

Supplementary Information for

Bisecting Lewis X in hybrid-type N-glycans of human brain revealed by deep structural glycomics

Johannes Helm^a, Clemens Gruber^a, Andreas Thader^{a§}, Jonathan Urteil^{a§}, Johannes Führer^{a%}, David Stenitzer^a, Daniel Maresch^{a&}, Laura Neumann^{a#}, Martin Pabst^{a©}, Friedrich Altmann^{a*}

^a Department of Chemistry, University of Natural Resources and Life Sciences Vienna, Muthgasse 18, 1190 Vienna, Austria.

Present addresses:

[§] Institute of Science and Technology Austria, 3400 Klosterneuburg, Austria

[§] BIOMAY AG, 1190 Wien, Austria

[%] VelaLabs GmbH, 1230 Wien, Austria

[&] Boehringer Ingelheim, 1120 Wien, Austria

[#] BakerHicks AG; 1120 Wien, Austria

[©] Delft University of Technology, Delft, The Netherlands

* Corresponding author: friedrich.altmann@boku.ac.at

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I. Supplementary Materials and Methods

Materials

Mouse brains were kindly donated by Dr. Boris Ferko (now Research Institute of Animal Production (RIAP) in Nitra, SK). Porcine brain was obtained from a local butcher. Samples from two human brains were kindly provided by Dr. Lena Hirtler (Medical University, Vienna, AT). Fungal β -galactosidase, bovine kidney fucosidase, jack bean α -mannosidase were from Sigma-Aldrich (Vienna, Austria) and α 1,6-mannosidase as well as α 1,3/4-specific fucosidase from New England Biolabs (Ipswich, MA, USA). UDP- $^{13}\text{C}_6$ -galactose was prepared from $^{13}\text{C}_6$ -galactose (Cambridge Isotope Laboratories, Tewksbury, MA, USA) with galactokinase (Sigma-Aldrich, Vienna, Austria) and recombinant galactose 1-phosphate uridylyltransferase as described¹. The biantennary N-glycan A⁴A⁴ with ^{13}C acetyl groups was purchased from Asparia glycomics (San Sebastian, Spain).

The biantennary N-glycan A⁴A⁴ with $^{13}\text{C}_2$ acetyl groups was purchased from Asparia glycomics (San Sebastian, Spain). $^{13}\text{C}_6$ -galactose was purchased from Cambridge Isotope Laboratories (Tewksbury, MA, USA).

N-glycan preparation from human and mouse brains

About 500 mg brain tissue (human or mouse brain) was cut into tiny pieces with the help of a scalpel. The pieces were transferred into a Falcon tube and mixed with 100 mM ammonium bicarbonate buffer containing 15 mM dithiothreitol (DTT) and 2.5 % sodium dodecyl sulfate in a total volume of 3.5 ml. After homogenization with an Ultra-Turrax T25 disperser the homogenate was boiled at 95°C for 5 min in order to eliminate enzymatic activities. After centrifugal clarification the supernatant was mixed with four volumes of methanol, one volume of chloroform and three volumes of water in the given order. After centrifugation of the mixture for 3 min at 2500 rpm, the upper phase was removed and another four volumes of methanol was added. After another centrifugation, the pellet was washed with methanol. The dried pellet was taken up in 50 mM ammonium acetate of pH 8.4 containing 1.25 M urea. For N-glycan release 2.5 U of PNGase F was added and the resulting mixture was incubated overnight at 37°C. This reaction mixture was loaded onto a Hypersep C18 cartridge (25 mg; Thermo Scientific, Vienna) that had been previously washed with 500 μl of methanol, then 500 μl 50 % acetonitrile in 65 mM ammonium formate buffer (pH 3.0) and equilibrated twice with 500 μl 0.1 % formic acid. The flow-through of the applied sample was collected and subjected to centrifugal evaporation. Reduction of the glycans was carried out in 1 % sodium borohydride at room temperature overnight. Desalting was performed using HyperSep Hypercarb solid-phase extraction cartridges (25 mg) (Thermo Scientific, Vienna).

N-glycan preparation from pig brain, bovine fibrin and white beans

N-glycans from pig brain and white beans (ca. 50 g) were prepared by pepsin digestion, (glyco)-peptide extraction on a cation exchange resin and PNGase A treatment as previously described². Peptic glycopeptides from bovine fibrin were desialylated in 50 mM sulfuric acid for 1 h at 80 °C. After neutralization with NaOH and centrifugation the glycopeptides were enriched by gel filtration and deglycosylated². Reduction and final purification were done as described above.

N-glycan preparation from purified glycoproteins

In the case of human IgG, 100 mg glycoprotein was dissolved in 10 mL 50 mM ammonium acetate (pH 8.4) and brought to 95 °C for 10 min. After cooling, 0.2 mU peptide:N-glycosidase F was added and digestion was carried out overnight at 37 °C. Subsequently, the released N-glycans were acidified, reduced and recovered by passage over Hypersep C18 cartridge as described above for small scale brain glycan preparations. Human colostrum IgA (1 mg) was treated similarly.

IgG N-glycans were in part fractionated by semi-preparative HPLC on a Hypercarb column as described previously². The major components GnGnF⁶, A⁴GnF⁶, GnA⁴F⁶ and A⁴A⁴F⁶ eluted in this order³ and could be obtained as isolated fractions for the preparation of defined isomers.

Glycosyltransferases and glycosidases

Recombinant human α 1,2-fucosyltransferase (FucT-II) was purchased from Bio-technie (Minneapolis, USA), recombinant bovine α 1,3-galactosyltransferase from Chemily Glycoscience (Peachtree Corners, USA) and bovine milk β 1,4-galactosyltransferase from Sigma-Aldrich (Vienna, Austria). Bovine kidney fucosidase from bovine kidney and jack bean mannosidase were purchased from Sigma-Aldrich (Vienna, Austria). The β 1,4-specific galactosidase from *Aspergillus oryzae* was prepared as described⁴. α 1,3/4-specific fucosidase and α 1,6-specific mannosidase were purchased from NEB (Ipswich, MA, USA).

Human fucosyltransferase III (FucT-III) lacking the N-terminal 34 amino acids, human fucosyltransferase IV (FucT-IV) lacking the N-terminal 172 amino acids, fucosyltransferase VIII (FucT-VIII) from *Bos taurus* lacking the N-terminal 30 amino acids, human β 1,3-galactosyltransferase (b3GalT5) lacking the N-terminal 29 amino acids, *N*-acetylglucosaminyltransferase I (GnT-I) from rabbit lacking the N-terminal 105 amino acids and human *N*-acetylglucosaminyltransferase III (GnT-III) lacking the N-terminal 22 amino acids were recombinantly expressed with a N-terminal His₆-tag using a pVT-Bac vector and the baculovirus insect cell system as described previously⁵. The enzymes were purified by metal chelate chromatography. The buffer was changed to 25 mM Tris/HCl pH 7.4 supplemented with 100 mM NaCl and the volume was reduced to less than 1 mL with an Amicon 10 kDa cut-off membrane (SigmaAldrich, Vienna). The enzymes were directly used after purification or stored at 4 °C.

Preparation of ¹³C₆-UDP-Galactose

UDP-¹³C₆-galactose was prepared by incubation of ¹³C₆-galactose with galactokinase (Sigma-Aldrich, Vienna, Austria). Galactose-1-phosphate was converted to the nucleotide sugar in the presence of UDP-glucose by human galactose-1-phosphate uridylyltransferase, which was recombinantly expressed in *Escherichia coli* BL21 and purified via its His₆-tag. The UDP-¹³C₆-galactose was finally purified by PGC chromatography with a slightly alkaline buffer as described¹.

Biosynthesis of glycan structures

The reduced and dried glycans, prepared as described above, were used as scaffolds for the different glycosidases and glycosyltransferases. The non-labelled standards were biosynthesized according to Figure S1 and the isotope-labelled glycan standards were biosynthesized according to Figure S3. Fucosyltransferases were used with 1 mM GDP-fucose and 10 mM MnCl₂ in a total volume of 50 μ L in 25 mM Tris/HCl pH 7.4 + 100 mM NaCl. Bovine β -1,4-galactosyltransferase and human β -1,3-galactosyltransferase were used with 1 mM UDP-galactose or ¹³C₆-UDP-galactose (or 1 mM UDP-GalNAc) and 20 mM MnCl₂ for bovine β -1,4-galactosyltransferase and 2 mM MnCl₂ for human β -1,3-galactosyltransferase in a total volume of 50 μ L in 25 mM Tris/HCl pH 7.4 + 100 mM NaCl. *N*-acetylglucosaminyltransferases 1 and 3 were used with 1 mM UDP-GlcNAc and 20 mM MnCl₂ in 50 mM Tris/HCl pH 7.4. α 1,3-galactosyltransferase was used with 1 mM UDP-galactose or ¹³C₆-UDP-galactose and 10 mM MnCl₂ in 50 μ L of 25 mM Tris/HCl pH 7.4 + 100 mM NaCl. β -galactosidase from *Aspergillus oryzae* and fucosidase from bovine kidney were used in 0.1 M phosphate citrate buffer pH 5.0, α -mannosidase from jack bean was used in sodium acetate buffer pH 4.5 supplemented with 5 mM ZnCl₂. α 1,3/4-specific fucosidase and α 1,6-mannosidase were used according to the manufacturer's protocol.

All enzyme reactions were carried out overnight at 37 °C. After each enzyme-reaction step, the reaction mixtures were purified using carbon solid phase cartridges (Multi-Sep Hypercarb 25 mg, Thermo Scientific, Vienna) and the completeness of the enzymatic reaction was checked using PGC-LC-ESI-MS before further enzymatic processing. After the last enzymatic

processing step, the finished glycan standards were again purified using PGC-SPEs, dried by centrifugal evaporation, taken up in a small volume of HQ-water and stored at -20°C until measurement.

Mass spectrometric methods

The purified samples were loaded on a PGC-column (100 mm × 0.32 mm, 5 µm particle size, Thermo Scientific, Waltham, MA, USA) with 10 mM ammonium bicarbonate as the aqueous solvent A and 80 % acetonitrile in solvent A as solvent B. The gradient was as followed: 0 – 4.5 min 1 % B, from 4.5 – 5.5 min 8 % B, from 5.5 – 58 min 8 - 22 % B, from 58 – 62.5 min 22 - 30 % B, from 62.5 – 63.5 min 68 % B, followed by an equilibration period at 1 % B from 64 – 70 min. The flowrate was 6 µL/min. Detection was performed with an ion trap mass spectrometer equipped with the standard ESI source directly linked to the Thermo Ultimate 3000 UPLC system. MS-scans were recorded from 400 – 1600 m/z. All samples were measured with an ion trap instrument (amaZon speed ETD; Bruker, Bremen, Germany) in positive mode or, in the case for some brain glycan runs, in negative mode. The negative mode measurements were carried out with the ICC target set to 100000, maximum accumulation time set to 250 ms and a scan range from 600 – 1500 m/z. The scan mode was set to enhanced resolution and the SPS (Smart Parameter Settings) were set to target mass 950 m/z, compound stability 100% and trap drive level 100%. For MS/MS, the number of precursor ions was set to 3 with active exclusion (exclusion after 1 spectrum and release after 0.22 min). The absolute threshold was set to 10000 and the inclusion list was set from 700 – 1200 m/z. The scan mode for MS/MS was set to enhanced resolution with the ICC target set to 200000 and maximum accumulation time of 100 ms with isolation width set to 2 m/z. Smart frag was enabled in enhanced mode (start amplitude: 150%, end amplitude 200% and fragmentation time 35 ms). PAN was enabled with Low CID CutOff at 17% and time stretch at 250%. FxD was enabled with activation at 100%, decay at 100% and tickle level at 100%.

The positive mode measurements were carried out with the ICC target set to 165000, the maximum accumulation time set to 200 ms and a scan range from 600 – 1500 m/z. The scan mode was set to enhanced resolution and the SPS (Smart Parameter Settings) were set to target mass 850 m/z, compound stability 100 % and trap drive level 100%. For MS/MS, the number of precursor ions was set to 3 with active exclusion (exclusion after 1 spectrum and release after 0.25 ms). The absolute threshold was set to 20000 and the inclusion list to 700 – 1200 m/z. The scan mode for MS/MS was set to enhanced resolution with the ICC target set to 200000, the maximum accumulation time to 55 ms and the isolation width to 3 m/z. Smart Frag was enabled in enhanced mode (start amplitude 80%, end amplitude 120% and fragmentation time 20 ms). PAN and FxD was disabled for positive mode MS/MS.

Standard source settings (capillary voltage 4.5 kV, nebulizer gas pressure 0.5 bar, drying gas 5 L/min, 200 °C) were used. Instrument tuning was optimized for a low mass range (around 1500-2000 Da molecules). MS/MS was carried out in data-dependent acquisition mode (switching to MS/MS mode for eluted peaks). Data interpretation was done with DataAnalysis 4.0 (Bruker, Bremen, Germany).

Supporting Tables:

Table S1 Vi-min values of N-glycans of various compositions. This collection of isomers does by no means claim to be comprehensive. For a list of H5N4F1 glycans with consecutive numbers refer to Figure 1.

H5N4		H5N4F1		H5N4F1	
Proglycan-code	vi-min	Proglycan-code	vi-min	Proglycan-code	vi-min
M ³ A ⁴ bi	11.9	M ³ Gn(AF)-bi	11.2	A ³ (FA)	31.2
Man5Gnbi	13.0	M ³ A ⁴ F ⁶ bi	16.6	F ²⁻⁴ A ⁴	31.6
M ³ A ³ bi	13.7	Man5GnF ⁶ bi	17.5	Man5An ⁴ F ⁶	32.4
M ³ GnA-bi	15.7	M ³ (F ²⁻⁴)bi	18.5	(FA)A ⁴	32.5
Man5An	23.4	M ³ A ³ F ⁶ bi	18.8	F ²⁻⁴ A ³	32.9
A ⁴ A ⁴	27.9	A ⁴ A ⁴ F ³	19.6	A ⁴ F ²⁻⁴	34.1
A ⁴ A ³	29.3	A ⁴ A ³ F ³	19.8	(FA)A ³	34.5
A ³⁻⁴ Gn	30.4	M ³ Gn(F ²⁻⁴)bi	21.1	F ²⁻³ A ⁴	35.6
A ³ A ⁴	31.8	M ³ (F ²⁻³)bi	21.2	A ⁴ F ²⁻³	36.2
A ³ A ³	32.5	Man5(An ⁴ F ³)	21.8	A ⁴ A ⁴ F ⁶	36.2
GnA ³⁻⁴	33.4	M ³ GnF ⁶ A-bi	22.7	F ²⁻³ A ³	35.6
A ³⁻³ Gn	35.1	(A ³⁻⁴ F ³)Gn	23.5	A ³ F ²⁻³	37.2
GnA ³⁻³	35.9	A ⁴ (AF)	23.9	A ⁴ A ³ F ⁶	37.6
		A ³ A ⁴ F ³	24	A ³ F ²⁻⁴	37.8
		A ³ A ³ F ³	24	A ³⁻⁴ GnF ⁶	38.3
H5N4F2		(AF)A ⁴	25.4	A ³ A ⁴ F ⁶	39.6
M ³ GnF ⁶ (AF)-bi	15.0	Gn(A ³⁻⁴ F ³)	26.2	A ³ A ³ F ⁶	40.4
(AF)(AF)	20.9	(AF)A ³	26.5	GnA ³⁻⁴ F ⁶	41.1
(FA)(FA)	32.4	A ³ (AF)	27.9	A ³⁻³ GnF ⁶	42.5
(F ²⁻³)(F ²⁻³)	43.4	A ⁴ (FA)	27.9	GnA ³⁻³ F ⁶	44.1
(F ²⁻⁴)(F ²⁻⁴)	43.6				

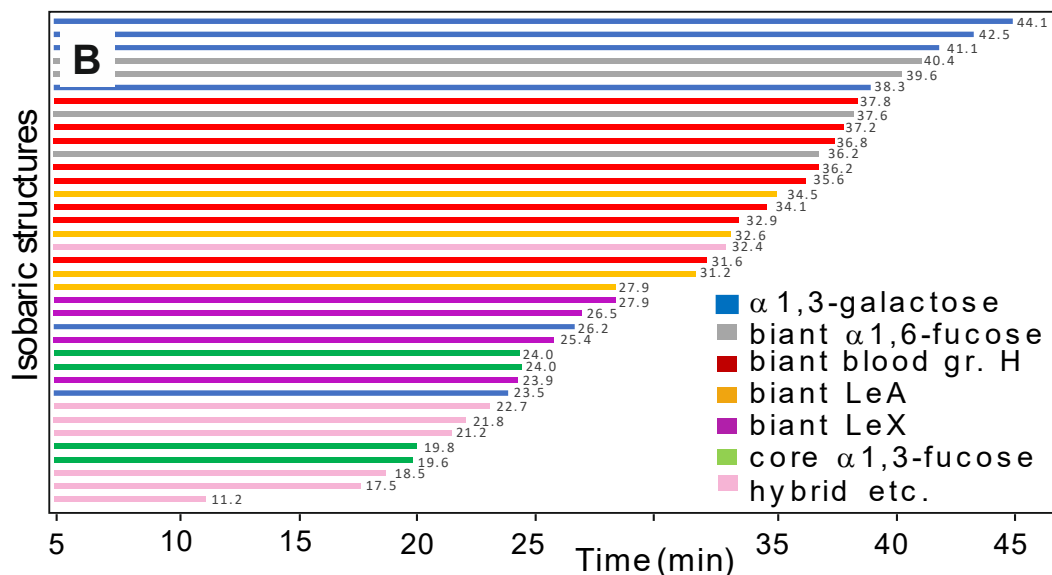


Table S2 Isomer assignment of IgA N-glycans by the glyco-TiGr approach. Experimental retention times of the peaks from Figure 6 are converted by linear interpolation using the Excel routine “TiGr calculation”. Values for virtual minutes (*vi-mins*) are compared to Table 1. Structures in bracket denote highly unlikely isomers with incidentally very similar retention time.

Peak Nr.	Exp.Rt. (min)	<i>Vi-min</i>	Close st hit	Δ (min)	Structure	Arbitrary number as in Figure 1
1	30.2	22.9	22.7	0.2	M ³ GnF ⁶ A-bi	27
2	31.2	23.9	23.9	0.0	A ⁴ (AF)	5
3	34.5	26.7	26.5	0.2	(AF)A ³	8
4	35.7	27.9	27.9	0.0	A ³ (AF), [(A ⁴ (FA)]	7, [9]
5	44.3	36.2	36.2	0.0	A ⁴ A ⁴ F ⁶ , [A ⁴ F ²⁻³]	1, [15]
6	46.0	37.6	37.6	0.0	A ⁴ A ³ F ⁶	2
7	49.4	40.4	40.4	0.0	A ³ A ³ F ⁶	4

II. Supplementary Figures

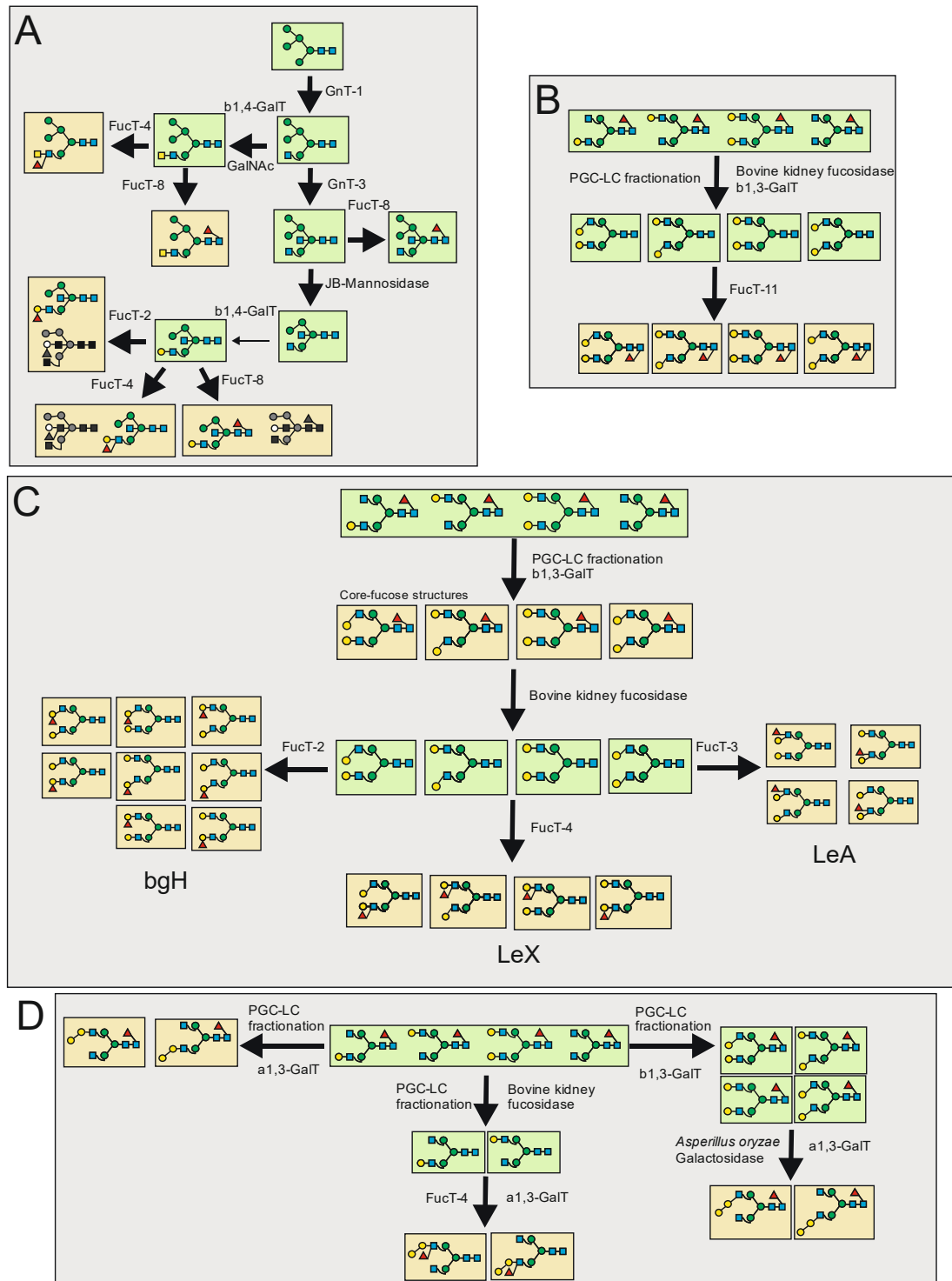


Figure S1 Pathways for biosynthesis of individual N-glycan structures with the composition H5N4F1; Panel **A** describes the biosynthesis of hybrid-type structures with Man5 from beans as starting point; Structures drawn in grey scales were unanticipated results. Panel **B** shows the pathway for plant type core α 1,3-core fucosylated structures from isolated IgG glycans as the starting point; Panel **C** gives the pathways for Lewis X, Lewis A, blood

group H and core α 1,6-fucosylated biantennary structures from isolated A^4GnF^6 , GnA^4F^6 , $A^4A^4F^6$ and $GnGnF^6$ glycans; Panel D shows the pathway for the α 1,3-galactosylated biantennary structures.

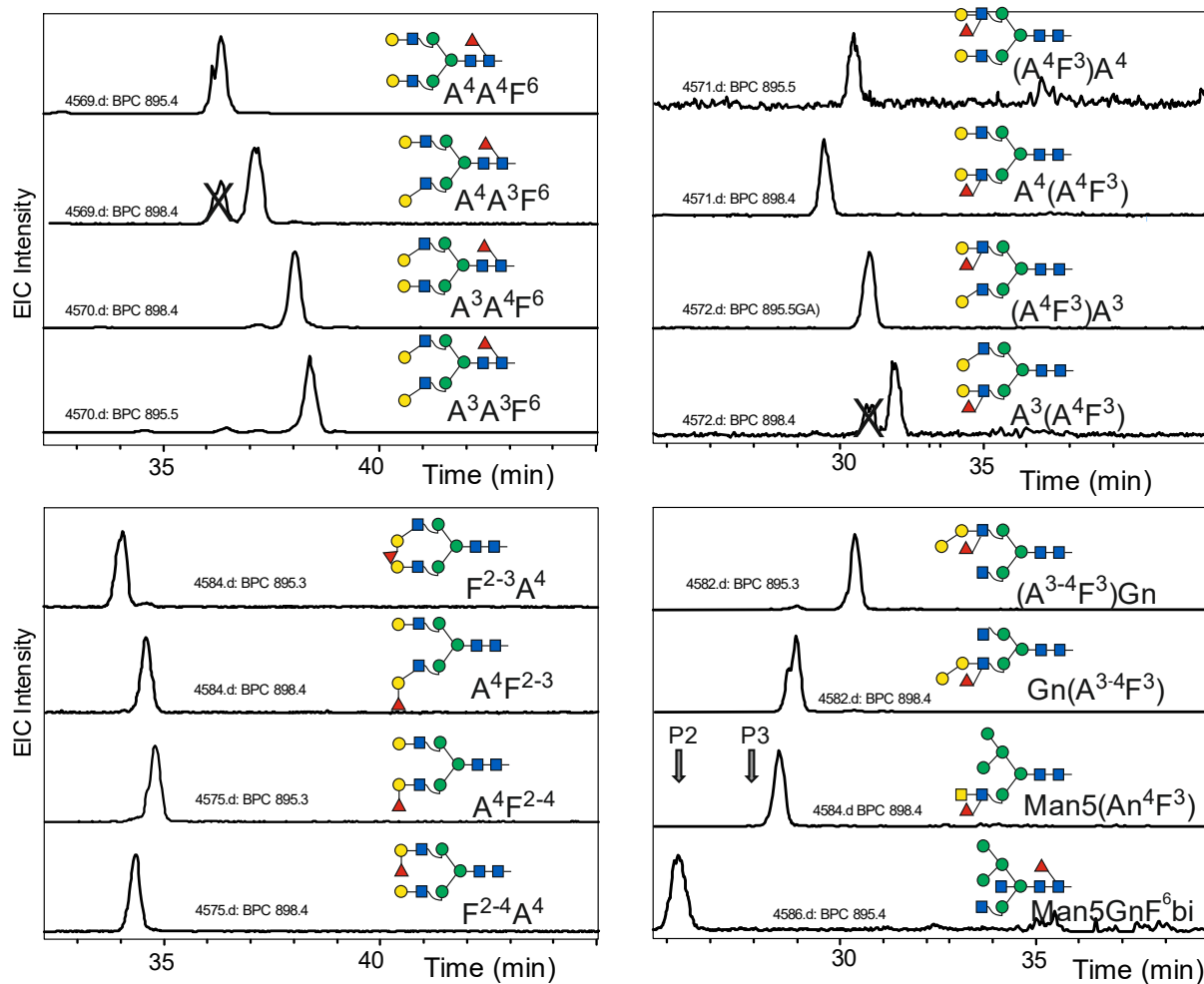


Figure S2 Examples of elution positions of individual reference glycans. Performed long before acquisition of the “mother chromatogram”, the elution times may deviate. In many cases, light and heavy (one $^{13}C_6$ -Gal) standards were co-injected as indicated by after the run number. Grey arrows in the lower right corner denote the positions of brain HSN4F1 peaks 2 and 3. Crossed-out peaks had aberrant isotope patterns.

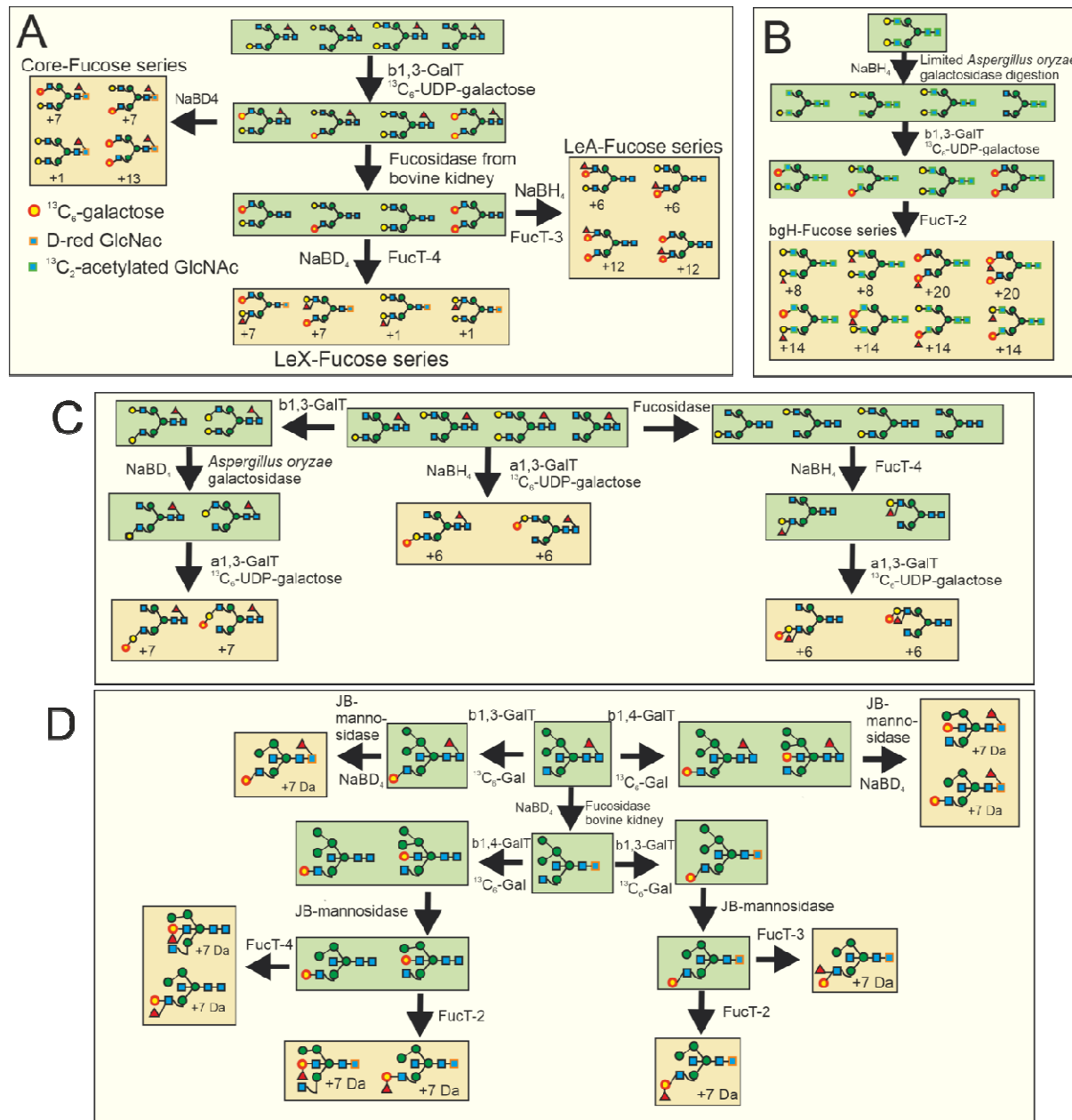


Figure S3 Biosynthesis pathways for isotope labelled N-glycans with the composition H5N4F1; Panel A shows the pathways for the biosynthesis of complex-type biantennary glycans (LeX-, LeA- and core-fucose) with A4GnF⁶, GnA⁴F⁶, A⁴A⁴F⁶ and GnGnF⁶ isolated from human IgG as the starting point; Panel B shows the pathway for the biosynthesis of the complex-type biantennary bgH glycans with $^{13}\text{C}_2$ -acetylated A⁴A⁴ as the starting point; Panel C shows the pathways for the biosynthesis of alpha-galactosylated complex-type biantennary structures with A⁴GnF⁶, GnA⁴F⁶, A⁴A⁴F⁶ and GnGnF⁶ isolated from human IgG as the starting point; Panel D shows the pathways for the biosynthesis of hybrid-type glycans with Man5GnF⁶bi isolated from pig brain as the starting point. Generation of a LeA determinant on hybrid-type glycans, however, failed, which reflects the recently described suppressive effect of bisecting GlcNAc on terminal modifications ⁶.

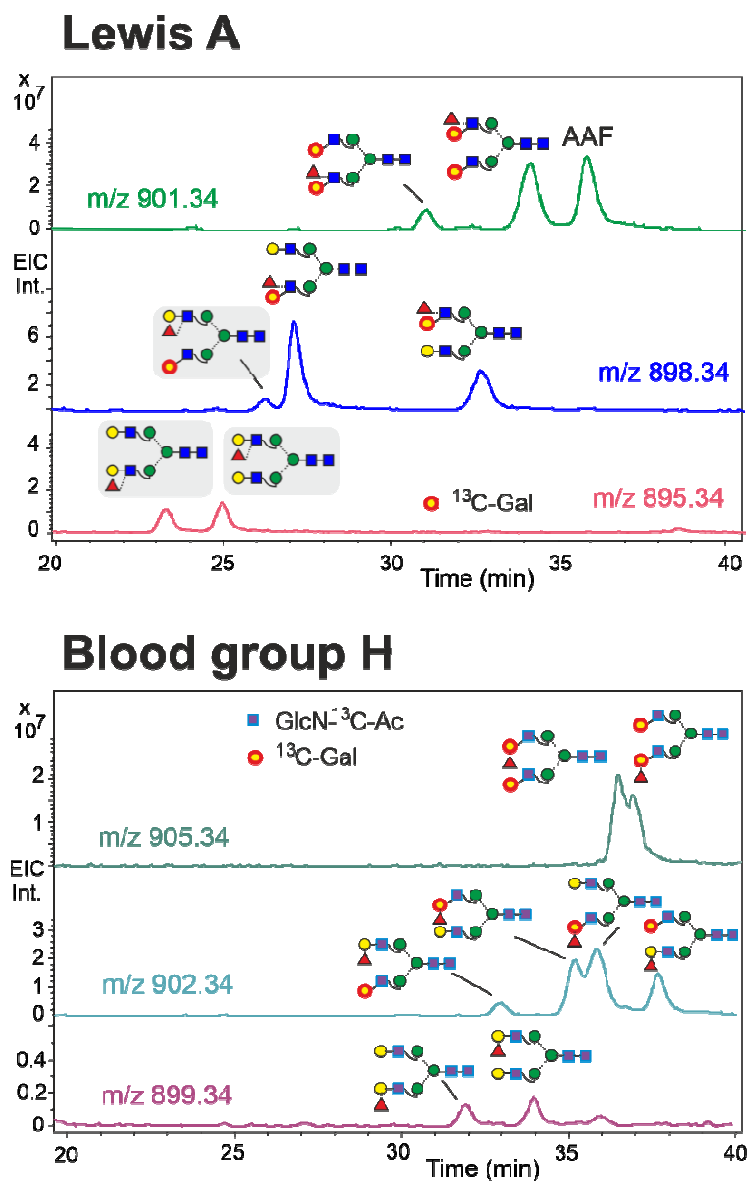


Figure S4 Determination of retention times of LeA and blood group H isomers.

Upper panel: Reaction of a NaBH_4 reduced, defucosylated mixture (A^4A^4 , A^4A^3 , A^3A^4 and A^3A^3) as shown in main text Figure 2C with FucT-3 generated four LeA isomers. Due to the dual activity of FucT-3, LeX isomers were also formed. These alternative products are shaded in grey. The peak designated AAF arises from the overlap with the isotopic pattern of the TiGr standard $\text{A}^4\text{A}^4\text{F}^6$.

Lower panel: The reaction scheme shown in Figure 2C was conducted with N-glycans harboring four $^{13}\text{C}_2$ -acetyl groups and FucT-2, which acts on type 1 and type 2 chains with a roughly five-fold preference for type 1 acceptor chains.

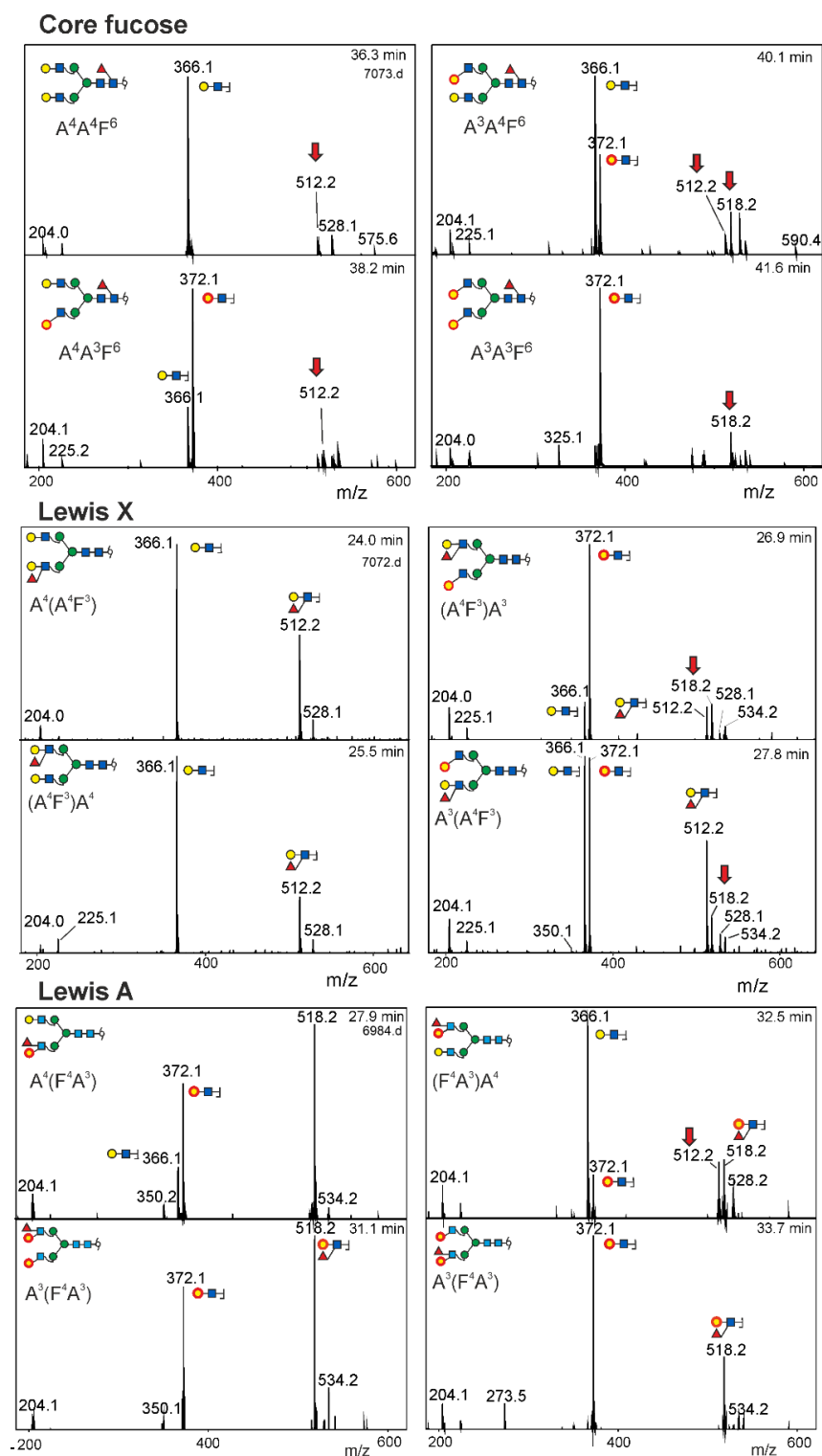


Figure S5 Relevant sections of the positive mode MS/MS spectra of fucosylated $^{13}\text{C}_6$ -galactose labelled standard N-glycans. The respective EICs are shown in main text Figure 2 and the SI Appendix, Figure 4. Note the different height of the disaccharide ions depending on their origin. Red arrows label fragments unquestionably resulting from re-arrangement.

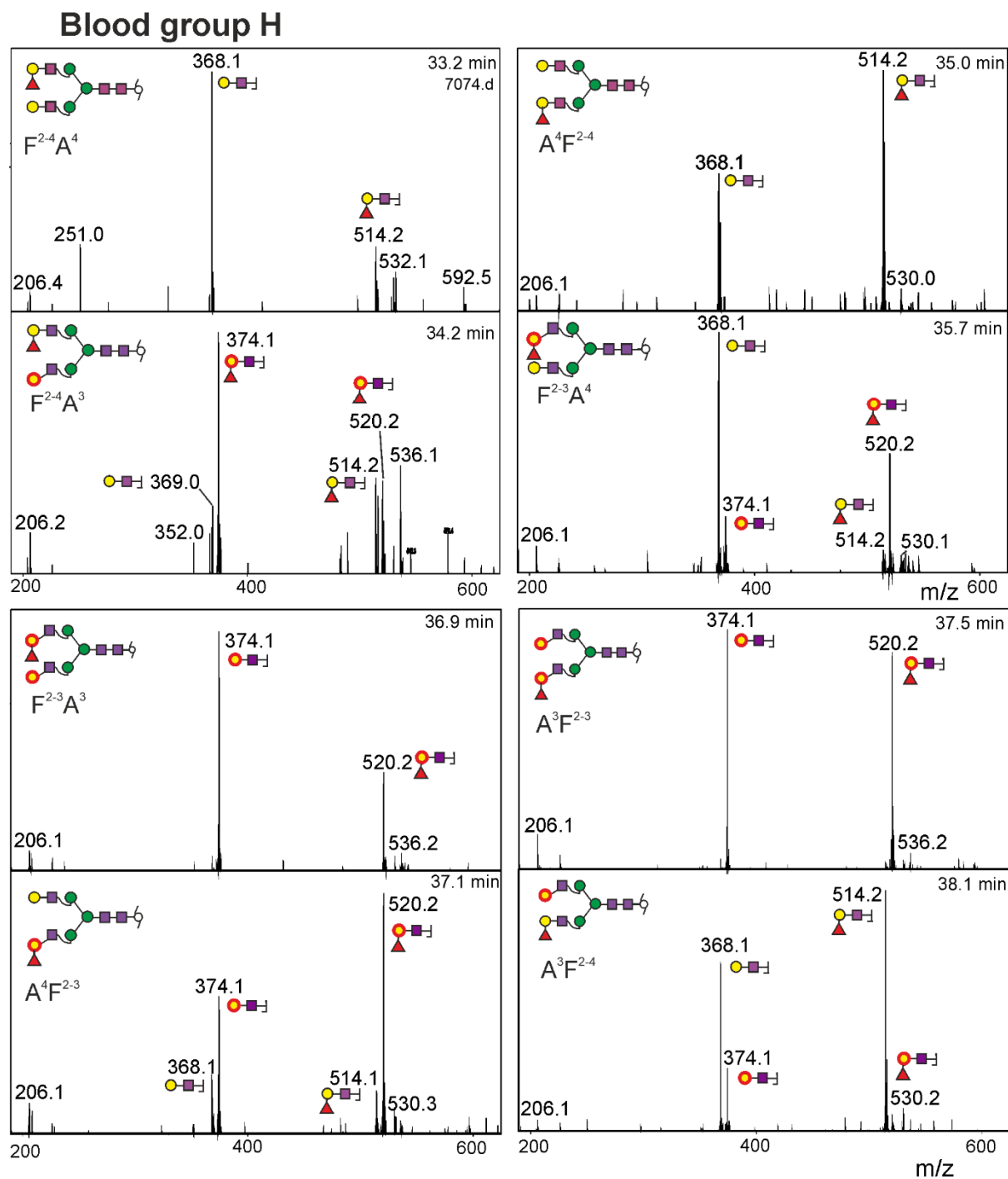


Figure S6 Relevant sections of the positive mode MS/MS spectra of $^{13}C_6$ -galactose (and $^{13}C_2$ -acetyl) labelled N-glycans with blood group H determinants. The respective EICs are shown in the SI Appendix, Figure 4. The purple squares GlcNAc with $^{13}C_2$ -labelled acetyl groups. Note the different height of the disaccharide ions depending on their origin.

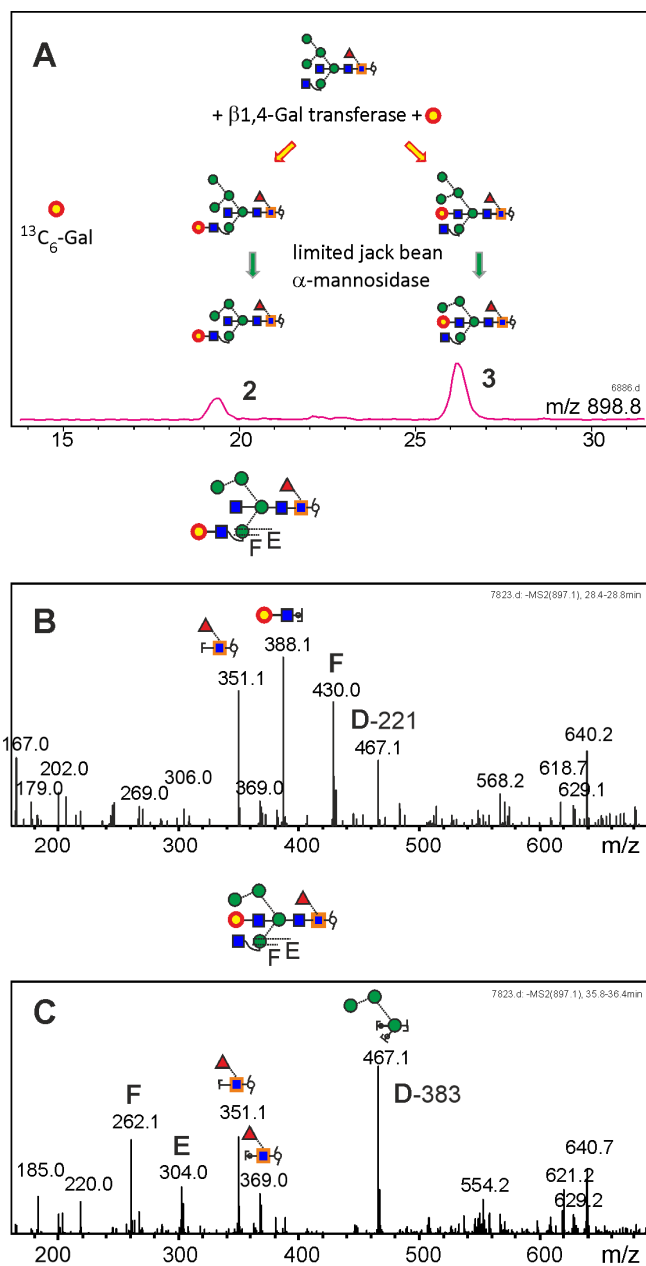


Figure S7 Negative ion CID of hybrid-type glycans after $^{13}\text{C}_6$ -Gal incorporation. The enzymatic cascade is shown in panel **A**. The spectra of peaks 2 and 3 (numbering as in main text Figure 3) are given in panels **B** and **C**. The spectra agree with the proposed structures as being Man4 glycans with core-fucose, a bisecting GlcNAc and galactose bound to the 3-arm in peak 2 but to the bisecting GlcNAc in peak 3. Note the very different terminal ions generated by the Gal-GlcNAc units. No E-ion is seen in panel **B**, instead the Gal-GlcNAc unit generated a very strong C-ion totally absent from the structure with the bisecting LacNAc. The mass of the ejected bisecting fragment of D-ions was determined in retrospect.

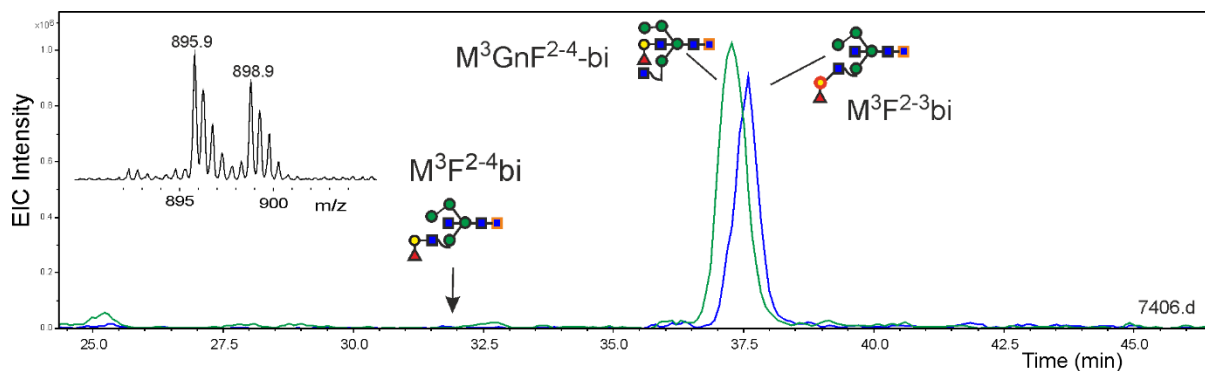


Figure S8 Hybrid-type products of FucT-3. The blue EIC is the product obtained from the conversion of Man⁵GnF⁶bi with b3GalT as shown in main text Figure 4 (peak 1). The green EIC shows - within the same LC run - the product obtained from brain peak 451c. The respective product for β1,4- galactose on the 3-arm elutes much earlier.

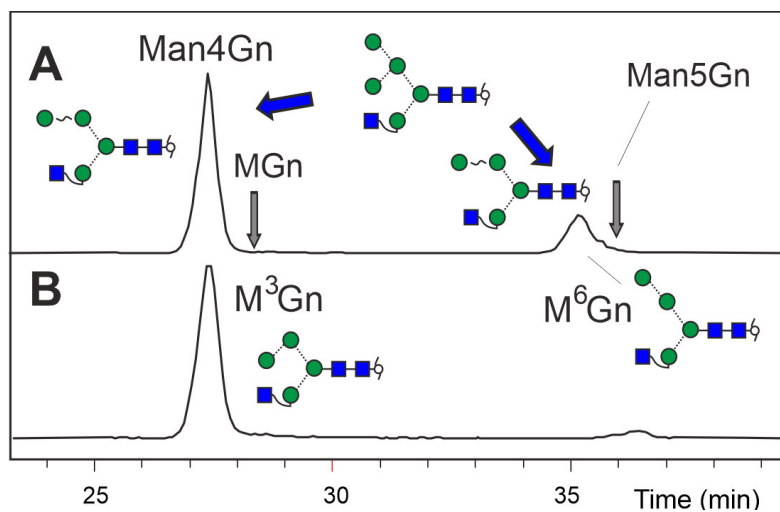


Figure S9 Determination of the exact structure of Man4Gn. Panel **A** shows the result of a limited digest of Man⁵Gn with jack bean α-mannosidase. Panel **B** depicts the same EICs trace after treatment with an α1,6-specific mannosidase. Obviously, the large peak in panel **A** was the isomer with the upper arm mannose in 3-linkage. Removal of the 6-linked mannose causes a profound forward shift on the PGC column, which is considered useful for concluding on the mannose arrangement in other Man⁴ / Man⁵ families. The elution positions of the substrate Man⁵Gn and the final product MGn are indicated by arrows. The bias towards M³Gn is more pronounced than reported previously⁷. Jack bean mannosidase then does not appear as stereospecific towards the two scissile mannose residues as it was inferred by X-ray crystallographic studies for Golgi α-mannosidase II⁸. The pronounced earlier elution of the Man⁴ structures as compared to their cognate Man⁵ precursor allows to assign the 6-branch of hybrid glycans as Man^α-3Man^α-6Man^β- (terminus term: M³) rather than Man^α-6Man^α-6Man^β- (terminus term: M⁶).

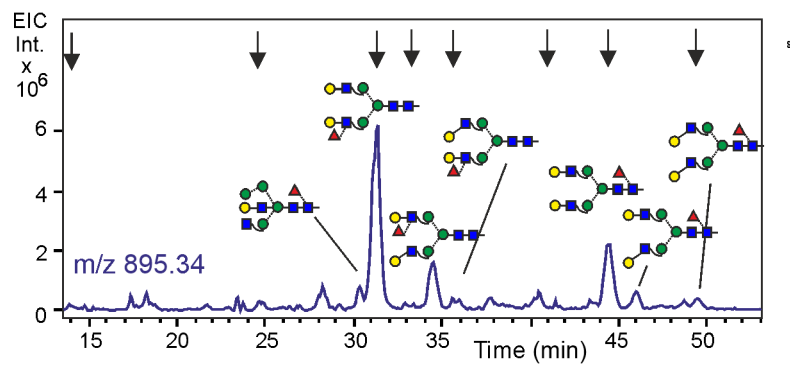


Figure S10. Analysis of multimeric IgA glycans of H5N4F1 composition by PGC-LC-ESI-MS/MS. Arrows at the top indicate elution positions of the glyco-TiGr standard mix. Only peaks with appropriate isotopic pattern are annotated.

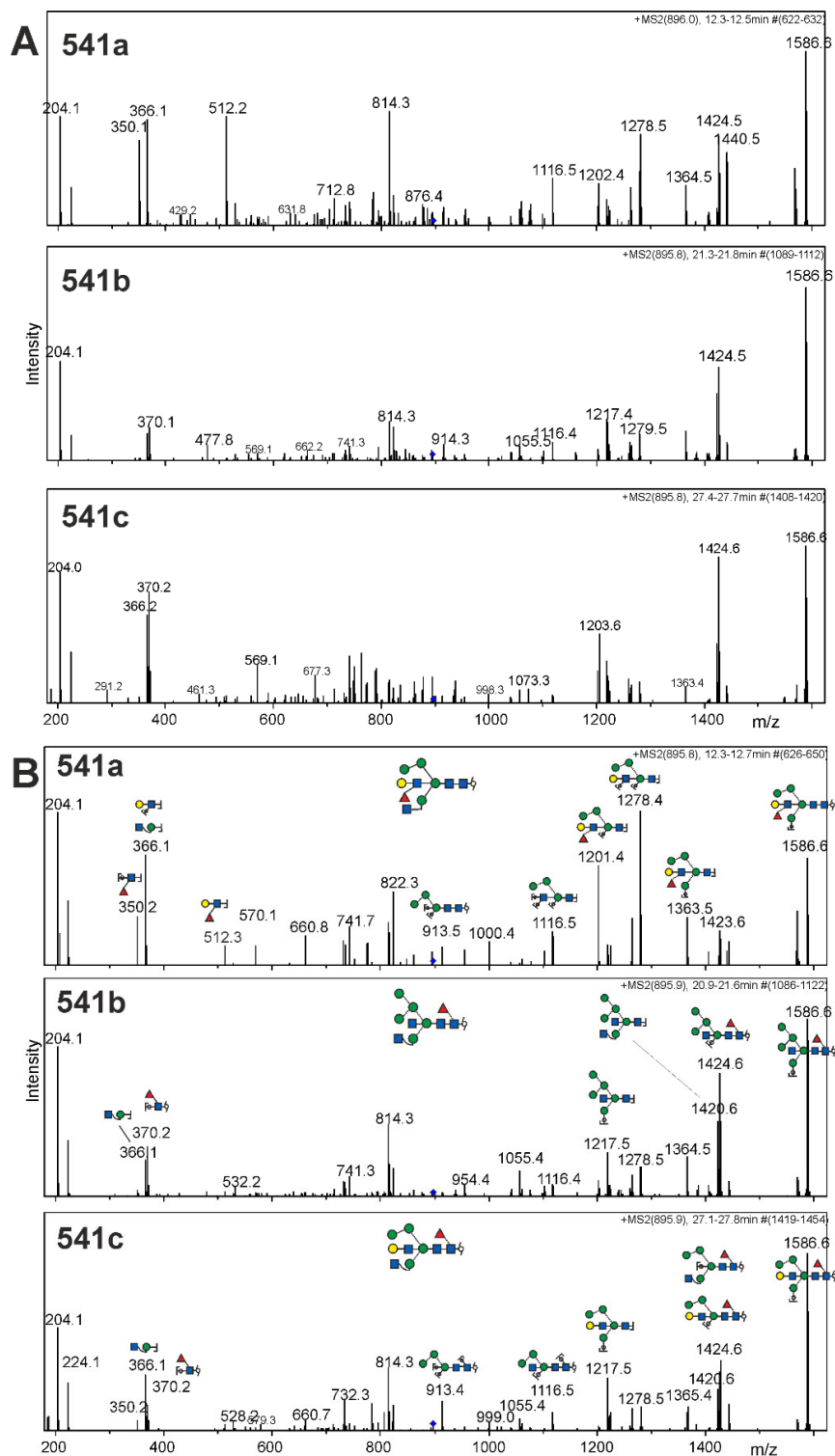


Figure S11 Positive mode CID MS/MS spectra of the hybrid-type HSN4F1 glycans of human (panel **A**) and porcine brain (panel **B**). Fragments obtained from $m/z = 895.9$ precursors ($MH^+ = 1789.67$) of peak 1, 2 and 3 are shown with tentative assignment of y and b fragment ions. Note the general dominance of the GlcNAc-loss fragment.

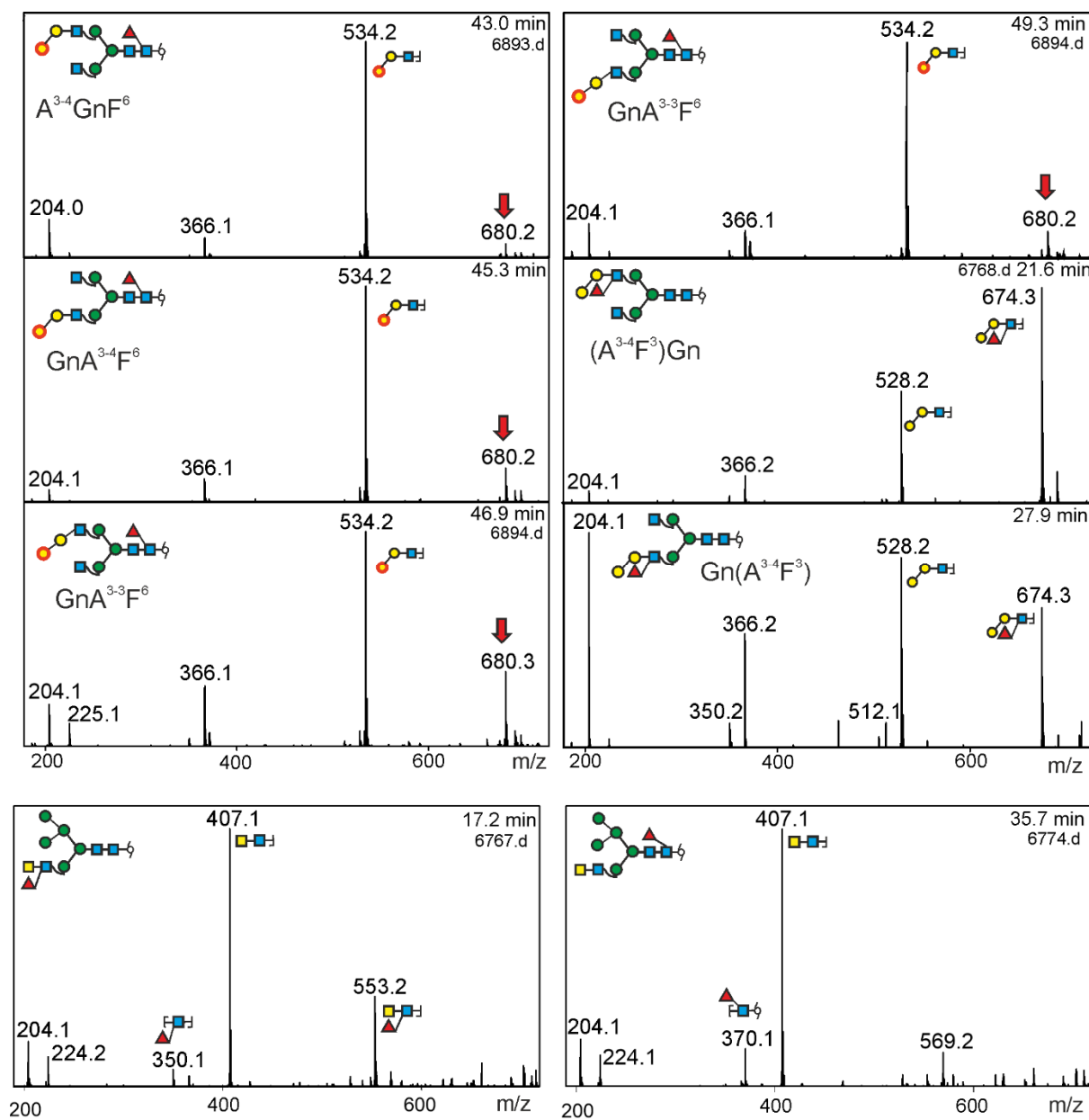


Figure S12 Relevant sections of the positive mode MS/MS spectra of alfa-galactose and of GalNAc containing N-glycans with core- or LeX-fucose. The core-fucosylated structures are $^{13}C_6$ -galactose labelled. Red arrows label fragments unquestionably resulting from re-arrangements.

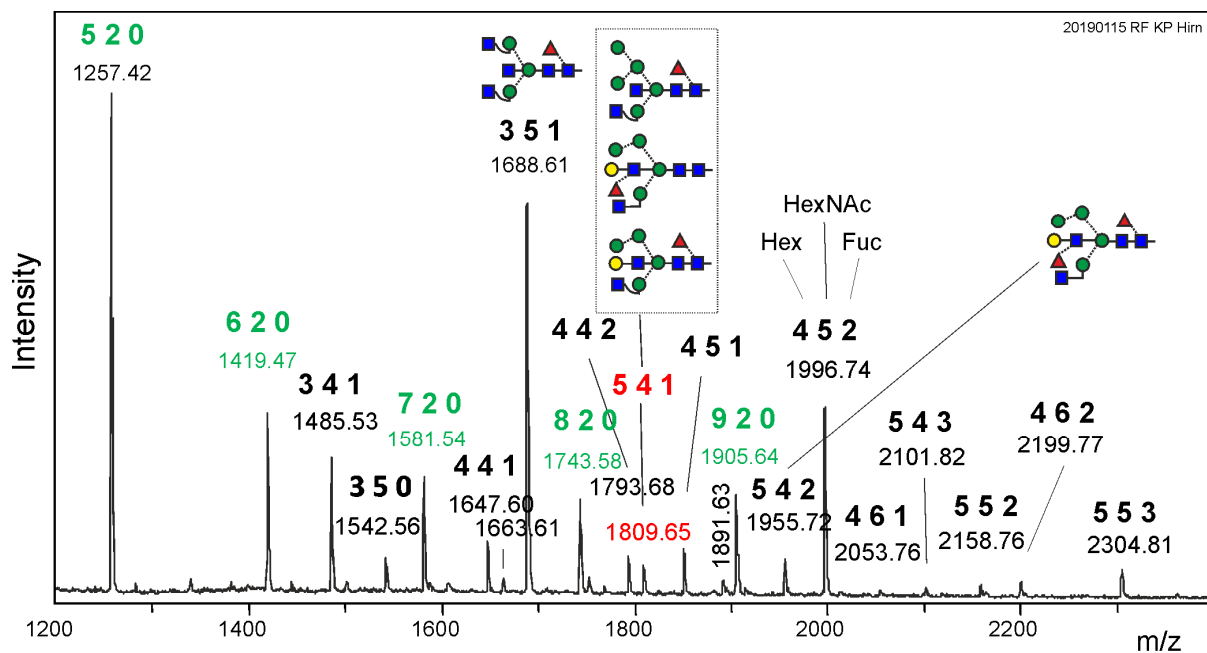


Figure S13 MALDI -TOF MS of neutral porcine brain N-glycans. Peaks are identified by the number of hexoses, N-acetylhexosamines and fucose residues, respectively. The peak for the composition 5 Hex, 4 HexNAcs and 1 Fuc is emphasized in red. Cartoons are drawn for selected major structures. Oligomannosidic glycans are annotated in green. Note that reflectron MALDI-TOF quenches the peak height with increasing analyte mass.

III. Exposition of the N-glycan nomenclature system “proglycan”

In brief: “Proglycan” lists the terminal tips of an N-glycan in counterclockwise manner. The 6-arm, then 3-arm, then core fucose and finally bisection are indicated. The **terminus terms** are given such that a minimal number of characters nevertheless results in complete and unambiguous definition of the structure.

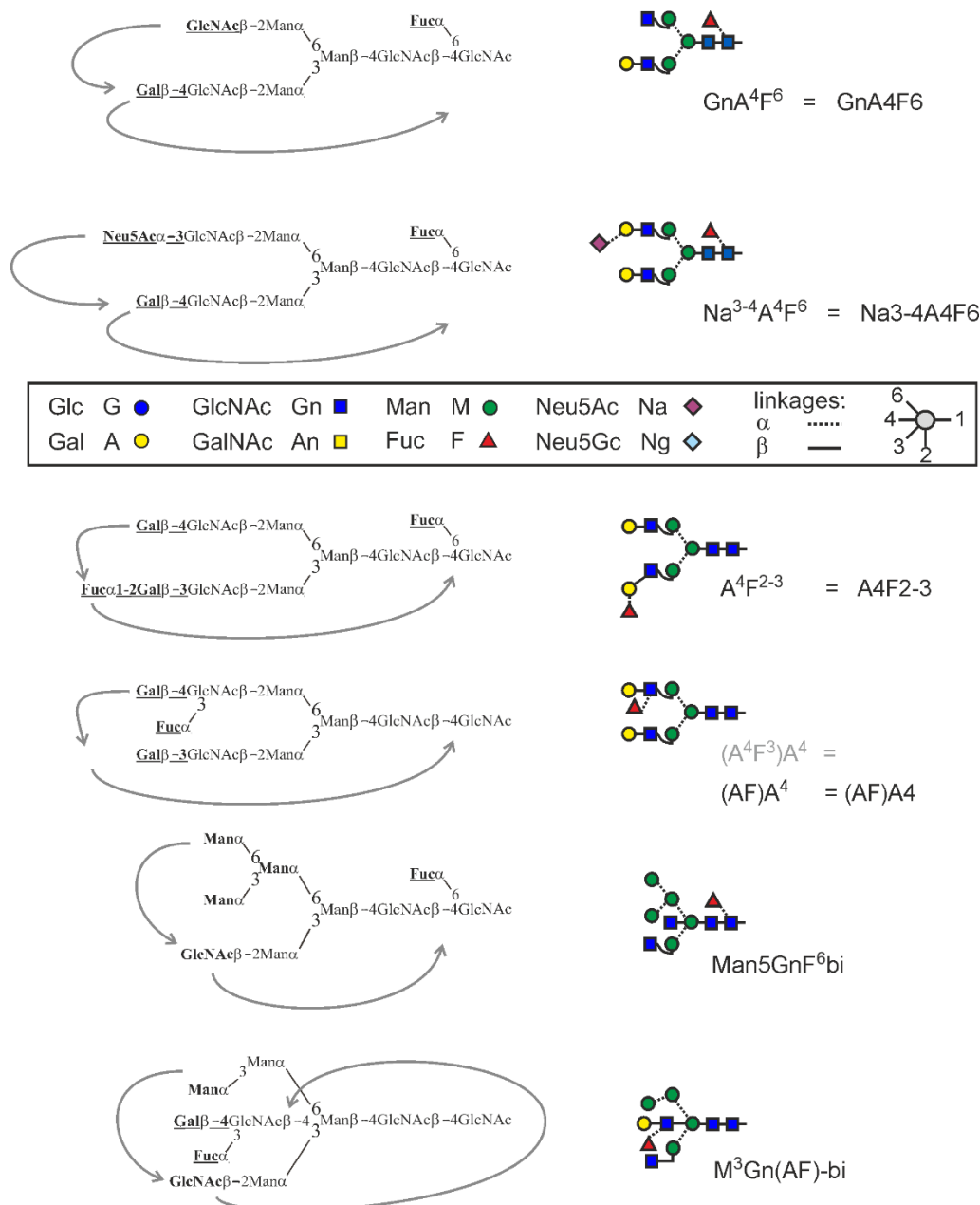


Figure S14 Outline of the Proglycan nomenclature

The system starts with the term GnGn for the simple diantennary glycan with two terminal GlcNAc residues as coined by Harry Schachter ⁹ and also used by others ¹⁰. Elongation of these antennae proceeds in a highly coordinated and defined manner. Thus, giving the very last residue of an antenna necessarily defines the following sequence. The residues are given by the one letter code, where A stands for galactose ¹¹. Modified monosaccharides such as N-acetylglucosamine are labelled by a second letter in small case, e.g. GlcNAc = Gn. In the case of sialic acids, Na and Ng stand for N-acetyl- or N-glycolylneuraminic acid, respectively.

The educated reader will immediately object that the situation is more complex as galactose is most often but not always found β 1,4-linked to GlcNAc and sialic acids may be linked to the 3 or the 6 position of galactose. These ambiguities are eliminated by superscripts. A⁴ stands for a Gal β 1-4GlcNAc β 1-2Man α 1-3 branch IF the **terminus term** A⁴ occupies the second position as in the figure below.

Sialic acid is usually linked to galactose: Na³-A⁴ could thus be written for the terminus of the 6-arm in the figure below. But we rather don't waste space for the self-evident. This **terminus term** Na³-A⁴ is written as Na^{3,4}. Fortunately, information is not lost together with formatting.

Fucosylation and bisecting GlcNAc are key issues of the current work. Core-fucosylation and bisection each have their own **terminus term** - F and bi.

The term F, however, is somewhat unclear in an environment dealing with insect and plant derived glycoproteins. Hence, it appears advisable to write F⁶ for full definition of a mammalian type N-glycan, while F³ denotes the core-1,3-fucose occurring in plants or insects.

Outer arm fucosylation occurs in three variants: the blood group H determinant Fuca1,2Gal, further Lewis A and Lewis X, where biosynthetic necessities always lead to branched structures. For the linear blood group H determinant, the IUPAC convention of connecting sugar by a line is adopted. Fuca(1-2)Gal β (1-3).... becomes F²-A³. It appears equally clear and catchier to just write F^{2,3}. For branched structures, brackets are used, however, such that both branching sugars are placed within the bracket. The antenna Gal β -4(Fuca-3)GlcNAc β ... becomes (A⁴F³) – the GlcNAc is self-evident. The linkage symbols are also self-evident so that a LeX determinant becomes (AF), whereas a LeA structure would be (FA).

The hyphen comes back in the admittedly very special case of substituted bisecting GlcNAc. The “bi” is then extend to A⁴-bi, or actually just A-bi as b3GalT does not act on the bisecting GlcNAc. Similarly, a LeX determinant is written as (AF)-bi to distinguish it from regular outer arm modifications.

We are fully aware that this system may appear unnecessary in the light of the numerous system used for decades ^{3, 12} or the highly sophisticated general annotation scheme for IT purposes ¹³. We nevertheless consider the Proglycan system the first and only one that condenses N-glycan structures into a – in most cases – handy and easy to understand short string,

List of possible terminus terms:in both first (6-arm) and second (3-arm) position:

Gn	a GlcNAc linked to the invariant pentasaccharide core
U	indicates no substituent of the β -mannose.
A	Galactose linked to GlcNAc, linkage not specified
A ⁴ / A4	Galactose β 1,4-linked to GlcNAc
A ³ / A3	Galactose β 1,3-linked to GlcNAc
(AF) / (A ⁴ F ³) / (A4F3) / Lx	Lewis X determinant
(FA) / (F ⁴ A ³) / (F4A3) / La	Lewis A determinant
F ²⁻³ / Lh ³	Blood group H determinant on type I chain
F ²⁻⁴ / Lh ⁴	Blood group H determinant on type II chain
Na	Sialic acid linked to Gal-GlcNAc, linkages not specified
Na ⁶⁻⁴ / Na6-4	Neu5Ac- α 2,6-Gal-1,4-GlcNAc-
Na ³⁻³ / Na3-3	Neu5Ac- α 2,3-Gal-1,3-GlcNAc-
(Na ⁶ Na ³⁻³)	Neu5Ac- α 2,6(Neu5Ac- α 2,3-Gal-1,3)-GlcNAc- (as in fetuin)

Possible in first (6-arm) position:

M	6-arm mannose of the invariant pentasaccharide core
M ³ / M3	a mannose in 3-linkage to 6-arm mannose of the core
M ⁶ / M6	a mannose in 6-linkage to 6-arm mannose of the core; rare
[GnGn]	GlcNAc- β 1,6-(GlcNAc- β 1,2-)Man
[A ⁴ A ⁴]	branched 6-arm with two Gal residues (in analogy to [GnGn])

Possible in second (3-arm) position:

M	3-arm mannose of the invariant pentasaccharide core
M ² / M2	a mannose in 2-linkage to the invariant pentasaccharide core
M ²⁻² / M2-2	two mannoses in series
[GnGn]	GlcNAc-b1,4-(GlcNAc-b1,2-)Man (in analogy to [GnGn])
[A ⁴ A ⁴]	branched 3-arm with two Gal residues (in analogy to [GnGn])

Possible in the extension positions: – if present; fucosylation before bisection

F ⁶ / F6	α 1,6-fucosylation of reducing end GlcNAc
F ³ / F3	α 1,3-fucosylation of reducing end GlcNAc
F ³ F ⁶ / F3F6	difucosylation of reducing end GlcNAc
X	β 1,2-xylosylation of the β -mannose (written before fucosylation)
bi	indicates presence of a bisecting GlcNAc
A-bi	bisecting LacNAc
(AF)-bi	bisecting Lewis X

Order of extension terms:

Xyl – substituents of reducing GlcNAc (3 before 6) – bisecting GlcNAc

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