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Supporting information for article:

Structural insights into human IgG1 interaction with FcγRI: no direct role of glycans in binding

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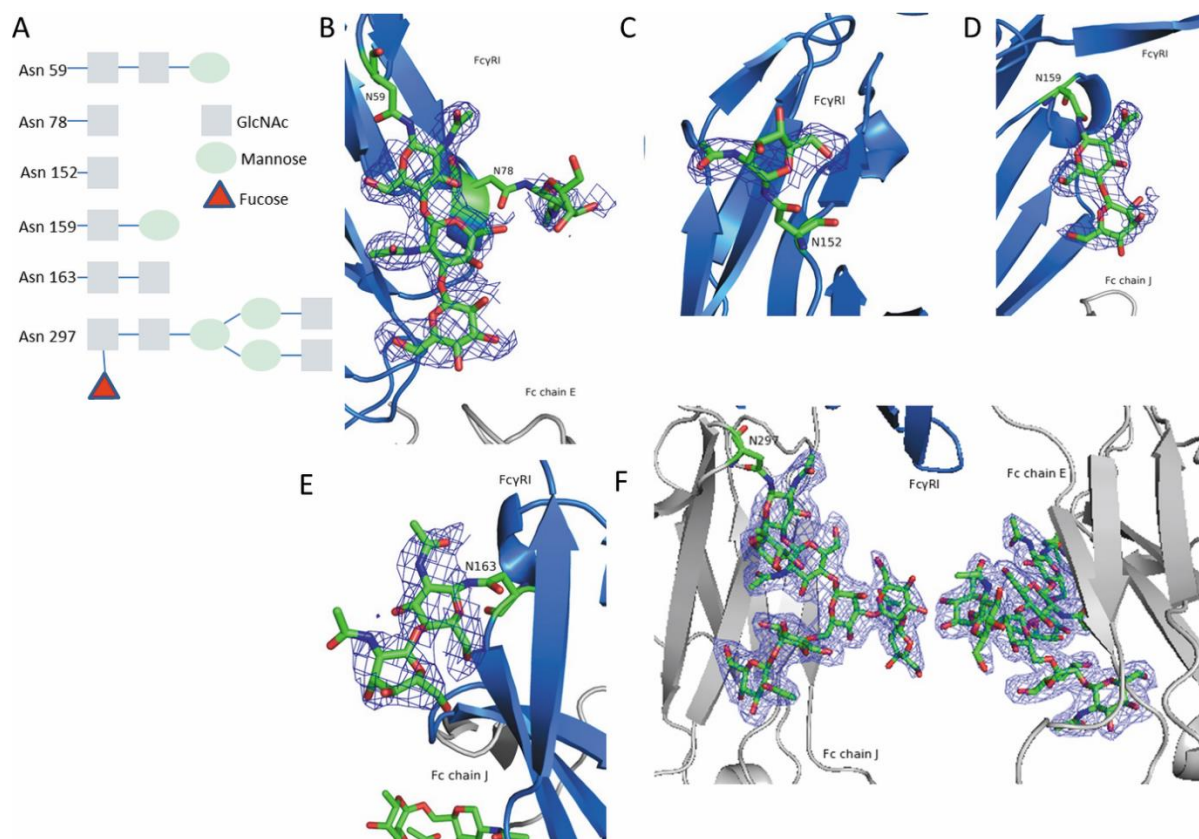


Figure S1 (A) Schematic representation of N-linked oligosaccharides attached to Fc γ RI and Fc, (B) Omit map showing oligosaccharides attached to Fc γ RI N59 and N78 in D1. SigmaA weighted $2mF_o - DF_c$ electron density map allowed the placement of GlcNAc-GlcNAc-Man near N59; however, the quality of that near N78 was considerably lower and only the first GlcNAc was placed, (C) Omit map showing one oligosaccharide attached to Fc γ RI N152 in D2. SigmaA weighted $2mF_o - DF_c$ electron density map allowed the placement of only one GlcNAc, (D) Omit map showing two oligosaccharides attached to Fc γ RI N159 in D2. SigmaA weighted $2mF_o - DF_c$ electron density map allowed the placement of GlcNAc-Man near N159; however, the quality of that around Man was considerably lower than for GlcNAc, (E) Omit map showing two oligosaccharides attached to Fc γ RI N163 in D2. SigmaA weighted $2mF_o - DF_c$ electron density map allowed the placement of GlcNAc-GlcNAc, (F) Omit map showing oligosaccharides attached to both Fc N297. SigmaA weighted $2mF_o - DF_c$ electron density map allowed the placement of bi-antennary glycans. Terminal galactose and sialic acid residues did not show in the electron density. All electron density maps are shown at 0.8σ .

Table S1 Summary of hydrogen bonds and electrostatic interactions formed between Fc γ RI and Fc.

Fc γ RI	Distance (Å)	Fc
A:LYS 130[N ζ] ^a	3.50	E:GLU 233[O ϵ 2]
A:LEU 131[N]	2.74	E:GLU 233[O]
A:LYS 173[N]	2.85	E:LEU 235[O]
A:HIS 174[N ϵ 2]	3.50	E:SER 239[O γ]
A:LEU 131[O]	3.07	E:LEU 235[N]
A:TYR 176[O η]	3.47	E:GLY 237[N]
A:ASN 134[N δ 2]	2.79	J:GLY 237[O]
A:LYS 145[N ζ]	3.07	J:GLU 269[O ϵ 2]
A:HIS 148[N ϵ 2]	3.22	J:ASP 265[O]
A:ARG 102[N η 2]	3.46	E:PRO 329[O]
A:LYS 130[N ζ]	3.50	E:233 GLU[O ϵ 2]
A:HIS 148[N δ 1]	3.30	J:267 SER[O γ]

^aLetters in bracket refer to the corresponding interacting atoms.

Table S2 Hydrogen bonds between FcyR1 D1 and D2 in unliganded and ligand-bound states.

D1	Hydrogen bond distance (Å) Unliganded	Hydrogen bond distance (Å) Ligand-bound	D2
A:VAL 31[N]	2.97	3.22	A:VAL 109[O]
A:VAL 31[O]	3.09	2.76	A:ARG 112[Nη2]
A:SER 32[O]	2.90	2.63	A:GLN 108[Nε2]
A:GLU 37[Oε2]	2.79	2.70	A:HIS 125[Nε2]
A:GLN 97[O]	2.79	2.68	A:ARG 112[Nη2]
A:GLU 99[Oε1]	3.37	2.95	A:ARG 112[Nη]