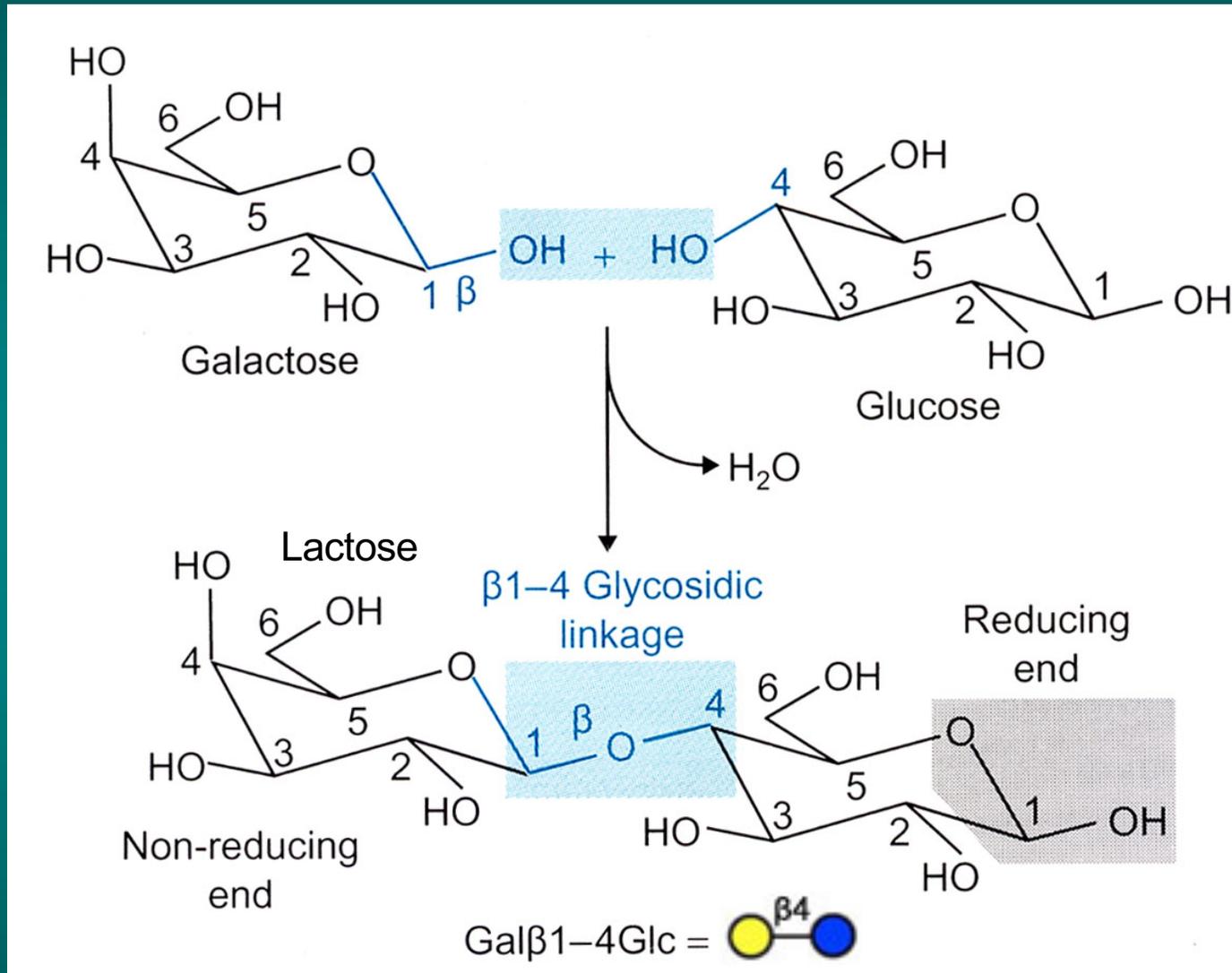
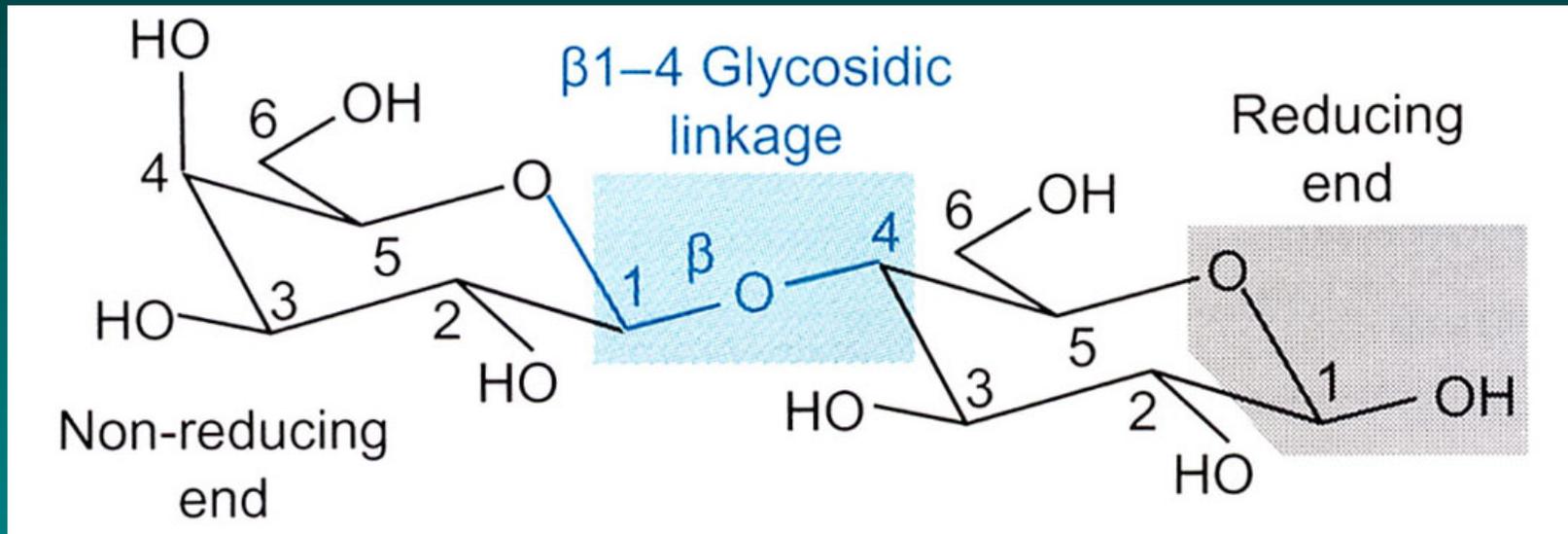


Glycosidic Bonds Link Sugars Together



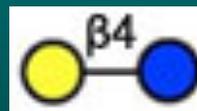
When glycosidic bond is formed the anomeric configuration is “locked”



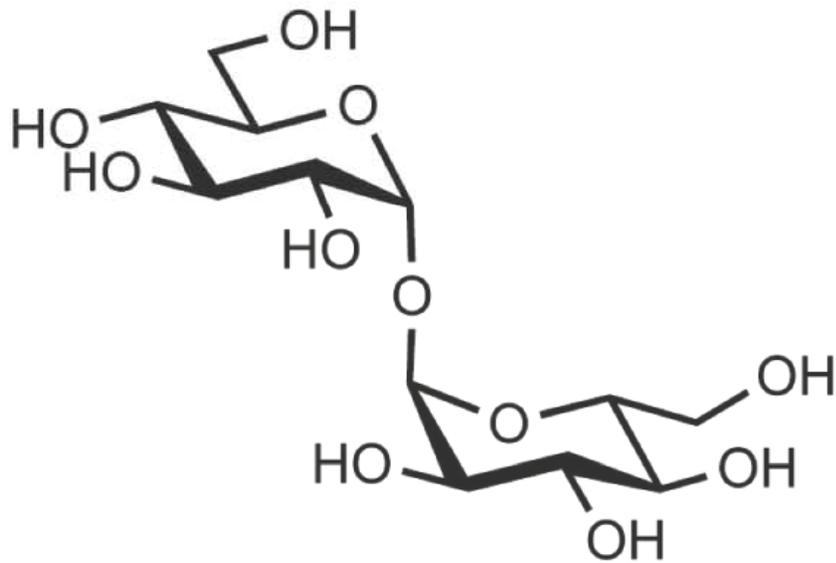
Nomenclature:

- Name the non-reducing (left-most) sugar (Gal)
- Name the anomeric configuration (β)
- Name the anomeric carbon number (1)
- Name the substituted carbon number (4)
- Name the substituted sugar (Glc)

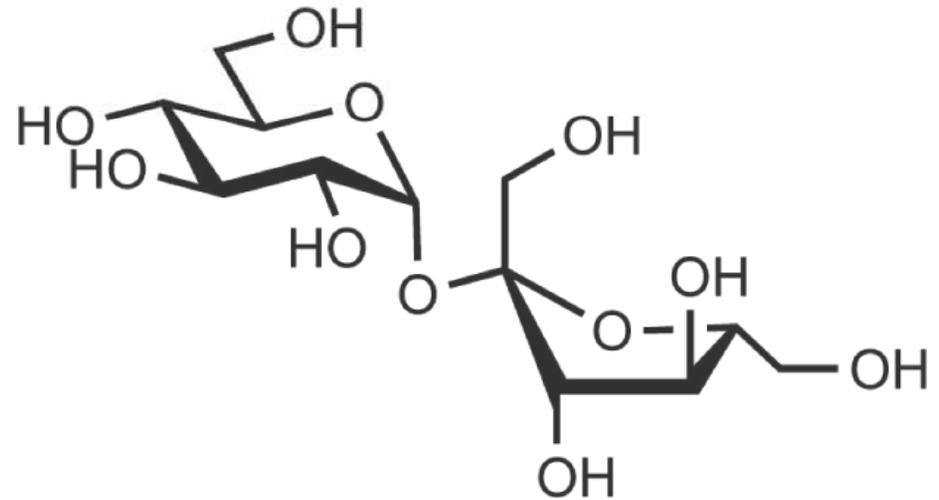
RESULT: Gal β 1-4 Glc



Two Common Non-Reducing Disaccharides

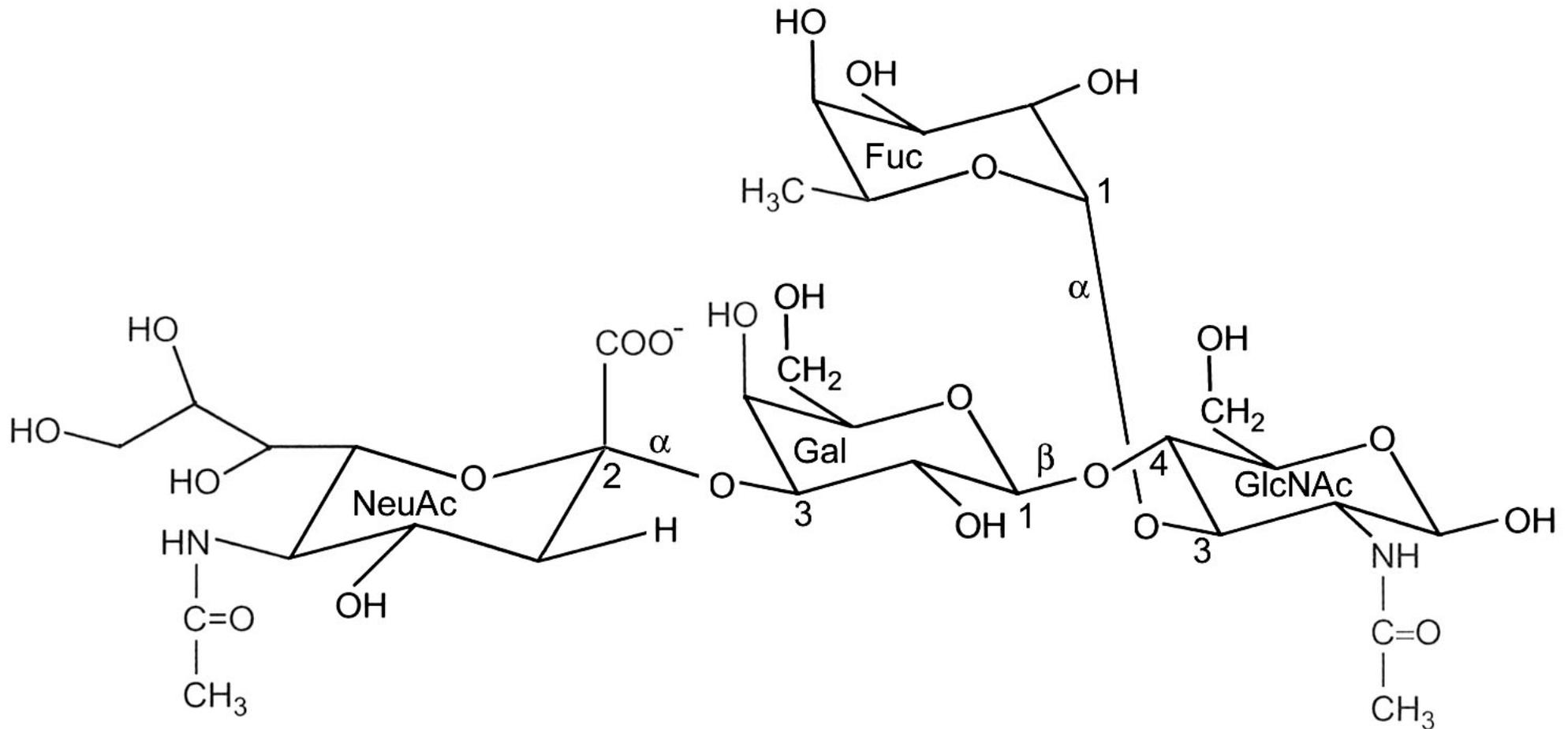


Glc α 1Glc α 1
(trehalose)

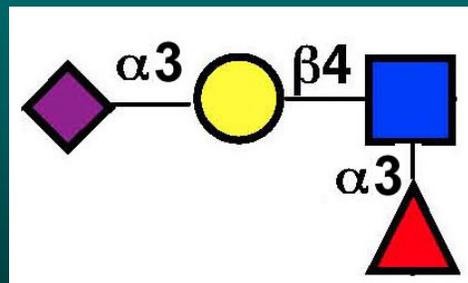


Glc α 2Fru β
(sucrose)

Nomenclature: Branches are Placed in Parentheses

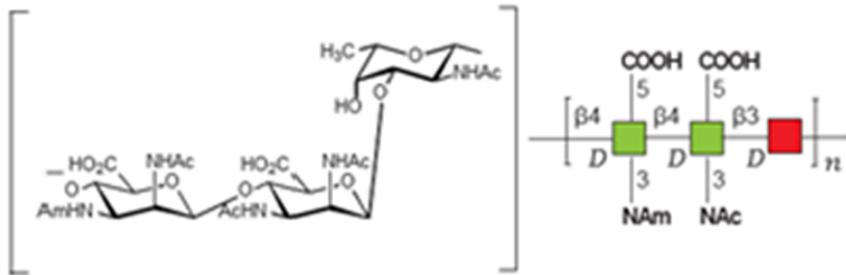


NeuAc α 2-3 Gal β 1-4 (Fuc α 1-3)
GlcNAc



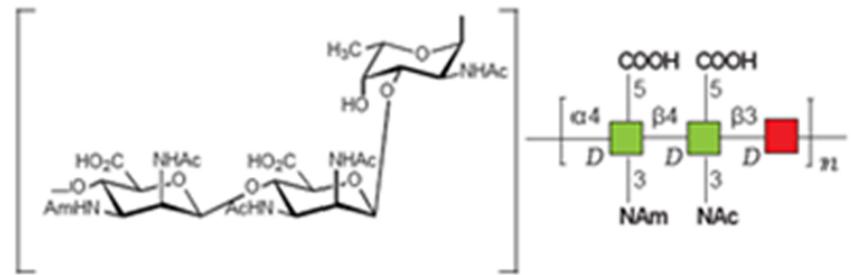
Examples of Complex Bacterial Polysaccharides

Pseudomonas aeruginosa O2a, O2b (IATS 16)



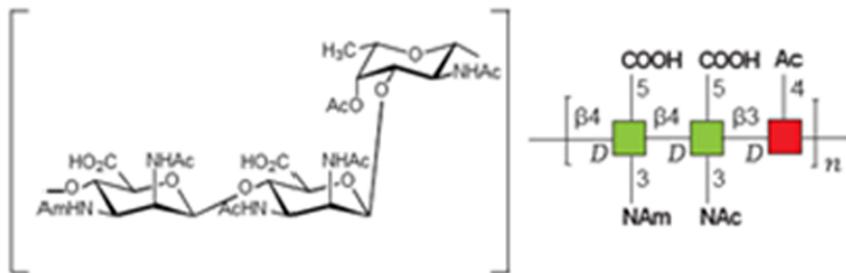
$[4\text{-}\beta\text{-D-ManpNAcA3NAc(1}\rightarrow\text{4)-}\beta\text{-D-ManpNAcA3NAc(1}\rightarrow\text{3)-}\beta\text{-D-FucpNAc(1}\rightarrow\text{4)-}]_n$

Pseudomonas aeruginosa O2a, O2d (IATS 5)



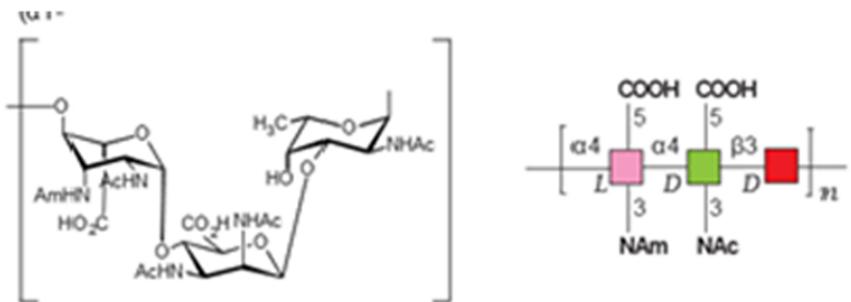
$[4\text{-}\beta\text{-D-ManpNAcA3NAc(1}\rightarrow\text{4)-}\beta\text{-D-ManpNAcA3NAc(1}\rightarrow\text{3)-}\alpha\text{-D-FucpNAc(1}\rightarrow\text{4)-}]_n$

Pseudomonas aeruginosa O2a, O2b, O2e



$[4\text{-}\beta\text{-D-ManpNAcA3NAc(1}\rightarrow\text{4)-}\beta\text{-D-ManpNAcA3NAc(1}\rightarrow\text{3)-}\beta\text{-D-FucpNAc4Ac(1}\rightarrow\text{4)-}]_n$

Pseudomonas aeruginosa O2 (IATS 18, FI 7)



$[4\text{-}\alpha\text{-L-GulpNAcA3NAc(1}\rightarrow\text{4)-}\beta\text{-D-ManpNAcA3NAc(1}\rightarrow\text{3)-}\alpha\text{-D-FucpNAc(1}\rightarrow\text{4)-}]_n$

Glycan Symbol Nomenclature

Neutral Hexoses - Circles; N-Acetylhexosamines - Squares

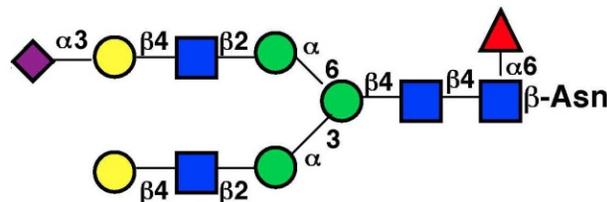
- Galactose stereochemistry: **Yellow (255,255,0)**  
- Glucose stereochemistry: **BLUE (0,0,250)**  
- Mannose stereochemistry: **GREEN (0,200,50)** 

Deoxysugar - Triangle; Penose - Star

- Fucose: **RED (250,0,0)** 
- Xylose: (5-pointed star) **ORANGE (250,100,0)** 

Acidic Sugars (Diamonds)

- Neu5Ac: **PURPLE (125,0,125)** 
- GlcA: **BLUE (0,0,250)/Upper segment** 



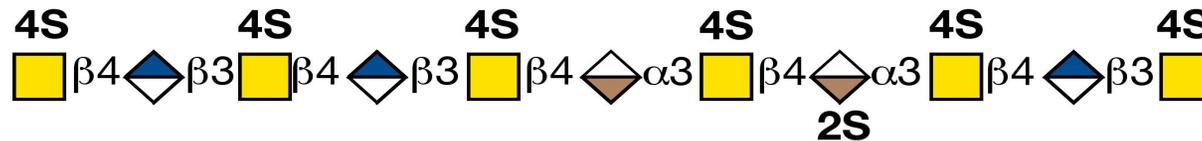
Symbolic Representation of Glycosaminoglycans

GlcNAc β 4GlcA β 3GlcNAc β 4GlcA β 3GlcNAc β 4GlcA β 3GlcNAc β 4GlcA β 3GlcNAc



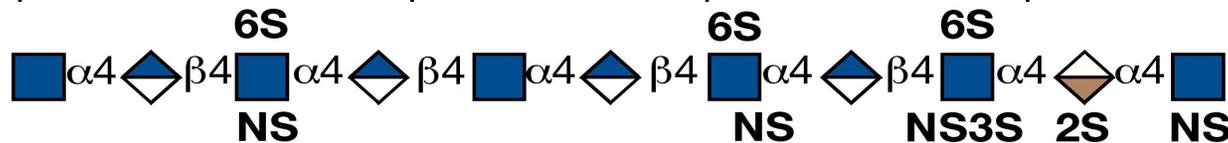
Hyaluronan

GalNAc4S β 4GlcA β 3GalNAc4S β 4IdoA α 3GalNAc4S β 4IdoA α 3GalNAc4S β 4IdoA2S α 3GalNAc4S β 4GlcA β 3GalNAc4S



Chondroitin/Dermatan Sulfate

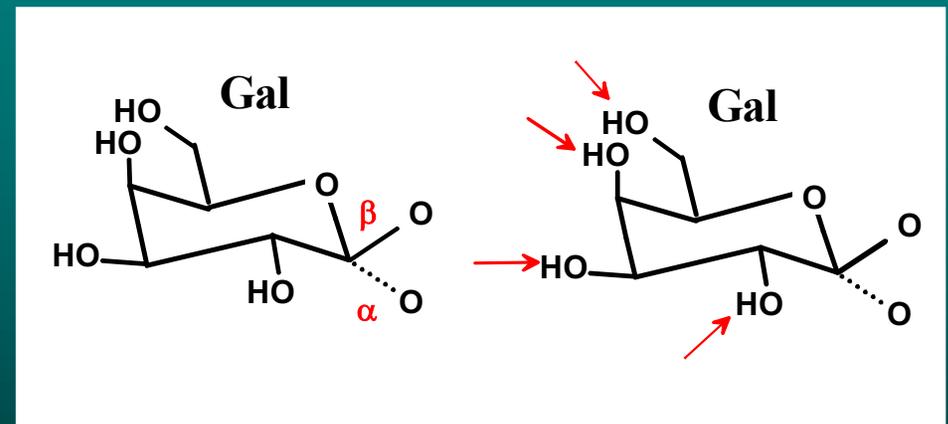
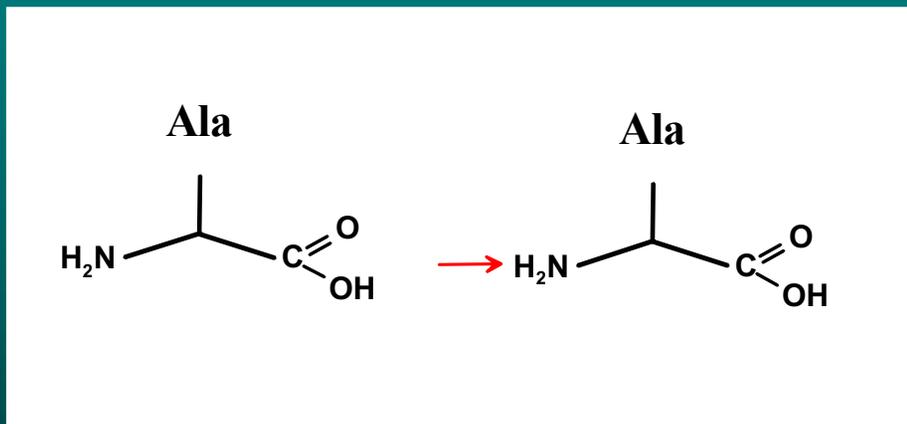
GlcNAc α 4GlcA β 4GlcNAcNS6S α 4GlcA β 4GlcNAc α 4GlcA β 4GlcNS6S α 4GlcA β 4GlcNS3S6S α 4IdoA2S α 4GlcNS



Heparan Sulfate/Heparin

Oligosaccharides: Molecular Diversity of Glycans

	<u>Polypeptides</u>	<u>Glycans</u>
Building blocks	amino acids	monosaccharides
Number of different monomers	20 common	9 common
Linkage sites per monomer	1	3-4
Possible linkage configurations	1	2
Possible homodimer structures	1	6-8
Linkage modes	linear	linear or branched



Man a1-4 Gal a1-3 Glc b1
Man a1-6 Gal a1-3 Glc b1
Man b1-2 Gal a1-3 Glc b1
Man b1-3 Gal a1-3 Glc b1
Man b1-4 Gal a1-3 Glc b1
Man b1-6 Gal a1-3 Glc b1
Man a1-2 Gal a1-4 Glc b1
Man a1-3 Gal a1-4 Glc b1
Man a1-4 Gal a1-4 Glc b1
Man a1-6 Gal a1-4 Glc b1
Man b1-2 Gal a1-4 Glc b1
Man b1-3 Gal a1-4 Glc b1
Man b1-4 Gal a1-4 Glc b1
Man b1-6 Gal a1-4 Glc b1
Man a1-2 Gal a1-6 Glc b1
Man a1-3 Gal a1-6 Glc b1

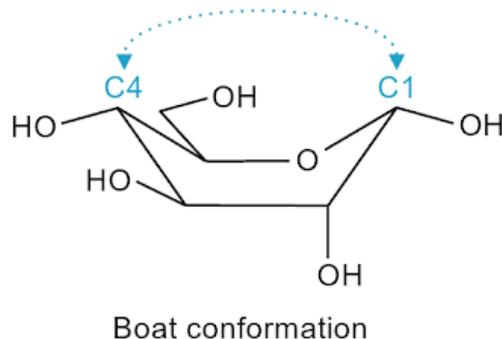
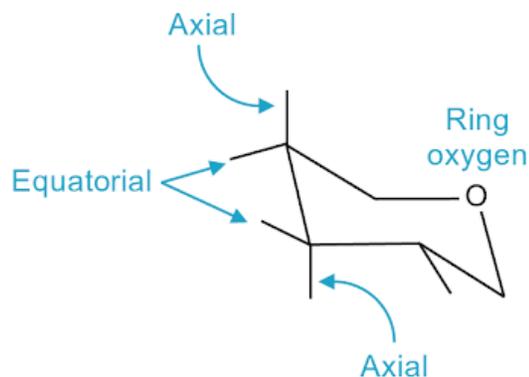
*Glycoproteins and glycolipids may contain ~3000 glycan determinants with an additional ~4000 theoretical pentasaccharide sequences in glycosaminoglycans

Cummings RD (2009) *Molecular BioSystems* 5, 1087

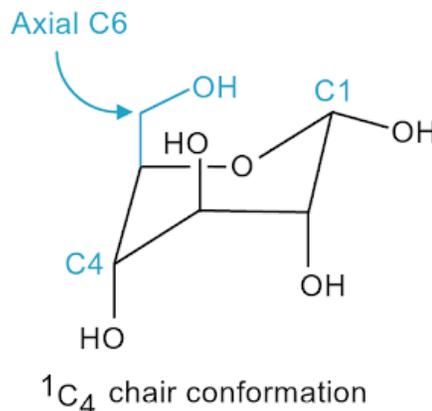
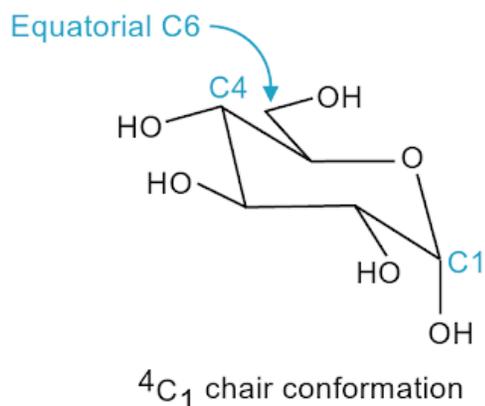
Types of Biomacromolecules

Macromolecule	Building Block	Aproximate Mass	Possible Variations in a Trimer
Protein	Amino acids	125 → 10⁴-10⁵	6
Nucleic Acid	Nucleotides	330 → 10³-10⁹	6
Lipid	Fatty acids	250 → 10³	NA
Carbohydrate	Monosaccharides	200 → 10²-10⁶	1,056 to 27,648!

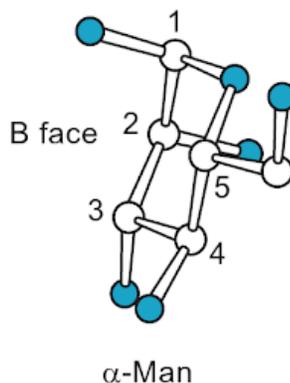
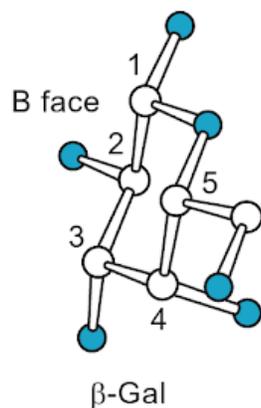
Monosaccharide Conformations



- crowding between H's at C1 and C4 destabilize the boat

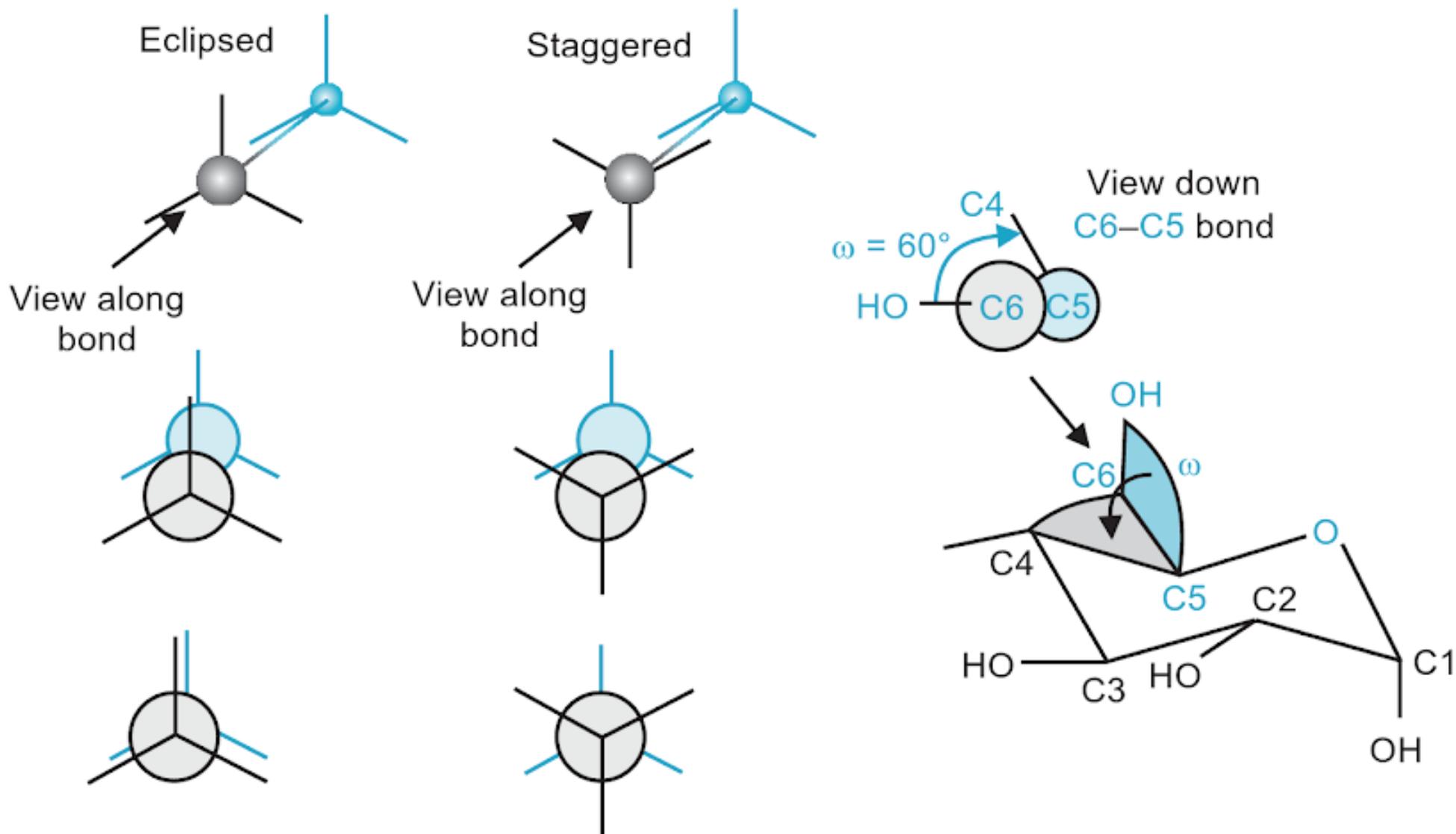


- hydroxyls at C2, C3 and C5 prefer to be equatorial

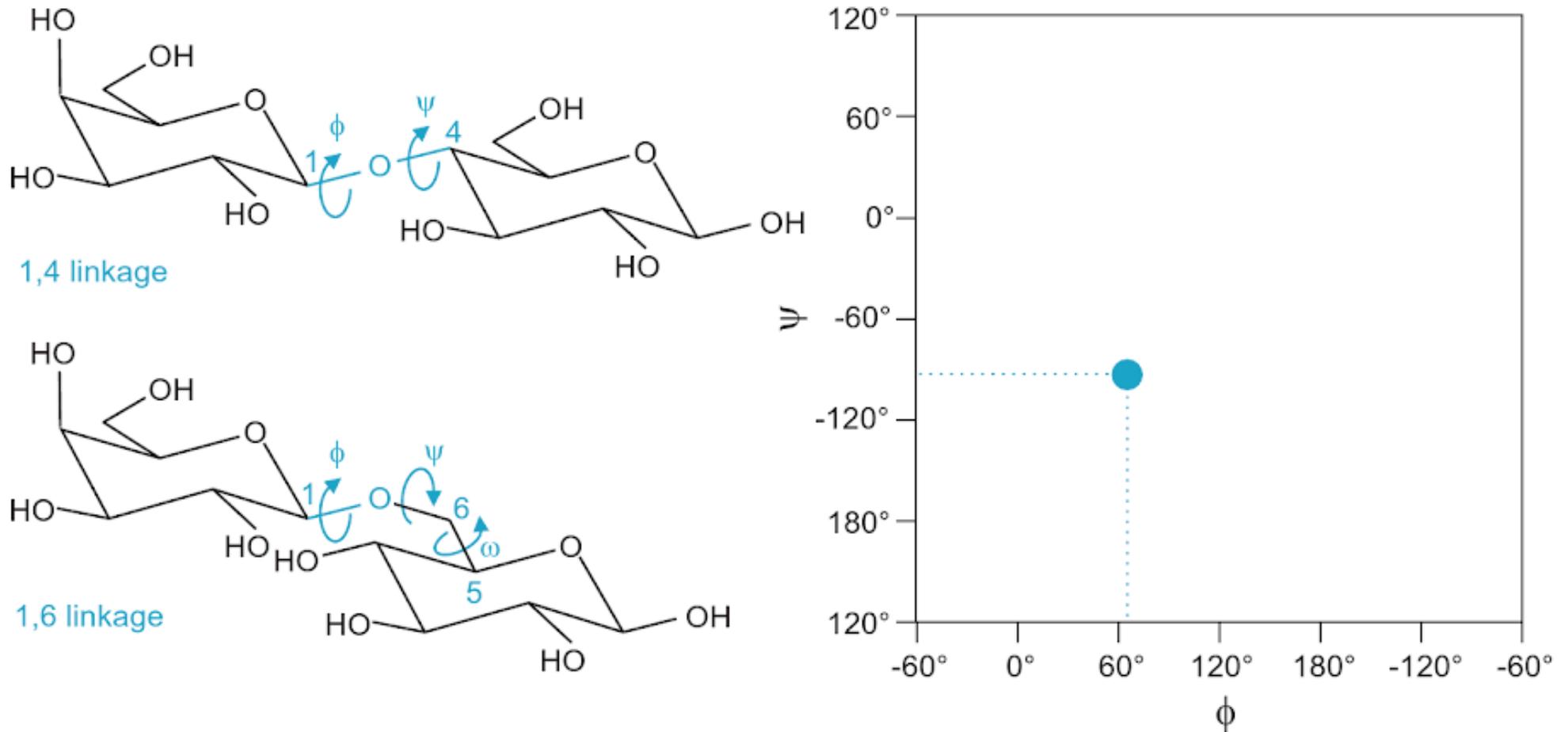


- the β face is the one where carbons are numbered in an anticlockwise arrangement

Newman Projections & Glycan Torsional Angles

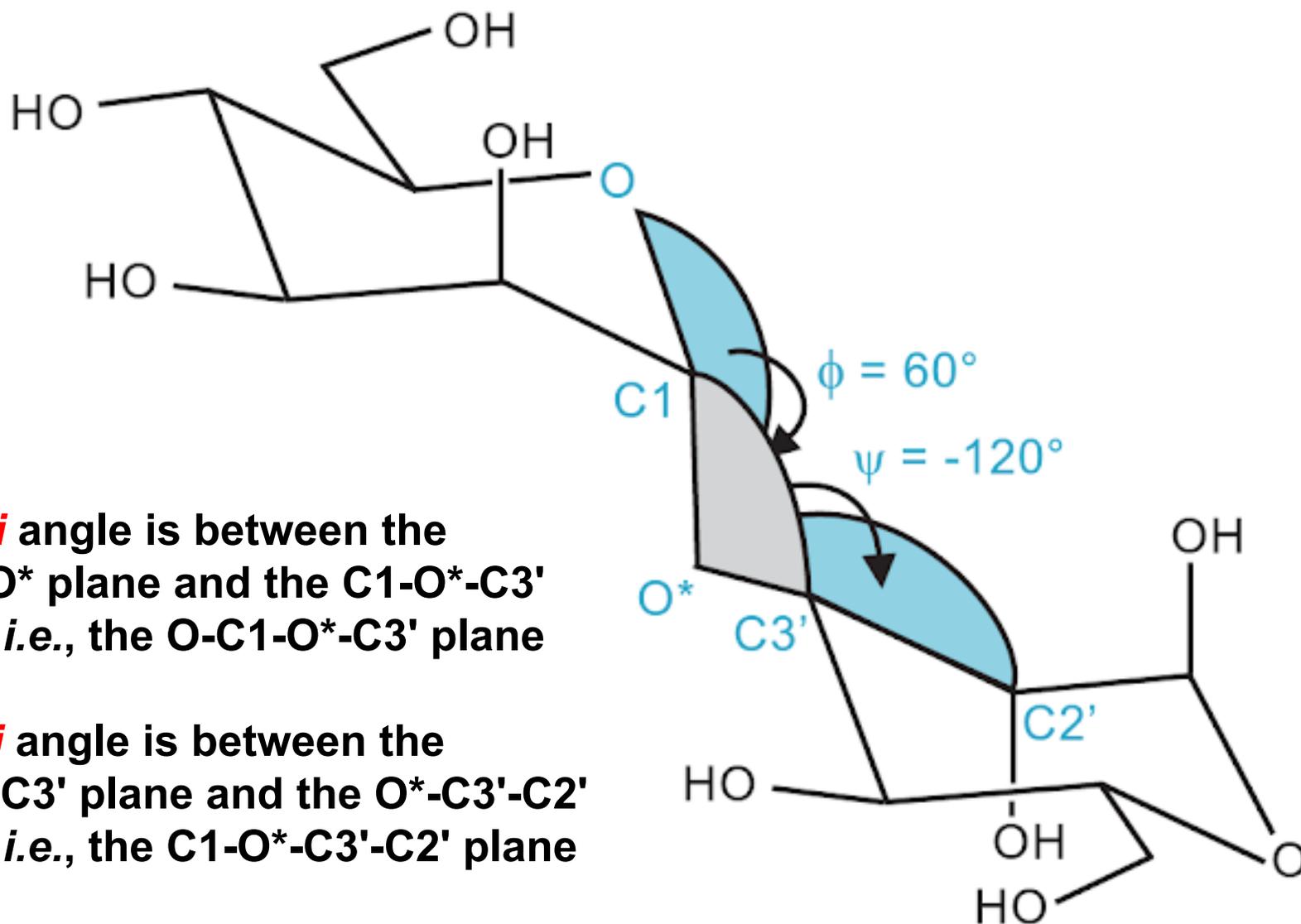


Glycosidic Linkages & Phi-Psi Plots



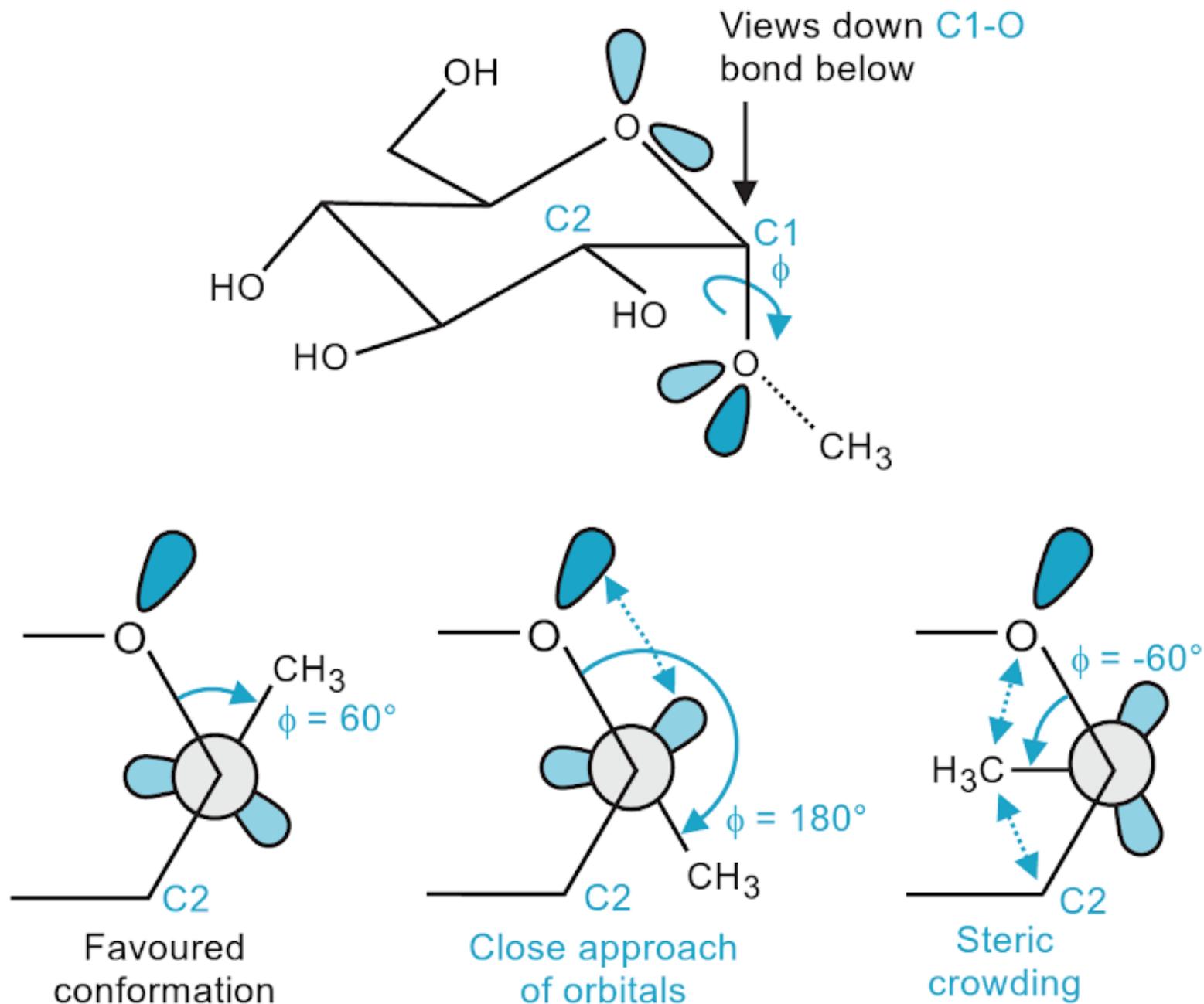
- an additional ω angle is required to describe a 1-6 linkage at the reducing monosaccharide

Definition of Linkage Torsion Angles

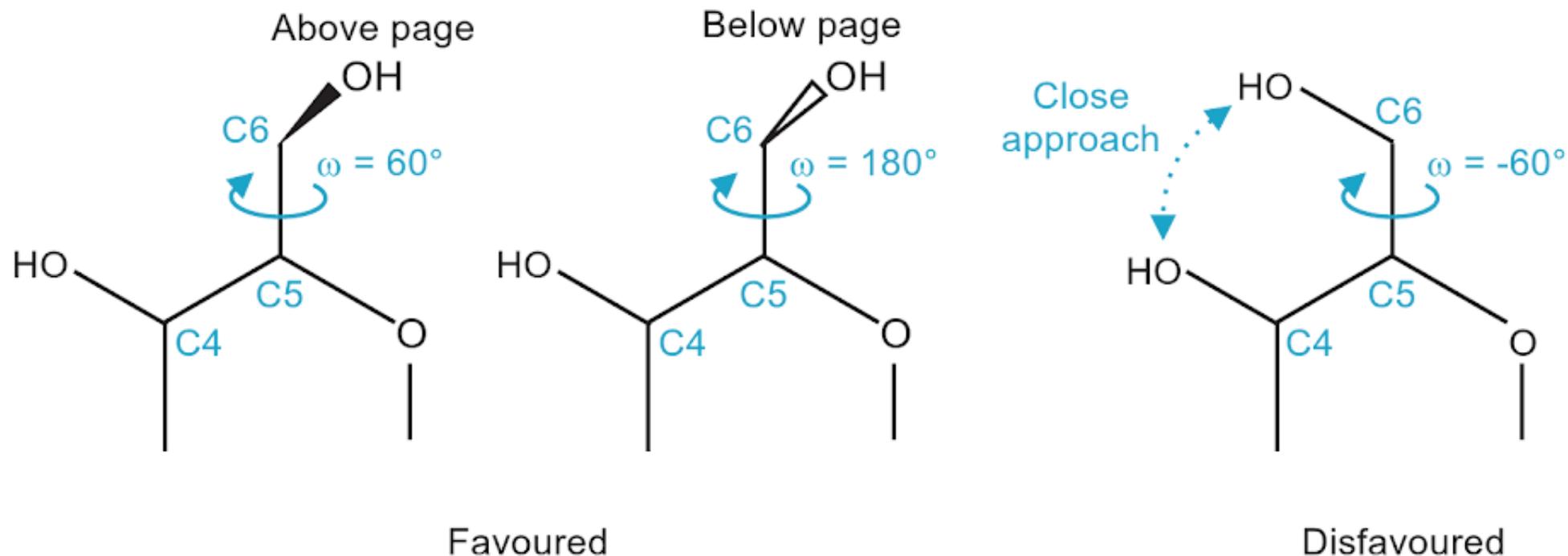


- the *phi* angle is between the O-C1-O* plane and the C1-O*-C3' plane, *i.e.*, the O-C1-O*-C3' plane
- the *psi* angle is between the C1-O*-C3' plane and the O*-C3'-C2' plane, *i.e.*, the C1-O*-C3'-C2' plane

Anomeric & Steric Effects for an α -Linkage

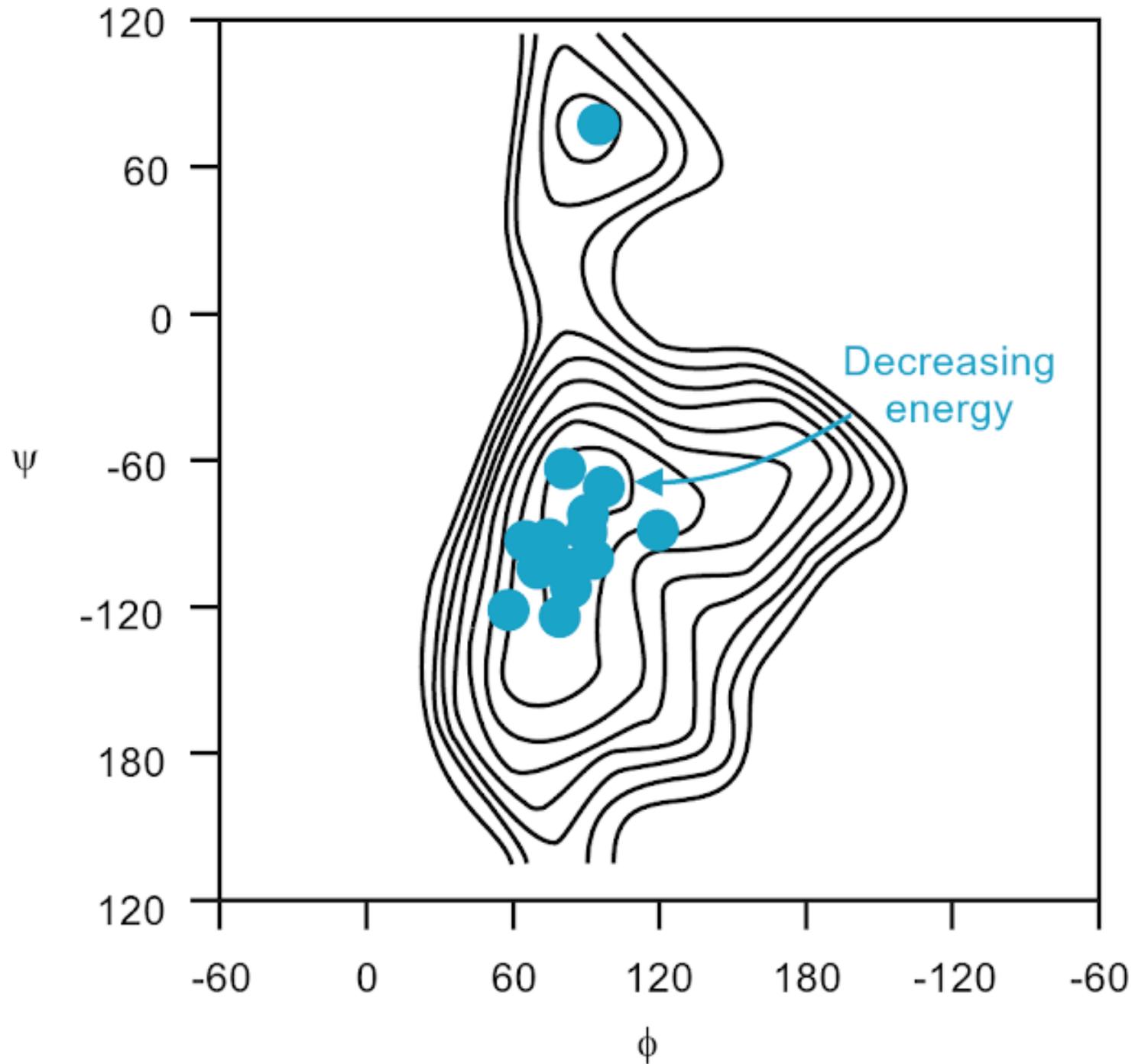


Conformational Constraint on the ω Angle

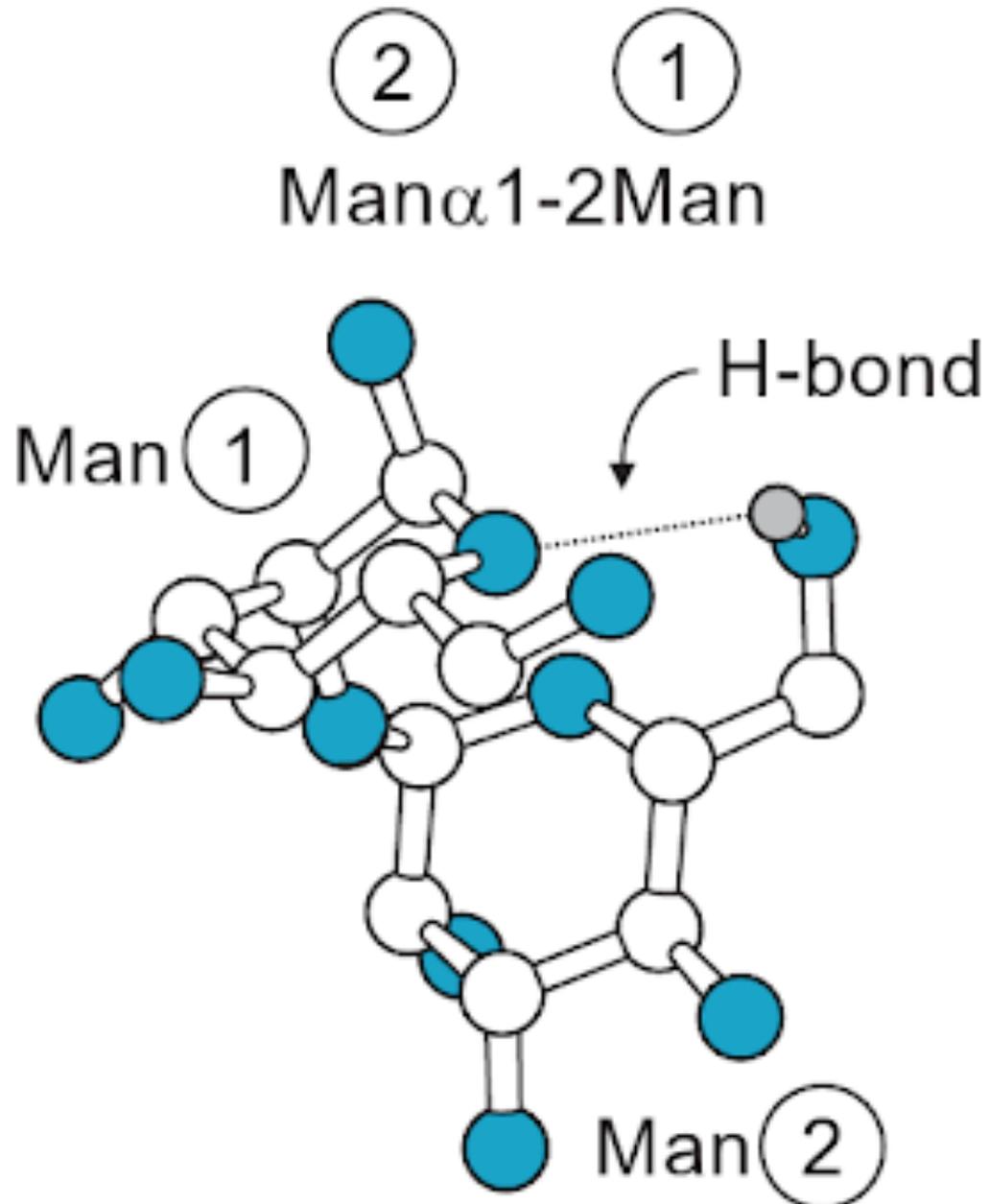


- the $\omega = -60$ angle is disfavoured due to steric clash between hydroxyl groups at C4 and C6

Energy Contour Map for Man $\alpha 1-3$ Man



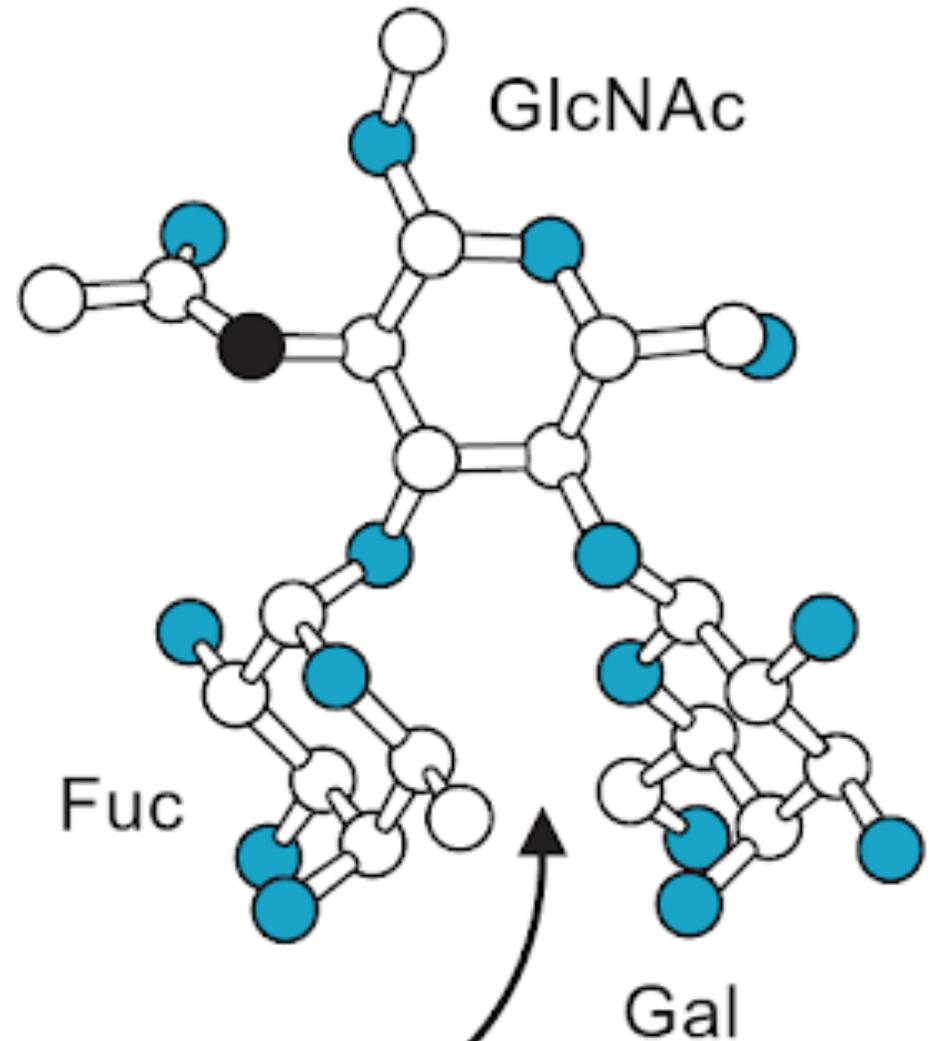
H-Bond Stabilization of a Man α 1-2Man Structure



Hydrophobic Packing between Apolar Faces

Lewis^X trisaccharide

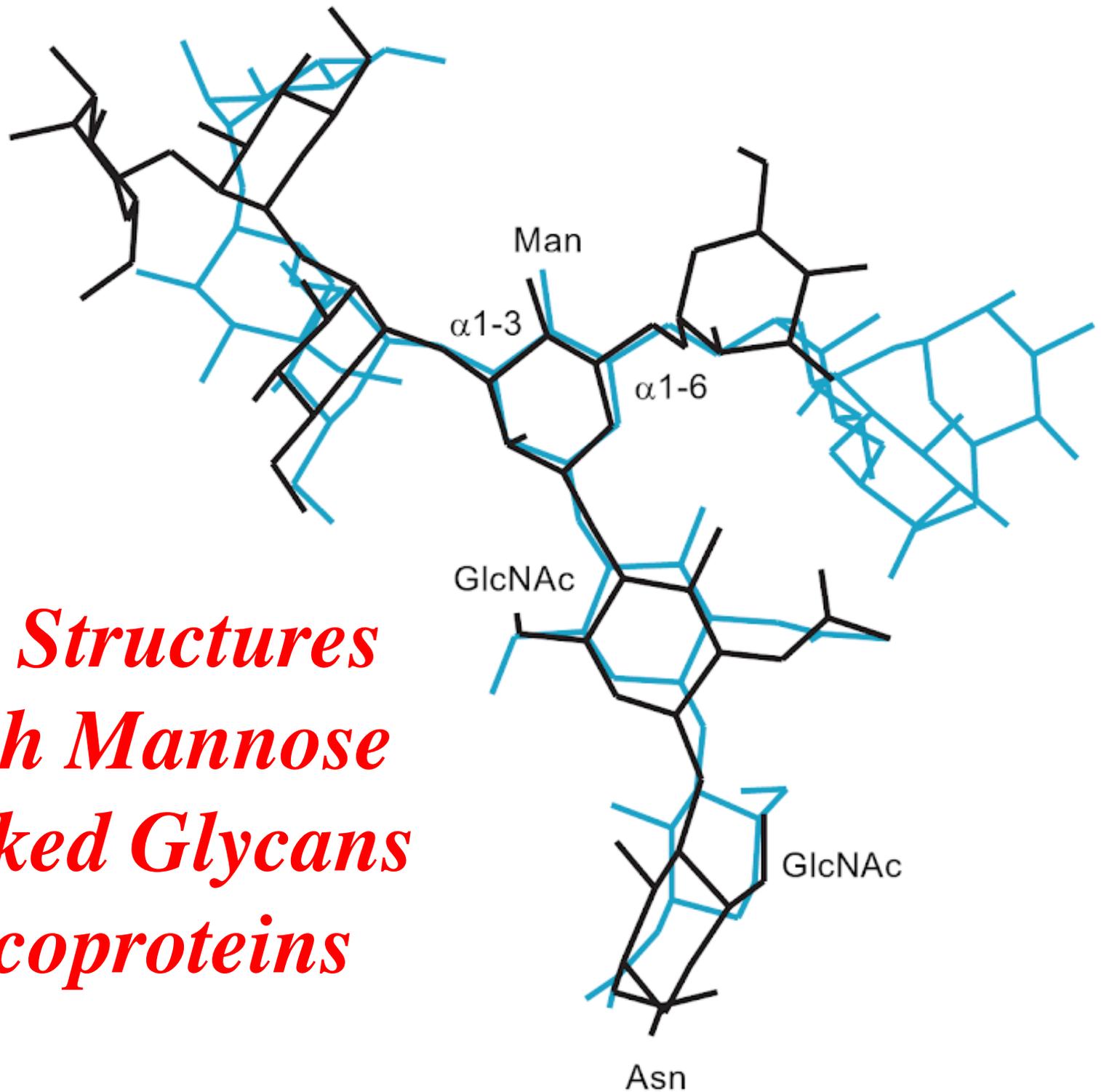
Gal β 1-4-GlcNAc
Fuc α 1-3-GlcNAc



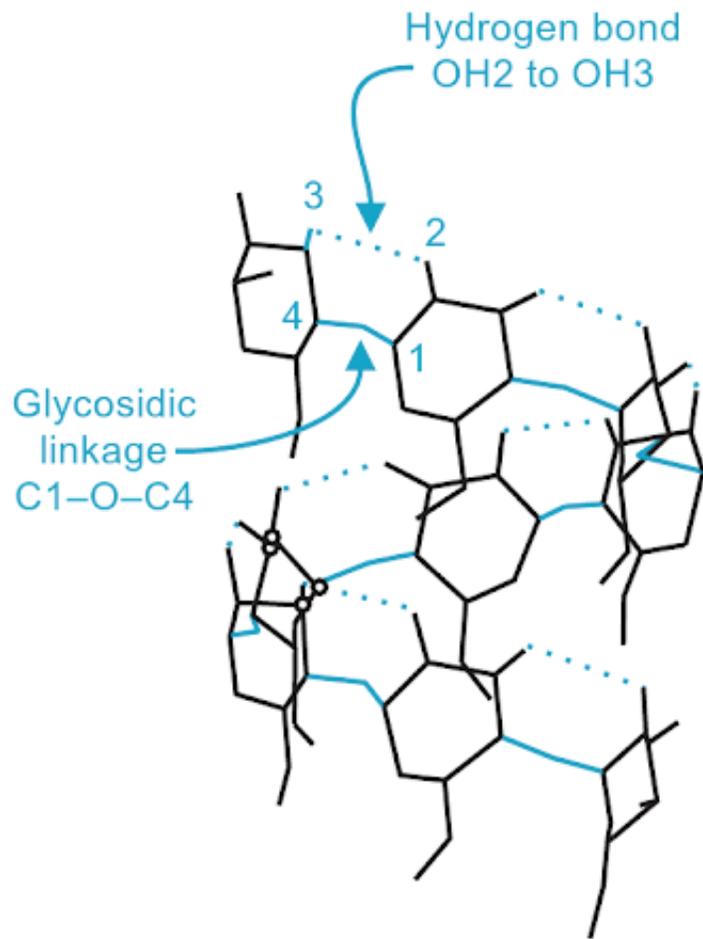
PDB: 2KMB

van der Waals
packing of planar faces

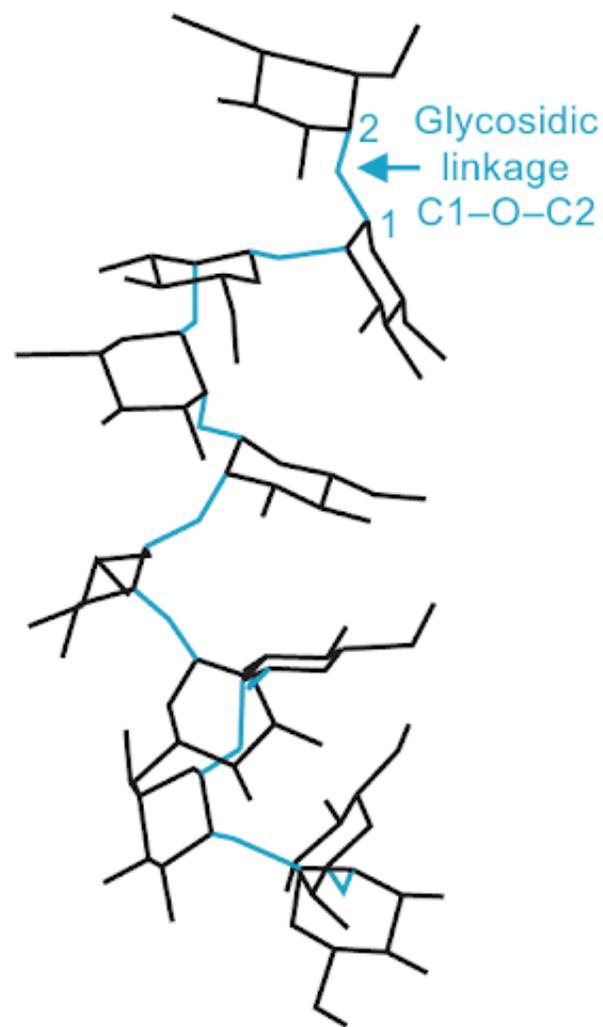
*X-Ray Structures
of High Mannose
N-Linked Glycans
in Glycoproteins*



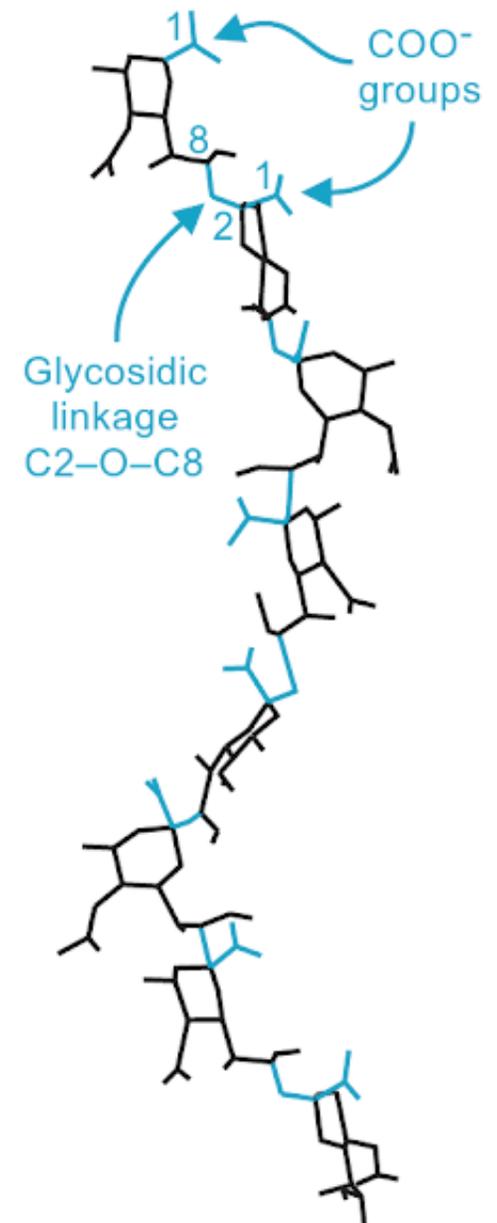
Helices in Polysaccharide Homopolymers



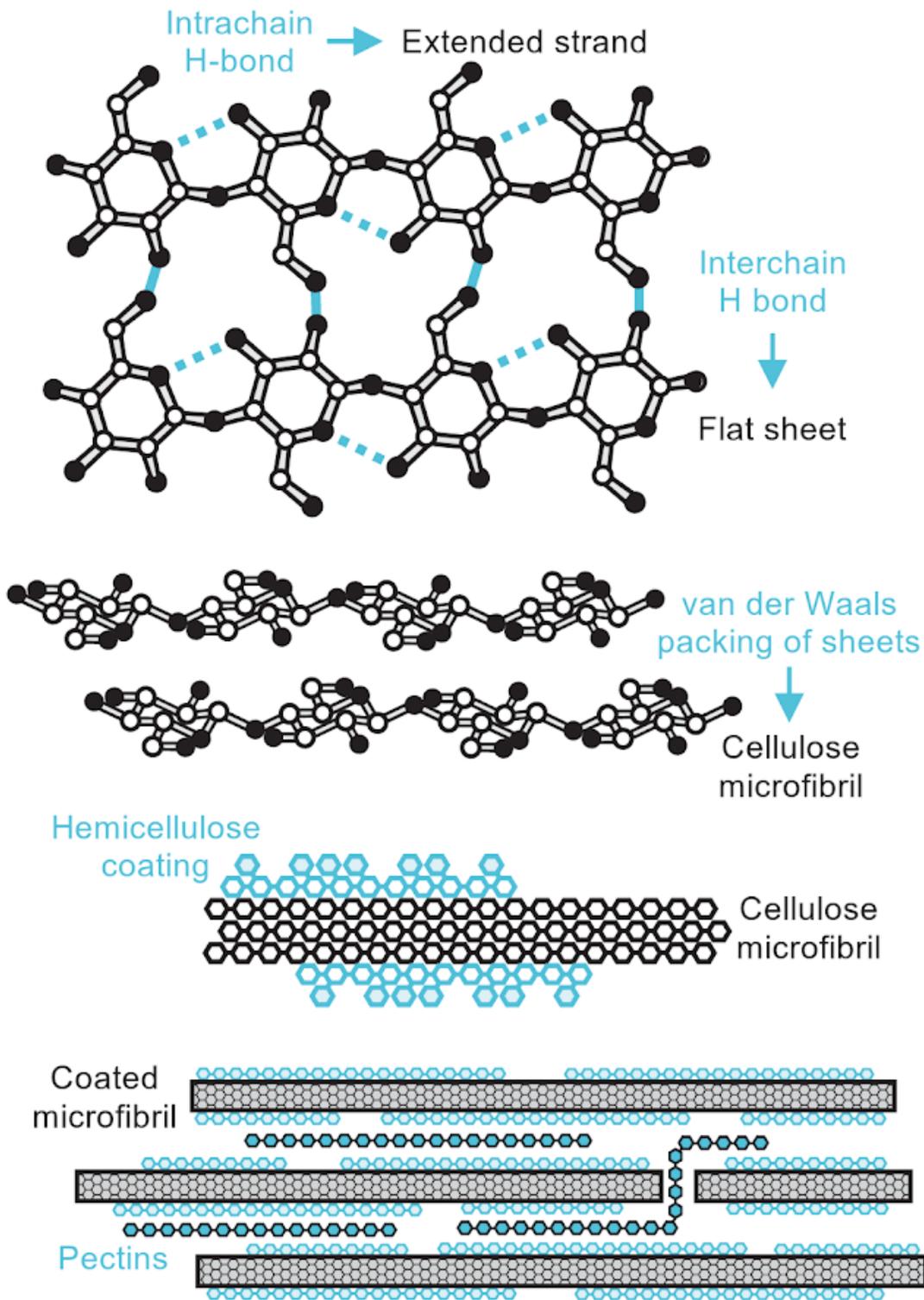
Amylose
(Glc α 1-4)_n



Mannan
(Man α 1-2)_n



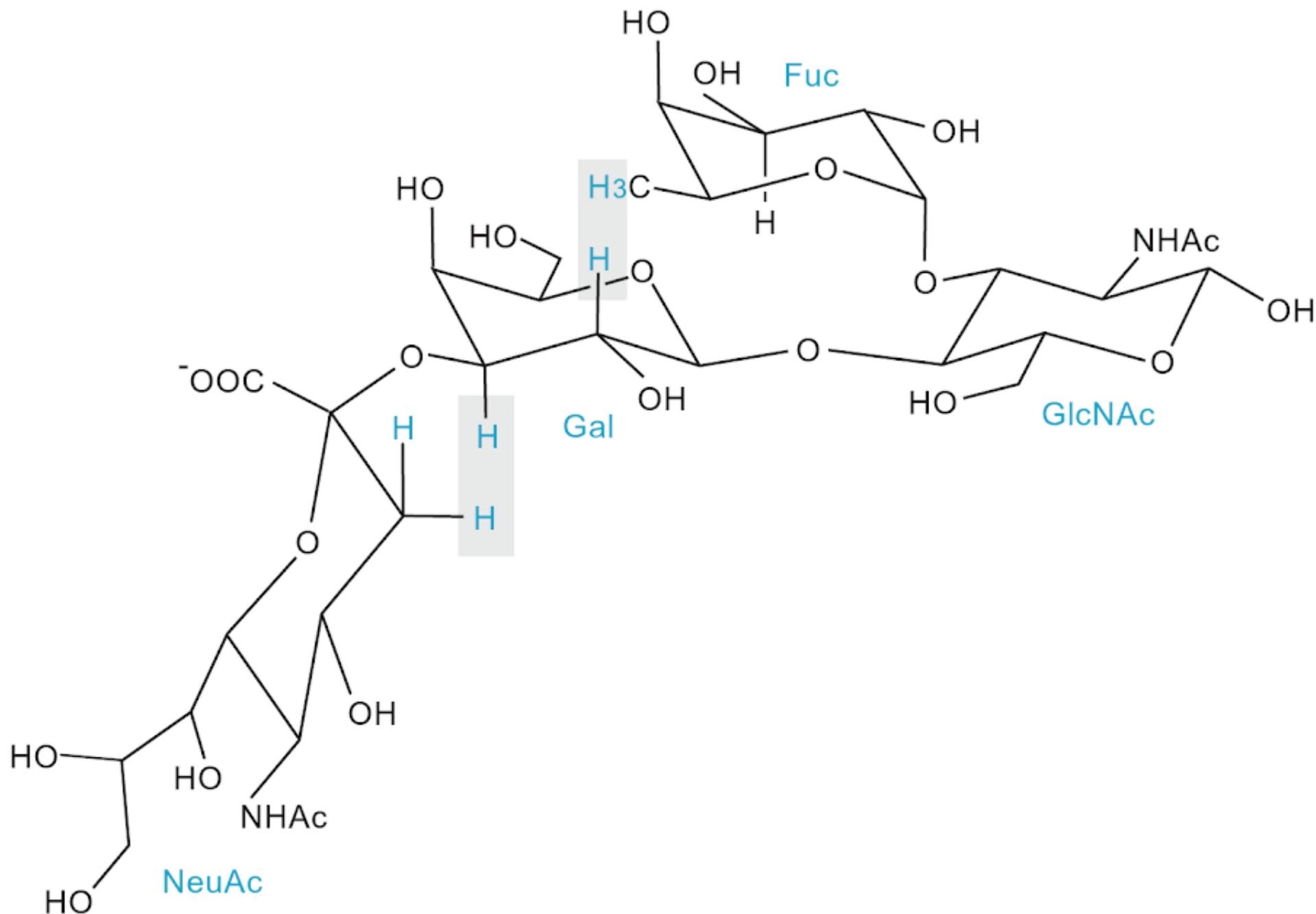
Polysialic acid
(NeuAc α 2-8)_n



Extended Conformations of Polysaccharides with β -Linked Residues found in many Plant Cell Walls

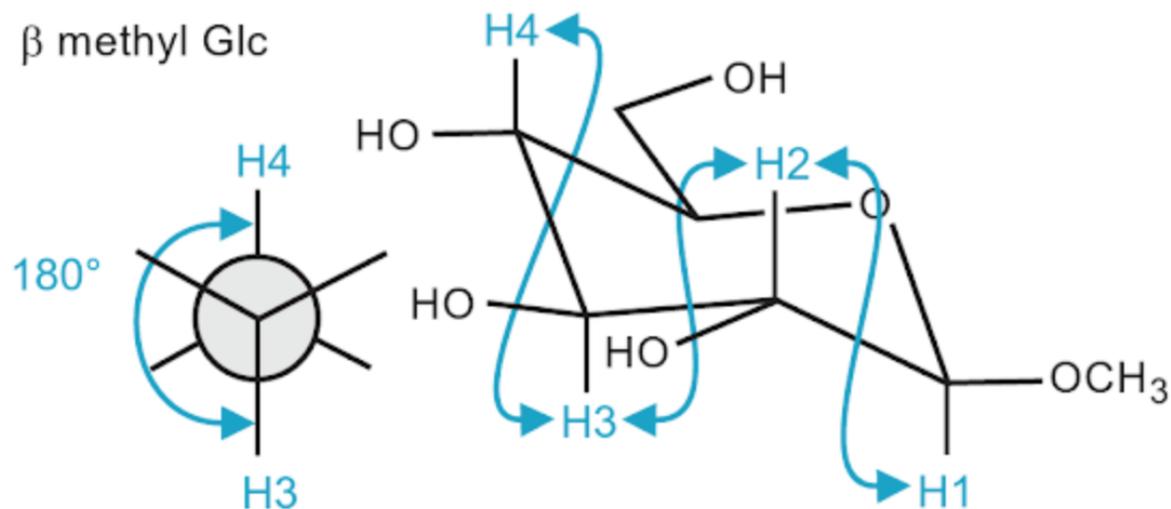
- examples include Cellulose, Pectins & Hemicellulose

NMR NOEs Establish Inter-Proton Distances

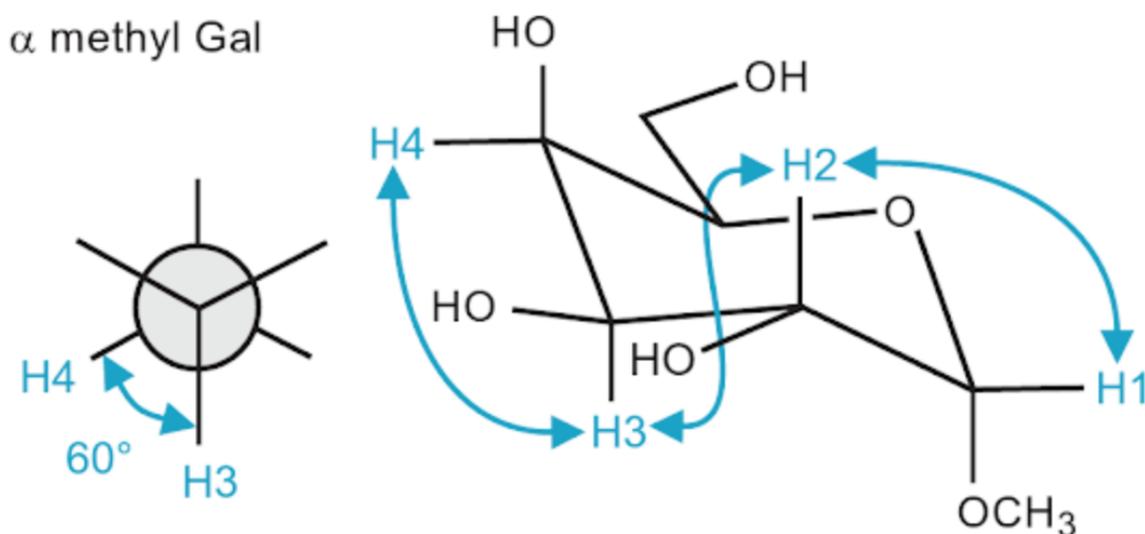


NMR Coupling Constants Set Torsional Values

trans =
large
coupling
constant



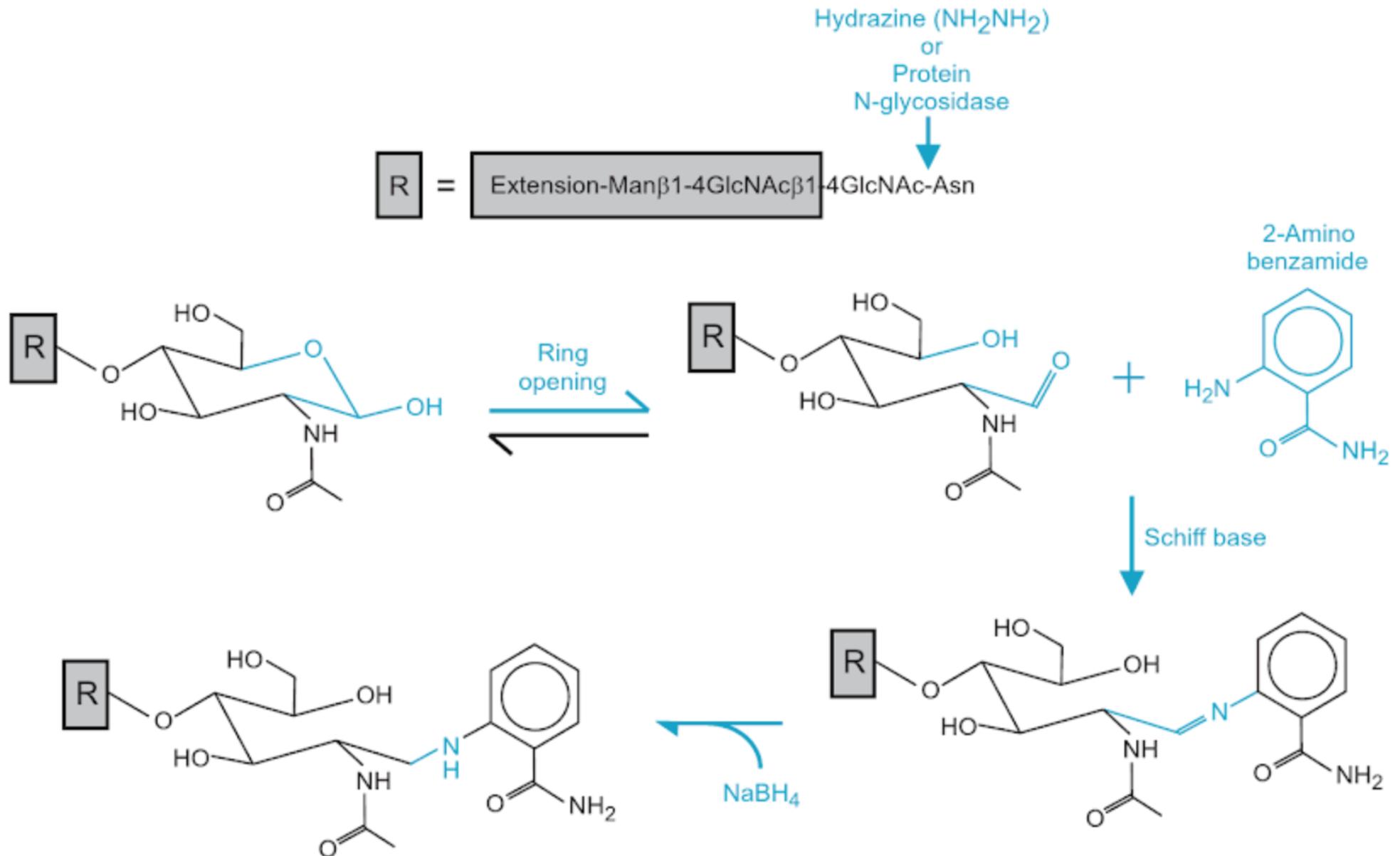
gauche =
small
coupling
constant



H2-H3-H4-H5 coupling
identifies monosaccharide
stereochemistry

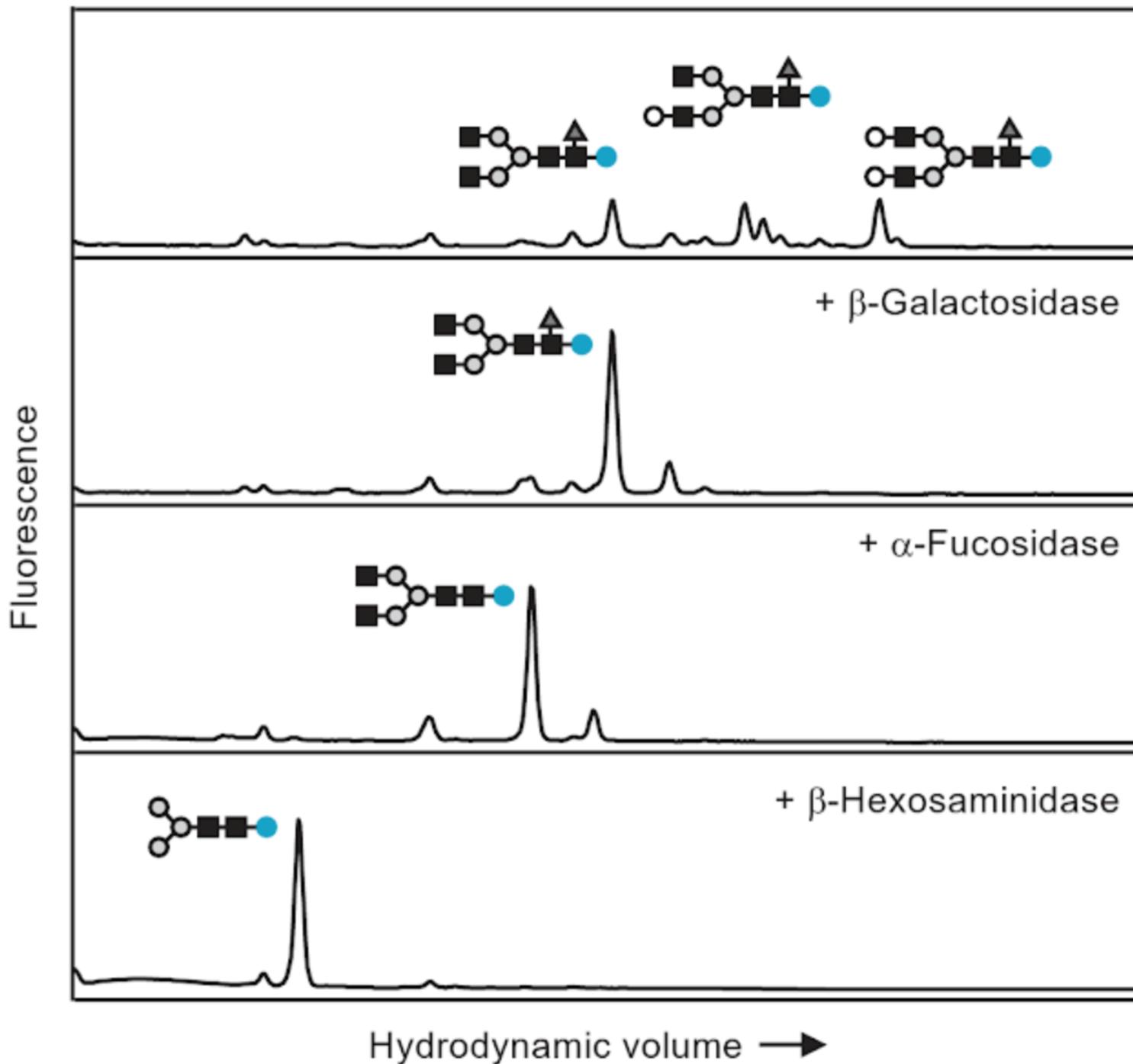
H1-H2 coupling
defines anomeric
configuration

Release & Labelling of N-Linked Glycans



Sequential Enzyme Digestion of End-Labelled Glycan

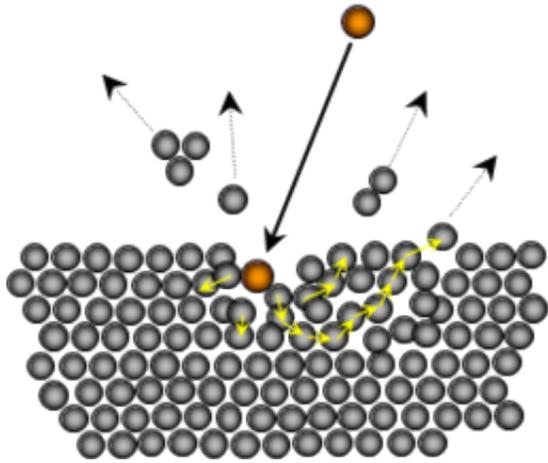
- GlcNAc
- Mannose
- Galactose
- ▲ Fucose
- 2-Amino benzamide



● upper (original) sample is glycans derived from IgG, which are then trimmed in stages to core structures

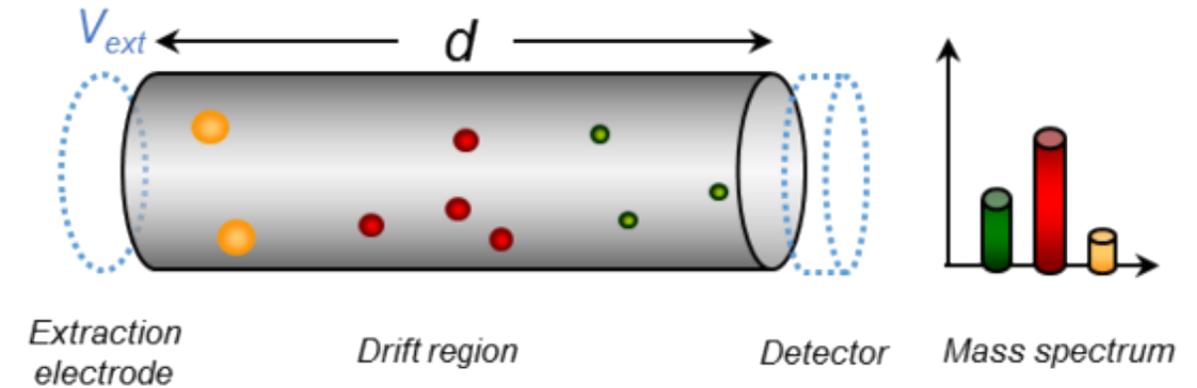
How Mass Spectrometry Works...

Collision Cascade



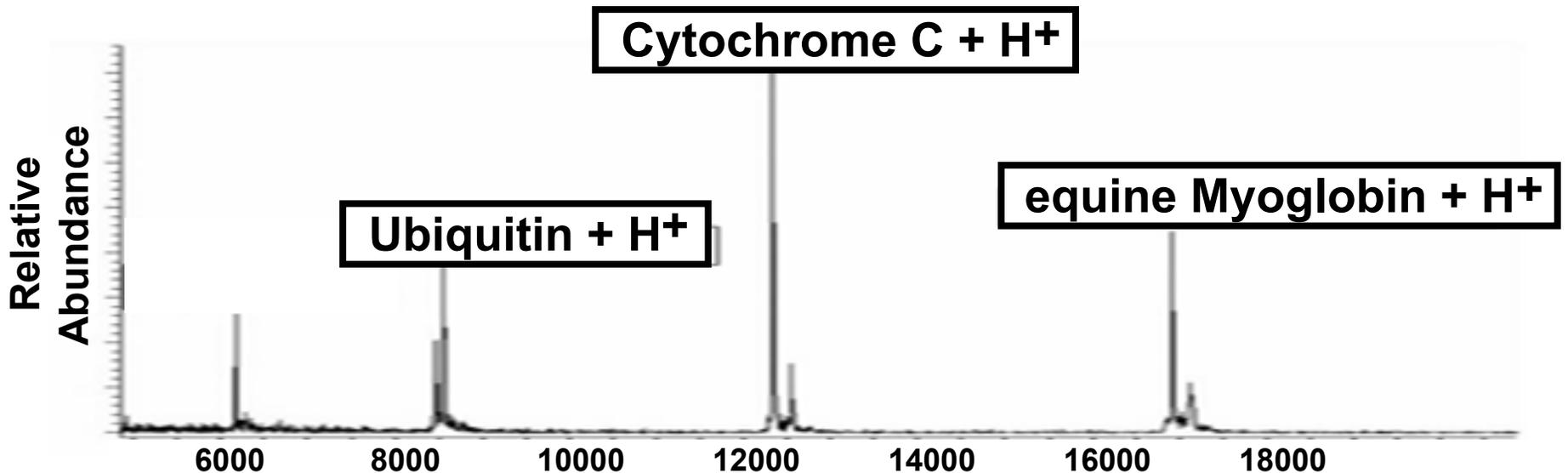
MALDI

Time-of-Flight Mass Analyzer

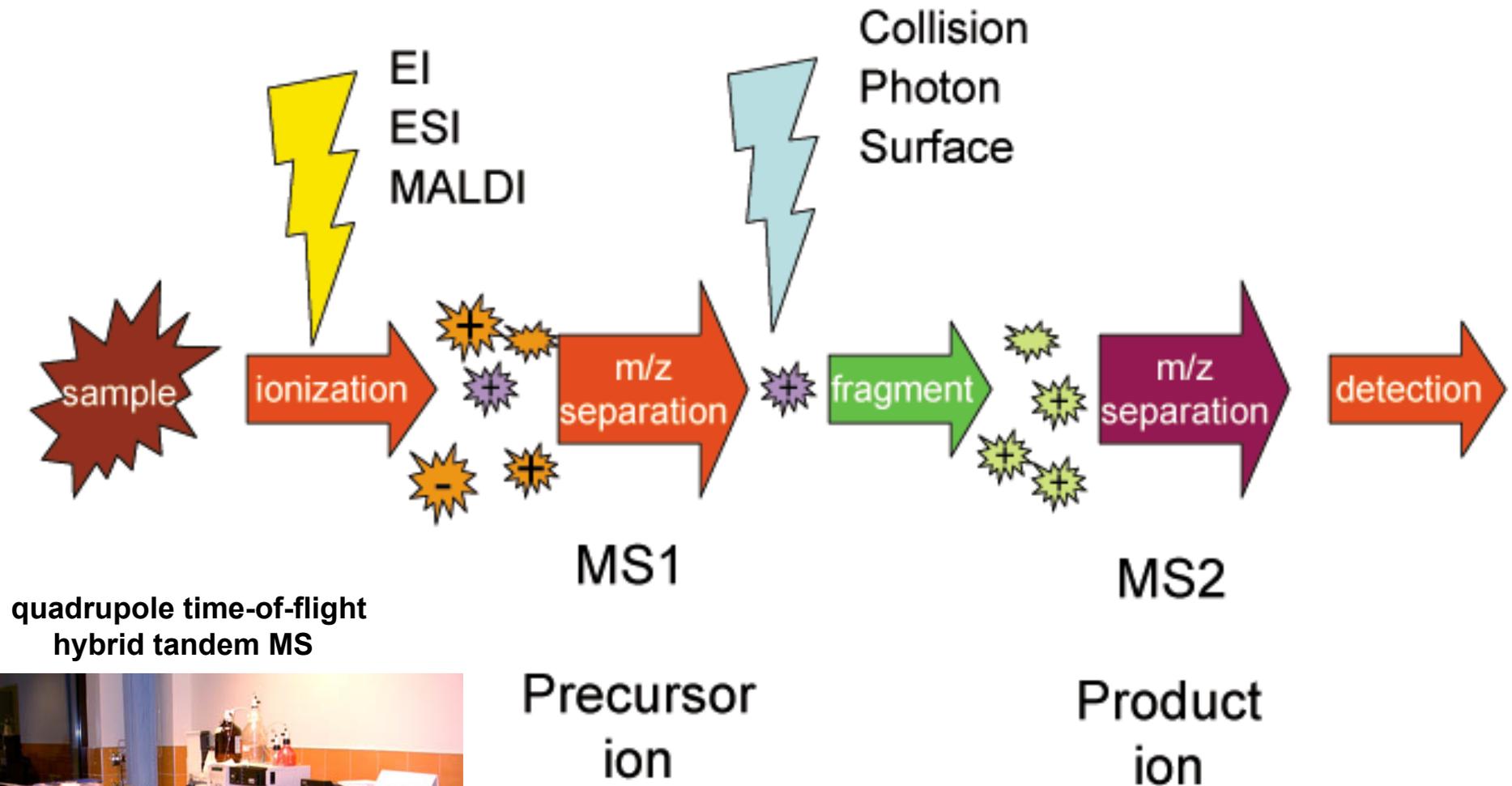


$$E = qV_{ext} = \frac{1}{2}mv^2$$

$$t = d \left(\frac{m}{2qV} \right)^{1/2} \propto m^{1/2}$$



Tandem Mass Spectrometry

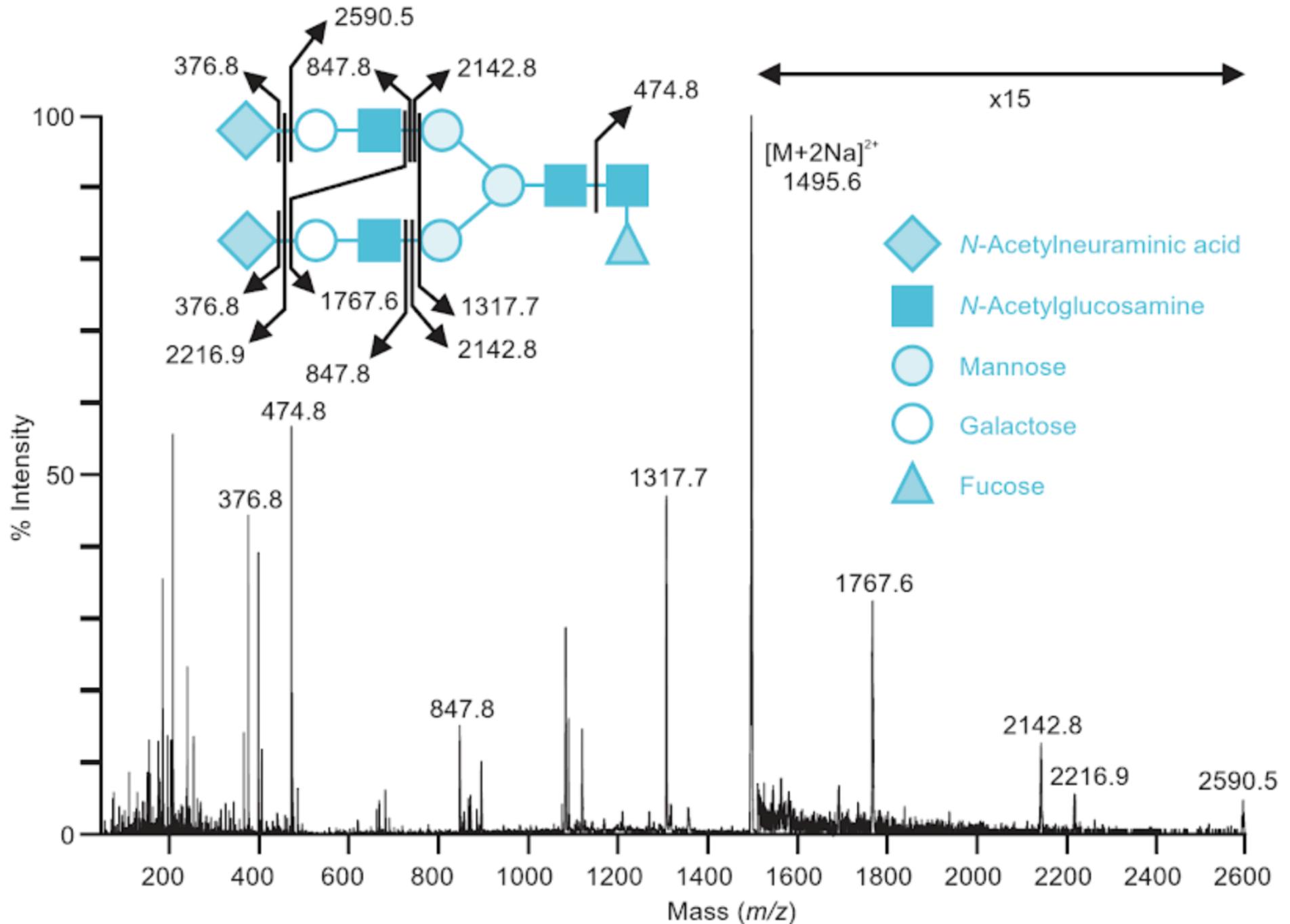


quadrupole time-of-flight
hybrid tandem MS

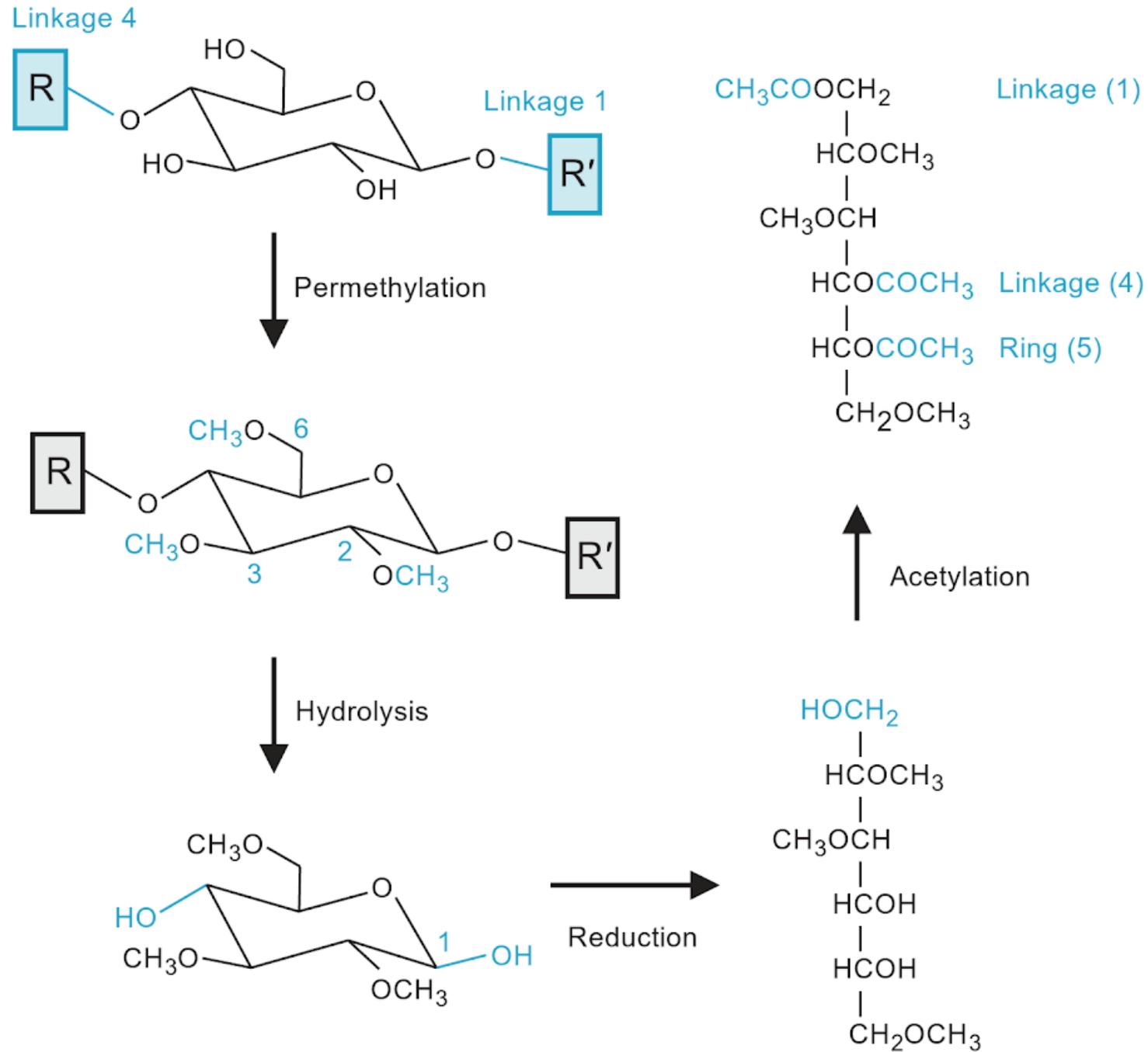


- the two mass spec stages can be separated in space (triple quad) or in time (*via* an ion trap)

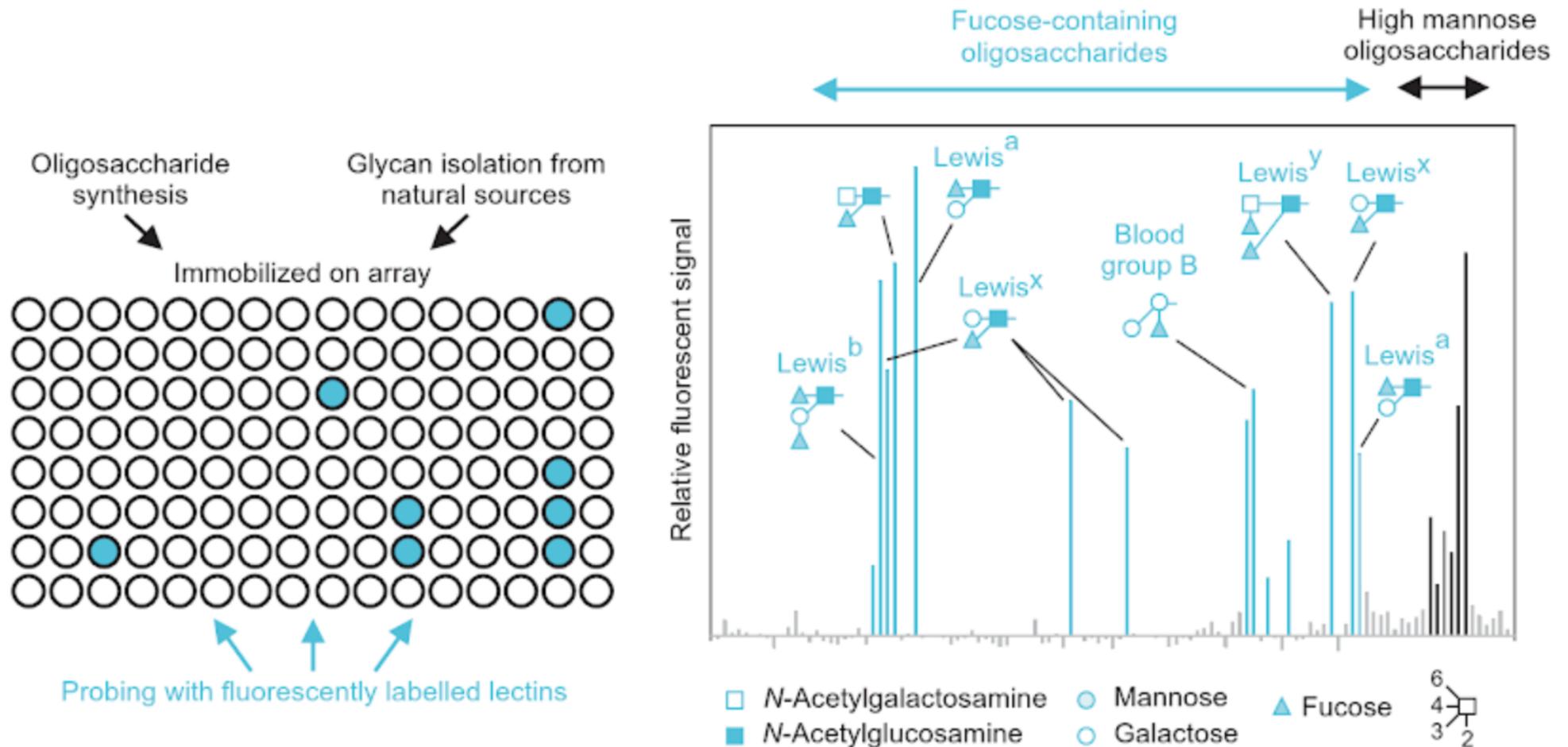
(Re)fragmentation of a Glycan by MS/MS Analysis



Permethylation/MS for Linkage Analysis



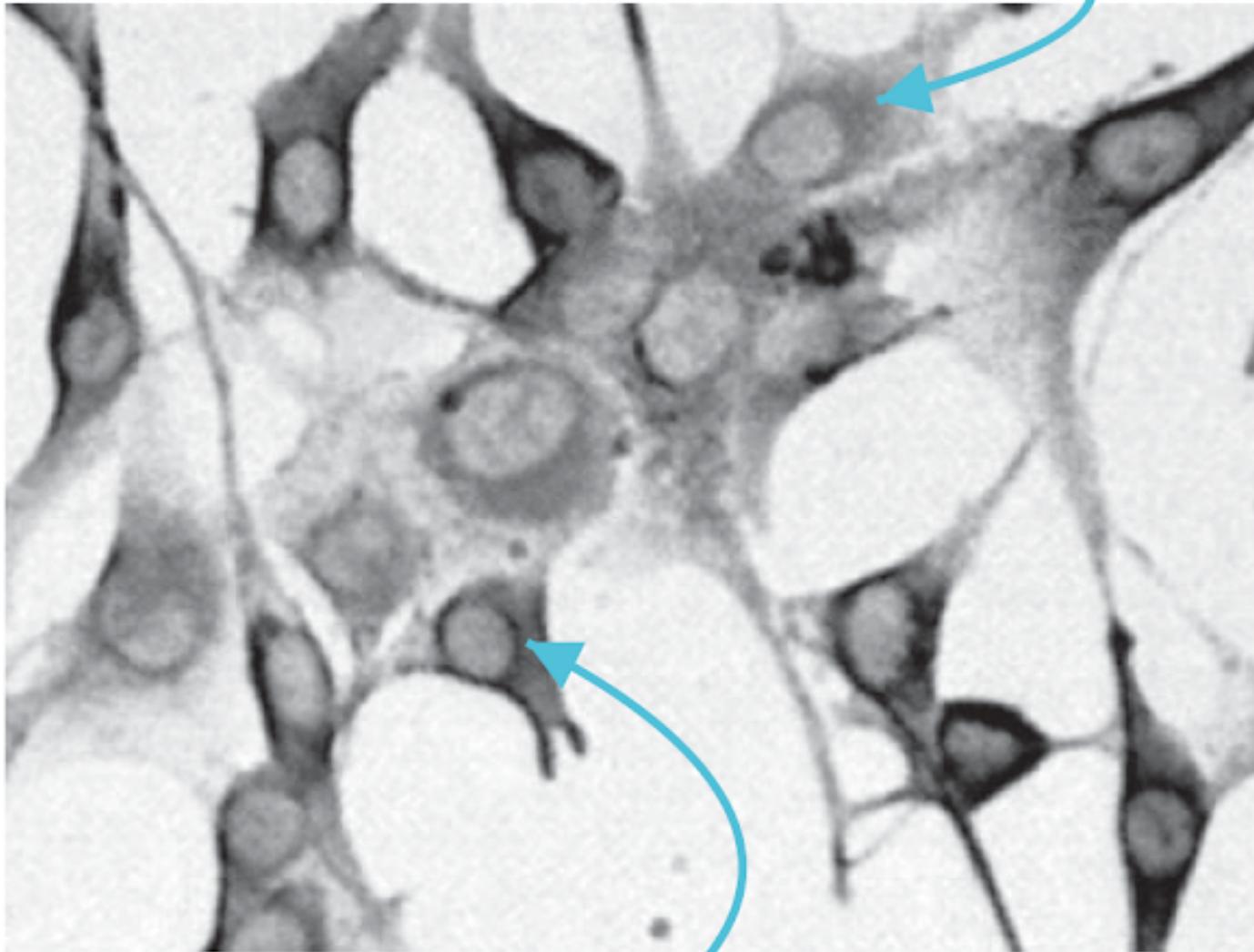
Binding Selectivity from a Glycan Array



Fluorescently labelled DC-SIGN (a Lectin) binds to glycans immobilized in individual wells. Binding to high mannose glycans, and those with a terminal fucose & galactose or GalNAc is evident.

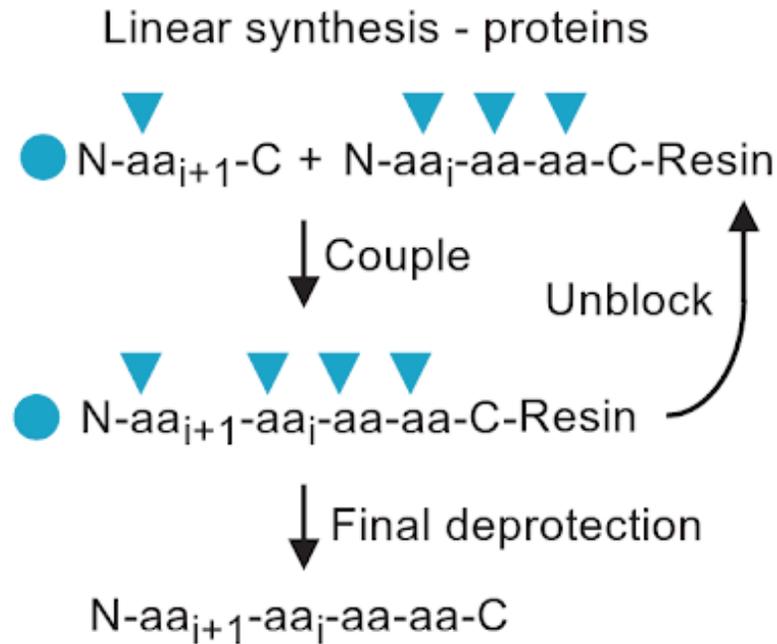
N-Linked Glycan Staining with Concanavalin A

Diffuse cytoplasmic staining
(endoplasmic reticulum)

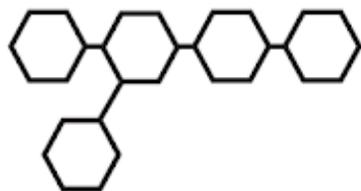


Perinuclear staining
(Golgi)

Chemical Synthesis: Peptides vs. Glycans

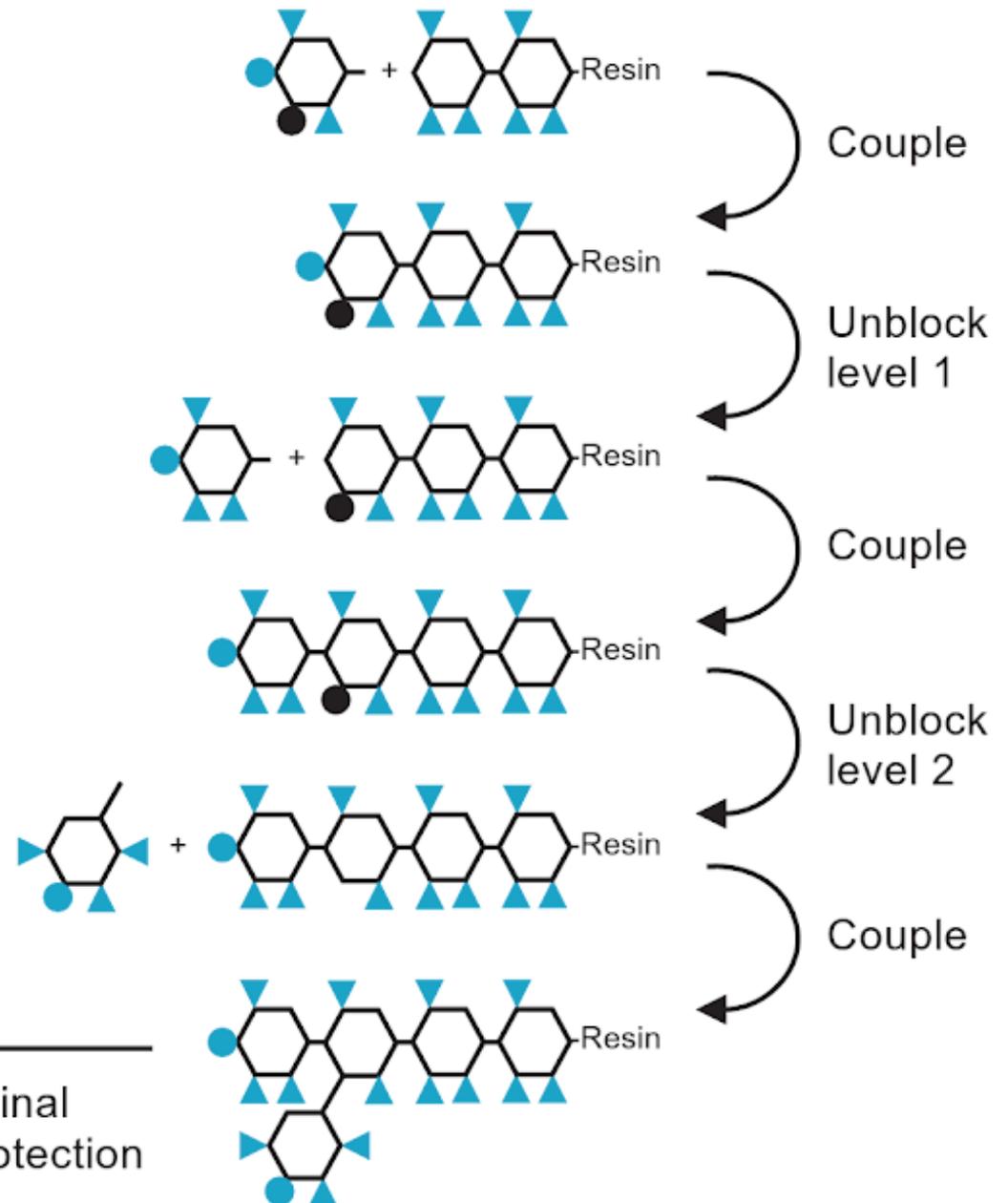


\bullet \bullet Blocking groups
 \blacktriangledown Side chain protection



Final deprotection

Branched synthesis - glycans



Enzymatic Addition of Sialic Acid to a Glycan

