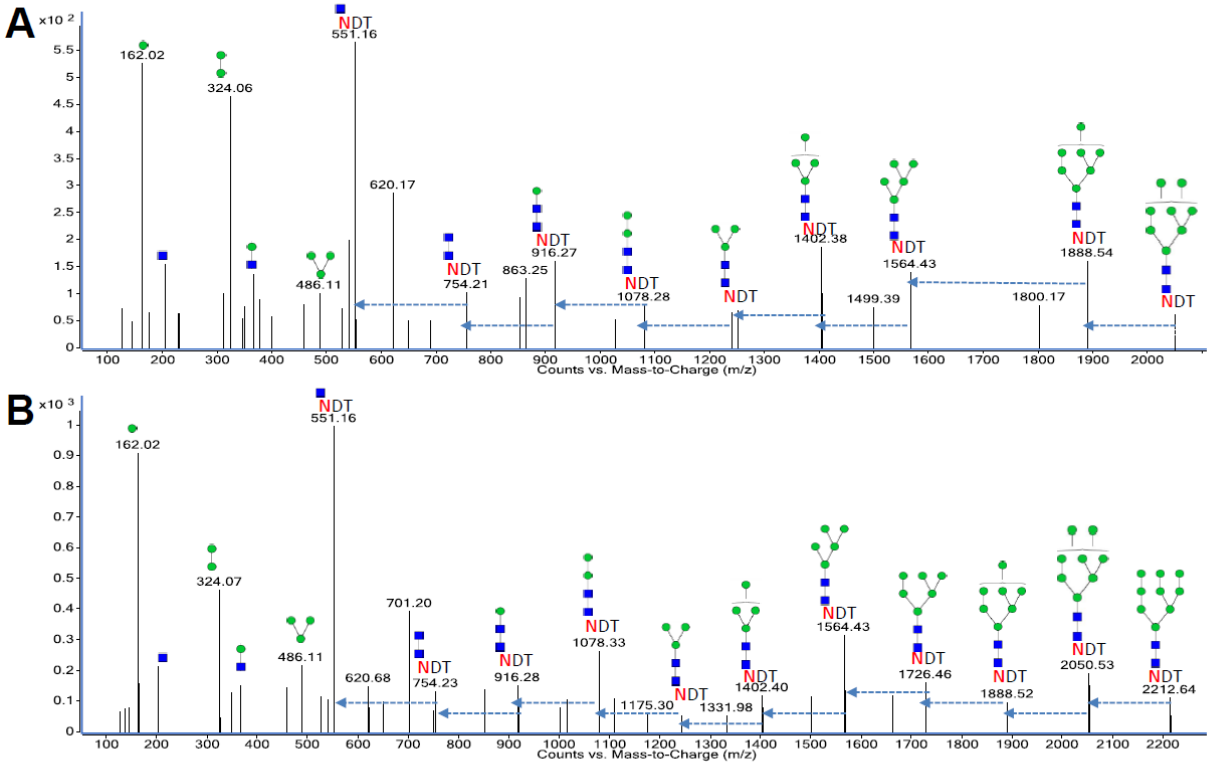

Figure S6