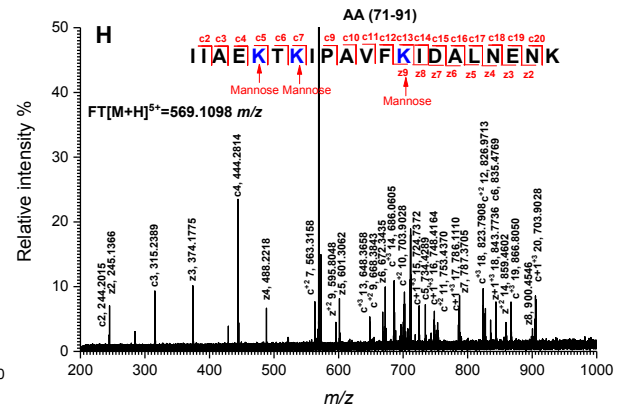
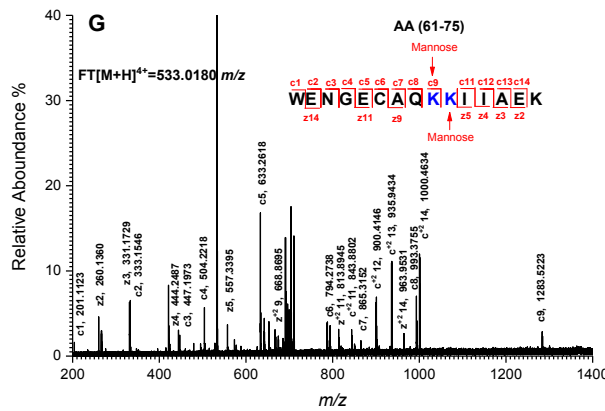
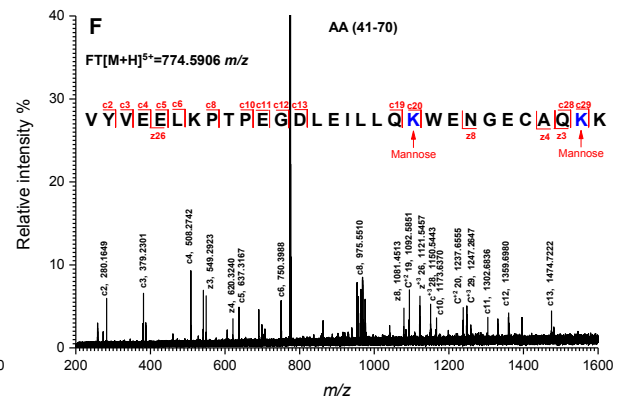
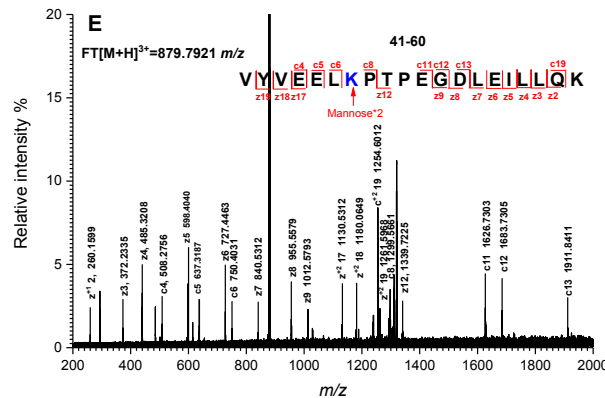
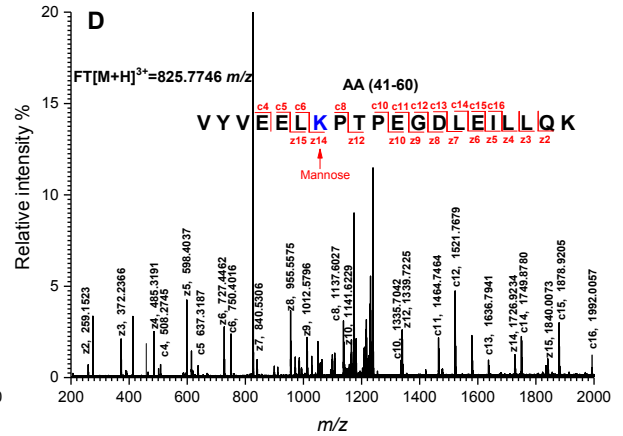
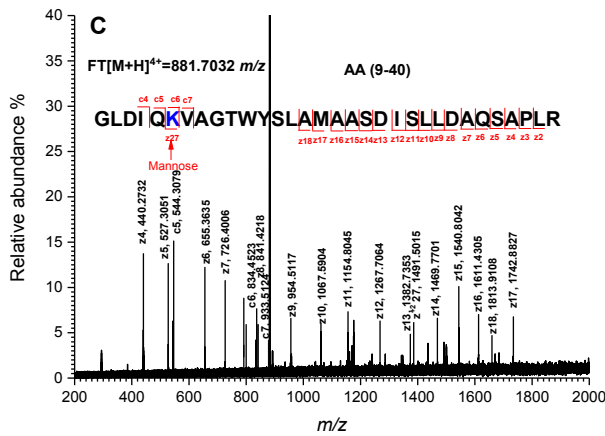
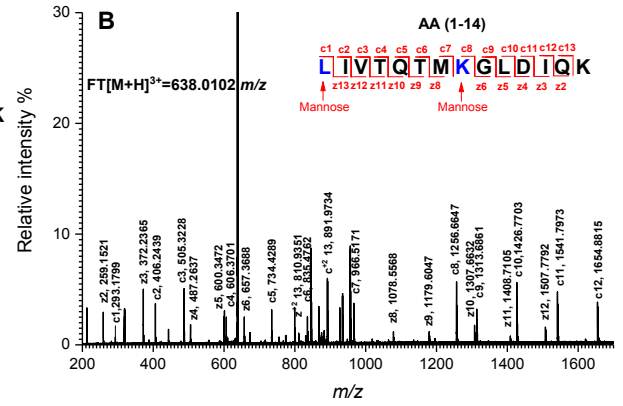
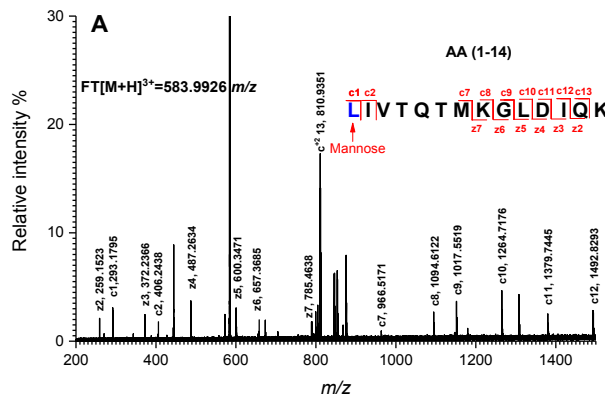


Table S1 The peptide mapping of native β -Lg (trypsin digestion).

Peptide location	m/z	Δm (ppm)	Sequence ^a
1-8	467.2753 ³⁺	-0.43	(-)LIVTQTMK(G)
9-14	673.3871 ¹⁺	-1.19	(K)GLDIQK(V)
15-40	903.1296 ³⁺	-0.66	(K)VAGTWYSLAMAASDISLLDAQSAPLR(V)
41-60	771.7569 ³⁺	-1.17	(R)VYVEELKPTPEGDLEILLQK(W)
41-70	886.9591 ⁴⁺	-1.13	(R)VYVEELKPTPEGDLEILLQKWENGEC*AQKK(I)
71-75	573.3601 ¹⁺	-0.87	(K)IIAEK(T)
76-91	601.0112 ³⁺	-1.50	(K)TKIPAVFKIDALNENK(V)
84-101	697.7145 ³⁺	-2.01	(K)IDALNENKVLVLDTDYKK(Y)
101-124	983.8052 ³⁺	-1.73	(K)KYLLFC*MENSAEPEQSLAC*QC*LVR(T)
125-138	545.9289 ³⁺	-1.65	(R)TPEVDDEALEKFDK(A)
142-148	419.2404 ²⁺	-3.34	(K)ALPMHIR(L)
149-162	858.9123 ²⁺	-1.75	(R)LSFNPTQLEEQC*HI(-)

^aC* means the alkylated cystine residue by iodoacetamide.



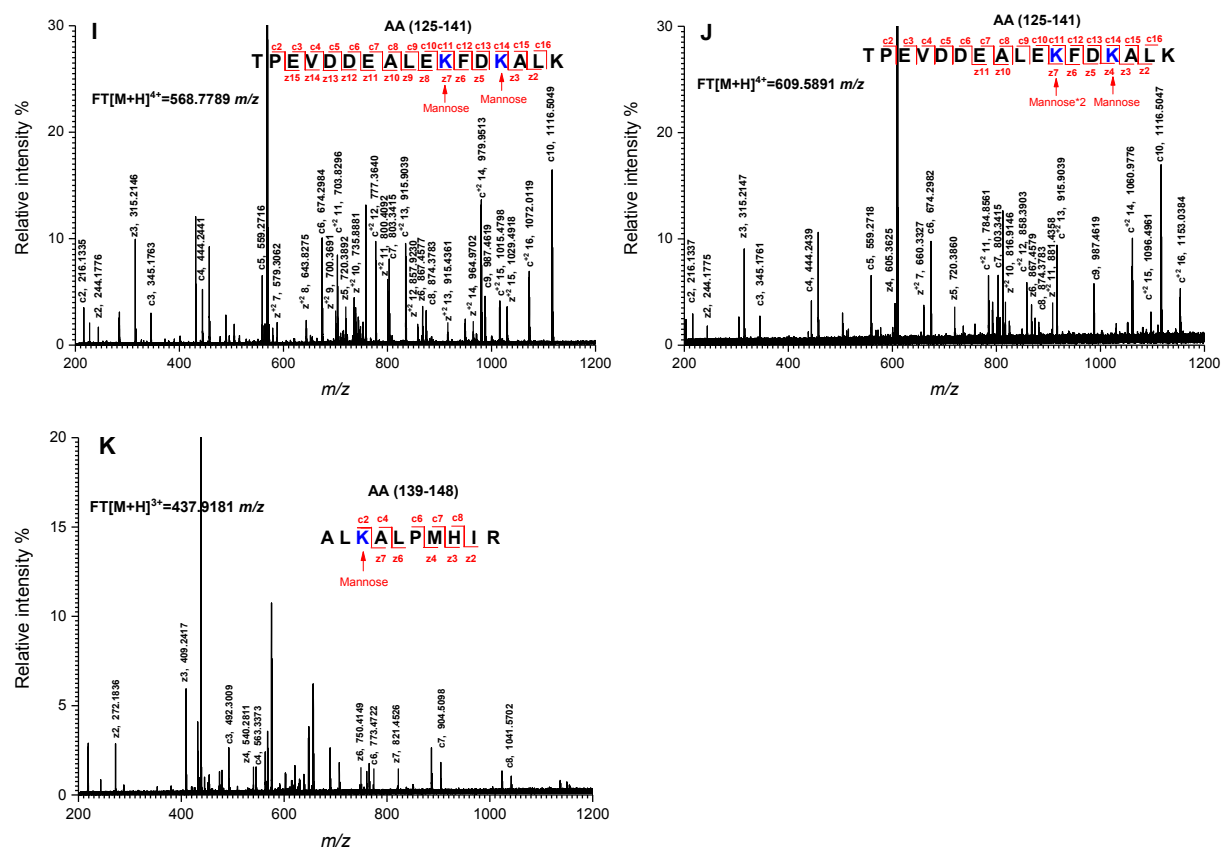


Fig. S1 ECD MS/MS spectra of the glycosylated peptides 1-14 (A & B), 9-14(C), 41-60 (D & E), 41-70(F), 61-75 (G), 71-91 (G), 125-141(I & J) and 139-148 (K). The sequence of each peptide is shown in the top of figure. The mass differences are exhibited with numbers and arrows. The determined glycation sites are highlighted by blue color and indicated by an arrow with symbol, in which "mannose" and "mannose*2" mean glycation site is added by one and two mannose molecules, respectively. The *c* and *z* ions are indicated by the numbers and lines.