

**$\alpha$ 2, 3-linkage of sialic acid to a GPI-anchor and an unpredicted GPI attachment site in human prion protein**

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Figure S1

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Table S1. Identified peptides of human PrP<sup>C</sup> from KI mouse brains after C18 column.

Fragment	Obsd. m/z	Calcd. m/z	Charge	Score	<i>P</i>
<u>Q</u> HTVTTT <u>T</u> K + Gln->pyro-Glu (N-term Q)	500.2590	998.5033	2	62	4.7e-006
QHTVTTT <u>T</u> K	508.7723	1015.5298	2	62	6.2e-006
ESQAY <u>Y</u> QR	522.7407	1043.4672	2	60	4.1e-006
Y <u>P</u> GQGS <u>P</u> GGNR	545.2571	1088.4999	2	55	1.8e-005
GEN <u>F</u> TETD <u>V</u> K	570.2645	1138.5142	2	60	4.5e-006
R <u>P</u> K <u>P</u> GGWNTGGSR	457.2410	1368.7011	3	48	0.00011
VVEQ <u>M</u> CITQYER	778.3681	1554.7170	2	28	0.011
VVEQ <u>M</u> CITQYER + Oxidation (M)	786.3632	1570.7120	2	70	5.5e-007
GEN <u>F</u> TETD <u>V</u> K <u>M</u> MER + 2 Oxidation (M)	573.5829	1717.7287	3	21	0.022
<u>H</u> MAGAAAAGAVVGG <u>L</u> GGY <u>M</u> LG <u>S</u> AMSRPIHFGSDYE	768.9607	3839.7818	5	38	0.00046
DR + 3 Oxidation (M)					

Table S2. Identified peptides of human PrP<sup>C</sup> from KI mouse brains after HILIC column.

Fragment	Obsd. m/z	Calcd. m/z	Charge	Score	<i>P</i>
<u>Q</u> HTVTTTTK + Gln->pyro-Glu (N-term Q)	500.2587	998.5033	2	57	1.5e-005
QHTVTTTTK	508.7716	1015.5298	2	27	0.024
ESQAYYQR	522.7411	1043.4672	2	60	4.3e-006
YPGQGSPGGNR	545.2562	1088.4999	2	50	4.3e-005
GENFTETDVK	570.2640	1138.5142	2	54	1.6e-005
VVEQMCITQYER	778.3660	1554.7170	2	70	6.6e-007
VVEQMCITQYER + Oxidation (M)	786.3628	1570.7120	2	79	6.5e-008
YPNQVYYRPMDEYSNQNNFVHDCVNITIK	906.1686	3620.6453	4	19	0.028

Table S3. LC-ESI-MS/MS analysis of GPI-anchor in human PrP<sup>C</sup> from KI mouse brains.

Fragment	Calcd. m/z	Charge	Calcd. m/z	Peak intensity		% Total
				2 <sup>+</sup> or 3 <sup>+</sup>	Total	
G-GPI core	1211.3 <sup>+</sup>	2 <sup>+</sup>	606.2	ND*	0	0
		3 <sup>+</sup>	404.4	ND		
G-GPI core + 4th Man	1373.4 <sup>+</sup>	2 <sup>+</sup>	687.2	ND	0	0
		3 <sup>+</sup>	458.5	ND		
G-GPI core + GalNAc	1414.4 <sup>+</sup>	2 <sup>+</sup>	707.7	ND	0	0
		3 <sup>+</sup>	472.1	ND		
G-GPI core + GalNAc + 4th Man	1576.4 <sup>+</sup>	2 <sup>+</sup>	788.7	2.54 E <sup>3</sup>	2.54 E <sup>3</sup>	34.5
G-GPI core + GalNAc + Gal		3 <sup>+</sup>	526.1	ND		
G-GPI core + GalNAc + Gal + 4th Man	1738.5 <sup>+</sup>	2 <sup>+</sup>	869.8	2.78 E <sup>3</sup>	2.78 E <sup>3</sup>	37.7
		3 <sup>+</sup>	580.2	ND		
G-GPI core + GalNAc + Gal + Neu5Ac	1867.5 <sup>+</sup>	2 <sup>+</sup>	934.3	1.24 E <sup>3</sup>	1.28 E <sup>3</sup>	17.4
		3 <sup>+</sup>	623.2	4.42 E <sup>1</sup>		
G-GPI core + GalNAc + Gal + Neu5Ac + 4th Man	2029.6 <sup>+</sup>	2 <sup>+</sup>	1015.3	5.87 E <sup>2</sup>	7.63 E <sup>2</sup>	10.4
		3 <sup>+</sup>	677.2	1.76 E <sup>2</sup>		
GS-GPI core	1298.3 <sup>+</sup>	2 <sup>+</sup>	649.7	ND	0	0
		3 <sup>+</sup>	433.4	ND		
GS-GPI core + 4th Man	1460.4 <sup>+</sup>	2 <sup>+</sup>	730.7	ND	0	0
		3 <sup>+</sup>	487.5	ND		
GS-GPI core + GalNAc	1501.4 <sup>+</sup>	2 <sup>+</sup>	751.2	ND	0	0
		3 <sup>+</sup>	501.1	ND		
GS-GPI core + GalNAc + 4th Man	1663.5 <sup>+</sup>	2 <sup>+</sup>	832.2	ND	0	0
GS-GPI core + GalNAc + Gal		3 <sup>+</sup>	555.2	ND		
GS-GPI core + GalNAc + Gal + 4th Man	1825.5 <sup>+</sup>	2 <sup>+</sup>	913.3	ND	0	0
		3 <sup>+</sup>	609.2	ND		
GS-GPI core + GalNAc + Gal + Neu5Ac	1954.6 <sup>+</sup>	2 <sup>+</sup>	977.8	ND	0	0
		3 <sup>+</sup>	652.2	ND		
GS-GPI core + GalNAc + Gal + Neu5Ac + 4th Man	2116.6 <sup>+</sup>	2 <sup>+</sup>	1058.8	ND	0	0
		3 <sup>+</sup>	706.2	ND		
Total					7.36 E <sup>3</sup>	100

\* ND: Not detected

Table S4. Identified peptides of human PrP<sup>C</sup> from human brains after HILIC column.

Fragment	Obsd. m/z	Calcd. m/z	Charge	Score	<i>P</i>
<u>Q</u> HTVTTTTK + Gln->pyro-Glu (N-term Q)	500.2595	998.5033	2	44	0.00025
ESQAYYQR	522.7402	1043.4672	2	39	0.00042
YPGQGSPGGR	545.2570	1088.4999	2	42	0.00038
VVEQMCITQYER + Oxidation (M)	786.3609	1570.7120	2	29	0.0055

Table S5. LC-ESI-MS/MS analysis of GPI-anchor in human PrP<sup>C</sup> from human brains.

Fragment	Calcd. m/z	Charge	Calcd. m/z	Peak intensity		% Total
				2 <sup>+</sup> or 3 <sup>+</sup>	Total	
G-GPI core	1211.3 <sup>+</sup>	2 <sup>+</sup>	606.2	ND*	0	0
		3 <sup>+</sup>	404.4	ND		
G-GPI core + 4th Man	1373.4 <sup>+</sup>	2 <sup>+</sup>	687.2	ND	0	0
		3 <sup>+</sup>	458.5	ND		
G-GPI core + GalNAc	1414.4 <sup>+</sup>	2 <sup>+</sup>	707.7	ND	0	0
		3 <sup>+</sup>	472.1	ND		
G-GPI core + GalNAc + 4th Man	1576.4 <sup>+</sup>	2 <sup>+</sup>	788.7	2.18 E <sup>2</sup>	2.18 E <sup>2</sup>	8.5
G-GPI core + GalNAc + Gal		3 <sup>+</sup>	526.1	ND		
G-GPI core + GalNAc + Gal + 4th Man	1738.5 <sup>+</sup>	2 <sup>+</sup>	869.8	1.29 E <sup>3</sup>	1.29 E <sup>3</sup>	50.3
		3 <sup>+</sup>	580.2	ND		
G-GPI core + GalNAc + Gal + Neu5Ac	1867.5 <sup>+</sup>	2 <sup>+</sup>	934.3	3.58 E <sup>1</sup>	3.58 E <sup>1</sup>	1.4
		3 <sup>+</sup>	623.2	ND		
G-GPI core + GalNAc + Gal + Neu5Ac + 4th Man	2029.6 <sup>+</sup>	2 <sup>+</sup>	1015.3	1.02 E <sup>3</sup>	1.02 E <sup>3</sup>	39.8
		3 <sup>+</sup>	677.2	ND		
GS-GPI core	1298.3 <sup>+</sup>	2 <sup>+</sup>	649.7	ND	0	0
		3 <sup>+</sup>	433.4	ND		
GS-GPI core + 4th Man	1460.4 <sup>+</sup>	2 <sup>+</sup>	730.7	ND	0	0
		3 <sup>+</sup>	487.5	ND		
GS-GPI core + GalNAc	1501.4 <sup>+</sup>	2 <sup>+</sup>	751.2	ND	0	0
		3 <sup>+</sup>	501.1	ND		
GS-GPI core + GalNAc + 4th Man	1663.5 <sup>+</sup>	2 <sup>+</sup>	832.2	ND	0	0
GS-GPI core + GalNAc + Gal		3 <sup>+</sup>	555.2	ND		
GS-GPI core + GalNAc + Gal + 4th Man	1825.5 <sup>+</sup>	2 <sup>+</sup>	913.3	ND	0	0
		3 <sup>+</sup>	609.2	ND		
GS-GPI core + GalNAc + Gal + Neu5Ac	1954.6 <sup>+</sup>	2 <sup>+</sup>	977.8	ND	0	0
		3 <sup>+</sup>	652.2	ND		
GS-GPI core + GalNAc + Gal + Neu5Ac + 4th Man	2116.6 <sup>+</sup>	2 <sup>+</sup>	1058.8	ND	0	0
		3 <sup>+</sup>	706.2	ND		
Total					2.56 E <sup>3</sup>	100

\* ND: Not detected

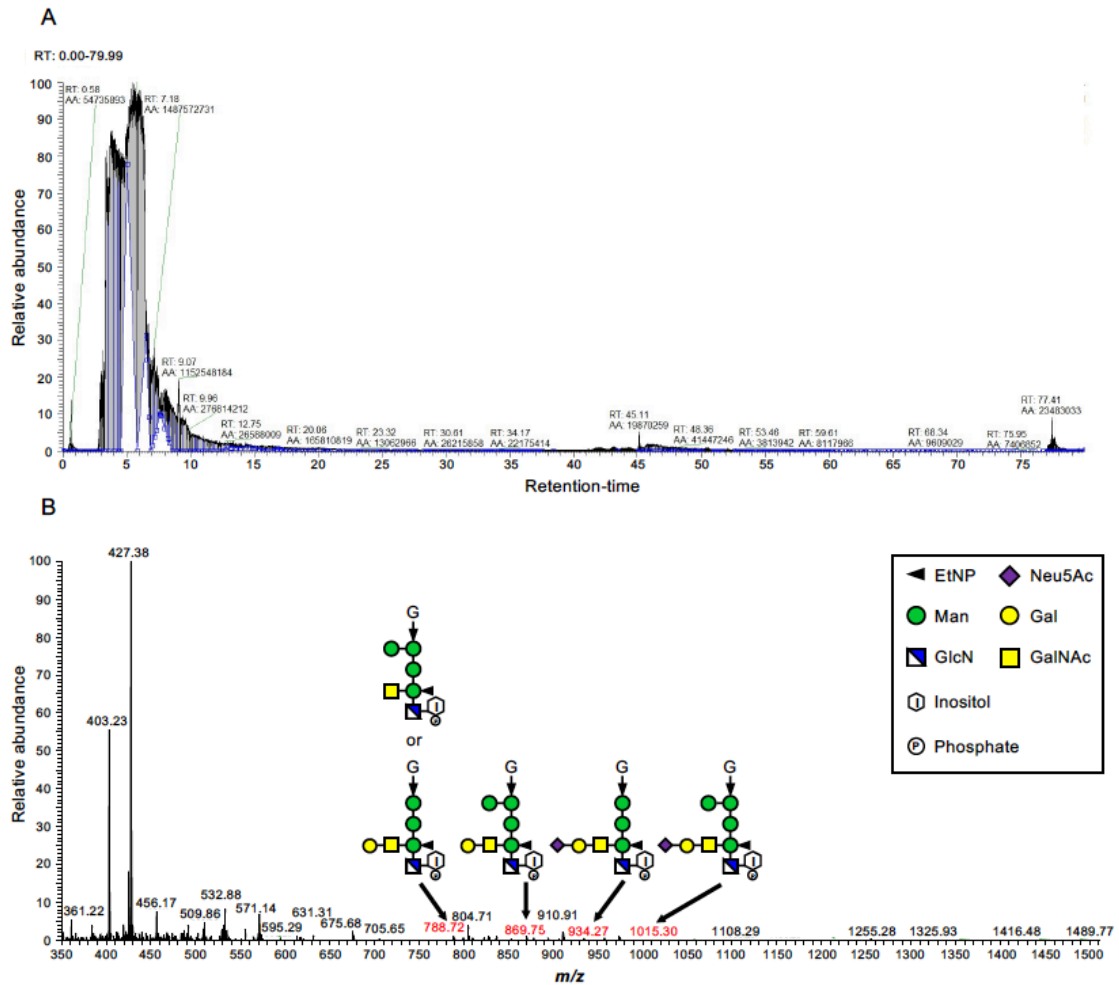


Figure S1: LC-ESI-MS analysis of purified human PrP<sup>C</sup> from KI mouse brains.

A. Total ion chromatogram (TIC) of LC-ESI-MS analysis of purified human PrP<sup>C</sup> from KI mouse brains. B. Total MS spectrum of purified human PrP<sup>C</sup> from KI mouse brains. An average MS spectrum was obtained based on retention-time from 49.75 min to 77.01 min. The  $m/z$  value of the spectrum ranged from 350 to 1500. The peptides containing GPI-glycan were highlighted by red and corresponding structures were shown by schematics. Glycan symbols are according to Symbol Nomenclature for Glycans (42).

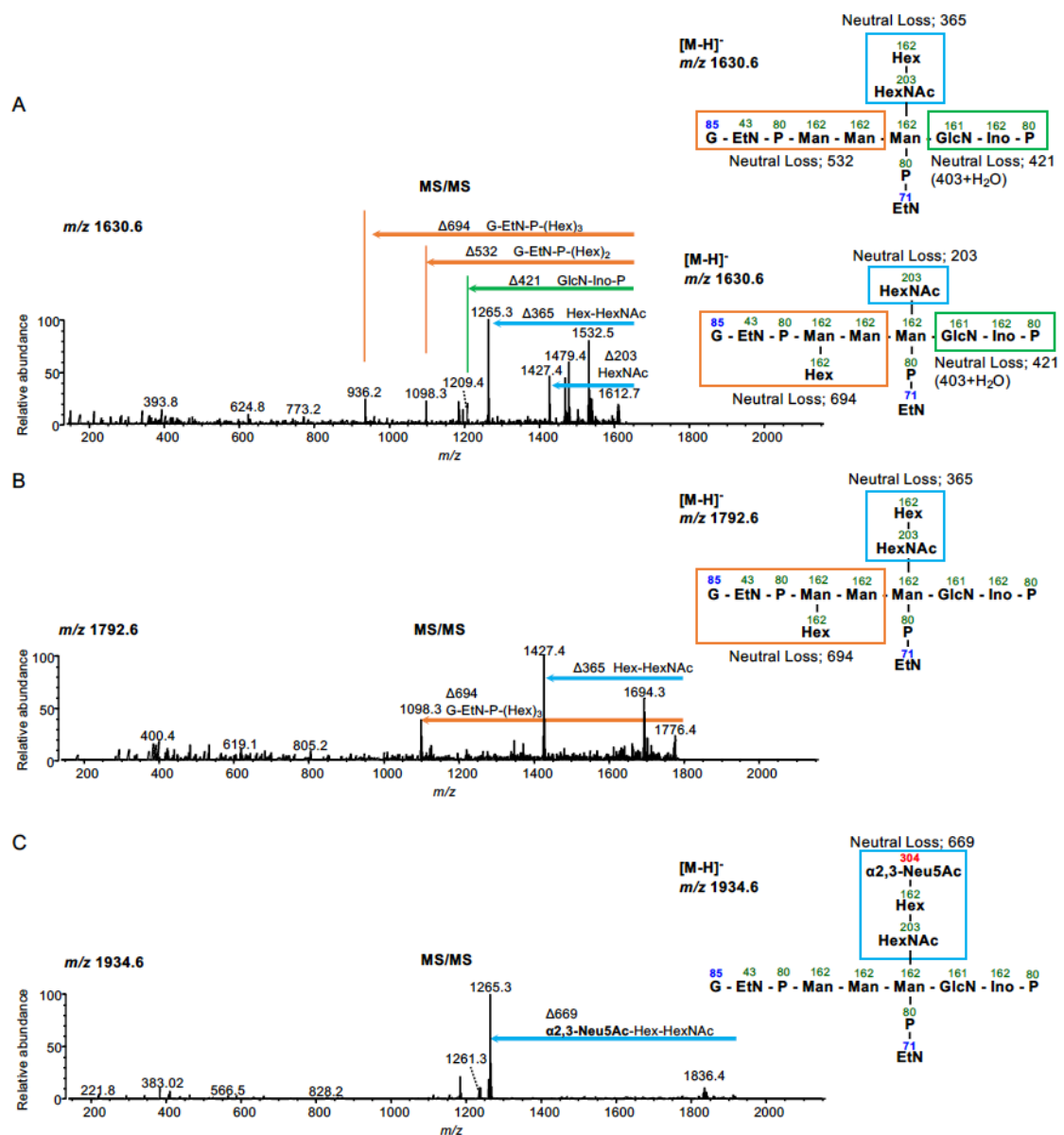


Figure S2: Linkage analysis of sialic acid on GPI-anchor by SALSA method using MALDI-MS. A. The MS/MS spectrum of a C-terminal peptide with GPI containing HexNac and Hex is shown. A 365 Da loss indicates the loss of Hex (Gal) and HexNac (GalNac). A 203 Da loss indicates the loss of HexNac (GalNac). B. The MS/MS spectrum of a C-terminal peptide with GPI containing Hex and HexNac-Hex is shown. 365 Da loss indicates the loss of Hex (Gal) and HexNac (GalNac). C. The MS/MS spectrum of a C-terminal peptide with GPI containing HexNac-Hex-Neu5Ac is shown. 669 Da loss indicates the loss of  $\alpha 2,3$ -linked Sia, Hex (Gal) and HexNac (GalNac).