

The amino groups of lysine of plasma proteins are susceptible to a non-enzymatic reaction with glucose under physiological conditions. This glycation process ultimately can lead to diabetes complications, oxidative stress and aging process. Due to fact that diabetic patients have high glucose concentration, the amount of glycated proteins can be used as a marker of disease progression. Glycation degree for different lysine residues vary and depend from protein location, lysine reactivity and glucose concentration. We have studied glycation profile of most abundant plasma protein albumin. The degree of glycation for each site was defined as the percentage of glycated to sum of glycated + non-glycated lysines. To get most comprehensive profile two MS instruments were used: timsTOF-Pro and Q-trap. Ion mobility was used as an additional separation dimension; PASEF MS/MS scans for fragmentations in timsTOF. Q-trap instrument was used in two different modes: CID/HCD and neutral-loss. In-vitro glycated HSA and plasma from diabetic and non-diabetic patients were reduced/alkylated and digested by Glu-C. The peptide mixture were separated in a nano-flow C18 system or HxSIL C18 in a MeCN/H₂O linear gradient depend from MS platform. Raw data was analyzed using PEAKS X or Proteome Discoverer. All discovered glycation peptides were manually validated. In summary, we created glycation profile for serum albumin that can be used in the future as hyperglycemia biomarker.