

Supplementary Information for

Biological recognition of mirror-image glycans

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General Biological methods

Expression and purification of human lectins

Bacterial expression constructs were generated in pET-24a. Recombinant human galectin-1 (Gal-1) (UniProt P09382) and galectin-8 (Gal-8) (UniProt O00214) were synthesized and cloned by Twist Bioscience. Galectin-1 was cloned with a C-terminal His6 tag and AviTag, and galectin-8 was cloned with an N-terminal AviTag and a C-terminal His6 tag.

Mammalian expression constructs were generated in pcDNA3.1. Human MGL (CLEC10A construct lacking residues 1–119; UniProt J3KR22), MBL (MBL2; UniProt P11226), DN-SPD (surfactant protein D construct lacking residues 24–45; UniProt P35247), intelectin-1 (ITLN1; UniProt Q8WWA0) and REG4 (UniProt Q9BYZ8) were synthesized as described previously [bioRxiv 2026.02.23.707224; PMID 40421735] and cloned by Twist Bioscience with an N-terminal AviTag and His6 tag. CL-K1 (UniProt Q9BWP8) and CRP (UniProt P02741) were cloned identically, but with a C-terminal AviTag and His6 tag. All construct sequences were verified by Sanger sequencing (Quintara Biosciences).

Galectin-1 and galectin-8 were expressed in *E. coli* D3 cells from pET-24a vectors. In brief, liter-scale cultures were grown to mid-log phase ($OD_{600} = 0.3–0.5$), induced with 0.4 mM IPTG and incubated for 16 h at 18 °C. Cells were collected by centrifugation ($3000\times g$, 30 min), and pellets were stored at -20 °C until purification. Pellets were resuspended in Ni-NTA loading buffer (20 mM sodium phosphate, 500 mM NaCl, 20 mM imidazole, pH 7.4), lysed using B-PER II reagent (Thermo Fisher Scientific, 78260), and clarified by centrifugation ($24,000\times g$, 60 min).

MGL, MBL, SP-D, CL-K1, CRP, intelectin-1 (ITLN-1) and REG4 were expressed transiently in Expi293F cells using the ExpiFectamine™ 293 Transfection Kit (Thermo Fisher Scientific, A14524) according to the manufacturer's instructions. Conditioned medium was harvested 3–5 d after transfection by centrifugation and passed through a 0.2 μ m PES filter.

Filtered His₆-tagged proteins were loaded onto a Ni-NTA column (Cytiva), washed with loading buffer and eluted using a gradient to elution buffer (20 mM sodium phosphate, 500 mM NaCl, 500 mM imidazole, pH 7.4). Fractions were analyzed on stain-free tris-glycine gels. Purified galectins were dialyzed overnight at 4 °C into PBS containing 7 mM β -mercaptoethanol, and mammalian-expressed lectins were dialyzed overnight at 4 °C (20 mM HEPES, 150 mM NaCl and 1 mM EDTA, pH 7.4) using 10 kDa MWCO Slide-A-Lyzer dialysis cassettes (Thermo Fisher Scientific). Protein concentrations were determined by A280 using extinction coefficients and molecular weights calculated with ProtParam. Proper folding was confirmed by differential scanning fluorimetry or circular dichroism before use.

Protein biotinylation

AviTag-bearing lectins were biotinylated using an enzymatic BirA biotinylation kit (Avidity) according to the manufacturer's recommendations for 2 h at 30 °C. Biotinylated proteins were desalted using Zeba desalting spin columns (Thermo Fisher Scientific, 89882), and biotinylation was confirmed by streptavidin gel-shift. Biotinylated human Siglec-15 (SG5-H82E9) was obtained from ACROBiosystems.

Construction of mirror-LiGA

Construction and isolation of "silent" double-barcoded phages (SDB phage), conjugation of glycans to monoclonal SDB phages, and preparation of LiGA can be found in previous

publications^{1,2}. Phage glycosylated with mirror-image glycans were prepared by reacting clonal SDB phages ($\sim 10^{13}$ PFU ml⁻¹) with glycan-NHS ester in borate buffer (100 mM, pH 8.0) at room temperature for 1 h, followed by purification of glycophages using a Zeba column (Thermo Fisher Scientific, 89882). This conjugation process was repeated to allow glycan ultra-high density displaying. Resulting glycophages were analyzed using MALDI-TOF MS and stored in 1:1 (v/v) PBS:glycerol at -20°C . MALDI-TOF MS spectra of SDB phages modified with mirror-image glycans are shown in Supplementary Figs. S6-S7. Composition of the mirror-LiGA is listed in Supplementary Table S1.

Generation of fluorescently labeled glycophages for lectin microarray

Phages ($\sim 10^{13}$ PFU ml⁻¹) were labelled with TAMRA-NHS ester (0.2 mM, Lumiprobe, 17120) in borate buffer (100 mM, pH 8.0) for 3 h at room temperature and purified using Zeba desalting spin column. Fluorescent phages were then glycosylated by incubating with glycan-NHS esters in borate buffer, purified using Zeba desalting spin columns, and stored in 1:1 (v/v) PBS:glycerol at -20°C . MALDI-TOF MS spectra of TAMRA-labeled glycophages can be found in Supplementary Fig. S8.

Analyzing glycosylated phages using MALDI-TOF mass spectrometry

Chemical modifications on phages were analyzed by MALDI-TOF MS using an AB Sciex Voyager Elite MALDI mass spectrometer equipped with a MALDI-TOF pulsed nitrogen laser (337 nm; 3-ns pulse up to 300 μJ per pulse) operating in full-scan MS in positive ionization mode. For sample preparation, a matrix solution (0.7 μl , 10 mg ml⁻¹ sinapinic acid in 4:1, v/v, acetone:methanol) was spotted on a 100-spot MALDI target plate (stainless steel) and allowed to dry. Phage samples were prepared by mixing a phage solution (2 μl in water or PBS, avoiding high salt or glycerol) with a layer 2 matrix (4 μl , 10 mg ml⁻¹ sinapinic acid in 1:1, v/v, 0.1% TFA in water:acetonitrile). The phage-matrix mixture (2 μl) was then deposited onto the dried first matrix layer and allowed to dry. The dried phage sample spots were rinsed with 0.1% TFA in water (3 $\times$ 10 μl) prior to analysis.

Binding of mirror-LiGA to purified GBPs

A protein solution (50 μl , 50 μg ml⁻¹) prepared in HEPES-buffered saline solution (HBS; 20 mM HEPES, 150 mM NaCl, 2 mM CaCl₂, pH 7.4) was added to a high-binding 96-well plate (Corning, CLS3369). The plate was sealed with tape (Thermo Fisher Scientific, 15036) and incubated overnight at 4°C . The next day, wells were washed with HBS containing 0.1% (v/v) Tween-20 (HBST; 3 $\times$ 200 μl), blocked with HBS containing 1% (w/v) BSA (HBSB; 200 μl), and then washed with HBST (3 $\times$ 200 μl), after which a LiGA solution (50 μl , 10^8 PFU in HBS) was added and incubated at room temperature for 1 h. Wells were then washed with HBST (2 $\times$ 200 μl) and HBS solution alone (1 $\times$ 200 μl). Bound phages were eluted with acid (50 μl , 10 mM HCl, 9 min, room temperature) and neutralized with 5 $\times$ Phusion HF buffer (25 μl ; Thermo Fisher Scientific, F518L). Eluted phage samples were quantified by qPCR and submitted for deep sequencing. Detailed sequencing data can be found in Supplementary Table S2.

Binding of clonal fluorescent glycophages to lectin microarray

Glass slide printed with lectin microarray (manufactured in the Mahal laboratory at the University of Alberta) was thawed at room temperature and hydrated in ethanolamine/boric acid buffer (50 mM ethanolamine, 100 mM boric acid) for 1 h. The slide was sequentially washed with PBS containing 0.01% Tween-20 (PBST) and PBS, and dried on a slide spinner.

Fluorescent glycoprophages (50 μ l in PBS:glycerol solution) were mixed with binding buffer (50 μ l; PBST supplemented with 0.1 mM CaCl_2) and incubated with the lectin microarray at 30 $^\circ\text{C}$ for 1 h. Arrays were washed with PBST (2 $\times$ 150 μ l) and PBS (2 $\times$ 150 μ l), briefly dipped in deionized water, dried on a slide spinner, and scanned at 532 nm using a GenePix 4400A Microarray Scanner. Fluorescence values were extracted using GenePix Pro 7 software, and active binding was defined as background-subtracted fluorescence above 1,000 AU. Composition of the lectin microarray can be found in Supplementary Tables S3–4.

Inhibition of mirror-LiGA binding to purified DC-SIGN by free sugars

A protein solution (50 μ l, 50 $\mu\text{g ml}^{-1}$ in HBS) was added to a high-binding 96-well plate, sealed with tape, and incubated overnight at 4 $^\circ\text{C}$. The next day, wells were washed (HBST; 3 $\times$ 200 μ l), blocked (HBSB; 200 μ l), and washed (HBST; 3 $\times$ 200 μ l), after which a LiGA solution (50 μ l, 10^8 PFU in HBS containing 0–500 mM free glycans) was added and incubated at room temperature for 1 h. Wells were washed with HBST containing corresponding concentrations of soluble glycan (2 $\times$ 200 μ l) and HBS solution alone (1 $\times$ 200 μ l). Bound phages were eluted with acid (50 μ l, 10 mM HCl, 9 min, room temperature) and neutralized with 5 $\times$ Phusion HF buffer (25 μ l). Eluted phage samples were quantified by qPCR and submitted for deep sequencing. Detailed sequencing data can be found in Supplementary Table S2.

Inhibition of mirror-LiGA binding to DC-SIGN⁺ cells by free glycans

Stable transfected DC-SIGN⁺ Raji cells cultured in complete medium (RPMI-1640 basal medium supplemented with 10% Fetal Bovine Serum (FBS), 1% Penicillin/Streptomycin, and 1 $\times$ GlutaMAX) were harvested at confluence and aliquoted (1 $\times$ 10^6 cells) to FACS tubes (Corning, 352054). Cells were pelleted (300 $\times$ g, 5 min), resuspended in LiGA solution (100 μ l, 10^8 PFU in HBSB containing 0–500 mM free glycans), and incubated on ice for 1 h. Cells were then washed with HBS containing 0.1% BSA and corresponding concentrations of soluble glycan (2 $\times$ 3 ml), then washed with HBS solution alone (1 $\times$ 800 μ l). Cells were then pelleted (300 $\times$ g, 5 min, 4 $^\circ\text{C}$), resuspended in lysis buffer (1 $\times$ Phusion HF buffer containing 0.1 mg ml^{-1} RNase A, 50 μ l) and vortexed at maximum speed. The cell lysate was centrifuged (2,000 $\times$ g, 3 min), and the supernatant was treated with proteinase K (0.1 mg ml^{-1} , 55 $^\circ\text{C}$, 10 min) and heat-inactivated (95 $^\circ\text{C}$, 10 min). After pelleting cell debris (21,000 $\times$ g, 3 min), the supernatant containing bound phage DNA was collected and submitted for deep sequencing. Detailed sequencing data can be found in Supplementary Table S2.

Binding of mirror-LiGA to human PBMCs and isolated T cells

Cryopreserved peripheral blood mononuclear cells (PBMCs) and isolated human peripheral blood CD4⁺ and CD8⁺ T cells from healthy adult donors (STEMCELL Technologies, 70025.2, 70026, 70027) were thawed in pre-warmed complete medium consisting of RPMI supplemented with 10% FBS, 100 U ml^{-1} penicillin, 100 $\mu\text{g ml}^{-1}$ streptomycin, non-essential amino acids (Gibco, 11140-050) and 55 μM 2-mercaptoethanol and allowed to recover overnight at 37 $^\circ\text{C}$ under 5% CO_2 .

The next day, cells were treated with active or heat-inactivated sialidase (from *Vibrio cholerae*, 550 mU) for 45 min at 37 $^\circ\text{C}$. The heat-inactivated controls were prepared by incubating the enzyme at 60–65 $^\circ\text{C}$ for 30 min. Cells were then washed with FACS buffer (Ca^{2+} - and Mg^{2+} -free HBSS supplemented with 1% BSA and 2 mM EDTA) and pelleted (300 $\times$ g, 10 min).

For LiGA binding to pre-isolated CD4⁺ and CD8⁺ T cells, cells were resuspended in LiGA solution (100 μ l, 10⁸ PFU in HBSB) and incubated on ice for 1 h. Cells were then washed with HBS supplemented with 0.1% BSA (2 $\times$ 3 ml) and HBS solution alone (1 $\times$ 800 μ l). Cell-bound phage DNA was collected by following treatment as described in Inhibition of mirror-LiGA binding to cells by free glycans.

For LiGA binding and flow-cytometric sorting of bulk PBMCs, cells were first stained with Zombie Violet viability dye diluted 1:1500 in PBS (BioLegend, 423113) for 10 mins at room temperature. The viability dye was quenched by washing cells with FACS buffer. Cells were then incubated with Fc-receptor blocking solution diluted 1:250 in FACS buffer (BioLegend, 422302) for 10 mins on ice, followed by incubation with phenotyping antibodies and LiGA for 1 h on ice. Cells were washed with FACS buffer and then sorted into monocyte, B-cell, NK-cell, CD4⁺ T-cell, and CD8⁺ T-cell populations using a five-way sort on a BD FACSymphony S6 (Centre for Immune Analytics, University of Toronto). Phenotyping antibodies used were as follows: anti-CD14 (BioLegend, 367123), anti-CD19 (BioLegend, 302237), anti-CD56 (BioLegend, 318355), anti-CD3 (BioLegend, 570470), anti-CD4 (BioLegend, 344685), and anti-CD8 (BioLegend, 344739). After sorting, cell-bound phage DNA was collected by following RNase A-proteinase K treatment as described in Inhibition of mirror-LiGA binding to cells by free glycans. All collected DNA samples were submitted for deep sequencing. Detailed sequencing data can be found in Supplementary Table S2.

Binding of mirror-LiGA to human serum IgM repertoire

Goat anti-human IgM (50 μ l, 20 μ g ml⁻¹ in PBS; Jackson Immuno Research, 109-005-043) was added to a high-binding plate, sealed, and incubated at room temperature for 2 h. Wells were then washed with PBST (2 $\times$ 200 μ l), blocked with 1% BSA in PBS for 1 h, and washed with PBST (3 $\times$ 200 μ l). Human serum samples (50 μ l, 1:100 diluted in PBS; Lori J. West lab, University of Alberta) were added to the well plate, sealed, and incubated overnight at 4 °C. On the next day, wells were washed with PBST (2 $\times$ 200 μ l), then mirror-LiGA (50 μ l, 10⁸ PFU ml⁻¹ in PBS) was added and incubated at room temperature for 1.5 h. Wells were washed with PBST (3 $\times$ 200 μ l), then bound phages were eluted from wells with acid, neutralized with 5 $\times$ Phusion HF buffer, and submitted for deep sequencing. Detailed sequencing data can be found in Supplementary Table S2.

Mapping biodistribution of mirror-LiGA in live mice

All animal procedures were approved by the University of Alberta Animal Care committee in accordance with the Canadian Council on Animal Care guidelines (AUP00002467). Mice were maintained under pathogen-free conditions at the University of Alberta animal facility.

Mirror-LiGA (0.2 ml, 1 $\times$ 10¹¹ PFU ml⁻¹ in PBS) was injected into the tail vein of 10–12-week-old male C57BL/6J mice. After 20 min of circulation, blood (0.1 ml) was collected from the tail vein into heparin-coated tubes. Upon anesthetization, mice were perfused with PBS, then liver and spleen were collected and kept in ice-cold PBS on ice. Blood samples were centrifuged (300 $\times$ g, 5 min, 4 °C) to separate plasma and red blood cells (RBCs).

Organs were minced into ~2 mm pieces using a single-edge razor blade and transferred into a 40 μ m cell strainer (Fisher Scientific, 22-363-547) fitted onto a 50 ml Falcon tube. Tissues were homogenized by gently grinding with the plunger of a 3 ml syringe while rinsing with ice-cold PBS (5 ml). The resulting cell suspension was centrifuged (300 $\times$ g, 5 min, 4 °C), resuspended in

RBC Lysis Buffer (5 ml, 1:10; Invitrogen, 00-430-54), and incubated at room temperature for 5 min. Cells were washed with ice-cold PBS (20 ml), pelleted (300×g, 5 min, 4 °C), resuspended in FACS buffer (5 ml for liver and 1ml for spleen), and counted.

An aliquot of splenocytes (1×10^7 cells in FACS buffer) was stained with an antibody cocktail on ice for 1 h and sorted into B-cell and T-cell populations on a Sony MA900 (Flow Core, University of Alberta). The antibody cocktail consisted of anti-mouse CD3 (1:100; Invitrogen, 11-0032-80) and anti-mouse CD19 (1:100; Invitrogen, 17-0193-80).

Cell-bound phage DNA was collected from homogenized tissues, sorted splenic T and B cells, plasma, and RBCs by following RNase A-proteinase K treatment as described in Inhibition of mirror-LiGA binding to cells by free glycans and then submitted for deep sequencing. Detailed sequencing data can be found in Supplementary Table S2.

Data analysis and statistics

Sequencing data were processed as previously described². Read counts were assigned to individual silent double-barcoded (SDB) phage clones according to their DNA barcode sequences. To account for differences in sequencing depth and sample recovery, a defined set of unmodified SDB phages (blanks) was spiked into the tested mirror-LiGA prior to any glycan-binding measurements and was used as internal standards. Sample-specific normalization factors were calculated from the internal-standard read counts using the relative log expression (RLE) method implemented in edgeR³. These normalization factors were then applied to the complete library, and normalized abundances were expressed as counts per million (CPM).

For each experimental comparison, normalized glycoprobe abundances in the test samples were compared with those in the designated reference samples (typically the naïve/input LiGA library) using edgeR³. Read counts were modeled using negative-binomial generalized linear models. Dispersion was estimated with robust estimation, and differential abundance was evaluated using the edgeR quasi-likelihood framework (glmQLFit and glmQLFTest). Low-abundance barcodes were identified using filterByExpr and were excluded from interpretation of statistical significance.

Enrichment was expressed as fold change (FC) relative to the reference condition. edgeR reports the difference between test and reference conditions as log₂ fold change (log₂FC), and linear fold change was calculated as $FC = 2^{\log_2 FC}$. Thus, $FC = 1$ indicates no change relative to the reference, $FC > 1$ indicates enrichment, and $FC < 1$ indicates depletion. Where multiple SDB phage clones encoded the same glycan structure and display density, each SDB was analyzed independently by edgeR; for glycan-level graphical summaries, the median log₂FC across the corresponding SDBs was used and converted to linear FC.

Statistical significance was determined from the quasi-likelihood F-test. P values were adjusted for multiple comparisons using the Benjamini–Hochberg procedure to control the false discovery rate (FDR). For graphical summaries in which multiple SDBs encoded the same glycan and display density, the median FDR of the corresponding SDBs was used. $FDR < 0.05$ is denoted by an asterisk, whereas $0.05 \leq FDR < 0.25$ is denoted by a dot.

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reduced pressure. The residue was diluted with water and extracted with DCM. The combined organic layers were washed with 1N HCl (aq) and brine, dried over Na₂SO₄, filtered, and concentrated under reduced pressure to give compound **S1** (0.43 g, 99%) as a mixture of α/β pyranose anomers (3:1). The product was used for the next step without further purification. ¹H NMR (400 MHz, CDCl₃): δ 6.05 (d, J = 1.9 Hz, 1H, H-1 α), 5.35–5.31 (m, 2H, H-3 α , H-4 α), 5.26–5.22 (m, 1H, H-2 α), 4.30–4.23 (m, 1H, H-6' α), 4.13–4.00 (m, 2H, H-6, H-5), 2.19 (s, 3H, COCH₃), 2.15 (s, 3H, COCH₃), 2.06 (s, 3H, COCH₃), 2.02 (s, 3H, COCH₃), 1.98 (s, 3H, COCH₃) ppm.

Phenyl 2,3,4,6-tetra-*O*-acetyl-1-thio-L-mannopyranoside (**S2**)

To a solution of compound **S1** (0.43 g, 1.10 mmol) in DCM (5.5 ml) was added a solution of thiophenol (PhSH, 0.17 ml, 1.66 mmol) in DCM (5.5 ml) via syringe. The reaction mixture was cooled in an ice bath, and BF₃·OEt₂ (0.42 mL, 3.33 mmol) was added dropwise. The ice bath was then removed, and the reaction mixture was stirred at room temperature for 16 h. The reaction mixture was then diluted with water and extracted with DCM. The combined organic layers were washed with saturated aqueous NaHCO₃ solution and brine, dried over Na₂SO₄ and concentrated under reduced pressure. The residue was purified by column chromatography (EtOAc/hexanes = 1:2 to 1:1) to afford compound **S2** (0.32 g, 49%) as a mixture of α/β pyranose anomers (10:1). ¹H NMR (400 MHz, CDCl₃) δ 7.48–7.45 (m, 2H, H-arom.), 7.32–7.27 (m, 3H, H-arom.), 5.48–5.47 (m, 2H, H-1, H-2), 5.32–5.28 (m, 2H, H-3, H-4), 4.54–4.50 (m, 1H, H-5), 4.28 (dd, J = 12.2, 5.9 Hz, 1H, H-6), 4.08 (dd, J = 12.2, 2.4 Hz, 1H, H-6'), 2.13 (s, 3H, COCH₃), 2.05 (s, 3H, COCH₃), 2.03 (s, 3H, COCH₃), 2.00 (s, 3H, COCH₃).

5-Chloropentyl 2,3,4,6-tetra-*O*-acetyl- α -L-mannopyranosyl-(1 $\rightarrow$ 2)-3,4,6-tri-*O*-acetyl- α -L-mannopyranoside (**S3**)

To a solution of Compound **S2** (0.1 g, 0.23 mmol, 1.0 equiv.) and 1-chloropentanol (28.4 μ l, 0.24 mmol, 1.05 equiv.) in DCM (1.2 ml) were stirred at room temperature in the presence of 4 Å MS (0.1 g) for 30 min. After cooling to -15 °C, N-iodosuccinimide (63.1 mg, 0.28 mmol, 1.2 equiv.) and trifluoromethanesulfonic acid (4.1 μ l, 0.05 mmol, 0.2 equiv) were slowly added and stirring continued at -15 °C for 1 h. The reaction mixture was allowed to warm to room temperature and then acetic anhydride (55 μ l, 2.5 equiv.) added. After 30 min, the molecular sieves were filtered through cotton and then washed with EtOAc. The filtrate was diluted with H₂O, extracted with EtOAc and washed with ice-cold 10% Na₂S₂O₅ (aq) and brine, the organic layer was dried over Na₂SO₄, filtered, and concentrated under reduced pressure. The crude product was purified by column chromatography (EtOAc/hexane = 1:3 to 1:1) to give compound **S3** (50.4 mg, 29%). ¹H NMR (400 MHz, CDCl₃) δ 5.36 (dd, J = 10.0, 3.4 Hz, 1H, H-3'), 5.30–5.20 (m, 4H, H-4, H-3, H-2', H-4'), 4.88 (br s, 2H, H-1, H-1'), 4.21–4.05 (m, 5H, H-5, H-6a,b, H-6a',b'), 3.98–3.97 (m, 1H, H-2), 3.88–3.85 (m, 1H, H-5'), 3.67 (td, J = 8.0, 6.3 Hz, 1H, H-1b''), 3.51 (t, J = 6.6 Hz, 2H, H-5''), 3.41 (td, J = 8.0, 6.2 Hz, 1H, H-1a''), 2.10, 2.09, 2.04, 2.03, 2.00, 1.99, 1.96 (7 s, 21H, 7 $\times$ COCH₃), 1.79–1.72 (m, 2H, H-4''), 1.62–1.56 (m, 2H, H-2''), 1.50–1.45 (m, 2H, H-3'').

5-Azidopentyl 2,3,4,6-tetra-*O*-acetyl- α -L-mannopyranosyl-(1 $\rightarrow$ 2)-3,4,6-tri-*O*-acetyl- α -L-mannopyranoside (**S4**)

To a solution of compound **S3** (50.4 mg, 0.07 mmol) in anhydrous DMF (1.0 ml) was added sodium azide (6.8 mg, 0.11 mmol). The reaction mixture was stirred under an argon atmosphere at 80 °C for 16 h. After cooling to room temperature, the reaction mixture was diluted with water and extracted with Ethyl ether. The combined organic layers were washed with water and brine, dried over Na₂SO₄, filtered, and concentrated under reduced pressure to give compound **S4** (47.5 mg, 93%). The product was used for the next step without further purification. ¹H NMR (400 MHz,

CDCl₃) δ 5.36 (dd, J = 10.0, 3.4 Hz, 1H, H-3'), 5.31-5.21 (m, 4H, H-4, H-3, H-2', H-4'), 4.88 (br s, 2H, H-1, H-1'), 4.20-4.06 (m, 5H, H-5, H-6a,b, H-6a',b'), 3.98-3.97 (m, 1H, H-2), 3.88-3.84 (m, 1H, H-5'), 3.67 (td, J = 8.1, 6.4 Hz, 1H, H-1b''), 3.40 (td, J = 8.0, 6.3 Hz, 1H, H-1a''), 3.25 (t, J = 6.7 Hz, 2H, H-5''), 2.11, 2.09, 2.04, 2.00, 1.99, 1.96 (6 s, 21H, 7 $\times$ COCH₃), 1.62-1.55 (m, 4H, H-4'', H-2''), 1.44-1.38 (m, 2H, H-3'').

5-Azidopentyl α -L-mannopyranosyl-(1 $\rightarrow$ 2)- α -L-mannopyranoside (S5)

To a solution of compound **S4** (47.5 mg, 0.06 mmol) in anhydrous MeOH (0.6 ml) at 0 °C was added NaOMe in MeOH (0.5 M, 25.4 μ l, 0.01 mmol). The reaction mixture was stirred at 0 °C until completion. The reaction was neutralized with 1 N HCl (aq), and the solvent was removed under reduced pressure. The resulting crude was dissolved in water and acetonitrile, followed by centrifugation, and purified by semi-preparative HPLC using an Agilent 1200 or 1260 Infinity system equipped with a Zorbax C8 column (Zorbax Rx, 9.4 mm $\times$ 250 mm). Solvent A was H₂O, and solvent B was ACN. The purification was performed at a flow rate of 3 ml min⁻¹ with a gradient of 5–90% B over 30 min. The product-containing fractions were collected and lyophilized to give compound **S5** (21.0 mg, 73%). [α]_D²⁵ = -50.1 (c 0.38, CD₃OD). IR (ATR) ν _{max} 3406, 2930, 2866, 2099, 1457, 1132, 1061, 1030 cm⁻¹. ¹H NMR (400 MHz, CD₃OD) δ ppm 5.00 (s, 1H, H-1), 4.91 (d, J = 1.64 Hz, 1H, H-1'), 3.92 (dd, J = 3.2, 1.8 Hz, 1H, H-2'), 3.81-3.79 (m, 1H, H-2), 3.78–3.74 (m, 3H, H-6a',b', H-3), 3.70-3.59 (m, 5H, H-3', H-5', H-6a, H-1''), 3.55-3.37 (m, 4H, H-6b, H-4, H-4', H-5), 3.26-3.23 (m, 2H, H-5''), 1.61-1.53 (m, 4H, H-2'', H-4''), 1.45-1.39 (m, 2H, H-3''); ¹³C NMR (400 MHz, CD₃OD) δ ppm 104.17, 99.90, 80.66, 74.98, 74.64, 72.41, 72.19, 71.85, 69.04, 68.82, 68.37, 63.13, 63.05, 52.36, 30.10, 29.67, 24.56; HRMS (ESI) m/z : [M + H]⁺ calcd for C₁₇H₃₁N₃O₁₁ 454.2031, found 454.2023.

5-[4-(2-Carboxyethyl)-1H-1,2,3-triazol-1-yl]pentyl α -L-mannopyranosyl-(1 $\rightarrow$ 2)- α -L-mannopyranoside (S6)

To a solution of compound **S5** (3.4 mg, 7.50 μ mol) and 4-pentynoic acid (0.9 mg, 6.3 μ mol) in H₂O (1.4 ml) was added a premixed solution containing CuSO₄ (aq) (0.1 equiv., 40 mM), tris(triazolyl)amine ligand **S7** (0.1 equiv., 40 mM in DMSO), and sodium ascorbate (aq) (2.0 equiv., 800 mM). The reaction mixture was stirred at room temperature for 1 h. The resulting crude was dissolved in water and acetonitrile, followed by centrifugation, and purified by semi-preparative HPLC using an Agilent 1200 or 1260 Infinity system equipped with a Zorbax C8 column (Zorbax Rx, 9.4 mm $\times$ 250 mm). Solvent A was H₂O, and solvent B was ACN. The purification was performed at a flow rate of 3 ml min⁻¹ with a gradient of 5–90% B over 50 min. The product-containing fractions were collected and lyophilized to give compound **S6** (4.1 mg, 99%). [α]_D²⁵ = -34.3 (c 0.19, D₂O). IR (ATR) ν _{max} 3377, 3099, 2937, 1682, 1557, 1417, 1204, 1131, 1060, 1031 cm⁻¹. ¹H NMR (400 MHz, D₂O) δ ppm 7.84 (s, 1H, =CH), 5.08 (s, 1H, H-1), 5.03 (d, J = 1.04 Hz, 1H, H-1'), 4.42 (t, 2H, J = 6.74 Hz, H-5''), 4.09-4.08 (m, 1H, H-2'), 3.92-3.49 (m, 13H, H-2, H-6a',b', H-3, H-3', H-5', H-6a, H-1'', H-6b, H-4, H-4', H-5), 3.03 (t, 2H, J = 7.10 Hz, H-1'''), 2.77 (t, 2H, J = 7.10 Hz, H-2'''), 1.96-1.89 (m, 2H, H-4''), 1.65-1.57 (m, 2H, H-2''), 1.37-1.27 (m, 2H, H-3''); ¹³C NMR (400 MHz, D₂O) δ ppm 102.36, 98.12, 78.76, 73.29, 72.78, 70.34, 69.97, 67.58, 66.98, 66.94, 61.15, 60.93, 50.30, 28.99, 27.79, 22.31, 20.38; HRMS (ESI) m/z : [M + H]⁺ calcd for C₂₂H₃₇N₃O₁₃ 552.2399, found 552.2365.

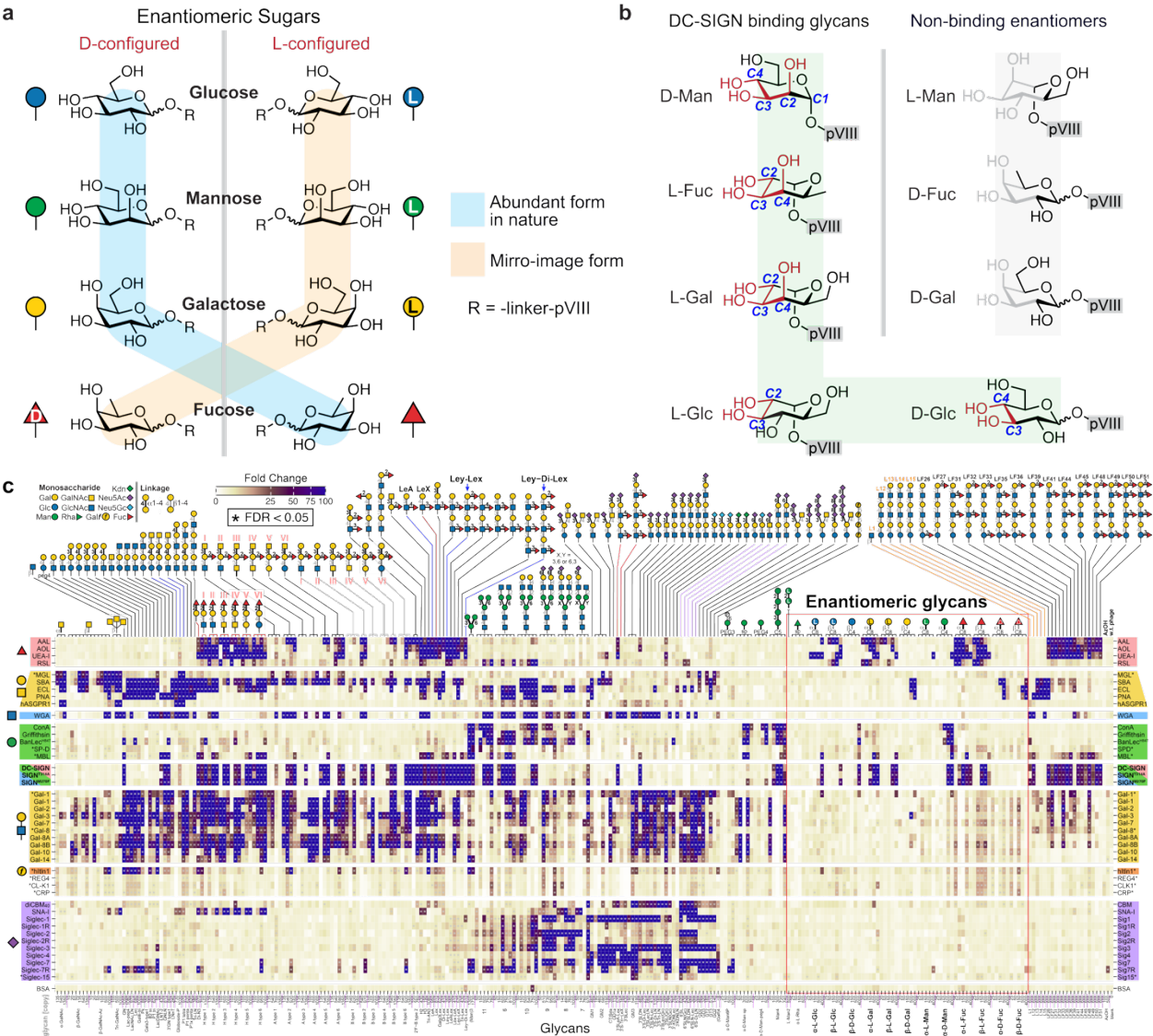


Fig. S1: Recognition of enantiomeric glycans by diverse glycan-binding proteins.

a, Structure of tested enantiomeric sugars in mirror-LiGA. **b**, Oriented DC-SIGN binding glycans and their enantiomers. Both D- and L-Glc showed binding to DC-SIGN at displaying density 4,000 glycans per virion. **c**, Binding profiles of purified glycan-binding proteins (GBPs) against the LiGA comprising canonical glycans and enantiomeric glycans displayed at multiple densities. The panel includes 37 unique lectins, five point-mutant Siglecs in which the conserved arginine in the carbohydrate-binding pocket was substituted with alanine to disrupt sialoglycan binding, and two point-mutant DC-SIGN variants (T314A and M270F) with increased and decreased binding, respectively, to canonical DC-SIGN ligands relative to wild-type DC-SIGN. Fold change (FC), defined as the enrichment of each glycopage after lectin binding relative to its abundance in the input LiGA library, is indicated by the color scale. Asterisks denote statistically significant enrichment at a false discovery rate (FDR) < 0.05. $n = 4$ for each tested protein.

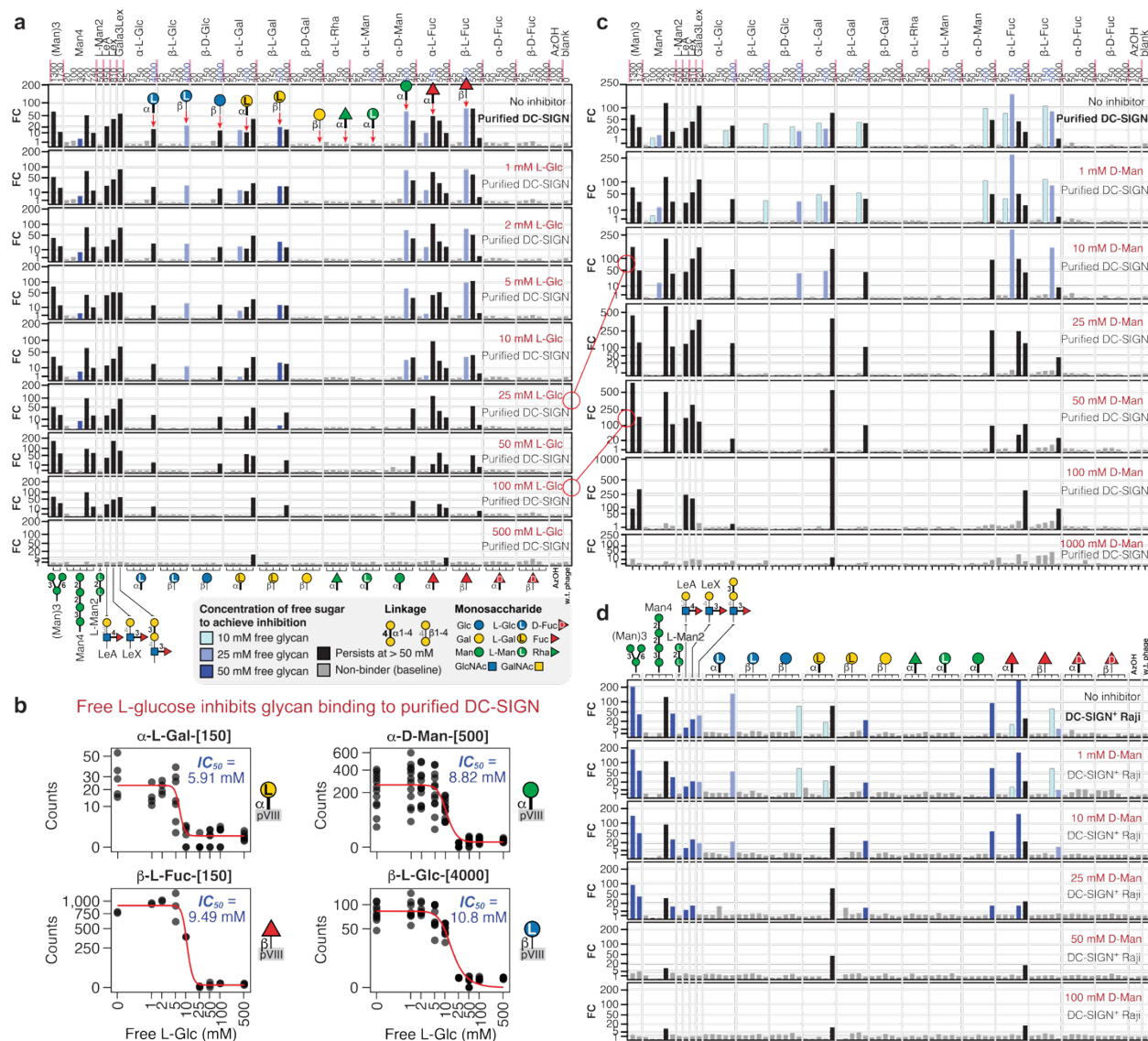


Fig. S3. Inhibition of DC-SIGN glycan binding by free L-glucose and D-mannose.

a, Inhibition of binding of LiGA to purified DC-SIGN extracellular domain (ECD) by increasing concentrations of free L-glucose (L-Glc). Fold-change (FC) values are shown for individual glycoproteins at each inhibitor concentration; $n = 3$. Glycans are grouped by structure and linkage, and the color scale indicates the free-glycan concentration required to reduce binding. **b**, Representative inhibition curves derived from sequencing read counts of selected glycoproteins incubated with purified DC-SIGN ECD in the presence of increasing concentrations of free L-Glc. Red curves show fitted inhibition profiles, and the corresponding IC_{50} values are indicated. **c**, Inhibition of binding of LiGA to purified DC-SIGN ECD by increasing concentrations of free D-mannose (D-Man); $n = 3$. **d**, Inhibition of binding of LiGA to DC-SIGN⁺ Raji cells by increasing concentrations of free D-Man. FC values are shown for individual glycoproteins at each inhibitor concentration.

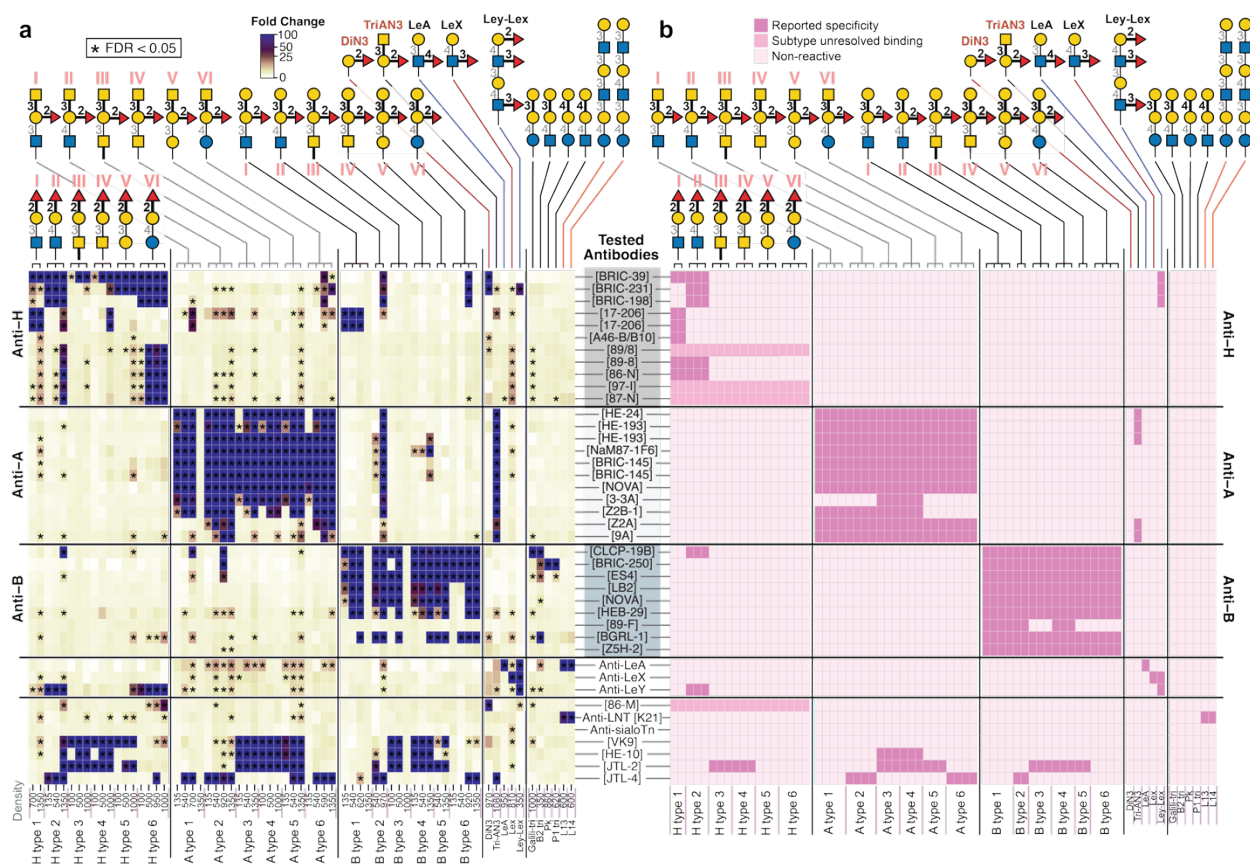


Fig. S4. Comparison of glycan-binding specificities of tested antibodies.

a, Glycan-binding profiles of anti-carbohydrate antibodies measured by LiGA. Antibodies were grouped based on reported specificities. Fold change (FC), defined as the enrichment of each glycoprotein after lectin binding relative to its abundance in the input LiGA library, is indicated by the color scale. $n = 4$ for each antibody. **b**, Semi-qualitative assessment data adapted from previous publications or provided from were converted to a heat-map representation. Reported specificity measured by ELISA¹²: A46-B/B10 (anti-HBGA), Z2B-1 (anti-HBGA), 89-F (anti-HBGB), JTL-2, and JTL-4. Reported specificity measured by neoglycoprotein glycan microarray^{13,14}: HE-10, HE-24 (anti-HBGA), HE-193 (anti-HBGA), Z2A (anti-HBGA), 9A (anti-HBGA), CLCP-19B (anti-HBGB), 7LE (anti-Lewis A), and F3 (anti-Lewis Y). Reported specificity measured by multiplex bead immunoassay (Luminex)¹⁵: Nova anti-A, Nova anti-B, JTL-2, and JTL-4. Specificity of all other antibodies were cited from suppliers. We did notice that reported specificity varies between assays. For example, HE-10 was previously reported to bind H type 3/4/5, A type 3/4/5, and B type 3/4/5¹⁶, whereas Gildersleeve and coworkers observed binding of HE-10 to A type 3/4, with no detectable binding to A type 5, B type 5, and H type 3/4/5¹³. Similarly, JTL-2 was reported to bind A/B type 3/4 and JTL-4 to bind A/B type 2 by ELISA¹², whereas multiplex bead immunoassays revealed additional binding of JTL-2 to A/B type 5 and of JTL-4 to A type 6¹⁵.

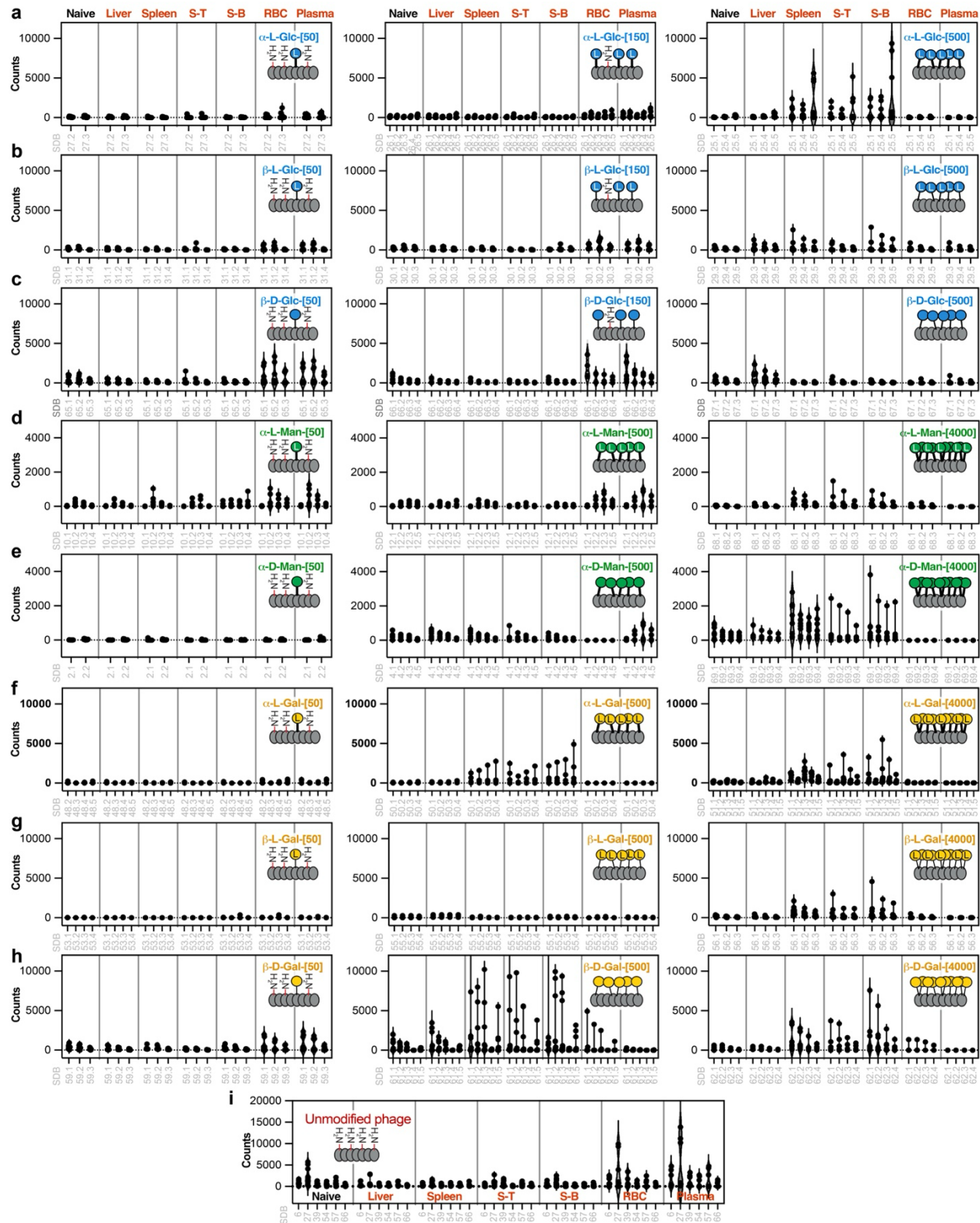


Fig. S5. Biodistribution of phages displaying enantiomeric glycans.

a to h, Illumina sequencing read counts of DNA barcodes corresponding to phages displaying α -L-glucose **a**, β -L-glucose **b**, β -D-glucose **c**, α -L-mannose **d**, α -D-mannose **e**, α -L-galactose **f**, β -L-galactose **g**, or β -D-galactose **h**, at the indicated glycan densities following LiGA injection and circulation in mice. For each glycan, phages displaying low, medium, and high glycan densities are shown from left to right; the number of glycan copies per phage virion is indicated in brackets (e.g., [50], [150], and [500]). Count, or read count, denotes the number of Illumina sequencing reads containing a particular phage DNA barcode. Counts are shown for the naïve input LiGA and for phages recovered from liver, spleen, FACS-sorted splenic T cells (S-T), FACS-sorted splenic B cells (S-B), red blood cells (RBC), and plasma. **i**, Read counts of unmodified phage controls recovered from the same compartments. Two to five silent double-barcoded (SDB) phage clones encoding each glycan-density combination were included to mitigate potential barcode-dependent PCR amplification bias. Naïve, input LiGA library injected into each mouse; S-T, FACS-sorted splenic T cells; S-B, FACS-sorted splenic B cells; RBC, red blood cells; $n = 11$.

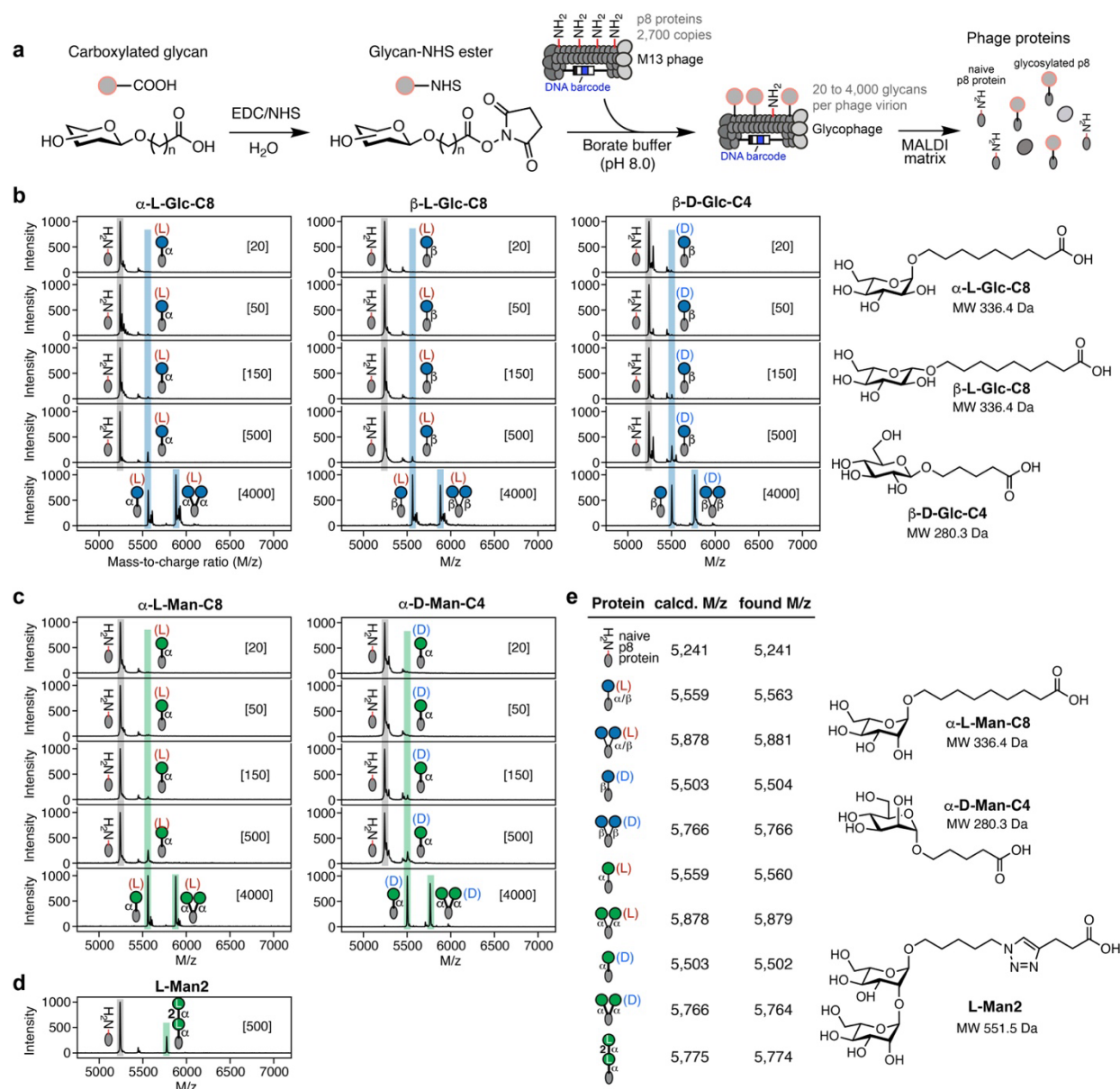


Fig. S6. MALDI-TOF MS of clonal phages displaying enantiomeric glucose (Glc), mannose (Man), and α -1,2-L-mannobiose (L-Man2).

a, Schematic of producing silent-barcoded glycophages by EDC/NHS-mediated coupling and MALDI-TOF MS analysis. Two amino groups can be glycosylated per pVIII (p8) protein: N-terminal amino group on Ala1 and ϵ -amino group on Lys8. The distance between nearest glycans displayed on phage has been shown in Fig. 1d. **b**, MALDI-TOF mass spectra of phages displaying enantiomeric Glc at the indicated glycan densities. **c**, MALDI-TOF mass spectra of phages displaying enantiomeric Man at the indicated glycan densities. **d**, MALDI-TOF mass spectrum of phage displaying L-Man2. Numbers in brackets indicate the calculated number of glycan copies per phage virion from the Numbers in brackets indicate the calculated number of glycan copies per phage virion and was estimated from the relative MALDI peak heights of pVIII species. **e**, Calculated and observed m/z values for unmodified and glycosylated pVIII species.



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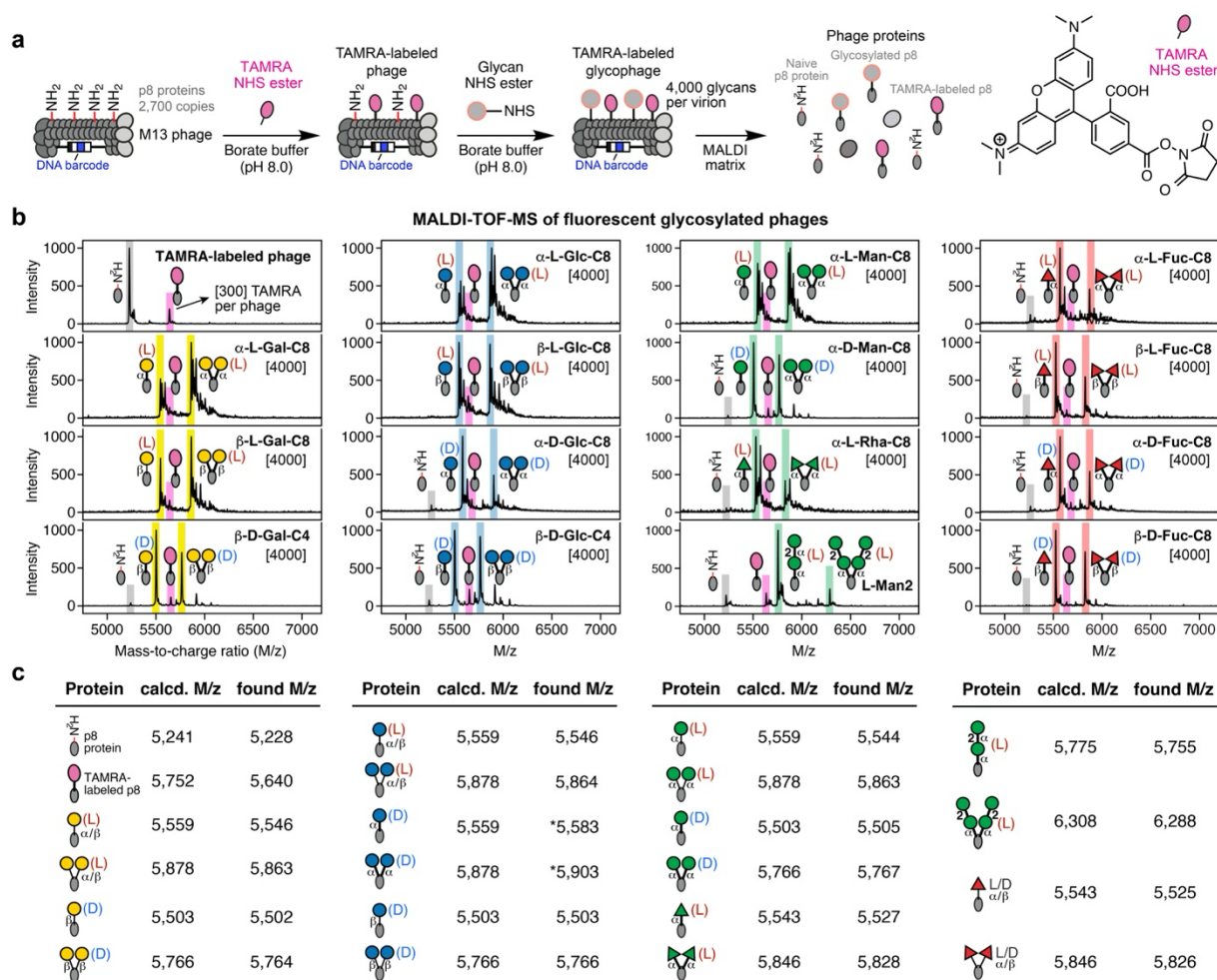


Fig. S8. MALDI-TOF MS analysis of fluorescently labeled clonal glycopheages.

a, Schematic of producing fluorescent glycopheages. A large batch of clonal M13 phage was labeled with TAMRA-NHS ester, purified by PEG precipitation, and aliquoted for subsequent conjugation with different glycans. **b**, MALDI-TOF mass spectra of TAMRA-labeled phages displaying the indicated glycans at high display density. Numbers in brackets indicate the calculated number of TAMRA or glycan copies per phage virion. Glycan display density was estimated from the relative MALDI-TOF MS peak heights of pVIII species, weighted by the number of glycans conjugated to each pVIII species, and multiplied by 2,700 pVIII copies per virion. **c**, Calculated and observed m/z values for unmodified, TAMRA-labeled, and glycosylated pVIII species. Asterisks indicate species with an approximately +16-Da offset from the calculated m/z.

Common name	Displaying density (# of glycans per phage)	Chemical structure
a-GalNAc	[135], [540], [1350]	GalNAc(α -O-butyl-COOH
b-GalNAcAz	[10], [20], [50], [100], [500], [1000]	GalNAc(β -P3
b-GalNAc	[10], [20], [50], [100], [500], [1000]	GalNAc(β -O-PEG3-COOH
Tri-GalNAc	[100], [500], [1000]	(β -D-GalNAc-sp)3-NHCO-PEG5-COOH
GN	[1050]	GlcNAc(β -Sp
Lac-peg4	[1080]	Gal β 1-4Glc(β -P4
LacNAc, LN	[970]	Gal β 1-4GlcNAc(β -Sp
Lec	[680]	Gal β 1-3GlcNAc(β -Sp
Galili-tri	[1000]	Gala1-3Gal β 1-4Glc(β -Sp
Pk	[860]	Gala1-4Gal β 1-4Glc(β -Sp
Gala3-type1	[350]	Gala1-3Gal β 1-3GlcNAc(β -Sp
B2 tri	[350]	Gala1-3Gal β 1-4GlcNAc(β -Sp
P1 tri	[620]	Gala1-4Gal β 1-4GlcNAc(β -Sp
LacDiNAc	[50]	GalNAc β 1-4GlcNAc(β -Sp
LNT-2	[430]	GlcNAc β 1-3Gal β 1-4Glc(β -Sp
GNLN	[810]	GlcNAc β 1-3Gal β 1-4GlcNAc(β -Sp
3'GN type1	[860]	GlcNAc β 1-3Gal β 1-3GlcNAc(β -Sp
LNnT	[240]	Gal β 1-4GlcNAc β 1-3Gal β 1-4Glc(β -Sp
Globoside-P	[730], [1030]	GalNAc β 1-3Gala1-4Gal β 1-4Glc(β -Sp
P1 tetra	[970]	GalNAc β 1-3Gala1-4Gal β 1-4GlcNAc(β -Sp
P1 penta	[620]	Gala1-4Gal β 1-4GlcNAc β 1-3Gal β 1-4Glc(β -Sp
P1x penta	[620]	Gal β 1-3GalNAc β 1-3Gala1-4Gal β 1-4GlcNAc(β -Sp
Tri-LN	[380]	Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β 1-3(β -Sp
Di-N3	[970]	Fuca1-2Gal(β -Sp
H type 1	[700]	Fuca1-2Gal β 1-3GlcNAc(β -Sp
H type 1	[135], [1350]	Fuca1-2Gal β 1-3GlcNAc(β -X-COOH
H type 2	[540]	Fuca1-2Gal β 1-4GlcNAc(β -Sp
H type 2	[135], [540], [1350]	Fuca1-2Gal β 1-4GlcNAc(β -X-COOH
H type 3	[100], [500], [1000]	Fuca1-2Gal β 1-3GalNAc(α -X-COOH
H type 4	[100], [500], [1000]	Fuca1-2Gal β 1-3GalNAc(β -X-COOH
H type 5	[100], [500], [1000]	Fuca1-2Gal β 1-3Gal(β -X-COOH
2'FL	[950]	Fuca1-2Gal β 1-4Glc(β -Sp
H type 6	[100], [500], [1000]	Fuca1-2Gal β 1-4Glc(β -X-COOH
A tetra type 1	[700]	GalNAca1-3[Fuca1-2]Gal β 1-3GlcNAc(β -Sp
A type 1	[135], [540], [1350]	GalNAca1-3[Fuca1-2]Gal β 1-3GlcNAc(β -X-COOH
A tetra type 2	[920]	GalNAca1-3[Fuca1-2]Gal β 1-4GlcNAc(β -Sp
A type 2	[135], [540], [1350]	GalNAca1-3[Fuca1-2]Gal β 1-4GlcNAc(β -X-COOH
A type 3	[135], [540], [1350]	GalNAca1-3[Fuca1-2]Gal β 1-3GalNAc(α -X-COOH
A type 4	[100], [500], [1000]	GalNAca1-3[Fuca1-2]Gal β 1-3GalNAc(β -X-COOH
A type 5	[135], [540], [1350]	GalNAca1-3[Fuca1-2]Gal β 1-4Gal(β -X-COOH
A tetra type 6	[590]	GalNAca1-3[Fuca1-2]Gal β 1-4Glc(β -Sp
A type 6	[135], [540], [1350]	GalNAca1-3[Fuca1-2]Gal β 1-4Glc(β -X-COOH
B tetra type 1	[620]	Gala1-3[Fuca1-2]Gal β 1-3GlcNAc(β -Sp
B type 1	[135], [540], [1350]	Gala1-3[Fuca1-2]Gal β 1-3GlcNAc(β -X-COOH
B tetra type 2	[970]	Gala1-3[Fuca1-2]Gal β 1-4GlcNAc(β -Sp
B type 2	[540]	Gala1-3[Fuca1-2]Gal β 1-4GlcNAc(β -X-COOH
B type 3	[100], [500], [1000]	Gala1-3[Fuca1-2]Gal β 1-3GalNAc(α -X-COOH
B type 4	[135], [540], [1350]	Gala1-3[Fuca1-2]Gal β 1-3GalNAc(β -X-COOH
B type 5	[540], [1350]	Gala1-3[Fuca1-2]Gal β 1-3Gal(β -X-COOH

B tetra type 6	[920]	Gala1-3[Fuca1-2]Galβ1-4Glc(β-Sp
B type 6	[135], [540], [1350]	Gala1-3[Fuca1-2]Galβ1-4Glc(β-X-COOH
2'F-B type 2	[220], [760]	Gala1-3[Fuca1-2]Galβ1-4[Fuca1-3]GlcNAc(β-Sp
H2	[430]	Fuca1-2Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAc(β-Sp
H3	[190]	Fuca1-2Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ1-3 Galβ1-4GlcNAc(β-Sp
Tri-AN3	[1080]	GalNAca1-3[Fuca1-2]Gal(β-Sp
LeA	[950]	Galβ1-3[Fuca1-4]GlcNAc(β-Sp
Lex	[810]	Galβ1-4[Fuca1-3]GlcNAc(β-Sp
Gala3Lex	[620]	Gala1-3Galβ1-4[Fuca1-3]GlcNAc(β-Sp
Di-Lex	[410]	Galβ1-4[Fuca1-3]GlcNAcβ1-3Galβ1-4[Fuca1-3] GlcNAcβ1-Sp
Ley-Lex	[350]	Fuca1-2Galβ1-4[Fuca1-3]GlcNAcβ1-3Galβ1-4[Fuca1-3] GlcNAc(β-Sp
LeALex	[350]	Galβ1-3[Fuca1-4]GlcNAcβ1-3Galβ1-4[Fuca1-3] GlcNAc(β-Sp
Lex-LeA	[410]	Galβ1-4[Fuca1-3]GlcNAcβ1-3Galβ1-3[Fuca1-4] GlcNAc(β-Sp
Lec-LeX	[570]	Galβ1-3GlcNAcβ1-3Galβ1-4[Fuca1-3]GlcNAc(β-Sp
Tri-Lex	[430]	Galβ1-4[Fuca1-3]GlcNAcβ1-3Galβ1-4[Fuca1-3] GlcNAcβ1-3Galβ1-4[Fuca1-3]GlcNAc(β-Sp
Ley-Di-Lex	[510]	Fuca1-2Galβ1-4[Fuca1-3]GlcNAcβ1-3Galβ1-4[Fuca1-3] GlcNAcβ1-3Galβ1-4[Fuca1-3]GlcNAc(β-Sp
(Man)3	[1300], [1730]	Mana1-6[Mana1-3]Man(α-S6
11	[50], [150], [500], [750], [780]	Mana1-6[Mana1-3]Manβ1-4GlcNAcβ1-4GlcNAc(β1-Sp
6	[50], [150], [500], [750], [810], [1000]	GlcNAcβ1-2Mana1-6[GlcNAcβ1-2Mana1-3]Manβ1-4 GlcNAcβ1-4GlcNAc(β1-Sp
10	[150], [150], [500], [540], [1000]	Galβ1-4GlcNAcβ1-2Mana1-6[Galβ1-4GlcNAcβ1-2 Mana1-3]Manβ1-4GlcNAcβ1-4GlcNAc(β1-Sp
9	[50], [510], [730], [950], [970]	Neu5Aca2-6Galβ1-4GlcNAcβ1-2Mana1-6[Neu5Aca2-6 Galβ1-4GlcNAcβ1-2Mana1-3]Manβ1-4GlcNAcβ1-4 GlcNAc(β1-Sp
GM1	[460]	Neu5Aca2-3[Galβ1-3GalNAcβ1-4]Galβ1-4Glc(β-Sp
GM2	[190], [460], [590], [1190]	Neu5Aca2-3[GalNAcβ1-4]Galβ1-4Glc(β-Sp
CTISda	[350]	Neu5Aca2-3[GalNAcβ1-4]Galβ1-4GlcNAc(β-Sp
GD1a	[110]	Neu5Aca2-3[Neu5Aca2-3Galβ1-3GalNAcβ1-4]Galβ1-4 Glc(β-Sp
3'S-Di-LeA	[160]	Neu5Aca2-3Galβ1-3[Fuca1-4]GlcNAcβ1-32(β-Sp
3'SLeA-Lex	[570]	Neu5Aca2-3Galβ1-3[Fuca1-4]GlcNAcβ1-3Galβ1-4 [Fuca1-3]GlcNAc(β-Sp
3'S-Tri-LeX	[160]	Neu5Aca2-3Galβ1-4[Fuca1-3]GlcNAcβ1-3Galβ1-4 [Fuca1-3]GlcNAcβ1-3Galβ1-4[Fuca1-3]GlcNAc(β-Sp
3'Slec	[430]	Neu5Aca2-3Galβ1-3GlcNAc(β-Sp
GM3	[190], [540], [1190]	Neu5Aca2-3Galβ1-4Glc(β-Sp
3'SLDN	[460]	Neu5Aca2-3GalNAcβ1-4GlcNAc(β-Sp
3'S-Di-Lec	[270]	Neu5Aca2-3Galβ1-3GlcNAcβ1-3Galβ1-3GlcNAc(β-Sp
3'SLecLN	[860]	Neu5Aca2-3Galβ1-3GlcNAcβ1-3Galβ1-4GlcNAc(β-Sp
3'SLN-Lec	[410]	Neu5Aca2-3Galβ1-4GlcNAcβ1-3Galβ1-3GlcNAc(β-Sp
3'S-Di-LN	[1350]	Neu5Aca2-3Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ1-Sp
3'STri-LN	[160]	Neu5Aca2-3Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ1-3 Galβ1-4GlcNAc(β-Sp
3'SLec (Gc)	[350]	Neu5Gca2-3Galβ1-3GlcNAc(β-Sp
3'SL (Gc)	[490]	Neu5Gca2-3Galβ1-4Glc(β-Sp
3'SLN (Gc)	[570]	Neu5Gca2-3Galβ1-4GlcNAc(β-Sp
3'-KDNLec	[760]	Kdna2-3Galβ1-3GlcNAc(β-Sp

3'KDNLN	[510]	Kdna2-3Galβ1-4GlcNAc(β-Sp
6'SL	[620]	Neu5Aca2-6Galβ1-4Glc(β-Sp
6'SLN (Gc)	[430]	Neu5Gca2-6Galβ1-4GlcNAc(β-Sp
6'SLDN	[620]	Neu5Aca2-6GalNAcβ1-4GlcNAc(β-Sp
6'SLN-Lec	[300]	Neu5Aca2-6Galβ1-4GlcNAcβ1-3Galβ1-3GlcNAc(β-Sp
6'S-Di-LN	[300]	Neu5Aca2-6Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ1-Sp
GD2	[460]	Neu5Aca2-8Neu5Aca2-3[GalNAcβ1-4]Galβ1-4Glc(β-Sp
GD3	[320]	Neu5Aca2-8Neu5Aca2-3Galβ1-4Glc(β-Sp
GT2	[160]	Neu5Aca2-8Neu5Aca2-8Neu5Aca2-3[GalNAcβ1-4]Galβ1-4Glc(β-Sp
GT3	[510]	Neu5Aca2-8Neu5Aca2-8Neu5Aca2-3Galβ1-4Glc(β-Sp
GQ2	[140]	Neu5Aca2-8Neu5Aca2-8Neu5Aca2-8Neu5Aca2-3[GalNAcβ1-4]Galβ1-4Glc(β-Sp
(Galf)4	[<8]	Galf β1-5Galf β1-5Galf β1-5Galf (β-S8
(Man)4	[20], [100], [300], [720], [740]	Mana1-2Mana1-2Mana1-3Man(α-S5
(L-Man)2	[500]	L-Mana1-2-L-Man(α-O-(CH ₂) ₅ -triazole-(CH ₂) ₂ -COOH
α-L-Rha	[20], [50], [150], [500]	L-Rha(α-Sp
α-L-Glc	[25], [50], [150], [500], [4000]	L-Glc(α-O-octyl-COOH
β-L-Glc	[25], [50], [150], [500], [4000]	L-Glc(β-O-octyl-COOH
β-D-Glc	[25], [50], [150], [500], [4000]	D-Glc(β-O-butyl-COOH
α-L-Gal	[25], [50], [150], [500], [4000]	L-Gal(α-O-octyl-COOH
β-L-Gal	[25], [50], [150], [500], [4000]	L-Gal(β-O-octyl-COOH
β-D-Gal	[25], [50], [150], [500], [4000]	D-Gal(β-O-butyl-COOH
α-L-Man	[25], [50], [150], [500], [4000]	L-Man(α-O-octyl-COOH
α-D-Man	[25], [50], [150], [500], [4000]	D-Man(α-O-butyl-COOH
α-L-Fuc	[25], [50], [150], [500], [4000]	L-Fuc(α-O-octyl-COOH
β-L-Fuc	[25], [50], [150], [500], [4000]	L-Fuc(β-O-octyl-COOH
α-D-Fuc	[25], [50], [150], [500], [4000]	D-Fuc(α-O-octyl-COOH
β-D-Fuc	[25], [50], [150], [500], [4000]	D-Fuc(β-O-octyl-COOH
AzOH	[100], [500]	2-Azidoethanol
blank	[0]	Unmodified M13 phage

Table S1. Chemical composition of the tested mirror-LiGA.

Linker abbreviations: Sp: -O-(CH₂)₂-N₃; S5: -O-(CH₂)₅-N₃; S6: -O-(CH₂)₆-N₃; S8: -O-(CH₂)₈-N₃; P3: -(O-CH₂-CH₂)₃-N₃; P4: -(O-CH₂-CH₂)₄-N₃; and -X-: -O-(CH₂)₈-S-(CH₂)₂-NHCO-(CH₂)₄-. Enantiomeric glycan-phage constructs were highlighted in pink. Conjugation of azido glycans to phage was performed as follows. Phages were first acylated with DBCO-NHS ester (Cayman Chemical, 40461) in 1:1 (v/v) PBS:glycerol, purified using Zeba spin desalting columns (7.0 kDa MWCO), and then conjugated to azido glycans by strain-promoted azide-alkyne cycloaddition (SPAAC). Carboxylate-containing glycans were conjugated to phage by activating the glycan carboxylate with EDC hydrochloride and NHS (1 equiv. each, relative to the glycan) in water, followed by amide coupling of the resulting glycan-NHS ester to phage in borate buffer (100 mM borate, 150 mM NaCl, pH 8.0).

LiGA	Target	Dataset	n	Sample type	Comments
NOA	AAL	20260205-87NOAaalPXA-EG	4	Purified lectin	Fig. 2 & Supplementary Fig. S1 (measured on Corning Easy-wash High binding 96 well-plate)
NOA	AOL*	20260212-87NOAaolPXA-EG	4	Purified lectin	
NOA	UEA-I	20260212-87NOAueaPXA-EG	4	Purified lectin	
NOA	RSL	20260212-87NOArslPXA-EG	4	Purified lectin	
NOA	MGL*	20260212-87NOAvaaaCYC-EG	3	Purified lectin	
NOA	SBA	20260205-87NOAzfaPXA-EG	4	Purified lectin	
NOA	ECL	20260212-87NOAaaaPXA-EG	4	Purified lectin	
NOA	PNA	20260212-87NOAyfaPXA-EG	4	Purified lectin	
NOA	ASGPR1	20260402-87NOAasgPAN-IF	4	Purified lectin	
NOA	WGA	20260212-87NOAwgalPXA-EG	4	Purified lectin	
NOA	ConA	20260205-87NOAcaPXA-EG	4	Purified lectin	
NOA	Griffithsin	20260430-87NOAowaPXA-EG	4	Purified lectin	
NOA	BanLec ^{H84T}	20260430-87NOAnwaPXA-EG	4	Purified lectin	
NOA	BanLec ^{H84T} *	20260205-87NOAkqaCYC-EG	3	Purified lectin	
NOA	SP-D*	20260212-87NOAvbaaCYC-EG	3	Purified lectin	
NOA	MBL*	20260212-87NOAhaaaCYC-EG	3	Purified lectin	
NOA	DC-SIGN ^{WT}	20260212-87NOAdcPXA-EG	4	Purified lectin	
NOA	DC-SIGN ^{T314A}	20260212-87NOAdctPXA-EG	4	Purified lectin	
NOA	DC-SIGN ^{M270F}	20260212-87NOAdcmPXA-EG	4	Purified lectin	
NOA	Galectin-1*	20260212-87NOAoqaCYC-EG	3	Purified lectin	
NOA	Galectin-1	20260529-87NOAgoULC-EG	4	Purified lectin	
NOA	Galectin-2	20260529-87NOAgadULC-EG	4	Purified lectin	
NOA	Galectin-3	20260529-87NOAgaULC-EG	4	Purified lectin	
NOA	Galectin-7	20260529-87NOAgsULC-EG	4	Purified lectin	
NOA	Galectin-8*	20260212-87NOAqaaaCYC-EG	3	Purified lectin	
NOA	Galectin-8A	20260529-87NOAgeiULC-EG	4	Purified lectin	
NOA	Galectin-8B	20260529-87NOAgebULC-EG	4	Purified lectin	
NOA	Galectin-10	20260529-87NOAgaeULC-EG	4	Purified lectin	
NOA	Galectin-14	20260529-87NOAghfULC-EG	4	Purified lectin	
NOA	hItln1*	20260212-87NOAgbaaCYC-EG	3	Purified lectin	
NOA	REG4*	20260212-87NOAzaaaCYC-EG	3	Purified lectin	
NOA	CL-K1*	20260212-87NOAiaaaCYC-EG	3	Purified lectin	
NOA	CRP*	20260212-87NOAfbaaCYC-EG	3	Purified lectin	
NOA	diCBM40	20260430-87NOAcjaPXA-EG	3	Purified lectin	
NOA	SNA-I	20260212-87NOAsnaPXA-EG	4	Purified lectin	
NOA	Siglec-1 ^{WT}	20260212-87NOAbiaPXA-EG	4	Purified lectin	
NOA	Siglec-1R	20260212-87NOAhqaPXA-EG	4	Purified lectin	
NOA	Siglec-2 ^{WT}	20260212-87NOAsigaPXA-EG	3	Purified lectin	
NOA	Siglec-2R	20260212-87NOAhqaPXA-EG	4	Purified lectin	
NOA	Siglec-3 ^{WT}	20260212-87NOAqsaPXA-EG	4	Purified lectin	
NOA	Siglec-4 ^{WT}	20260212-87NOAksaPXA-EG	4	Purified lectin	
NOA	Siglec-7 ^{WT}	20260212-87NOAsigbPXA-EG	3	Purified lectin	
NOA	Siglec-7R	20260212-87NOAsigcPXA-EG	4	Purified lectin	
NOA	Siglec-15 ^{WT} *	20260212-87NOAjqacCYC-EG	3	Purified lectin	
NOA	BSA	20260205-87NOAbsPXA-EG	4	Purified protein	
NOA	No target	20260212-87NOAooCYC-EG	3	Naïve LiGA	
NOA	hDC-SIGN+ Raji	20260306-87NOArjdNZC-FH	3	0 mM D-Man	Fig. 3 & Supplementary Fig. S3 (measured against cultured DC-SIGN+ Raji cells with gradient concentrations of free D-(+)-mannose)
NOA	hDC-SIGN+ Raji	20260306-87NOArjdBZC-FH	3	1 mM D-Man	
NOA	hDC-SIGN+ Raji	20260306-87NOArjdJZC-FH	3	10 mM D-Man	
NOA	hDC-SIGN+ Raji	20260306-87NOArjdIZC-FH	3	25 mM D-Man	
NOA	hDC-SIGN+ Raji	20260306-87NOArjdZCC-FH	3	50 mM D-Man	
NOA	hDC-SIGN+ Raji	20260306-87NOArjdCZC-FH	3	100 mM D-Man	
NOA	Purified hDC-SIGN	20260611-87NOAdcADCM-FH	3	0 mM D-Man	Supplementary Fig. S3 (measured against purified DC-SIGN ECD-coated Corning Easy-wash High binding 96-well plate with gradient concentrations of free D-(+)-mannose)
NOA	Purified hDC-SIGN	20260611-87NOAdcBDCM-FH	3	1 mM D-Man	
NOA	Purified hDC-SIGN	20260611-87NOAdcCDC-FH	3	10mM D-Man	
NOA	Purified hDC-SIGN	20260611-87NOAdcDDCM-FH	3	25 mM D-Man	
NOA	Purified hDC-SIGN	20260611-87NOAdcEDCM-FH	3	50mM D-Man	
NOA	Purified hDC-SIGN	20260611-87NOAdcFDCM-FH	3	0.1 M D-Man	
NOA	Purified hDC-SIGN	20260611-87NOAdcGDCM-FH	3	1 M D-Man	
NOA	Purified hDC-SIGN	20260514-87NOAdcACAA-FH	3	0 mM L-Glc	Supplementary Fig. S3 (measured on purified DC-SIGN ECD-coated Corning Easy-wash High binding 96-well plate and inhibited by gradient
NOA	Purified hDC-SIGN	20260514-87NOAdcBBAA-FH	3	1 mM L-Glc	
NOA	Purified hDC-SIGN	20260514-87NOAdcCBAA-FH	3	2 mM L-Glc	
NOA	Purified hDC-SIGN	20260514-87NOAdcDAAA-FH	3	5 mM L-Glc	
NOA	Purified hDC-SIGN	20260514-87NOAdcEBAA-FH	3	10 mM L-Glc	
NOA	Purified hDC-SIGN	20260514-87NOAdcFBAA-FH	3	25 mM L-Glc	

NOA	Purified hDC-SIGN	20260514-87NOAdcGBAA-FH	3	50 mM L-Glc	concentrations of free L-(-)-glucose)
NOA	Purified hDC-SIGN	20260514-87NOAdcHAAA-FH	3	0.1 M L-Glc	
NOA	Purified hDC-SIGN	20260514-87NOAdcIAAA-FH	3	1 M L-Glc	
NOA	Donor# 655	20260212-87NOAdbPXA-GG	3	Human serum	Fig. 4 (measured on anti-IgM precoated Corning Easy-wash High binding 96 well-plate)
NOA	Donor# 663	20260212-87NOAnhPXA-GG	3	Human serum	
NOA	Donor# 1471	20260320-87NOAicPXA-GG	3	Human serum	
NOA	Donor# 844	20260212-87NOAigPXA-GG	3	Human serum	
NOA	Donor# 788	20260320-87NOAdIPXA-GG	3	Human serum	
NOA	Donor# 794	20260212-87NOAenPXA-GG	3	Human serum	
NOA	Donor# 796	20260320-87NOAmmoPXA-GG	3	Human serum	
NOA	Donor# 1029	20260320-87NOAlePXA-GG	3	Human serum	
NOA	Donor# 1109	20260212-87NOArhPXA-GG	3	Human serum	
NOA	Donor# 1417	20260320-87NOAphPXA-GG	3	Human serum	
NOA	Donor# 1221	20260212-87NOArgPXA-GG	3	Human serum	
NOA	Donor# 791	20260320-87NOAifPXA-GG	3	Human serum	
NOA	Donor# 688	20260212-87NOAohPXA-GG	3	Human serum	
NOA	No target	20260212-87NOAooBO-GG	3	Naïve LiGA	
NOA	Anti-Lewis A [7LE]	20260402-87NOAalaPAN-IF	4	Purified Ab	Fig. 4 and Supplementary Fig. S4 (measured on Corning Easy-wash High binding 96 well-plate)
NOA	Anti-Lewis X [HI198]	20260402-87NOAalxPAN-IF	4	Purified Ab	
NOA	Anti-Lewis Y [F3]	20260402-87NOAalyPAN-IF	4	Purified Ab	
NOA	AntiH [BRIC39]	20260421-87NOAfvPAN-IF	4	Purified Ab	
NOA	AntiH [BRIC231]	20260421-87NOAtvaPAN-IF	4	Purified Ab	
NOA	AntiH [BRIC198]	20260430-87NOApvaPAN-IF	4	Purified Ab	
NOA	AntiH [17-206]	20260402-87NOAanhPAN-IF	4	Purified Ab	
NOA	AntiH [17-206].	20260421-87NOAwvaPAN-IF	4	Purified Ab	
NOA	AntiH [A46BB10]	20260402-87NOAyvaPAN-IF	4	Purified Ab	
NOA	AntiHo [89/8]	20260402-87NOAjuaPAN-IF	4	Purified Ab	
NOA	AntiH [89-8]	20260430-87NOArtaPAN-IF	4	Purified Ab	
NOA	AntiH [86-N]	20260430-87NOAuoaPAN-IF	4	Purified Ab	
NOA	AntiH [97-1]	20260430-87NOAgkaPAN-IF	4	Purified Ab	
NOA	AntiH [87-N]	20260430-87NOAkwaPAN-IF	4	Purified Ab	
NOA	AntiA [HE24]	20260402-87NOAhedPAN-IF	4	Purified Ab	
NOA	AntiA [HE193]	20260402-87NOAvgPAN-IF	4	Purified Ab	
NOA	AntiA [HE193].	20260421-87NOAataPAN-IF	4	Purified Ab	
NOA	AntiA [NaM871F6]	20260430-87NOAlqaPAN-IF	4	Purified Ab	
NOA	AntiA [BRIC145]	20260430-87NOAxwaPAN-IF	4	Purified Ab	
NOA	AntiA [BRIC145].	20260421-87NOAbriPAN-IF	4	Purified Ab	
NOA	AntiA [NOVA]	20260430-87NOAftwaPAN-IF	4	Purified Ab	
NOA	AntiA [3-3A]	20260430-87NOAeuaPAN-IF	4	Purified Ab	
NOA	AntiA [Z2B1]	20260421-87NOAzbbPAN-IF	4	Purified Ab	
NOA	AntiA [Z2A]	20260430-87NOAduaPAN-IF	4	Purified Ab	
NOA	AntiA [9A]	20260402-87NOAavaPAN-IF	4	Purified Ab	
NOA	AntiB [CLCP19B]	20260402-87NOAvvaPAN-IF	4	Purified Ab	
NOA	AntiB [BRIC250]	20260430-87NOAvwaPAN-IF	4	Purified Ab	
NOA	AntiB [ES4]	20260430-87NOAsuaPAN-IF	4	Purified Ab	
NOA	AntiB [LB2]	20260430-87NOAtwaPAN-IF	4	Purified Ab	
NOA	AntiB [NOVA]	20260430-87NOAglPAN-IF	4	Purified Ab	
NOA	AntiB [HEB29]	20260402-87NOAndPAN-IF	4	Purified Ab	
NOA	AntiB [89-F]	20260402-87NOAlpaPAN-IF	4	Purified Ab	
NOA	AntiB [BGR11]	20260402-87NOAkvaPAN-IF	4	Purified Ab	
NOA	AntiB [Z2H-2]	20260402-87NOAzahPAN-IF	4	Purified Ab	
NOA	[86-M]	20260421-87NOAetaPAN-IF	4	Purified Ab	
NOA	Anti-LNT [K21]	20260430-87NOAywaPAN-IF	4	Purified Ab	
NOA	Anti-SialoTn	20260430-87NOAqwaPAN-IF	4	Purified Ab	
NOA	[VK9]	20260430-87NOAblaPAN-IF	4	Purified Ab	
NOA	[HE10]	20260430-87NOAwwaPAN-IF	4	Purified Ab	
NOA	[JTL-2]	20260430-87NOAjvaPAN-IF	4	Purified Ab	
NOA	[JTL-4]	20260430-87NOAiuaPAN-IF	4	Purified Ab	
NOA	No target	20251218-87NOAooNA-IF	5	Naïve LiGA	
NOA	F-CD4-Δ	20260212-87NOAztahYC-EG	2	FACS-sorted cells	Fig. 5 (Human PBMCs derived primary immune cells)
NOA	M-CD4-Δ	20260212-87NOAjsaHYC-EG	2	FACS-sorted cells	
NOA	F CD4-S	20260212-87NOAztuYUC-EG	2	FACS-sorted cells	
NOA	M-CD4-S	20260212-87NOAjsaYUC-EG	2	FACS-sorted cells	
NOA	F-CD8-Δ	20260212-87NOAttaHYC-EG	2	FACS-sorted cells	
NOA	M-CD8-Δ	20260212-87NOAytaHYC-EG	2	FACS-sorted cells	
NOA	F-CD8-S	20260212-87NOAttaYUC-EG	2	FACS-sorted cells	
NOA	M-CD8-S	20260212-87NOAttaYUC-EG	2	FACS-sorted cells	

NOA	F-MO-Δ	20260212-87NOArnaHYC-EG	2	FACS-sorted cells	Fig. 5 (Human PBMCs derived primary immune cells)
NOA	M-MO-Δ	20260212-87NOAqtaHYC-EG	2	FACS-sorted cells	
NOA	F-MO-S	20260212-87NOArnaUYC-EG	2	FACS-sorted cells	
NOA	M-MO-S	20260212-87NOAqtaUYC-EG	2	FACS-sorted cells	
NOA	F-B-Δ	20260212-87NOApraHYC-EG	2	FACS-sorted cells	
NOA	M-B-Δ	20260212-87NOAdqaHYC-EG	2	FACS-sorted cells	
NOA	F-B-S	20260212-87NOApraUYC-EG	2	FACS-sorted cells	
NOA	M-B-S	20260212-87NOAdqaUYC-EG	2	FACS-sorted cells	
NOA	F-NK-Δ	20260212-87NOAxtaHYC-EG	2	FACS-sorted cells	
NOA	M-NK-Δ	20260212-87NOAfsaHYC-EG	2	FACS-sorted cells	
NOA	F-NK-S	20260212-87NOAxtaUYC-EG	2	FACS-sorted cells	
NOA	M-NK-S	20260212-87NOAfsaUYC-EG	2	FACS-sorted cells	
NOA	F-Iso.CD4-Δ	20260212-87NOAvtaQYC-EG	2	Isolated cells	
NOA	M-Iso.CD4-Δ	20260212-87NOAgiaQYC-EG	2	Isolated cells	
NOA	F-Iso.CD4-S	20260212-87NOAvtaTBC-EG	2	Isolated cells	
NOA	M-Iso.CD4-S	20260212-87NOAgiaQYC-EG	2	Isolated cells	
NOA	F-Iso.CD8-Δ	20260212-87NOAhtaHYC-EG	2	Isolated cells	
NOA	M-Iso.CD8-Δ	20260212-87NOAiqahHYC-EG	2	Isolated cells	
NOA	F-Iso.CD8-S	20260212-87NOAhtaTBC-EG	2	Isolated cells	
NOA	M-Iso.CD8-S	20260212-87NOAiqahHYC-EG	2	Isolated cells	
MEG	Liver (in vivo)	20241030-87MEGbiEYC-GL1	1	Mouse #1	Fig. 6 (mapping in vivo biodistribution of enantiomeric glycans in live mice)
MEG	Liver (in vivo)	20241030-87MEGbiEYC-GL2	1	Mouse #1	
MEG	Liver (in vivo)	20241030-87MEGbiEYC-GL3	1	Mouse #2	
MEG	Liver (in vivo)	20241030-87MEGbiEYC-GL4	1	Mouse #2	
MEG	Liver (in vivo)	20241030-87MEGbiEYC-GL5	1	Mouse #3	
MEG	Liver (in vivo)	20241030-87MEGbiEYC-GL6	1	Mouse #3	
MOX	Liver (in vivo)	20250707-87MOXbiYXC-GL1	1	Mouse #4	
MOX	Liver (in vivo)	20250707-87MOXbiYXC-GL2	1	Mouse #5	
MOX	Liver (in vivo)	20250707-87MOXbiYXC-GL3	1	Mouse #6	
MOY	Liver (in vivo)	20250716-87MOYbiYXC-DE1	1	Mouse #7	
MOY	Liver (in vivo)	20250716-87MOYbiYXC-DE2	1	Mouse #8	
MEG	Spleen (in vivo)	20241030-87MEGikEYC-GL1	1	Mouse #1	
MEG	Spleen (in vivo)	20241030-87MEGikEYC-GL2	1	Mouse #1	
MEG	Spleen (in vivo)	20241030-87MEGikEYC-GL3	1	Mouse #2	
MEG	Spleen (in vivo)	20241030-87MEGikEYC-GL4	1	Mouse #2	
MEG	Spleen (in vivo)	20241030-87MEGikEYC-GL5	1	Mouse #3	
MEG	Spleen (in vivo)	20241030-87MEGikEYC-GL6	1	Mouse #3	
MOX	Spleen (in vivo)	20250707-87MOXikYXC-GL1	1	Mouse #4	
MOX	Spleen (in vivo)	20250707-87MOXikYXC-GL2	1	Mouse #5	
MOX	Spleen (in vivo)	20250707-87MOXikYXC-GL3	1	Mouse #6	
MOY	Spleen (in vivo)	20250716-87MOYikYXC-DE1	1	Mouse #7	
MOY	Spleen (in vivo)	20250716-87MOYikYXC-DE2	1	Mouse #8	
PW	Spleen (in vivo)	20250926-87PWikYX-DE1	1	Mouse #9	
PW	Spleen (in vivo)	20250926-87PWikYX-DE2	1	Mouse #10	
PW	Spleen (in vivo)	20250926-87PWikYX-DE3	1	Mouse #11	
MEG	S-T (in vivo)	20241030-87MEGmaaFWA-GL1	1	Mouse #1	
MEG	S-T (in vivo)	20241030-87MEGmaaFWA-GL2	1	Mouse #1	
MEG	S-T (in vivo)	20241030-87MEGmaaFWA-GL3	1	Mouse #2	
MEG	S-T (in vivo)	20241030-87MEGmaaFWA-GL4	1	Mouse #2	
MEG	S-T (in vivo)	20241030-87MEGmaaFWA-GL5	1	Mouse #3	
MEG	S-T (in vivo)	20241030-87MEGmaaFWA-GL6	1	Mouse #3	
MOX	S-T (in vivo)	20250707-87MOXmaaFWA-GL1	1	Mouse #4	
MOX	S-T (in vivo)	20250707-87MOXmaaFWA-GL2	1	Mouse #5	
MOX	S-T (in vivo)	20250707-87MOXmaaFWA-GL3	1	Mouse #6	
MOY	S-T (in vivo)	20250716-87MOYmaaFWB-DE1	1	Mouse #7	
MOY	S-T (in vivo)	20250716-87MOYmaaFWB-DE2	1	Mouse #8	
PW	S-T (in vivo)	20250926-87PWmaaFWB-DE1	1	Mouse #9	
PW	S-T (in vivo)	20250926-87PWmaaFWB-DE2	1	Mouse #9	
PW	S-T (in vivo)	20250926-87PWmaaFWB-DE3	1	Mouse #10	
PW	S-T (in vivo)	20250926-87PWmaaFWB-DE4	1	Mouse #10	
PW	S-T (in vivo)	20250926-87PWmaaFWB-DE5	1	Mouse #11	
PW	S-T (in vivo)	20250926-87PWmaaFWB-DE6	1	Mouse #11	
MEG	S-B (in vivo)	20241030-87MEGmbaFWA-GL1	1	Mouse #1	
MEG	S-B (in vivo)	20241030-87MEGmbaFWA-GL2	1	Mouse #1	
MEG	S-B (in vivo)	20241030-87MEGmbaFWA-GL3	1	Mouse #2	
MEG	S-B (in vivo)	20241030-87MEGmbaFWA-GL4	1	Mouse #2	
MEG	S-B (in vivo)	20241030-87MEGmbaFWA-GL5	1	Mouse #3	

MEG	S-B (in vivo)	20241030-87MEGmbaFWA-GL6	1	Mouse #3	
MOX	S-B (in vivo)	20250707-87MOXmbaFWA-GL1	1	Mouse #4	
MOX	S-B (in vivo)	20250707-87MOXmbaFWA-GL2	1	Mouse #5	
MOX	S-B (in vivo)	20250707-87MOXmbaFWA-GL3	1	Mouse #6	
MOY	S-B (in vivo)	20250716-87MOYmbaFWB-DE1	1	Mouse #7	
MOY	S-B (in vivo)	20250716-87MOYmbaFWB-DE2	1	Mouse #8	
PW	S-B (in vivo)	20250926-87PWmbaFWB-DE1	1	Mouse #9	
PW	S-B (in vivo)	20250926-87PWmbaFWB-DE2	1	Mouse #9	
PW	S-B (in vivo)	20250926-87PWmbaFWB-DE3	1	Mouse #10	
PW	S-B (in vivo)	20250926-87PWmbaFWB-DE4	1	Mouse #10	
PW	S-B (in vivo)	20250926-87PWmbaFWB-DE5	1	Mouse #11	
PW	S-B (in vivo)	20250926-87PWmbaFWB-DE6	1	Mouse #11	
MOX	Plasma (in vivo)	20250707-87MOXcoBLD-GL1	1	Mouse #4	
MOX	Plasma (in vivo)	20250707-87MOXcoBLD-GL2	1	Mouse #5	
MOX	Plasma (in vivo)	20250707-87MOXcoBLD-GL3	1	Mouse #6	
MOY	Plasma (in vivo)	20250716-87MOYcoBLD-DE1	1	Mouse #7	
MOY	Plasma (in vivo)	20250716-87MOYcoBLD-DE2	1	Mouse #7	
MOY	Plasma (in vivo)	20250716-87MOYcoBLD-DE3	1	Mouse #8	
MOY	Plasma (in vivo)	20250716-87MOYcoBLD-DE4	1	Mouse #8	
MOX	RBC (in vivo)	20250707-87MOXcwYXC-GL1	1	Mouse #4	
MOX	RBC (in vivo)	20250707-87MOXcwYXC-GL2	1	Mouse #5	
MOX	RBC (in vivo)	20250707-87MOXcwYXC-GL3	1	Mouse #6	
MOY	RBC (in vivo)	20250716-87MOYcwYXC-DE1	1	Mouse #7	
MOY	RBC (in vivo)	20250716-87MOYcwYXC-DE2	1	Mouse #7	
MOY	RBC (in vivo)	20250716-87MOYcwYXC-DE3	1	Mouse #8	
MOY	RBC (in vivo)	20250716-87MOYcwYXC-DE4	1	Mouse #8	
MEG	No target	20241030-87MEGooBO-GL	3	Naïve LiGA	
MOX	No target	20250707-87MOXooBO-GL	3	Naïve LiGA	
MOY	No target	20250718-87MOYooBO-GL	3	Naïve LiGA	
PW	No target	20250926-87PWooBO-DE	3	Naïve LiGA	
MOX	hDC-SIGN+ Raji	20250610-87MOXrjdPANC-IF	5	Cultured cell line	Supplementary Fig. S2
MOX	hLangerin+ Raji	20250610-87MOXrjIPANC-IF	5	Cultured cell line	
MOX	WT Raji cells	20250610-87MOXehPANC-IF	5	Cultured cell line	
MOX	No target	20250610-87MOXooNA-EG	5	Naïve LiGA	

Table S2. Summary of LiGA data used in this work.

All deep sequencing datasets mentioned in this study are publicly available at <https://48hd.cloud/>. * indicates the tested protein was biotinylated. F, female; M, male; Δ, cells were treated with heat-deactivated sialidase; S, cells were treated with activate sialidase (from *Vibrio Cholerae*); MO, monocytes; B, B lymphocytes; NK, natural killer cells; S-T, splenic T lymphocytes; S-B, splenic B lymphocytes; RBC, red blood cells.

	Description*
Sample: Glycan-containing sample (e.g. glycan, glycoprotein, cell lysate, cell, glycopeptide, etc.)	
Description of Sample	Glycophage constructs
Sample preparation protocol	Glycophage construct samples were labeled with TAMRA prior to analysis on the lectin microarrays, and thus required no sample preparation.
Labeling protocol for sample detection	Samples are labelled with TAMRA.
Two-color reference (if used)	N/A
Assay protocol	Lectin microarrays are blocked with blocking buffer (50 mM ethanolamine and 100 mM boric acid) for one hour at room temperature. Slides are rinsed once with PBST (0.01%) and once with 1X PBS for 5 minutes each, then dried using a slide spinner. Each slide is mounted on a 24-well format hybridization cassette (Arrayit), in which each well contains a subarray. To each well, 50 μ l of sample was added, then diluted with 50 μ l PBST (with 0.1 mM Ca^{2+} to reach the final volume (100 μ l) and PBST concentration (0.005%). Slides are incubated in a hybridization oven on a rocker tray for one hour at 30°C in the dark. After hybridization, arrays are washed with PBST (0.01%) once for one minute, then once for five minutes. Arrays are lastly washed once with PBS for one minute, then once for ten minutes. Once finished, slides are removed from the cassette and briefly immersed in ultrapure water, then dried using a slide spinner.
2. Lectin Library	
General description of the lectin library used in the array	Lectin microarrays are generated in house.
List of lectins and/or glycan-binding proteins, their source, concentration, and buffer	Please see Table S4.
Modification of lectins	N/A
3. Immobilization Surface; e.g., Microarray Slide	
Immobilization surface	Nexterion Slide H Barcoded 3D Hydrogel Coated.
Manufacturer	Schott North America.
Custom preparation of the surface	N/A
4. Array Production	
Description of Arrayer	Nano-Plotter 2.1 piezoelectric printer (GeSim, Germany) with cooled microwell plate holder and cooled printing deck.
Lectin deposition	Triplicates of each lectin are printed onto each subarray.
Printing conditions	Dilute lectins to the pre-determined concentrations in the print buffer (final concentration of print buffer: 1 mM monosaccharide in PBS, 5 ng ml ⁻¹ Atto 532; Please see Supplemental Table 1 for the concentrations of lectins). Load the mixed solution to the microplate. Before printing, check the humidity of the print chamber. The humidity should be kept around 50% throughout the entire print. Ensure both microwell plate holder and printing deck are cooled. Adjust the cooling temperature based on ambient temperature and the temperature of the cooled slide deck surface, preventing moisture building up inside the print chamber. Once printing is complete, allow the slides to dry for at least one hour before vacuum sealing and storage at -20°C.
Array layout	Each microarray contains 21 subarrays (3 columns and 7 rows). In each subarray, triplicates of a lectin are printed, with six lectins in each row. The number of columns is 18, and the row number depends on how many lectin probes are printed on the arrays (i.e. 132 lectins require 22 rows).

Quality control	The well-characterized glycoproteins glycophorin, ovalbumin, asialofetuin, 1:1 A549:HEK293T cell lysate, human serum, fetuin, and RNase B are used for quality assurance of the printed microarrays.
5. Detector and Data Processing	
Instrument (scanner, flow cytometer)	Fluorescent Slide Scanner GenePix 4400A (Molecular Devices).
Instrument settings	A low resolution preview scan of the slide is performed to adjust photomultiplier tube (PMT) gain for the channel used (TAMRA: 532nm) so that the signals are not saturated and within the linear detection range. After adjusting PMT gain, slides are scanned in the given channel at 5 μ m resolution.
Image analysis software	GenePix Pro 7 (Molecular Devices).
Data processing and statistical analysis	Extracted data is processed for quality checks using Grubbs outlier test with $\alpha = 0.05$. Log2 values of the average signals are median-normalized over the individual subarray in each channel.
6. Lectin Microarray Data Presentation	
Data presentation and interpretation	Raw values output by Genepix Pro 7 software were thresholded by a cut-off of >2000 AU.
7. Data Location	
Data Location	https://doi.org/10.7303/syn76179151

Table S3. Lectin Microarray Information.

Lectin	Species/Origin	Print Conc. ($\mu\text{g ml}^{-1}$)	Rough Specificity /Inhibitory monosaccharide	Vendor/Source
AAA	<i>Anguilla anguilla</i> <i>agglutinin</i>	2000	Fucose	Vector
AAL	<i>Aleuria aurantia</i>	2000	Fucose	Medicago/Vector
ACA	<i>Amaranthus Caudatus</i>	2000	Gal- β 1,3-GalNAc	EY
AIA	<i>Artocarpus integrifolia</i>	2000	β 1,3-GalNAc	EY/Glycomatrix/Vector
AMA	<i>Allium moly</i>	2000	Oligo mannose	Vector
Anti-B.G. Lewis A	MAB mouse IgG1 [7LE]	undiluted	Lewis A	Abcam
Anti-B.G. Lewis B	MAB mouse IgM [2- 25LE]	undiluted	Lewis B	Abcam/Sigma
Anti-B.G. Lewis X	MAB mouse IgM [P12]	undiluted	Lewis X	Sigma
Anti-B.G. Lewis Y	MAB mouse IgM [F3]	undiluted	Lewis Y	Abcam
Anti-Blood Group A	MAB mouse IgM [HE- 193]	undiluted	Blood Group A	Thermo Fisher
Anti-Blood Group B	MAB mouse IgM [HEB- 29]	undiluted	Blood Group B	Abcam/ Thermo Fisher
Anti-Blood Group H	MAB mouse IgG3 [17- 206]	undiluted	Blood Group H	Thermo Fisher
Anti- Polysialic Acid	MAB mouse IgG2a [735]	undiluted	Polysialic Acid	Absolute Antibody
Anti-IgA	MAB IgG1 [KT41]	undiluted	IgA	Abcam
Anti-IgG	MAB IgG2a [KT131]	undiluted	IgG	Abcam
Anti-IgM	MAB IgG1[KT16]	undiluted	IgM	Abcam
AOL	<i>Aspergillus oryzae</i>	2000	Fucose	TCI America
ASA	<i>Allium sativum</i>	2000	Mannose	EY
BanLec H84T	<i>Musa acuminata</i>	2000	High Mannose	Generated in house
BC2L-A	<i>Burkholderia cenocepacia</i>	2000	Mannose	Elicityl
BPA/BPL	<i>Bauhinia purpurea</i>	2000	β -Gal / β -GalNAc	Vector
CA	<i>Colchicum autumnale</i>	2000	Bi-antennary N- linked glycans	EY
ConA	<i>Canavalia ensiformis</i>	2000	Tri-mannose core	Thermo Fisher/Vector
DBA	<i>Dolichos biflorus</i>	2000	GalNAc	Vector
diCBM40	engineered NanI from <i>Clostridium perfringens</i>	1500	α Sialylation	Generated in house
DSA	<i>Datura stramonium</i>	2000	LacNAc	Vector
ECA	<i>Erythrina cristagalli</i>	2000	LacNAc	EY/Vector
GafD	<i>Escherichia coli</i>	2000	GlcNAc	Generated in house
GNA/GNL	<i>Galanthus nivalis</i>	2000	Oligo mannose	Sigma/Vector
GS/GSL-I	<i>Griffonia simplicifolia-I</i>	2000	α -Gal / Lac	Vector
GS/GSL-II	<i>Griffonia simplicifolia-II</i>	2000	GlcNAc	Vector
HHL	<i>Hippeastrum hybrid</i>	2000	Oligo/High mannose	BioWorld
HPA	<i>Helix pomatia</i>	2000	Blood Group A	Sigma

LcH	<i>Lens culinaris</i>	2000	Core Fucose	EY/Medicago
LEA/LEL	<i>Lycopersicon esculentum</i>	2000	GlcNAc	Vector
LTL Lotus	<i>Lotus tetragonolobus</i>	2000	Fucose	EY/Vector
MAA/MAL-I	<i>Maackia amurensis-I</i>	2000	Sialylation/Sulfation	EY/Vector
MAA/MAL-II	<i>Maackia amurensis-II</i>	2000	Sialylation/Sulfation	Vector
MNA-G	<i>Morus nigra Morniga G</i>	2000	GalNAc	EY
MNA-M	<i>Morus nigra Morniga M</i>	2000	Oligo mannose / Gal	EY
MPA/MPL	<i>Maclura pomifera</i>	2000	β 1,3-GalNAc	Vector
NPA/NPL	<i>Narcissus pseudonarcissus</i>	2000	Oligo mannose	EY
PA-IL	<i>Pseudomonas aeruginosa</i>	2000	Gal	Generated in house
PA-IIL	<i>Pseudomonas aeruginosa</i>	2000	Fucose	Elicityl
PapGII	<i>Escherichia coli</i>	2000	Gal	Generated in house
PHA-E	<i>Phaseolus vulgaris Erythroagglutinin</i>	2000	Bisecting GlcNAc	Sigma/Vector
PHA-L	<i>Phaseolus vulgaris Leukoagglutinin</i>	2000	β 1,6 Branching N-Link glycans	Medicago/Vector
PhoSL	<i>Pholiota squarrosa</i>	2000	Core Fucose	Bio Basic
PNA	<i>Arachis hyogaea</i>	2000	Gal- β 1,3-GalNAc	EY/Vector
Recombinant Protein A	<i>Staphylococcus aureus</i>	2000	Immunoglobulins	Thermo Fisher
Recombinant Protein G	<i>Streptococcus</i> Group G	2000	Immunoglobulins	Sigma
Recombinant Protein L	<i>Peptostreptococcus magnus</i>	2000	Immunoglobulins	Thermo Fisher
PSA	<i>Pisum sativum</i>	2000	Core Fucose	Vector
PSL	<i>Polyporus squamosus</i>	2000	α 2,6 sialylation	TCI America
RCA120	<i>Ricinus Communis Agglutinin I</i>	2000	Gal / Lac	Vector
rGRFT	<i>Griffithsia</i>	1700	High mannose	Generated in house
Ricin B Chain	<i>Ricinus communis</i>	2000	Gal	Vector
RCA120	<i>Ricinus communis</i>	2000	Gal	Vector
RPA	<i>Robinia pseudoacacia</i>	2000	Multiantennary N-glycans with bisecting GlcNAc	EY
SBA	<i>Glycine max</i>	2000	LacdiNAc	Vector
SLBR-B	<i>Streptococcus gordonii M99</i>	2300	α 2,6 sialylation	Generated in house
SLBR-H	<i>Streptococcus gordonii DL1</i>	2000	α 2,3 sialylation	Generated in house
SLBR-N	<i>Streptococcus gordonii UB10712</i>	2000	α 2,3 sialylation	Generated in house
SNA	<i>Sambucus nigra</i>	2000	α 2,6 sialylation	EY/Vector
SNA-II	<i>Sambucus nigra-II</i>	2000	α 2 Fucose /oligo mannose	EY

STL	<i>Solanum tuberosum</i> <i>Agglutinin</i>	2000	LacNAc	Vector
TJA-II	<i>Trichosanthes japonica</i> - <i>II</i>	2000	α 2 Fucose	Aniara Diagnostica/Medicago
TL	<i>Tulipa sp.</i>	2000	GlcNAc	BioWorld
UDA	<i>Urtica dioica</i>	2000	GlcNAc / Oligo mannose	EY
UEA-I	<i>Ulex europaeus-I</i>	2000	α 2 Fucose	BioWorld/GeneTex/Vector
UEA-II	<i>Ulex europaeus-II</i>	2000	GlcNAc	EY/BioWorld
VVA	<i>Vicia villosa</i>	2000	Terminal GalNAc	Vector
WFA	<i>Wisteria floribunda</i>	2000	GalNAc- β 1,4	Vector
WGA	<i>Triticum vulgare</i>	2000	GlcNAc	GeneTex

Table S4. Lectins used in microarrays.

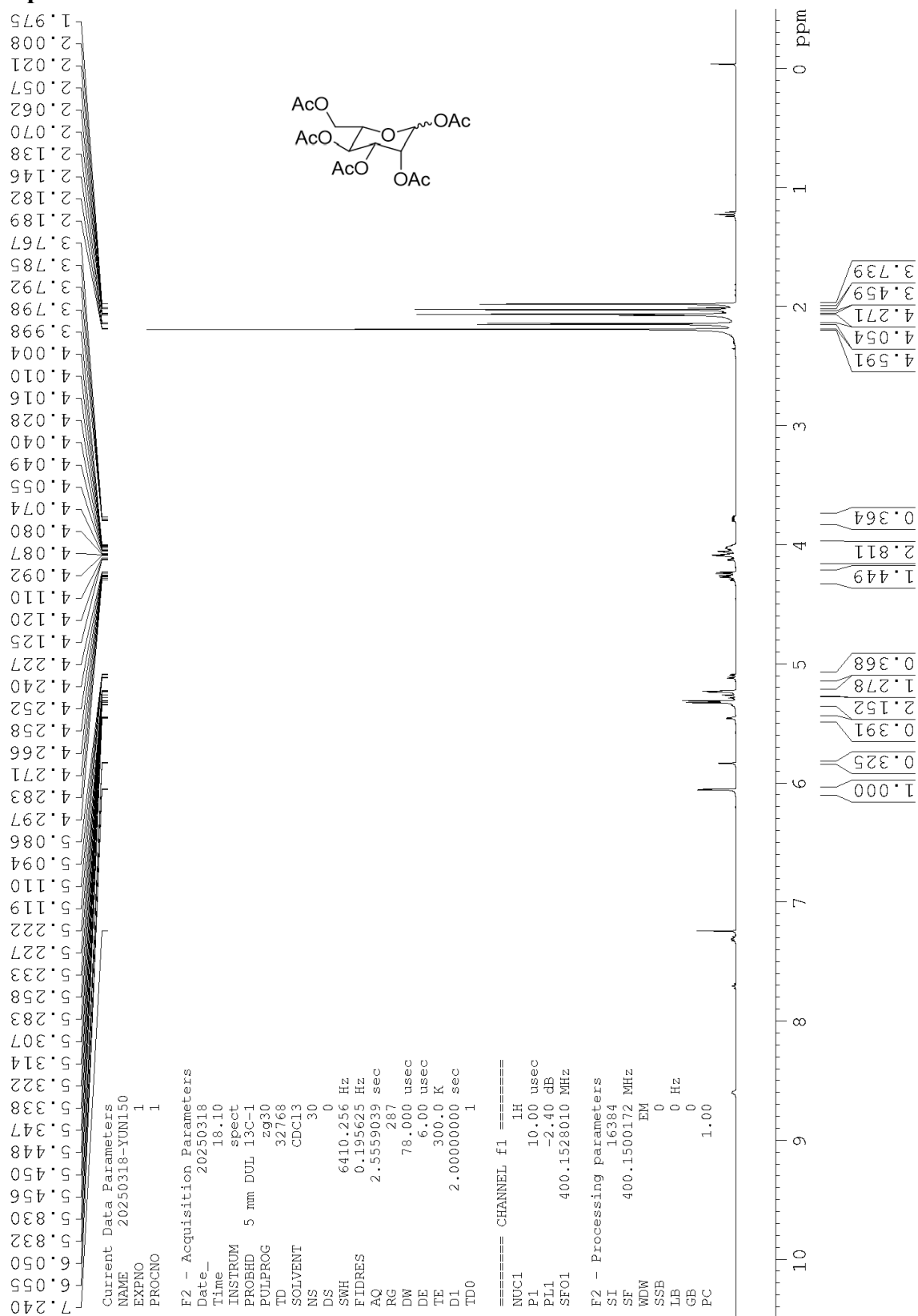
Glycan	Top	Bottom	HillSlope	N points	N concentration	Fit status	R ²	IC50 (mM)
Man3-[1300]	2615.147	0.000	1.688	14	6	OK	0.930	IC50 = 20.1 mM
Man3-[1730]	393.491	3.052	4.600	15	6	OK	0.887	IC50 = 31.3 mM
Man4-[20]	146.134	0.000	1.349	35	6	OK	0.461	IC50 = 18.7 mM
Man4-[100]	21.315	656.497	10.000	22	6	OK	0.414	IC50 = 150 mM
Man4-[300]	65.184	4.206	3.547	80	6	OK	0.801	IC50 = 8.49 mM
Man4-[720]	765.197	36.319	2.144	54	6	OK	0.520	IC50 = 13.3 mM
Man4-[740]	249.317	0.000	1.562	30	6	OK	0.951	IC50 = 14.1 mM
L-Man2-[500]	13.358	6.037	3.975	26	6	OK	0.305	IC50 = 2.9 mM
LeA-[950]	714.135	0.000	2.048	14	6	OK	0.870	IC50 = 35.8 mM
Lex-[810]	213.114	13.006	10.000	16	6	OK	0.960	IC50 = 25.2 mM
Gala3Lex-[620]	830.518	0.000	0.704	14	6	OK	0.928	IC50 = 2.81 mM
L-Glca-[150]	13.918	42.051	8.928	33	6	OK	0.255	IC50 = 13.5 mM
L-Glca-[500]	10.519	0.000	0.066	17	6	OK	0.478	IC50 = 0.01 mM
L-Glca-[4000]	447.668	0.000	0.433	68	6	OK	0.818	IC50 = 0.119 mM
L-Glcb-[20]	NA	NA	NA	68	6	Fit failed	NA	IC50: NA
L-Glcb-[50]	18.222	10.699	0.010	13	6	OK	0.119	IC50 = 297 mM
L-Glcb-[150]	19.694	22.534	10.000	35	6	OK	0.031	IC50 = 42.6 mM
L-Glcb-[500]	NA	NA	NA	37	6	Fit failed	NA	IC50: NA
L-Glcb-[4000]	10.918	7.031	0.010	12	6	OK	0.062	IC50 = 0.0167 mM
D-Glcb-[20]	23.955	40.680	0.010	72	6	OK	0.061	IC50 = 80.1 mM
D-Glcb-[50]	15.824	44.680	0.010	44	6	OK	0.169	IC50 = 227 mM
D-Glcb-[150]	25.750	44.194	0.010	56	6	OK	0.133	IC50 = 83.2 mM
D-Glcb-[500]	23.208	285.963	10.000	48	6	OK	0.277	IC50 = 130 mM
D-Glcb-[4000]	975.701	9.922	9.552	100	6	OK	0.465	IC50 = 6.81 mM
L-Gala-[500]	21.615	0.527	9.998	68	6	OK	0.922	IC50 = 6.16 mM
L-Gala-[4000]	827.225	0.000	1.605	89	6	OK	0.362	IC50 = 43.9 mM
L-Galb-[150]	13.743	10.447	10.000	6	6	OK	0.260	IC50 = 39.2 mM
L-Galb-[500]	32.089	26.113	2.759	61	6	OK	0.049	IC50 = 3.65 mM
L-Galb-[4000]	425.253	19.041	5.261	81	6	OK	0.504	IC50 = 23.7 mM
D-Galb-[20]	66.209	80.265	0.010	47	6	OK	0.009	IC50 = 0.0478 mM
D-Galb-[50]	42.471	31.009	10.000	52	6	OK	0.154	IC50 = 14.4 mM
D-Galb-[150]	25.808	343.174	10.000	71	6	OK	0.052	IC50 = 148 mM
D-Galb-[500]	52.584	31.886	10.000	54	6	OK	0.157	IC50 = 9.75 mM
D-Galb-[4000]	21.449	567.713	10.000	38	6	OK	0.210	IC50 = 150 mM
L-Mana-[20]	14.417	19.141	0.010	6	6	OK	0.121	IC50 = 94.4 mM
L-Mana-[150]	14.378	4.206	1.257	6	6	OK	0.983	IC50 = 0.971 mM
L-Mana-[500]	NA	NA	NA	23	6	Fit failed	NA	IC50: NA
L-Mana-[4000]	57.175	62.808	0.010	43	6	OK	0.002	IC50 = 0.0116 mM
D-Mana-[4000]	27.331	0.114	10.000	84	6	OK	0.774	IC50 = 21.3 mM
L-Fuca-[20]	32.860	39.690	10.000	14	6	OK	0.333	IC50 = 11 mM
L-Fuca-[150]	15.214	1.628	2.343	12	6	OK	0.855	IC50 = 2.74 mM
L-Fuca-[500]	1845.453	0.000	0.844	14	6	OK	0.869	IC50 = 5.8 mM
L-Fuca-[4000]	17.371	38.330	1.800	51	6	OK	0.156	IC50 = 1.46 mM
L-Fucb-[20]	21.257	16299.465	10.000	16	6	OK	0.497	IC50 = 199 mM
L-Fucb-[50]	35.034	27.901	2.921	12	6	OK	0.072	IC50 = 3.85 mM
L-Fucb-[150]	23.233	1323.536	10.000	12	6	OK	0.812	IC50 = 148 mM
L-Fucb-[500]	1696.232	46.143	10.000	14	6	OK	0.993	IC50 = 3.07 mM
L-Fucb-[4000]	105.472	3.584	6.666	43	6	OK	0.642	IC50 = 35.5 mM
D-Fuca-[20]	16.263	36.200	10.000	12	6	OK	0.705	IC50 = 11.3 mM
D-Fuca-[50]	NA	NA	NA	14	6	Fit failed	NA	IC50: NA
D-Fuca-[150]	48.703	25.575	3.218	6	6	OK	0.258	IC50 = 3.61 mM
D-Fuca-[500]	87.739	34.770	5.808	12	6	OK	0.415	IC50 = 3.57 mM
D-Fuca-[4000]	13.790	0.036	0.010	6	6	OK	0.278	IC50 = 0.013 mM
D-Fucb-[20]	62.438	21.547	8.316	12	6	OK	0.415	IC50 = 3.72 mM
D-Fucb-[500]	27.191	21.916	0.010	6	6	OK	0.168	IC50 = 0.0278 mM
D-Fucb-[4000]	22.935	19.580	0.010	14	6	OK	0.175	IC50 = 118 mM
AzOH-[100]	48.882	13.532	0.010	20	6	OK	0.180	IC50 = 0.0106 mM
AzOH-[500]	16.092	6.039	0.963	39	6	OK	0.092	IC50 = 50.9 mM

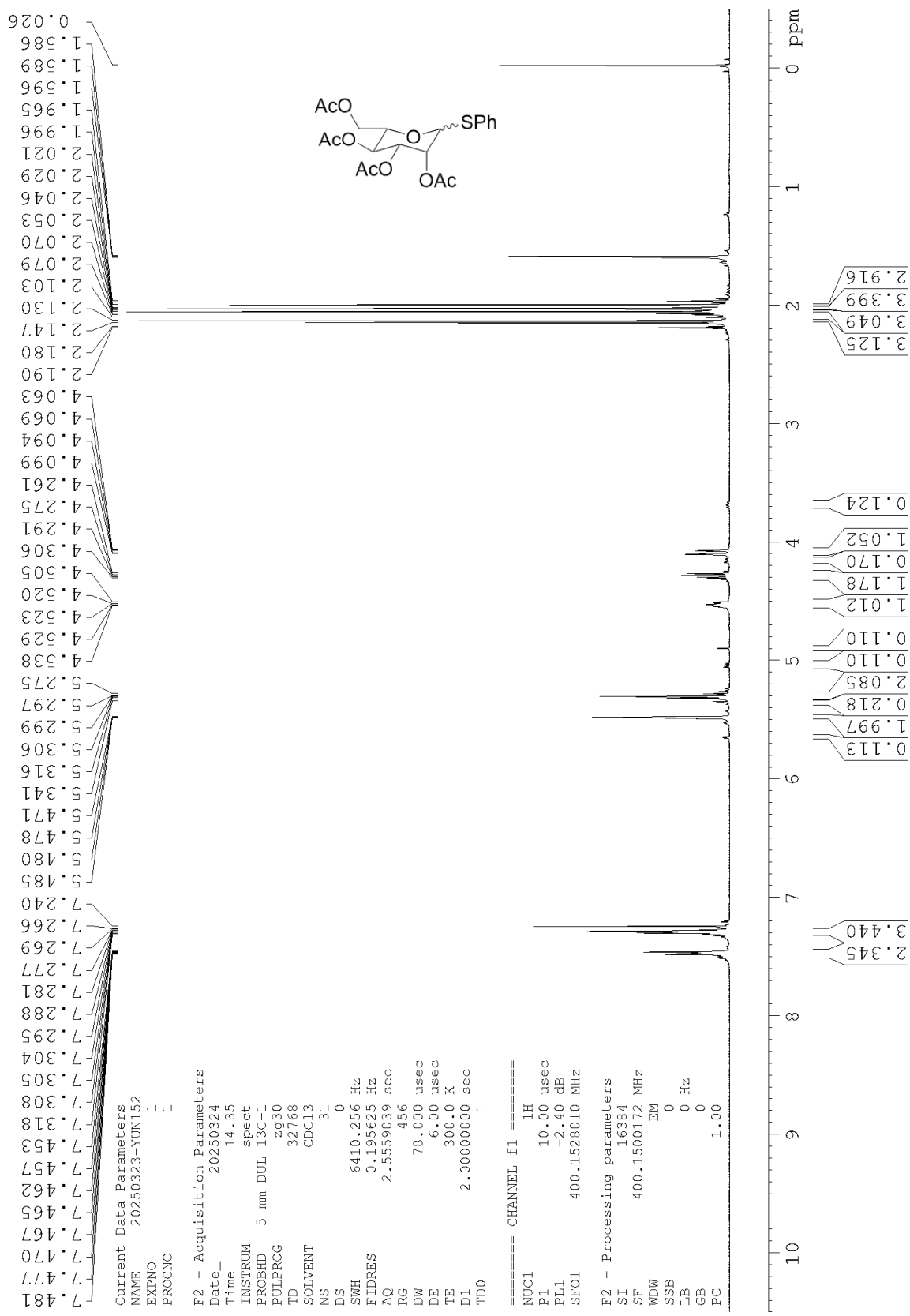
Table S5. Fitted IC₅₀ for inhibition of glycoproteins binding to DC-SIGN⁺ Raji by free D-Man. Mirror-LiGA was incubated with DC-SIGN⁺ Raji cells in the presence of increasing concentrations of free D-(+)-mannose. Sequencing counts for each glycoprotein were normalized to those of the internal standard (unmodified blank phage) and fitted to inhibition curves. Fitted IC₅₀ values with good fits ($R^2 > 0.75$) were highlighted in green, whereas those with moderate fits ($0.40 < R^2 \leq 0.75$) were highlighted in yellow. Glycans showing no enrichment in the absence of D-Man (0 mM) were excluded from the analysis. (Fig. 3 and fig. S3).

Glycan	Display density	MEG	MOX	MOY	PW
α -L-Man	[20]	Y	Y	Y	Y
α -L-Man	[50]	Y	Y	Y	Y
α -L-Man	[150]	Y	Y	Y	Y
α -L-Man	[500]	Y	Y	Y	Y
α -L-Man	[4000]	N	Y	Y	Y
α -D-Man	[20]	Y	Y	Y	Y
α -D-Man	[50]	Y	Y	Y	Y
α -D-Man	[150]	Y	Y	Y	Y
α -D-Man	[500]	Y	Y	Y	Y
α -D-Man	[4000]	N	Y	Y	Y
α -L-Glc	[20]	N	Y	Y	Y
α -L-Glc	[50]	N	Y	Y	Y
α -L-Glc	[150]	N	Y	Y	Y
α -L-Glc	[500]	N	Y	Y	Y
α -L-Glc	[4000]	N	N	N	N
β -L-Glc	[20]	N	Y	Y	Y
β -L-Glc	[50]	N	Y	Y	Y
β -L-Glc	[150]	N	Y	Y	Y
β -L-Glc	[500]	N	Y	Y	Y
β -L-Glc	[4000]	N	N	N	N
β -D-Glc	[20]	N	Y	Y	Y
β -D-Glc	[50]	N	Y	Y	Y
β -D-Glc	[150]	N	Y	Y	Y
β -D-Glc	[500]	N	Y	Y	Y
β -D-Glc	[4000]	N	N	Y	Y
α -L-Gal	[20]	N	Y	Y	Y
α -L-Gal	[50]	N	Y	Y	Y
α -L-Gal	[150]	N	Y	Y	Y
α -L-Gal	[500]	N	Y	Y	Y
α -L-Gal	[4000]	N	Y	Y	Y
β -L-Gal	[20]	N	Y	Y	Y
β -L-Gal	[50]	N	Y	Y	Y
β -L-Gal	[150]	N	Y	Y	Y
β -L-Gal	[500]	N	Y	Y	Y
β -L-Gal	[4000]	N	Y	Y	Y
β -D-Gal	[20]	N	Y	Y	Y
β -D-Gal	[50]	N	Y	Y	Y
β -D-Gal	[150]	N	Y	Y	Y
β -D-Gal	[500]	N	Y	Y	Y
β -D-Gal	[4000]	N	Y	Y	Y

Table S6. LiGA used in in vivo glycan binding profiling.

LiGA used for in vivo organ homing analysis of glycosylated phages in four independent campaigns: MEG (20241030; n = 3 mice, with each mouse sequenced twice), MOX (20250707; n = 3 mice), MOY (20250716; n = 2 mice), and PW (20250926; n = 3 mice). MEG, MOX, MOY, and PW are different LiGAs. **Y**, the glycosylated phage exists in the tested LiGA; N, the glycosylated phage absents in the tested LiGA.





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Current Data Parameters
NAME 20250323-YUN153-middle
```

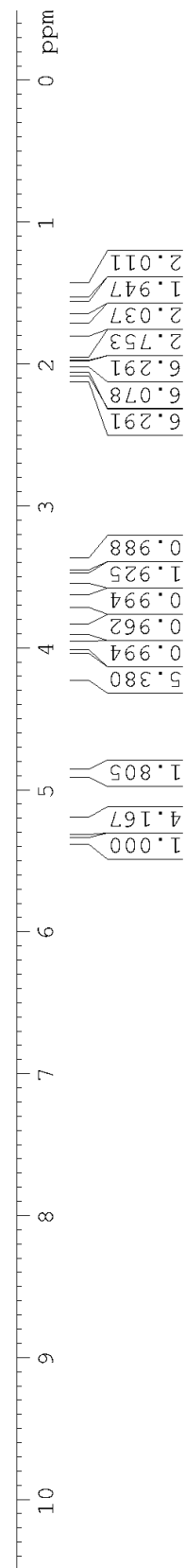
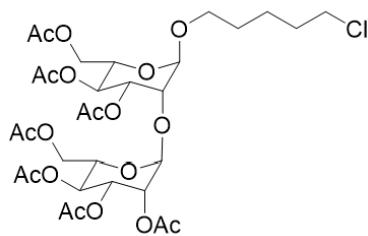
NAME	EXPNO	PROCNO
	1	1

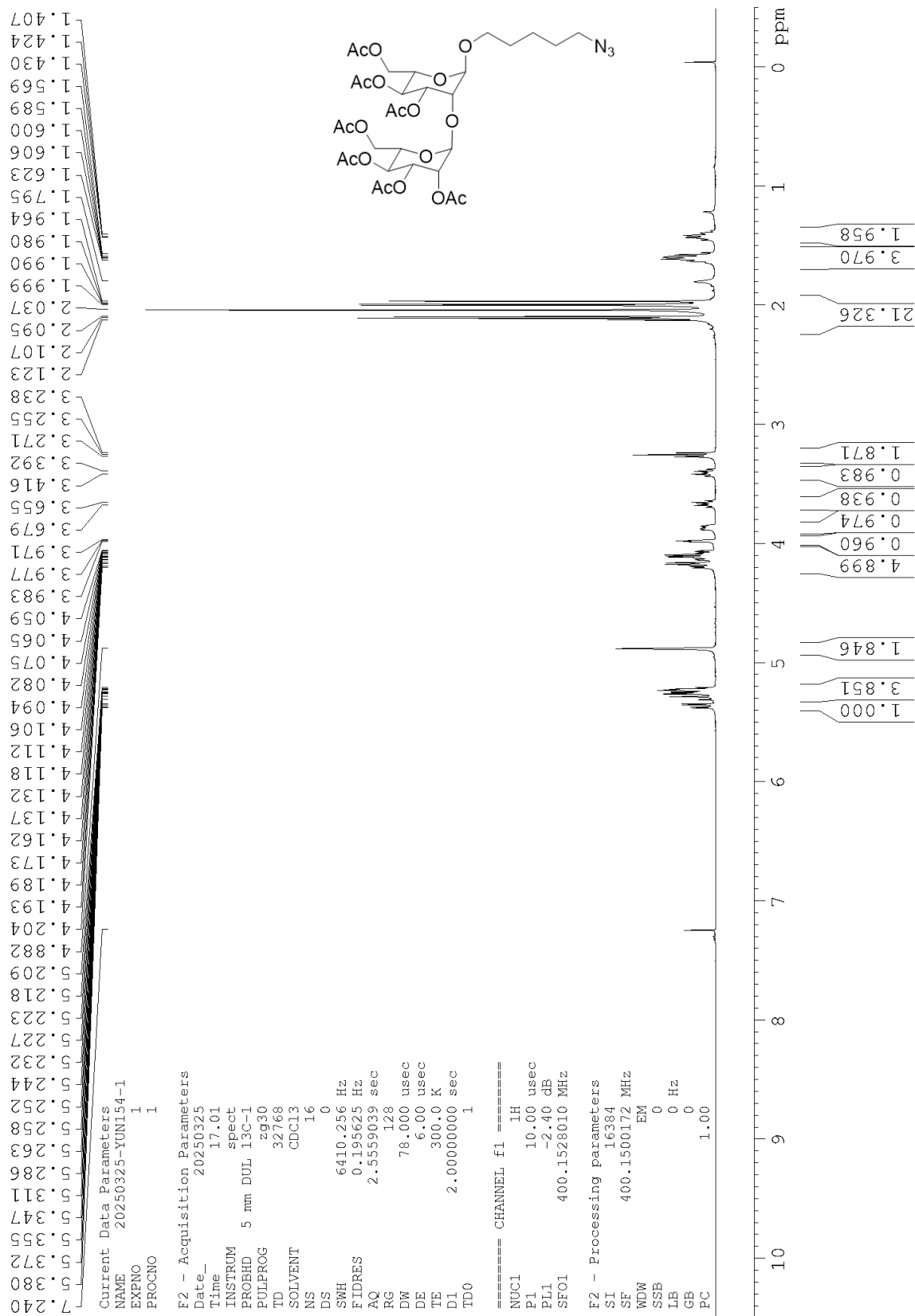
F2 - Acquisition Parameters

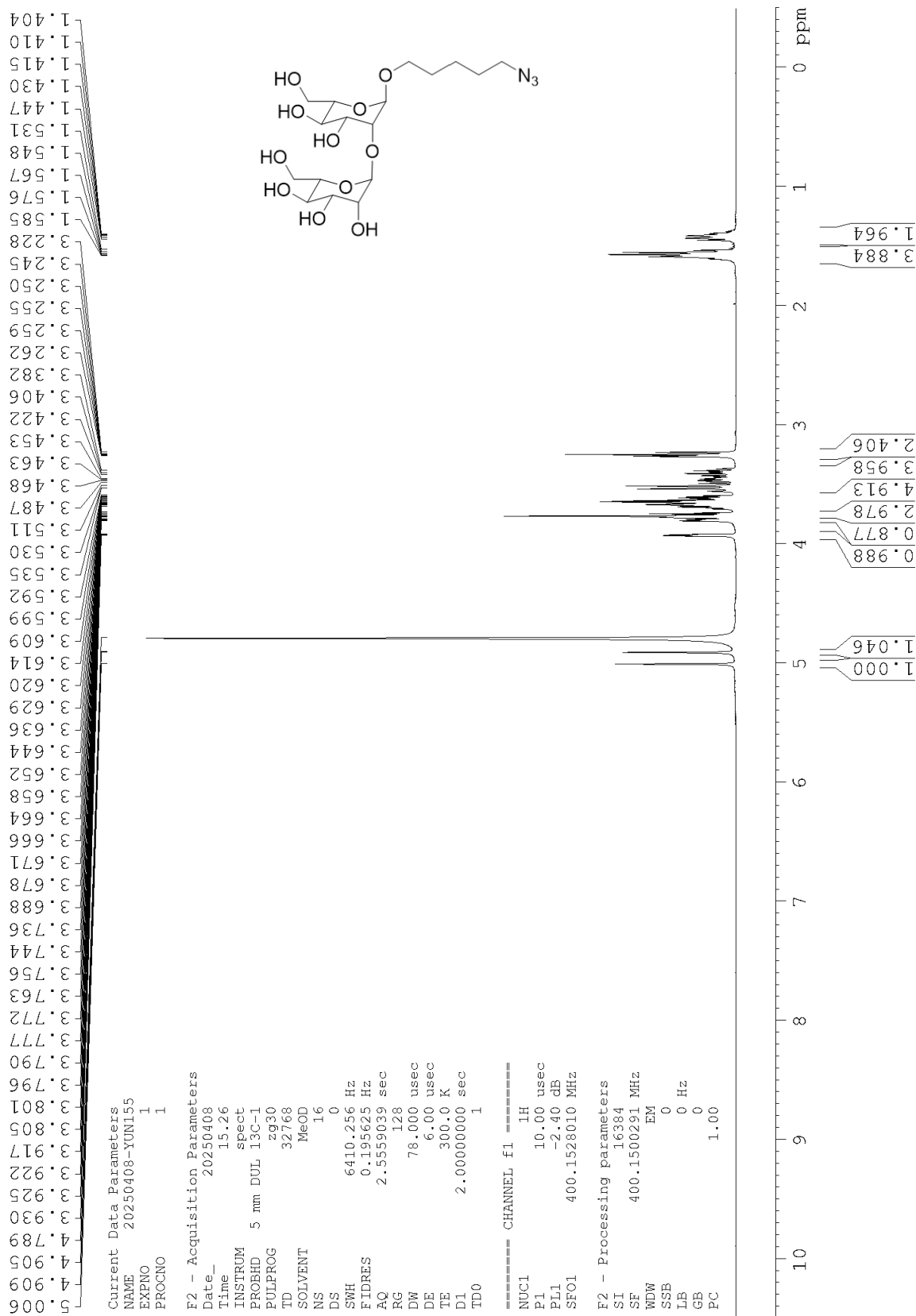
Date_	20250324	
Time	14.30	
INSTRUM	spect	
PROBHD	5 mm DUL 13C-1	
PULPROG	zg30	
TD	32768	
SOLVENT	CDCl3	
NS	27	
DS	0	
SWH	6410.256 Hz	
FIDRES	0.195625 Hz	
AQ	2.5559039 sec	
RG	101	
DW	78.000 usec	
DE	6.00 usec	
TE	300.0 K	
D1	2.00000000 sec	
TD0	1	

```
===== CHANNEL f1 =====
NUC1      1H
P1        10.00 usec
PL1       -2.40 dB
SFO1      400.1528010 MHz
```

F2 - Processing parameters	
SI	16384
SF	400.1500171 MHz
WDW	EM
SSB	0
LB	0 Hz
GB	0
PC	1.00







```

Current Data Parameters
NAME      20250408-YUN155
EXPNO     2
PROCNO    1

F2 - Acquisition Parameters
Date_     20250408
Time      15.29
INSTRUM   spect
PROBHD    5 mm DUL 13C-1
PULPROG   zgpg30
TD        65536
SOLVENT   MeOD
NS         91
DS         0
SWH        22727.273 Hz
FIDRES     0.346791 Hz
AQ         1.4417920 sec
RG         2050
DW         22.000 usec
DE         6.00 usec
TE         300.0 K
D1         2.00000000 sec
d11        0.03000000 sec
DELTA     1.89999998 sec
TD0        1

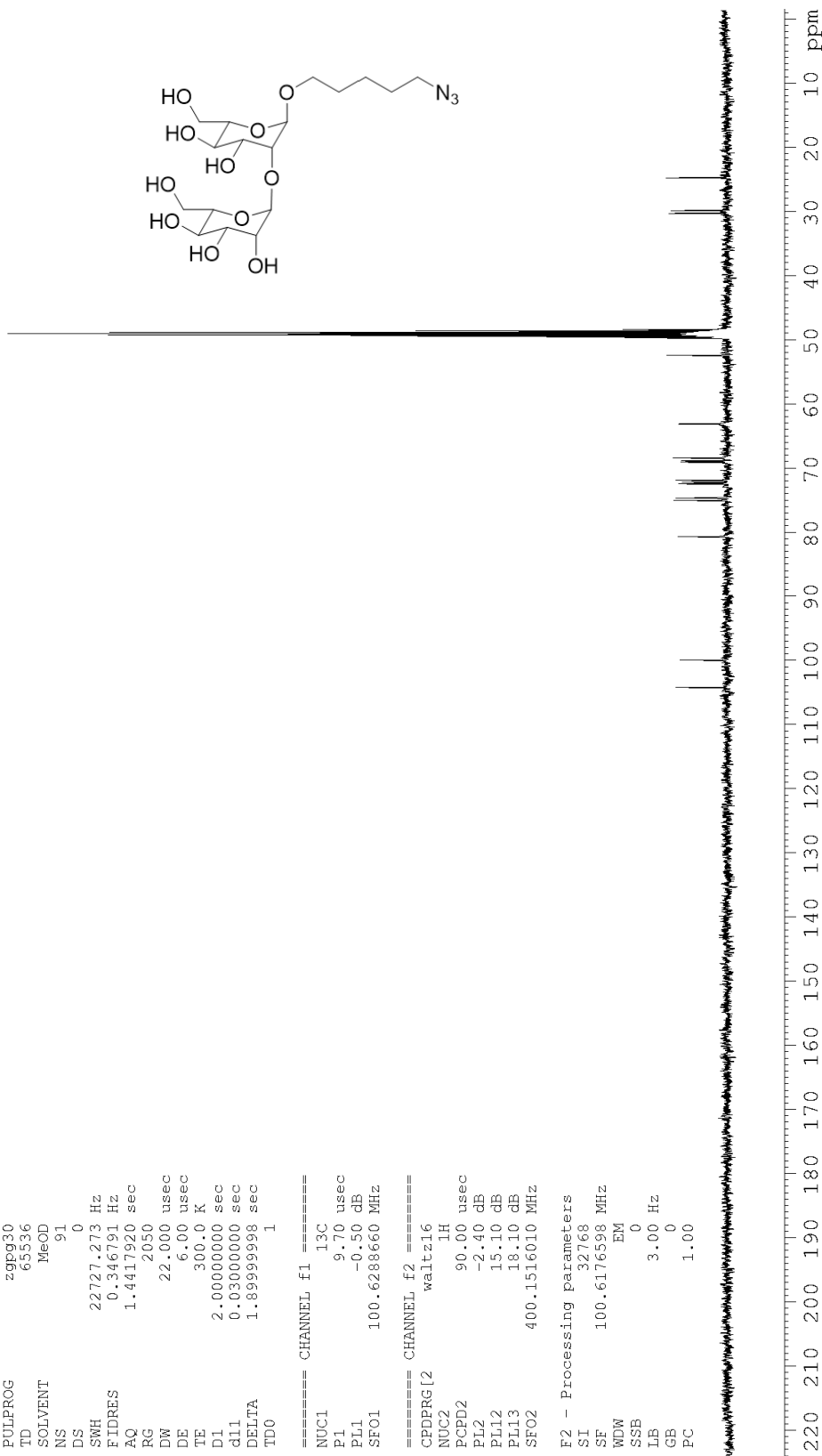
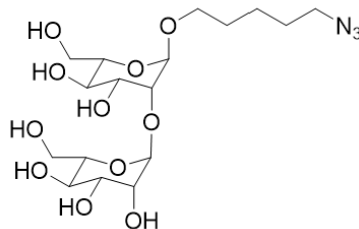
===== CHANNEL f1 =====
NUC1       13C
P1         9.70 usec
PL1        -0.50 dB
SFO1       100.6288660 MHz

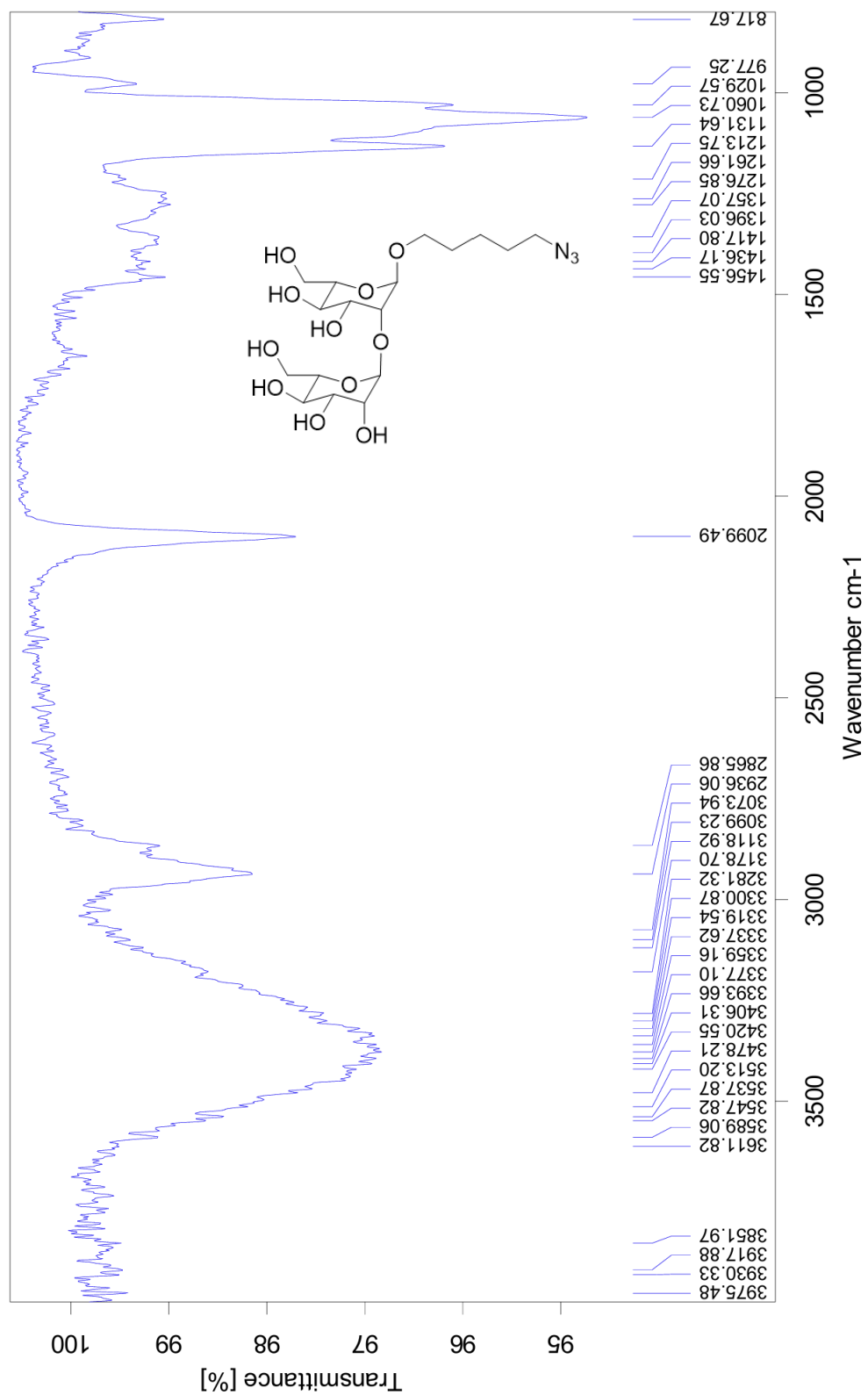
===== CHANNEL f2 =====
CPDPRG[2   waltz16
NUC2       1H
PCPD2      90.00 usec
PL2        -2.40 dB
PL12       15.10 dB
PL13       18.10 dB
SFO2       400.1516010 MHz

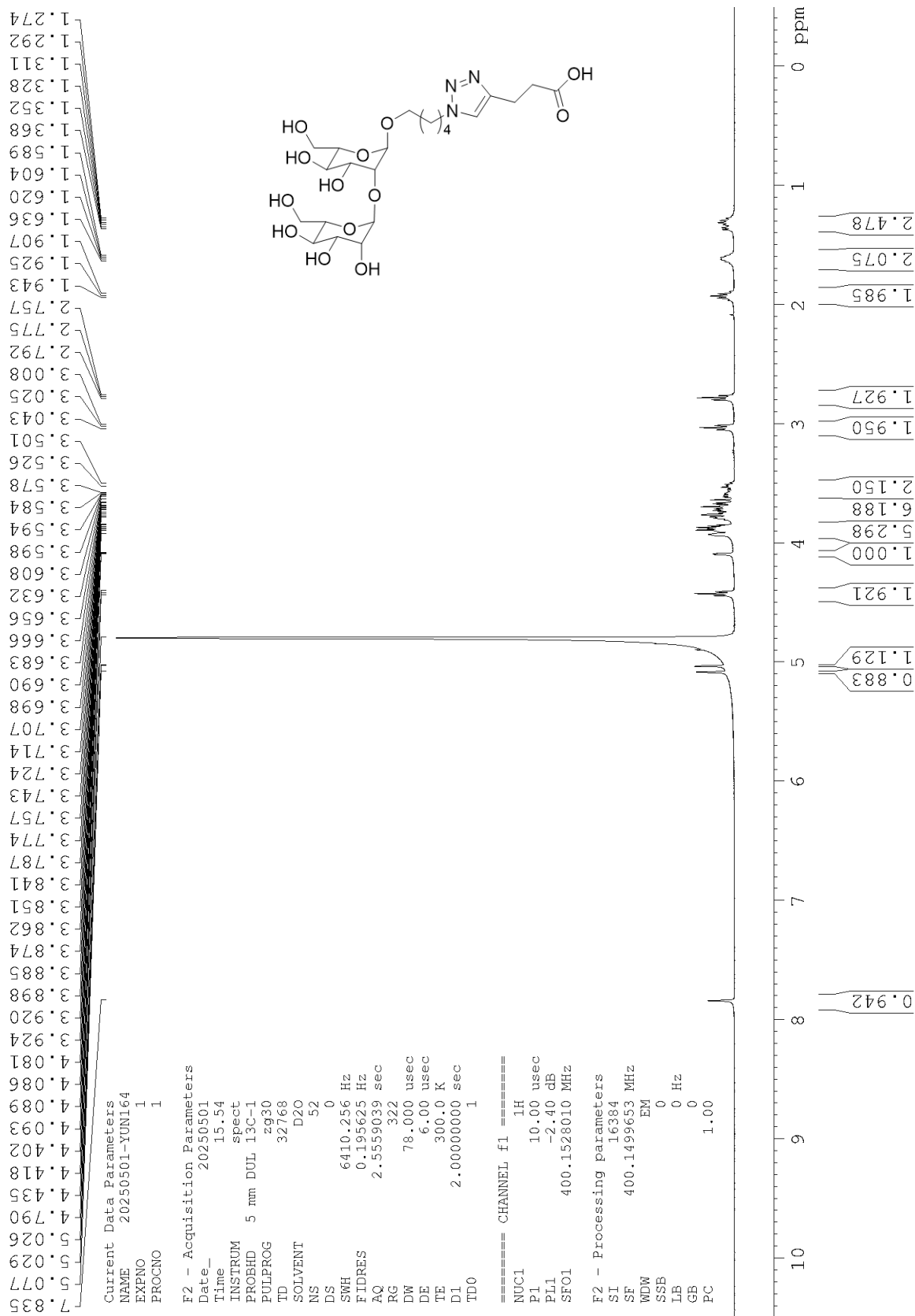
F2 - Processing parameters
SI         32768
SF         100.6176598 MHz
WDW        EM
SSB        0
LB         3.00 Hz
GB         0
PC         1.00

```

104.174
 99.900
 80.659
 74.982
 74.639
 72.408
 72.187
 71.852
 69.037
 68.823
 68.365
 63.127
 63.053
 52.365
 49.639
 49.426
 49.213
 49.000
 48.787
 48.574
 48.361
 30.102
 29.674
 24.558







```

Current Data Parameters
NAME      20250502-YUNI64-DATA
EXPNO     3
PROCNO    1

F2 - Acquisition Parameters
Date_     20250502
Time      8.26
INSTRUM   spect
PROBHD    5 mm DUL 13C-1
PULPROG   zgpg30
TD         65536
SOLVENT   D2O
NS         7458
DS         0
SWH        22727.273 Hz
FIDRES     0.346791 Hz
AQ         1.4417920 sec
RG         2050
DW         22.000 usec
DE         6.00 usec
TE         300.0 K
D1         2.00000000 sec
d11        0.03000000 sec
DELTA     1.89999998 sec
TD0        1

===== CHANNEL f1 =====
NUC1       13C
P1         9.70 usec
PL1        -0.50 dB
SFO1       100.6288660 MHz

===== CHANNEL f2 =====
CPDPRG[2   waltz16
NUC2        1H
PCPD2       90.00 usec
PL2         -2.40 dB
PL12        15.10 dB
PL13        18.10 dB
SFO2       400.1516010 MHz

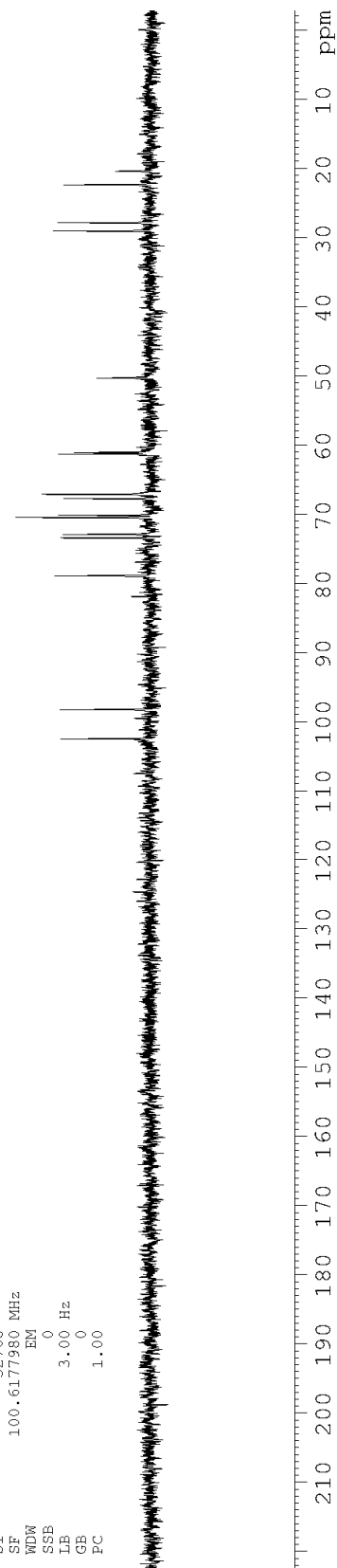
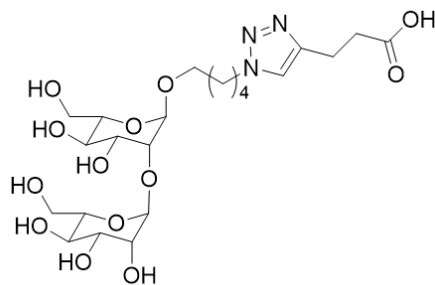
F2 - Processing parameters
SI         32768
SF         100.6177980 MHz
WDW        EM
SSB        0
LB         3.00 Hz
GB         0
PC         1.00

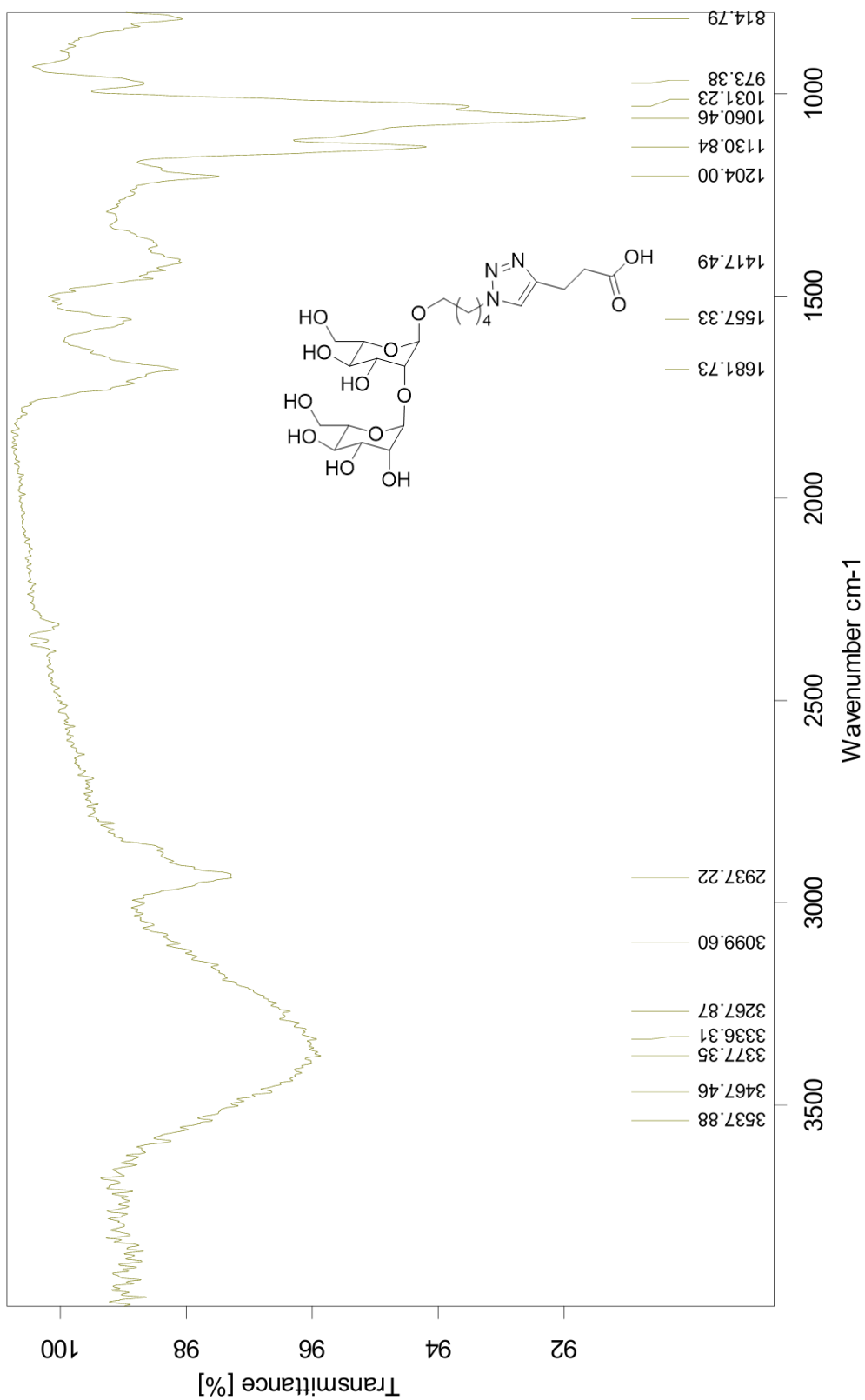
```

102.356
98.122

78.758
73.292
72.777
70.337
69.972
67.584
66.982
66.937
61.150
60.926
50.295

28.985
27.790
22.309
20.377





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