

# Structural characterisation and enzymatic fingerprinting of oligo and polysaccharides

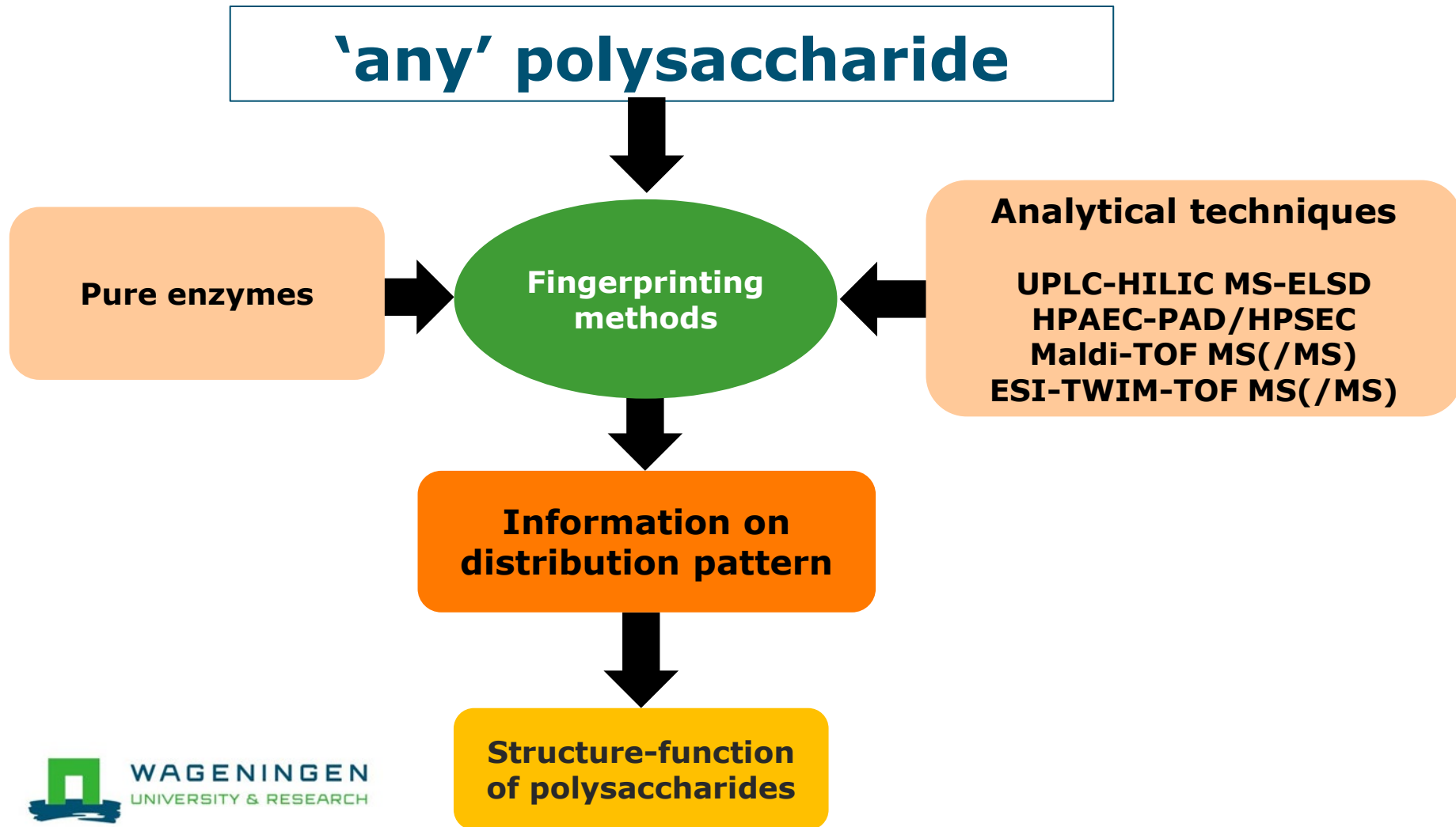
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Functionality of oligo and polysaccharides:  
the chemical fine structure matters!

# Fingerprinting polysaccharides to reveal the distribution of substituents → Our Approach



# Presentation outline

- Enzymatic fingerprinting of **pectin**
  - Enzymatic degradation
  - Identification and quantification of diagnostic oligosaccharides
  - Construction of parental polysaccharide molecules
- Characterisation of prebiotic oligosaccharides
  - Galactooligosaccharides----- PGC-MS identification

# Pectin plays an important role as:

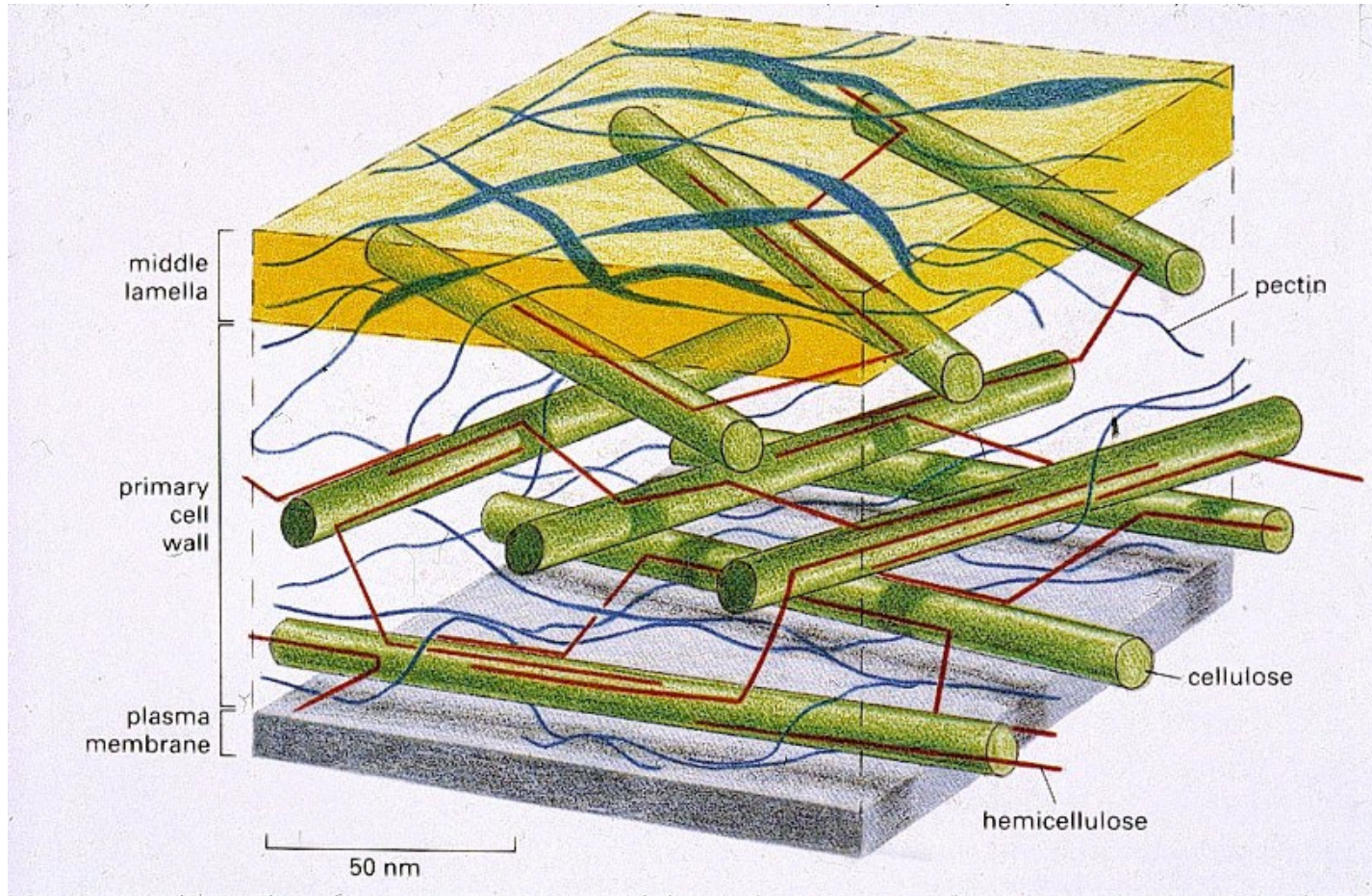
- Cell Wall component
  - Determine (partly) texture of tissues
  - Change during ripening of e.g., fruits (endogenous enzymes)
  - Change during processing due to depolymerization, de-esterification, solubilization, etc.
  - Present in by-products from agro-industry
- Texturizer in many fruit- & vegetable-based food products
- Ingredient for food industry
  - Modification during extraction and down-stream processing
  - Thickener and gelling agent
  - Stabilizer in fruit and milk beverages
- Health promoting component
  - Stimulation immune system
  - Fermentation by gut bacteria

# Pectin is part of the plant cell wall

- Pectin – charged, branched
- Hemicellulose – moderately branched, strong interaction with cellulose
- Cellulose
- Lignin – highly complex polymer of phenolic compounds
- Especially ‘pectin’ and ‘hemicellulose’ represent classes of polysaccharides with a broad range of chemical structures and a wide variation in size, charge, branching, etc

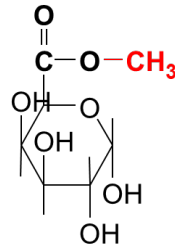
# model for the primary plant cell wall

McCann and Roberts (1991)

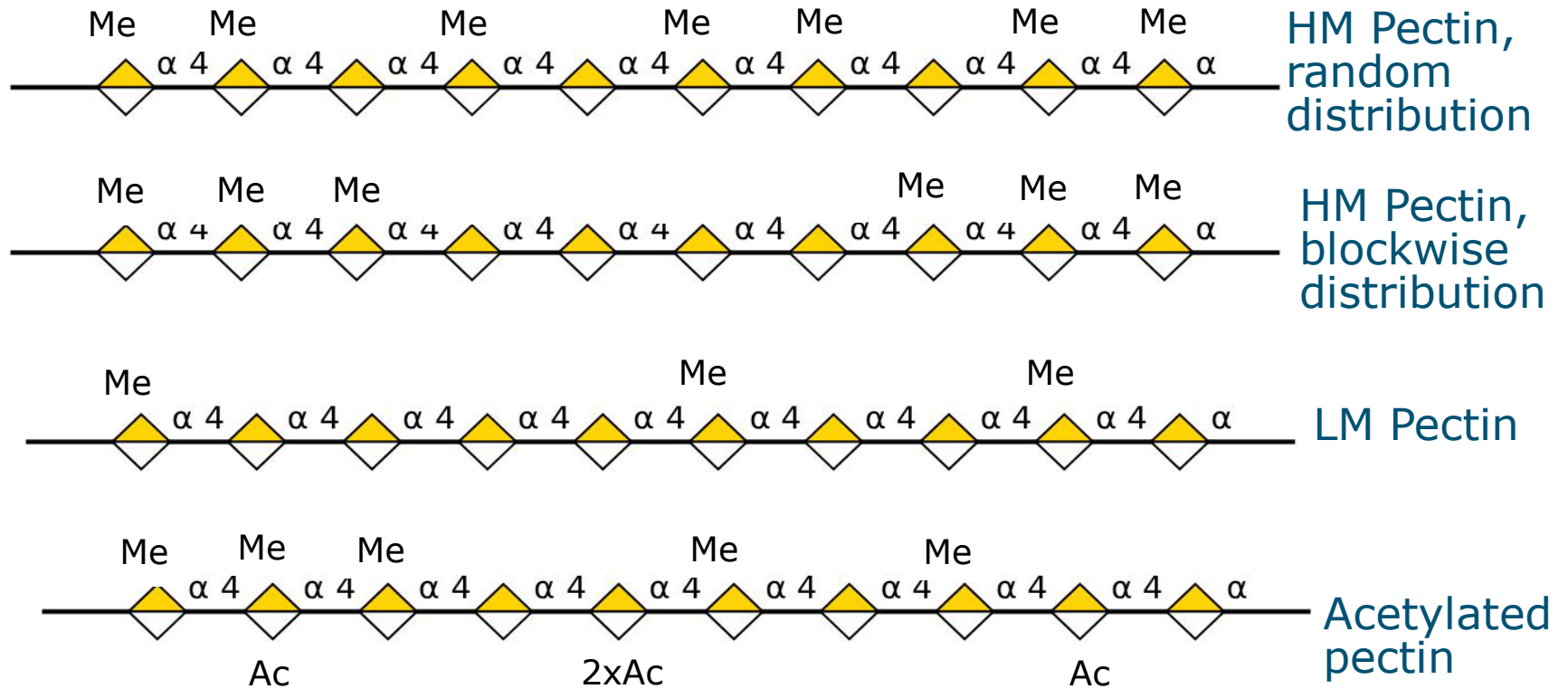
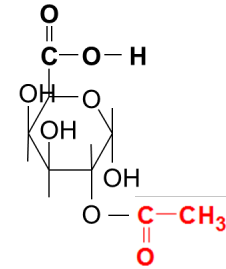


# Schematic structure of pectic polysaccharides

Homogalacturonan  
(HG)



Galacturonic acid





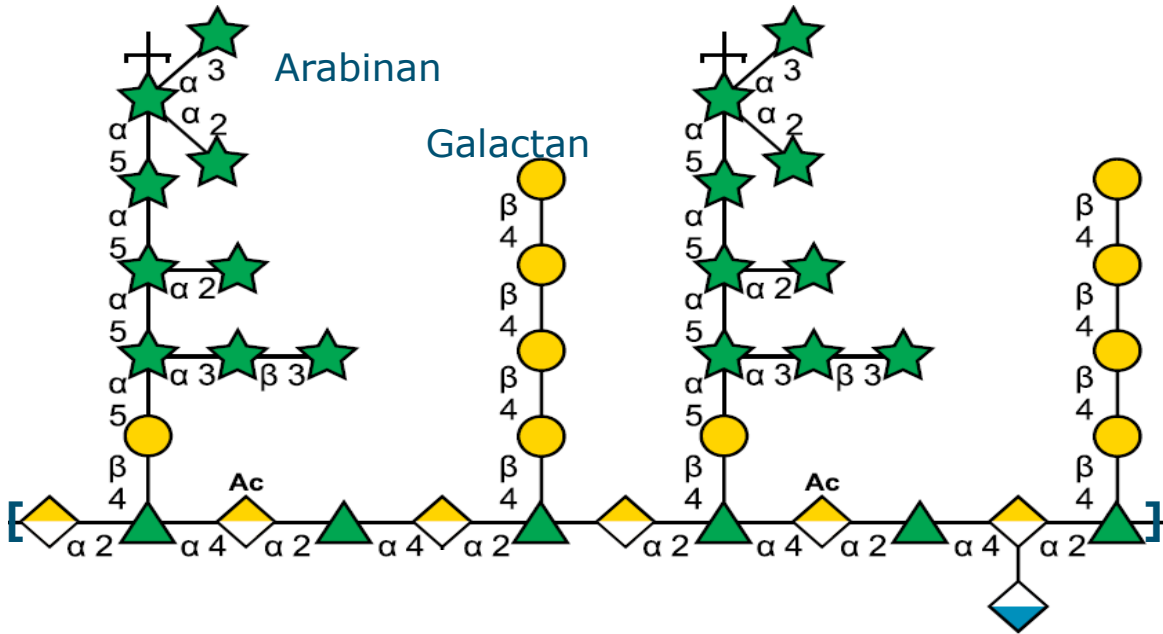
# Monosaccharide symbol nomenclature

SHAPE	White (Generic)	Blue	Green	Yellow	Orange	Pink	Purple	Light Blue	Brown	Red
Filled Circle	○ Hexose	● Glc	● Man	● Gal	● Gul	● Alt	● All	● Tal	● Ido	
Filled Square	◻ HexNAc	■ GlcNAc	■ ManNAc	■ GalNAc	■ GulNAc	■ AltNAc	■ AllNAc	■ TalNAc	■ IdoNAc	
Crossed Square	◻ Hexosamine	◻ GlcN	◻ ManN	◻ GalN	◻ GulN	◻ AltN	◻ AllN	◻ TalN	◻ IdoN	
Divided Diamond	◊ Hexuronate	◊ GlcA	◊ ManA	◊ GalA	◊ GulA	◊ AltA	◊ AllA	◊ TalA	◊ IdoA	
Filled Triangle	△ Deoxyhexose	▲ Qui	▲ Rha		▲ 6dGul	▲ 6dAlt		▲ 6dTal		▲ Fuc
Divided Triangle	△ DeoxyhexNAc	▲ QuiNAc	▲ RhaNAc			▲ 6dAltNAc		▲ 6dTalNAc		▲ FucNAc
Flat Rectangle	◻ Di-deoxyhexose	▬ Oli	▬ Tyv		▬ Abe	▬ Par	▬ Dig	▬ Col		
Filled Star	☆ Pentose		★ Ara	★ Lyx	★ Xyl	★ Rib				
Filled Diamond	◊ Deoxymonosonate		◆ Kdn				◆ Neu5Ac	◆ Neu5Gc	◆ Neu	◆ Sia
Flat Diamond	◊ Di-deoxymonosonate		◆ Pse	◆ Leg		◆ Aci		◆ 4eLeg		
Flat Hexagon	◻ Unknown	⬡ Bac	⬡ LDmanHep	⬡ Kdo	⬡ Dha	⬡ DDmanHep	⬡ MurNAc	⬡ MurNGc	⬡ Mur	
Pentagon	◻ Assigned	⬠ Api	⬠ Fru	⬠ Tag	⬠ Sor	⬠ Psi				

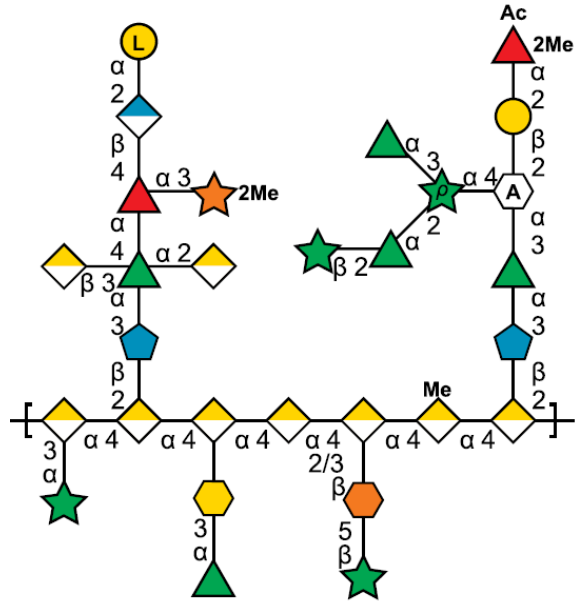
	D-Glucose $\rho$		D-Kdo		L-Arabinose $f$		L-Fucose $\rho$	<b>Me</b>	O-Methyl group
	D-Galactose $\rho$		D-Dha		L-Arabinose $\rho$		D-Galacturonic acid $\rho$	<b>2Me</b>	2-O-Methyl group
	L-Galactose $\rho$		D-Apiose $f$		D-Xylose $\rho$		D-Glucuronic acid $\rho$	<b>Ac</b>	O-Acetyl group
	D-Mannose $\rho$		L-Aceric acid		L-Rhamnose $\rho$		Lignin monomer		

# Schematic structure of pectic polysaccharides

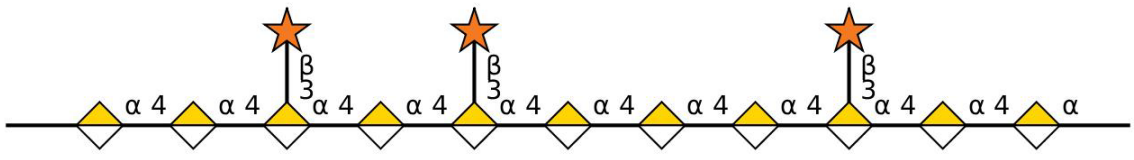
## Rhamnogalacturonan I (RG I)



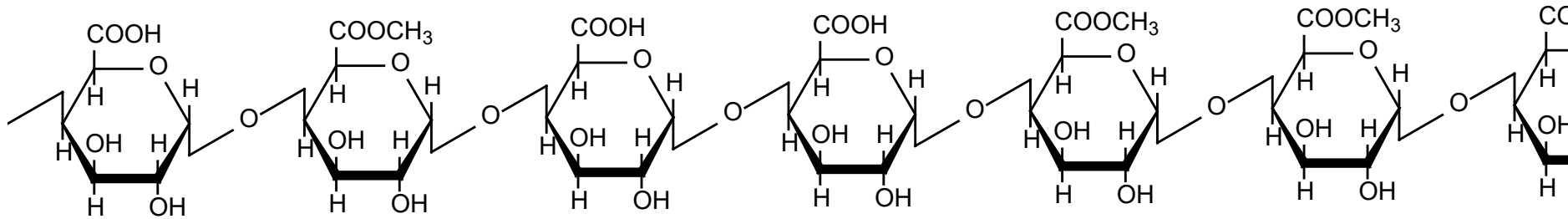
## Rhamnogalacturonan II (RG II)



## Xylogalacturonan



# Changing pectin characteristics in plant material



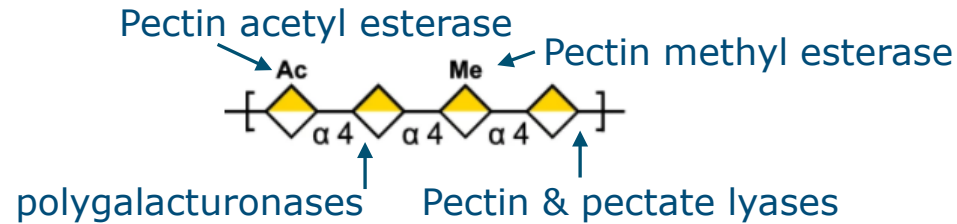
- Biosynthesis of fully methyl esterified pectin
- Tailoring of molecular weight, methyl esterification and interactions during growing/ripening/storage/processing
  - In planta : enzymes
  - During processing
    - @ home : chemically = cooking
    - @ industry : both chemically and enzymatically (processing aid!)

# Pectin structure

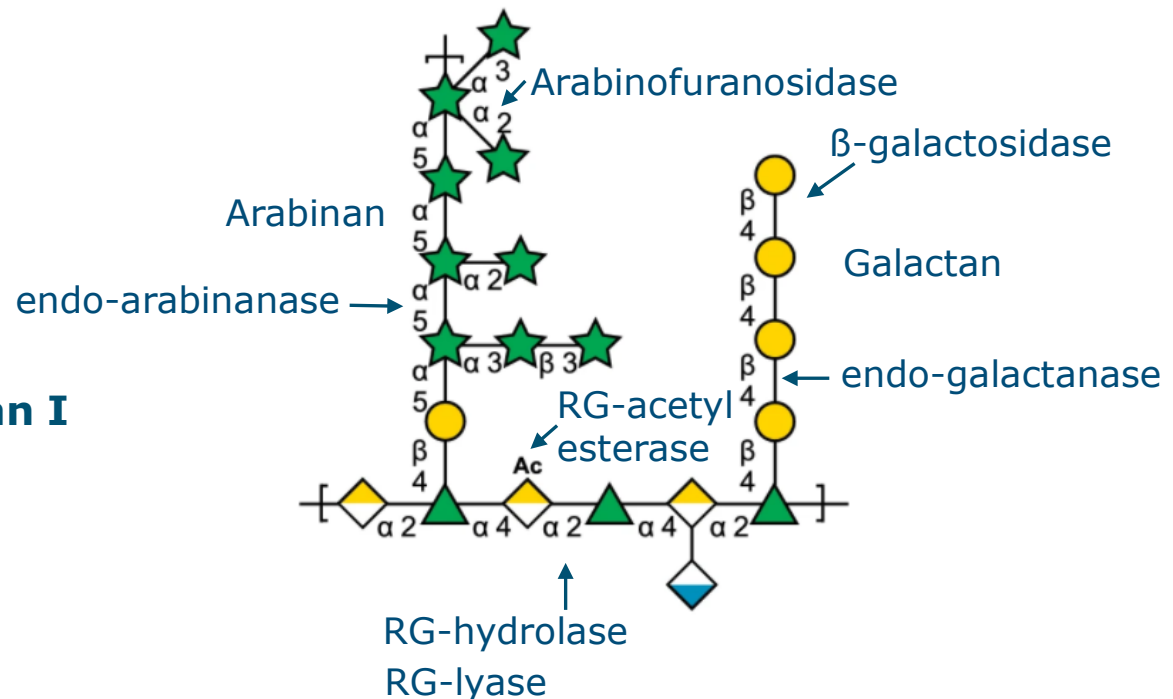
- Commercial pectin is extracted from citrus peel and apple pomace
- Commercial pectin is mainly homogalacturonan with methyl-esters
- Structure depends on:
  - origin raw material (orange, lemon, grapefruit, apple, sugar beet)
  - possible endogenous enzyme activity in raw material (pPME),
  - method of extraction,
  - sugar composition, DM, Mw, DB etc.
- Techno- and bio functionality strongly depends on level and distribution of methyl-esters

# Pectinases – a variety of enzymes

## Homogalacturonan



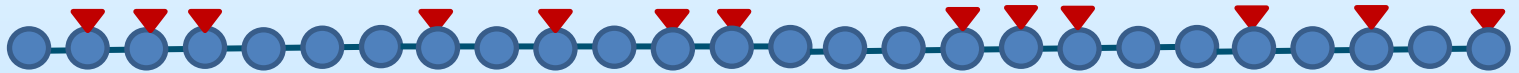
## Rhamnogalacturonan I



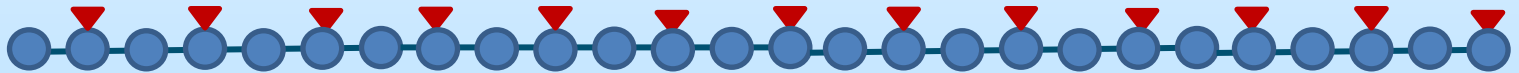
# Characterisation of pectins

Distribution of methyl esters: Homogalacturonan 50% DM

Random



Sequential



Blockwise



Combi

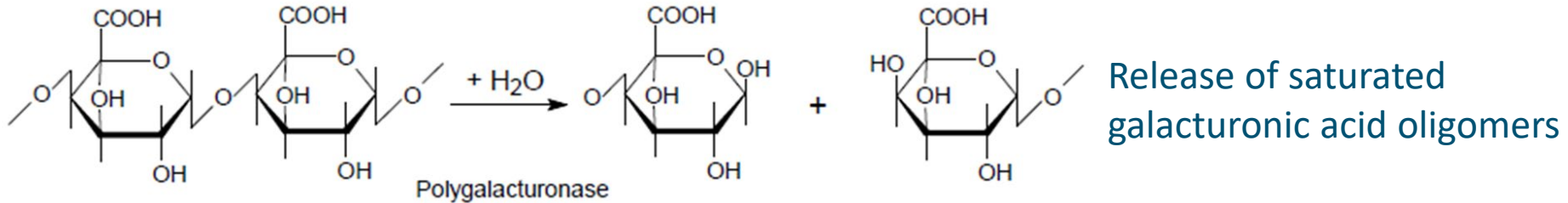


● = Galacturonic acid (GaIA)

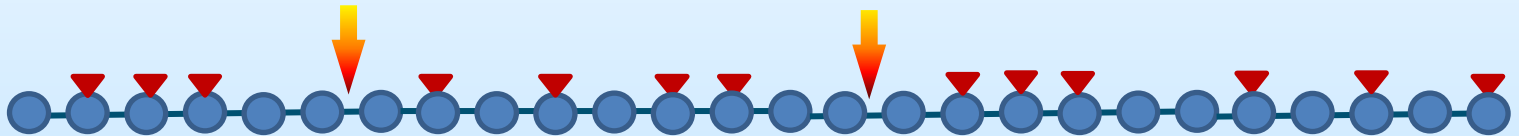
● = methyl-GaIA

# Homogalacturonan:

## Finger printing of methyl ester groups using PG



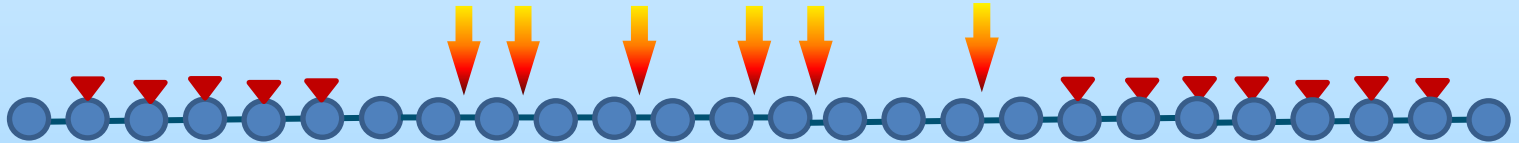
Random



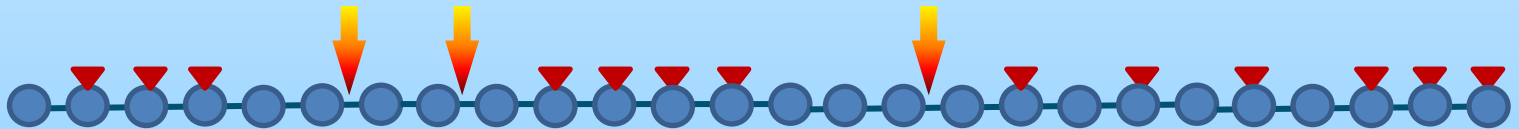
Sequential



Blockwise



Combi



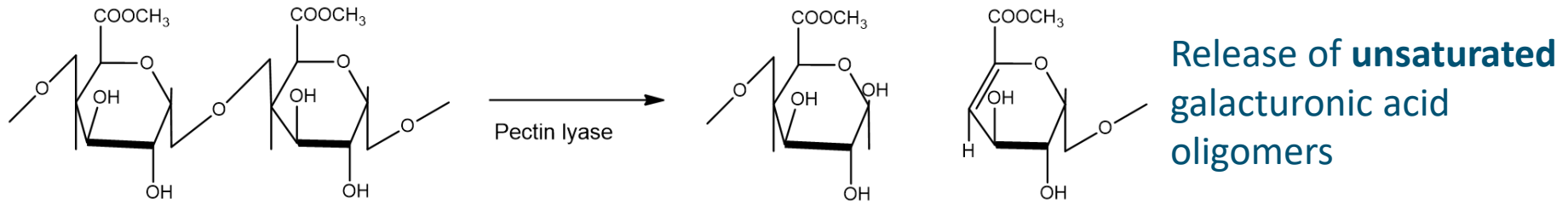
● = Galacturonic acid (GalA)

▼ = methyl-GalA

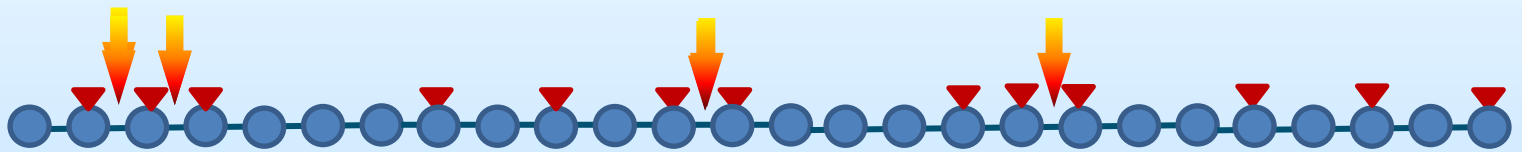
= site of attack endo-PG  
(*Kluyveromyces fragilis*)

# Homogalacturonan:

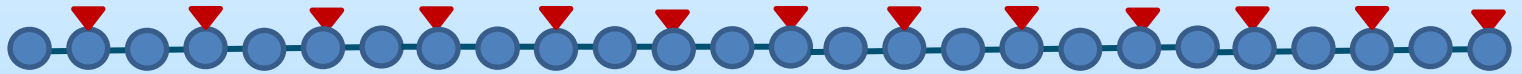
## Finger printing of methyl ester groups using PL



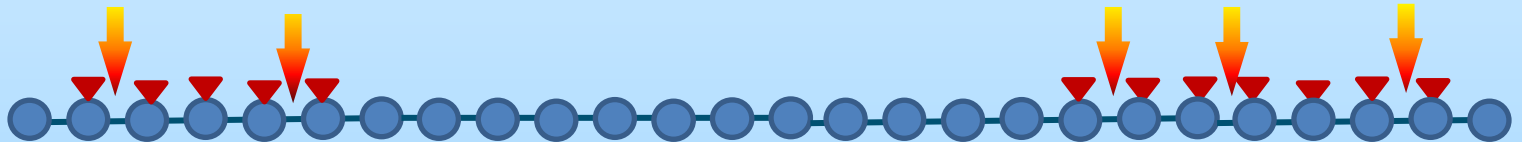
Random



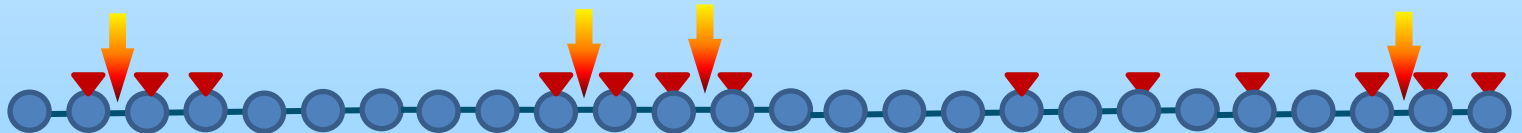
Sequential



Blockwise



Combi



● = Galacturonic acid (GalA)

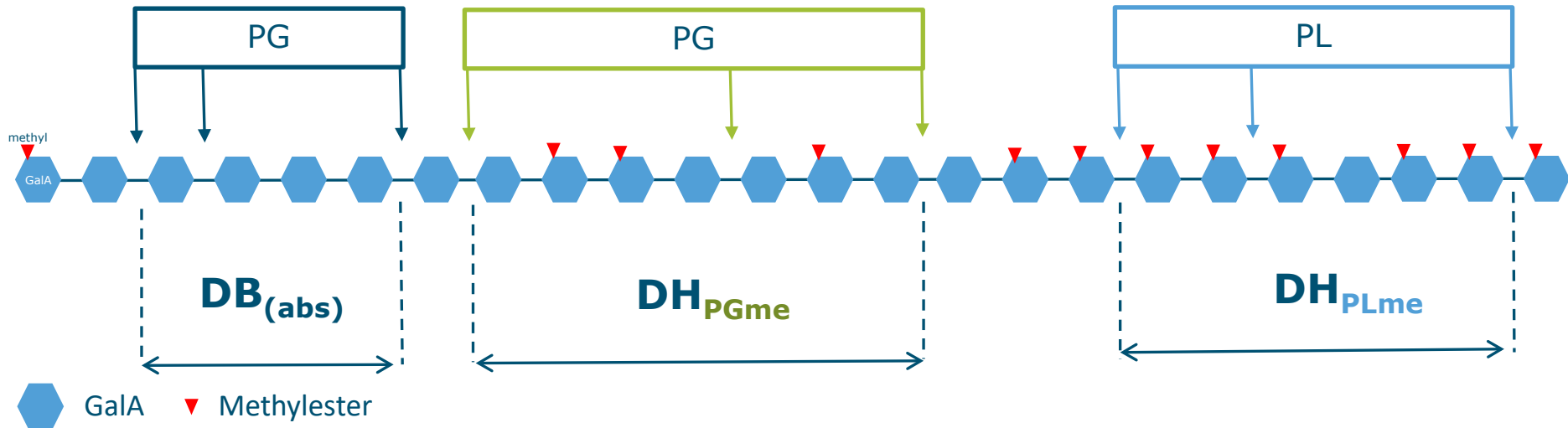
▼ = methyl-GalA

 = site of attack pectin lyase



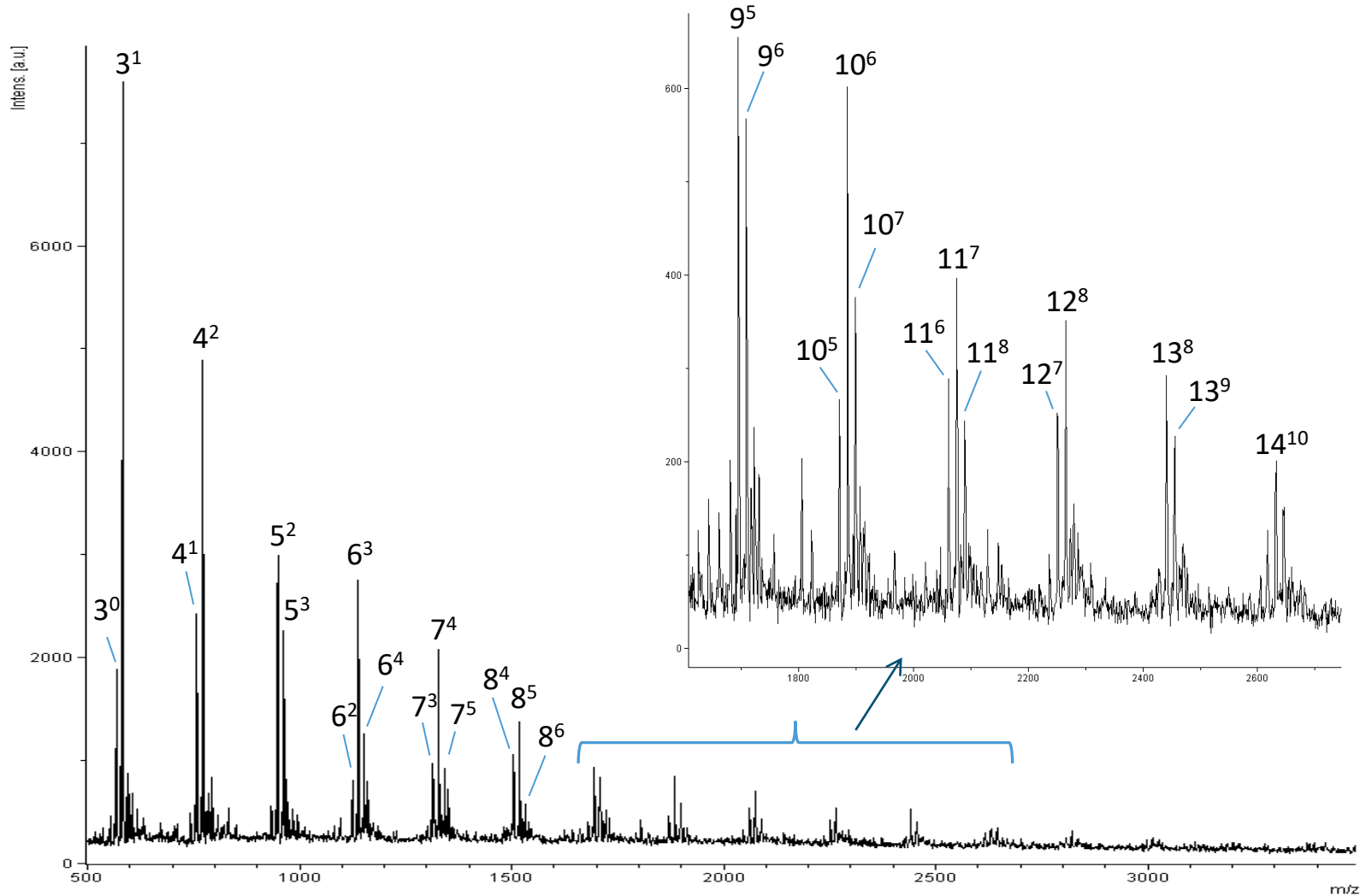
# Descriptive parameters

## Degree of Blockiness and Degree of Hydrolysis

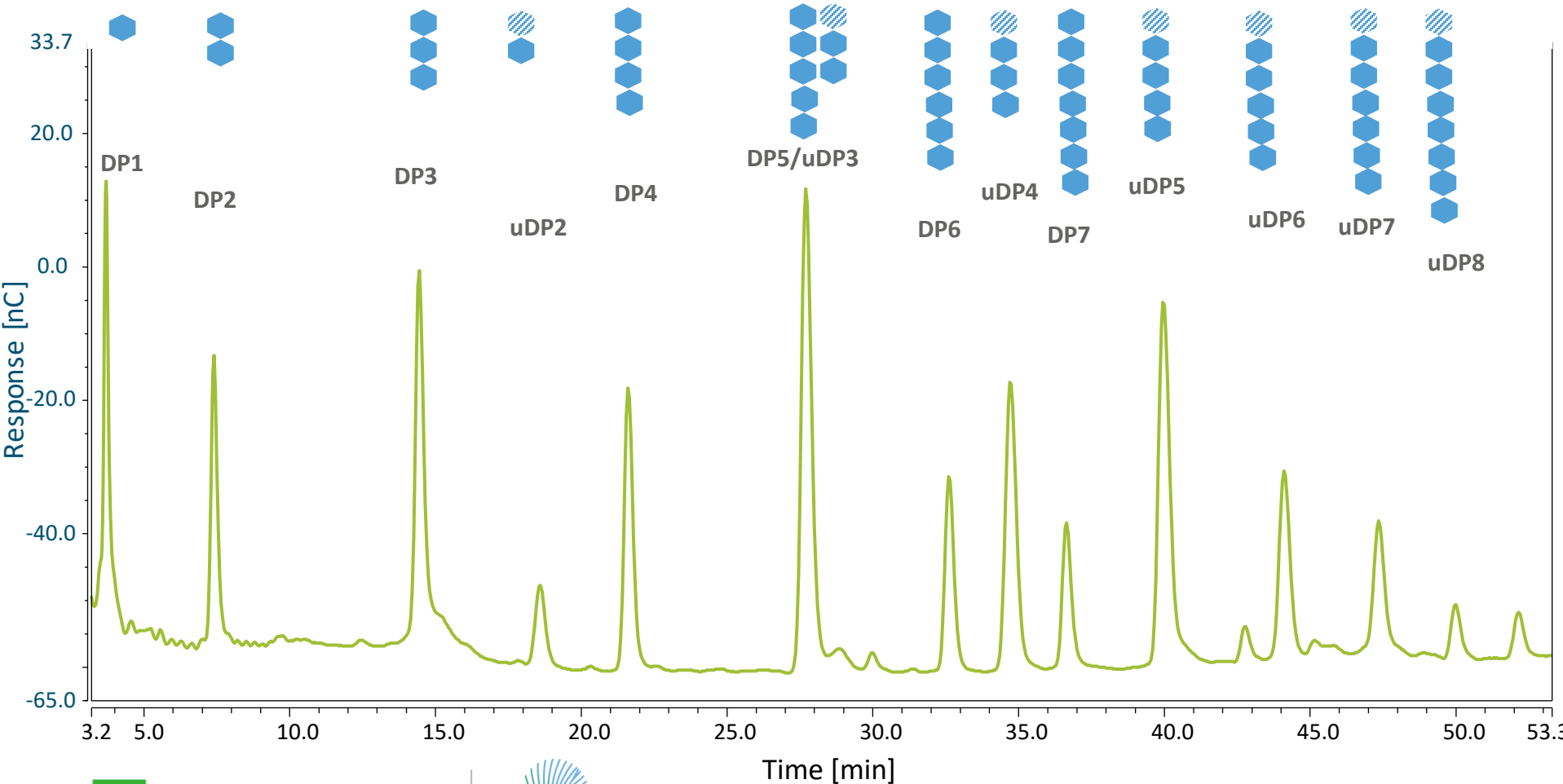


- **DB** quantifies unsubstituted mono-, di- and tri GalA oligomers as released by PG  
→ Information on non-esterified regions, relative to non-esterified GalA
- **DB absolute** → Information on non-esterified regions within pectin, relative to total GalA
- **DH<sub>PGme</sub>** represents PG released methylesterified segments  
→ Information on specific (partly) methyl esterified regions
- **DH<sub>PLme</sub>** represents PL released highly methylesterified oligomers from the pectin  
→ Information on highly methyl esterified regions

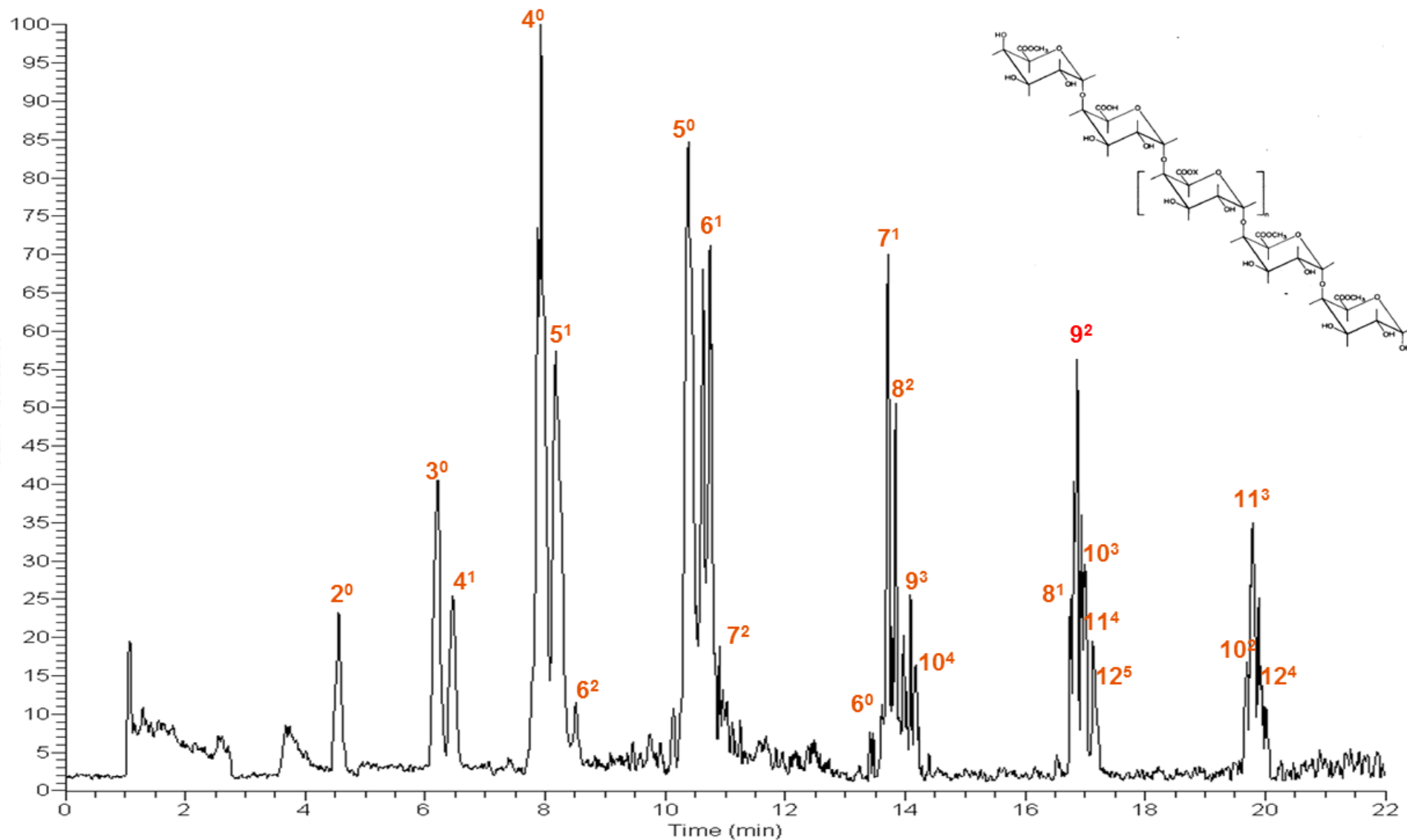
# MALDI TOF MS of random esterified DM70 pectin digested by endo-PG



# HPAEC-PAD elution profile of the DM~60 pectins after enzymatic degradation

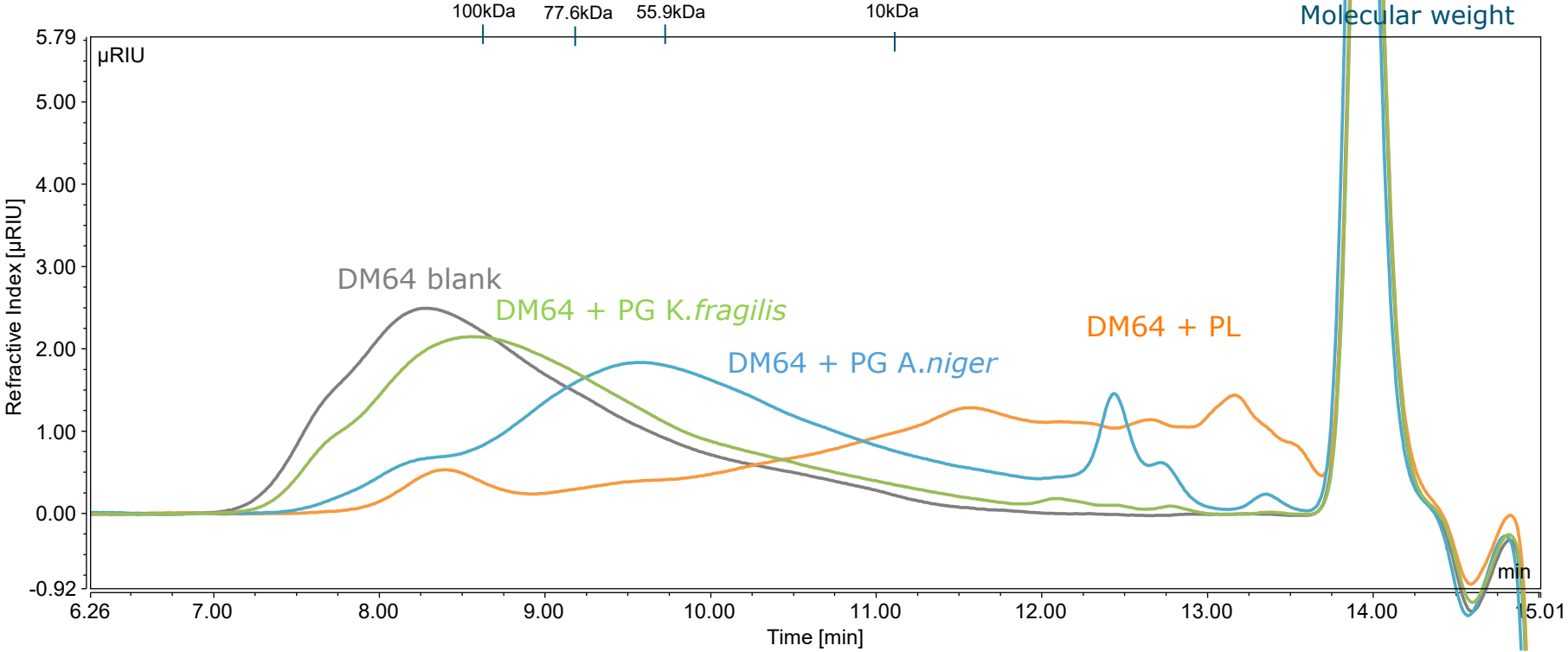


# HILIC HPLC-Iontrap-MS<sup>n</sup> method: methyl-esterified pectin oligomers



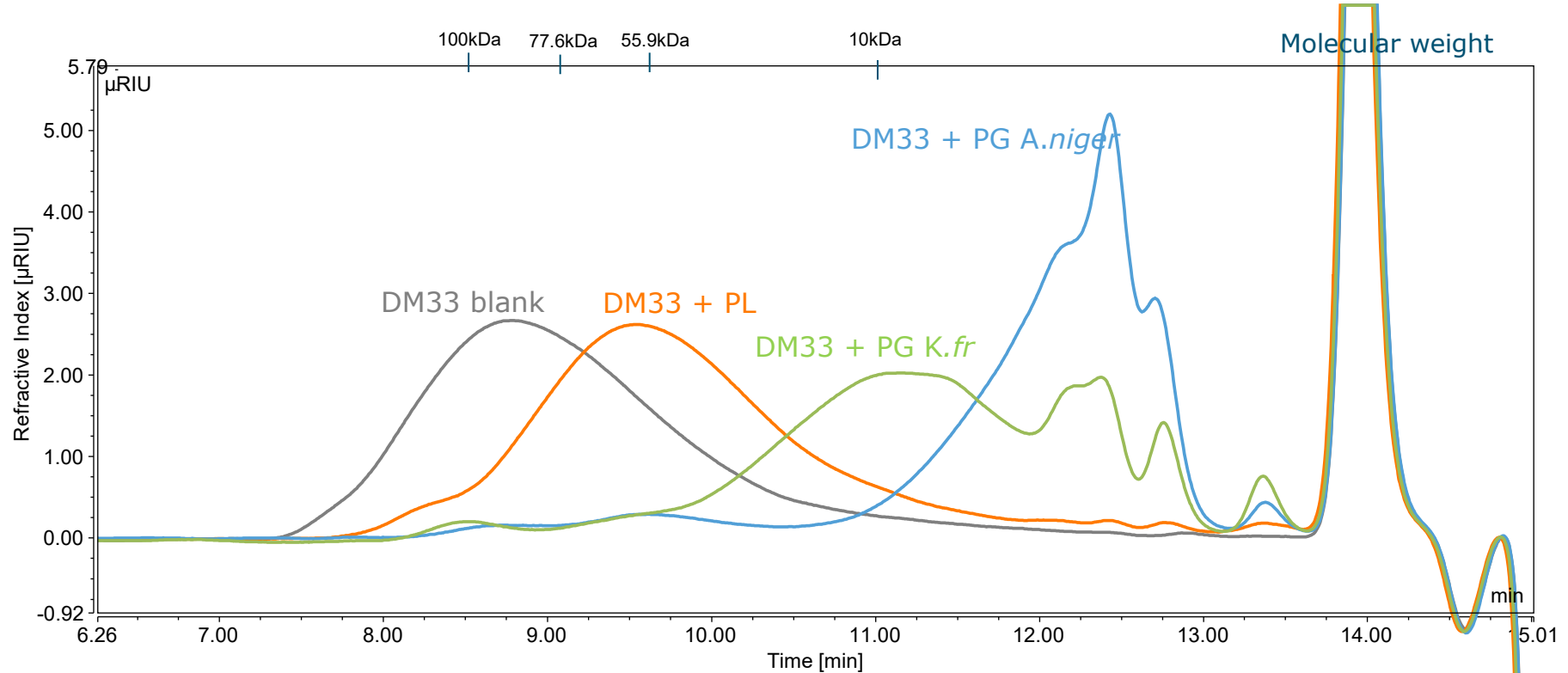
Influence of methylester groups: shift to earlier times **5<sup>1</sup> = GalA<sub>5</sub> 1methyl**

# HPSEC elution profiles of high esterified DM64 pectin incubated with PGs and a PL



PL degrades substantially HM pectin  
PG degrades HM pectin only slightly and degradation depends on origin of PG

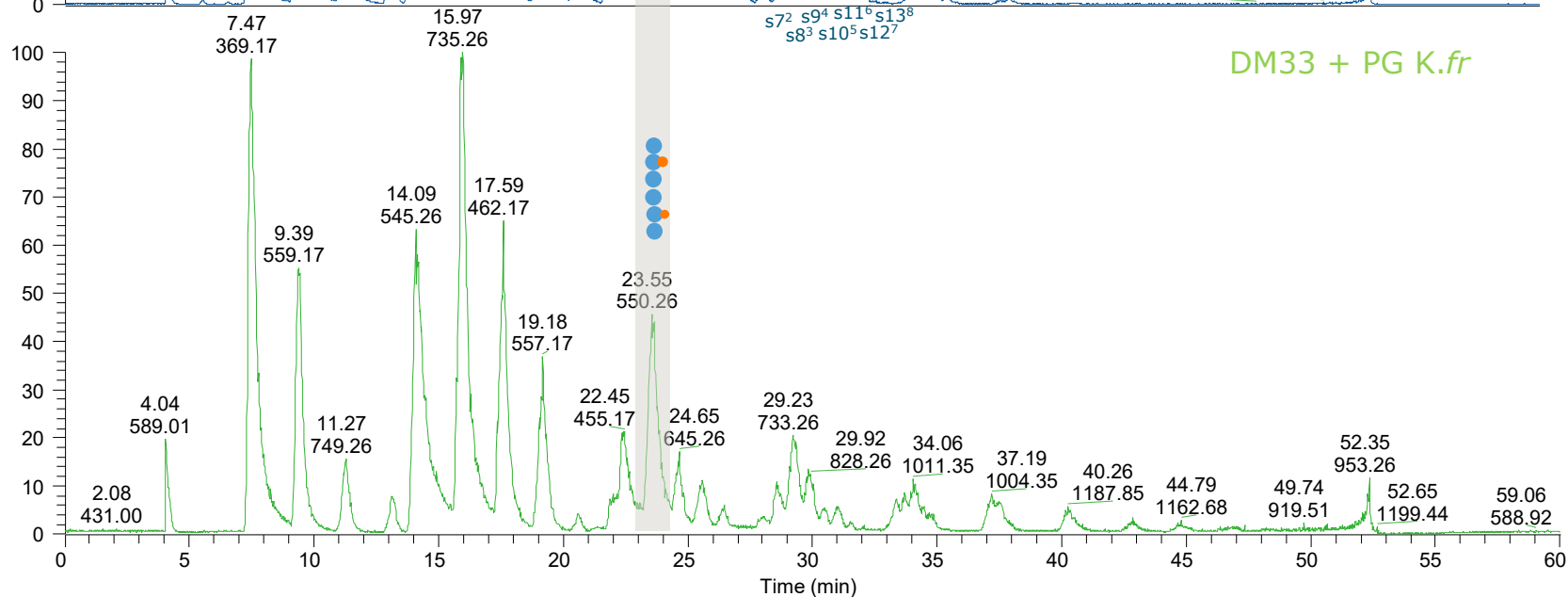
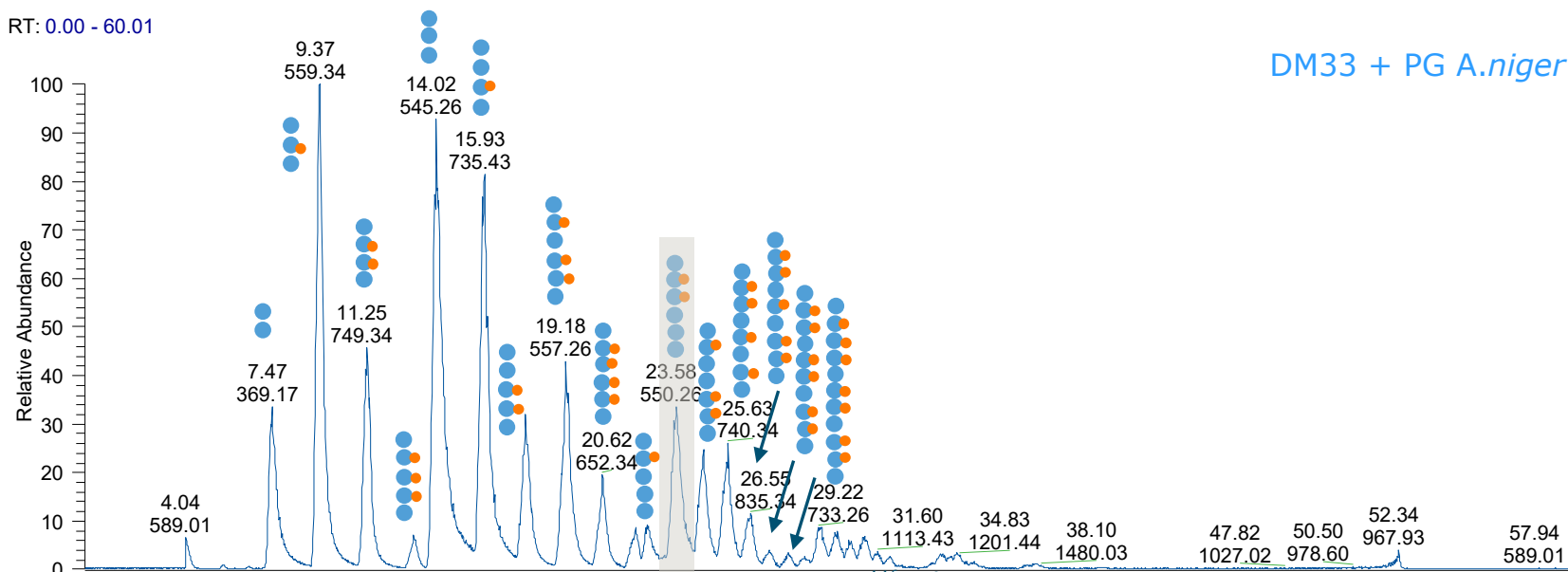
# HPSEC elution profiles of low esterified DM33 pectin after incubation with PGs and PL



Depending on PG's origin, different Mw profiles are obtained.  
PG degrades LM pectin much better than PL

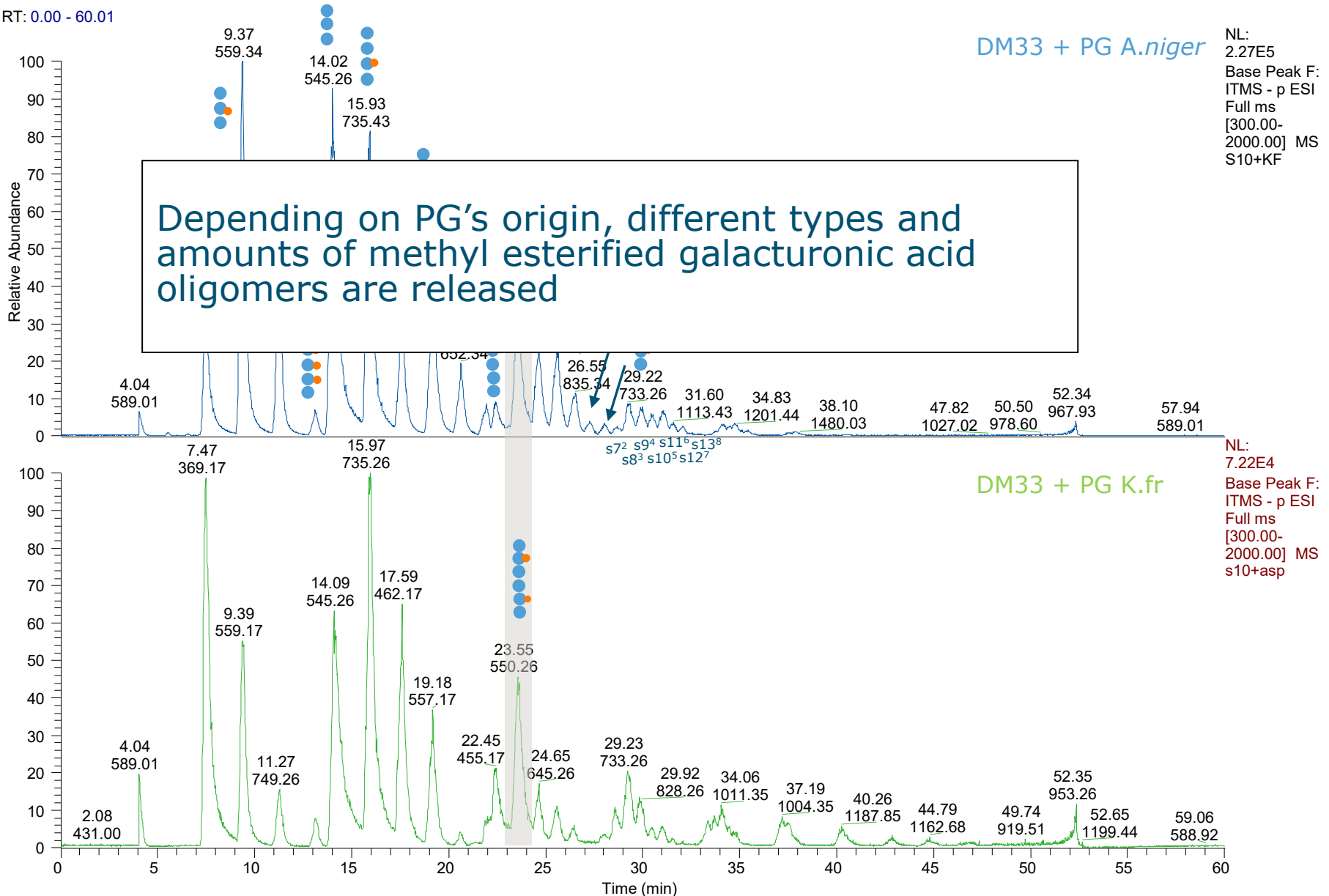
# HILIC LC-MS profiles of DM33 pectin incubated with PGs

RT: 0.00 - 60.01



# UPLC-MS profiles of DM33 incubated with PG from different origin

RT: 0.00 - 60.01

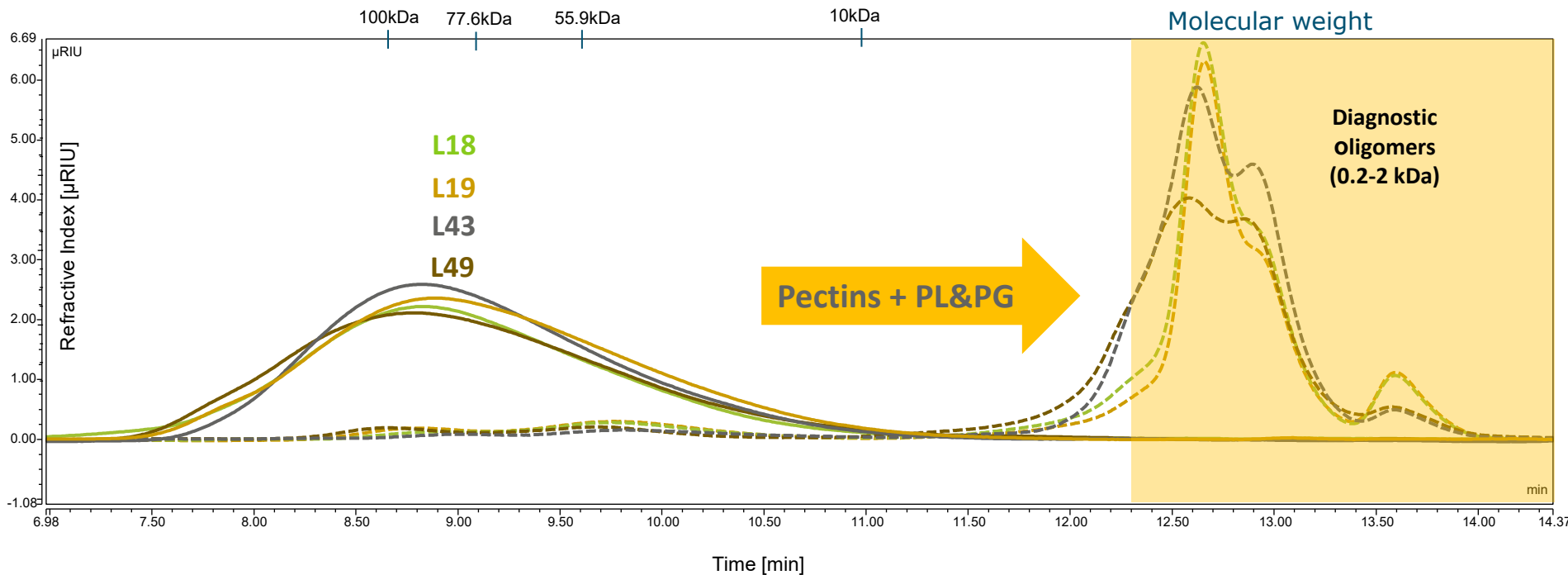




# HPSEC-RI elution profiles of Lemon pectins before and after enzymatic degradation by PG + PL

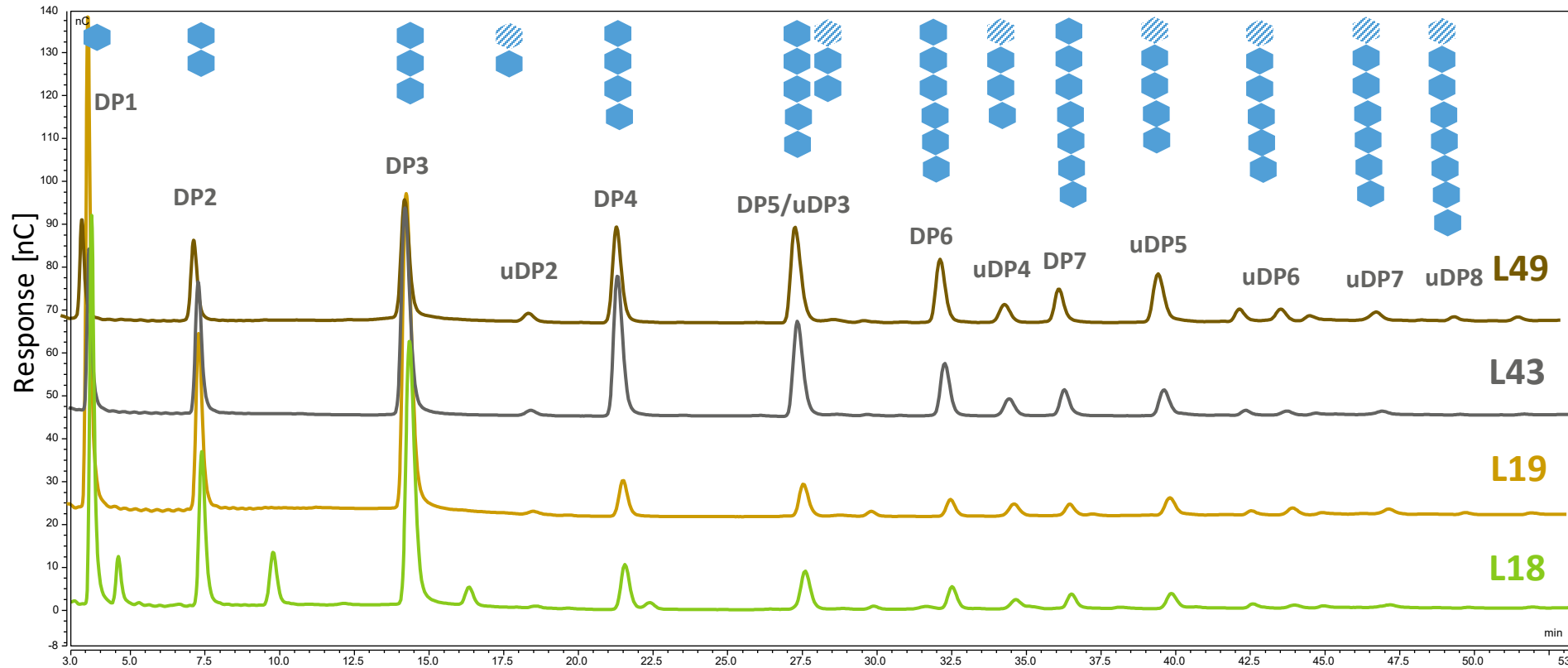
Two times 2 different commercial Lemon pectins:

2 x LM pectins  
2 x MM pectins



PG and PL digestion together completely degrade various pectins to mono-, and oligosaccharides

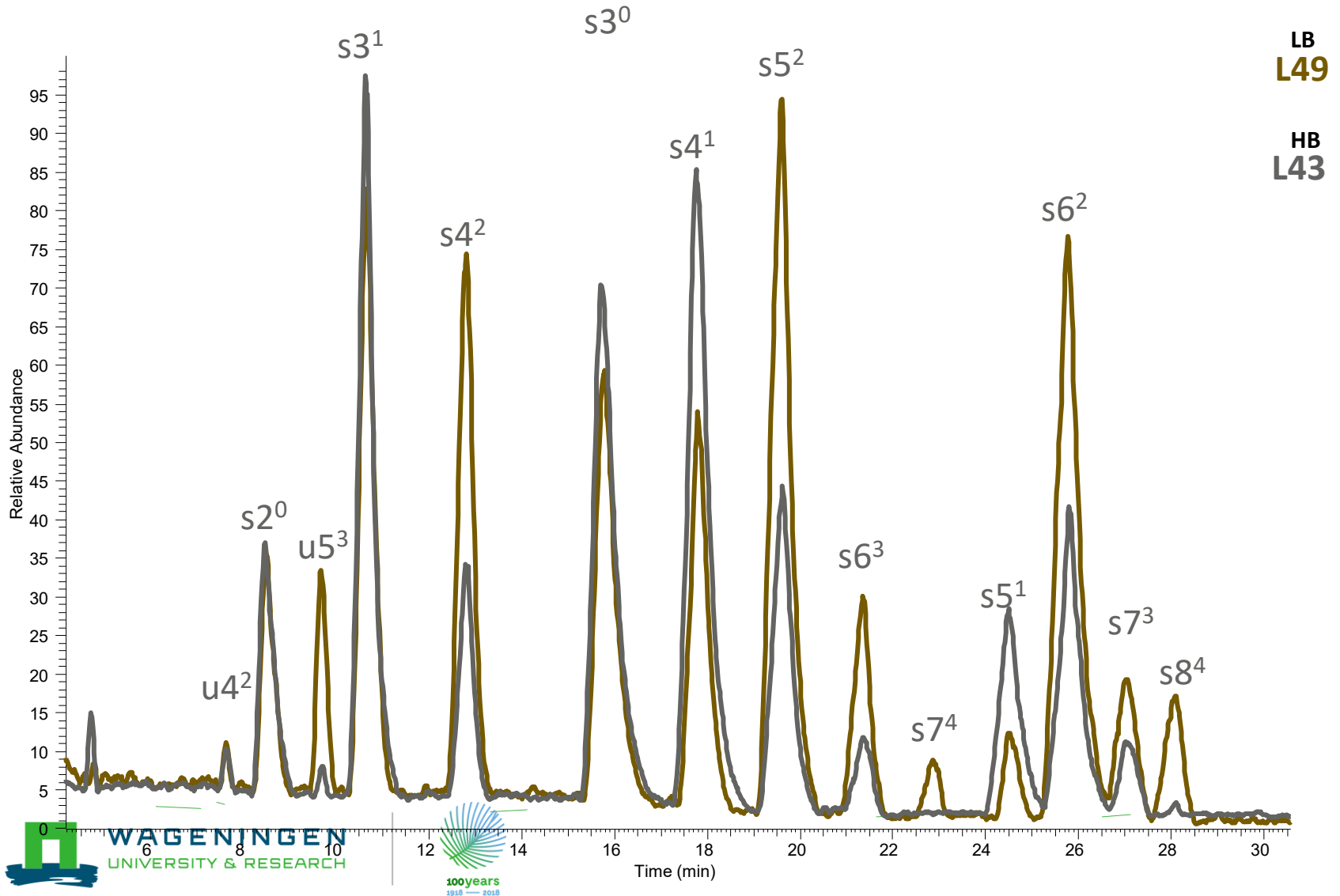
# HPAEC-PAD elution profile of the pectins after enzymatic degradation



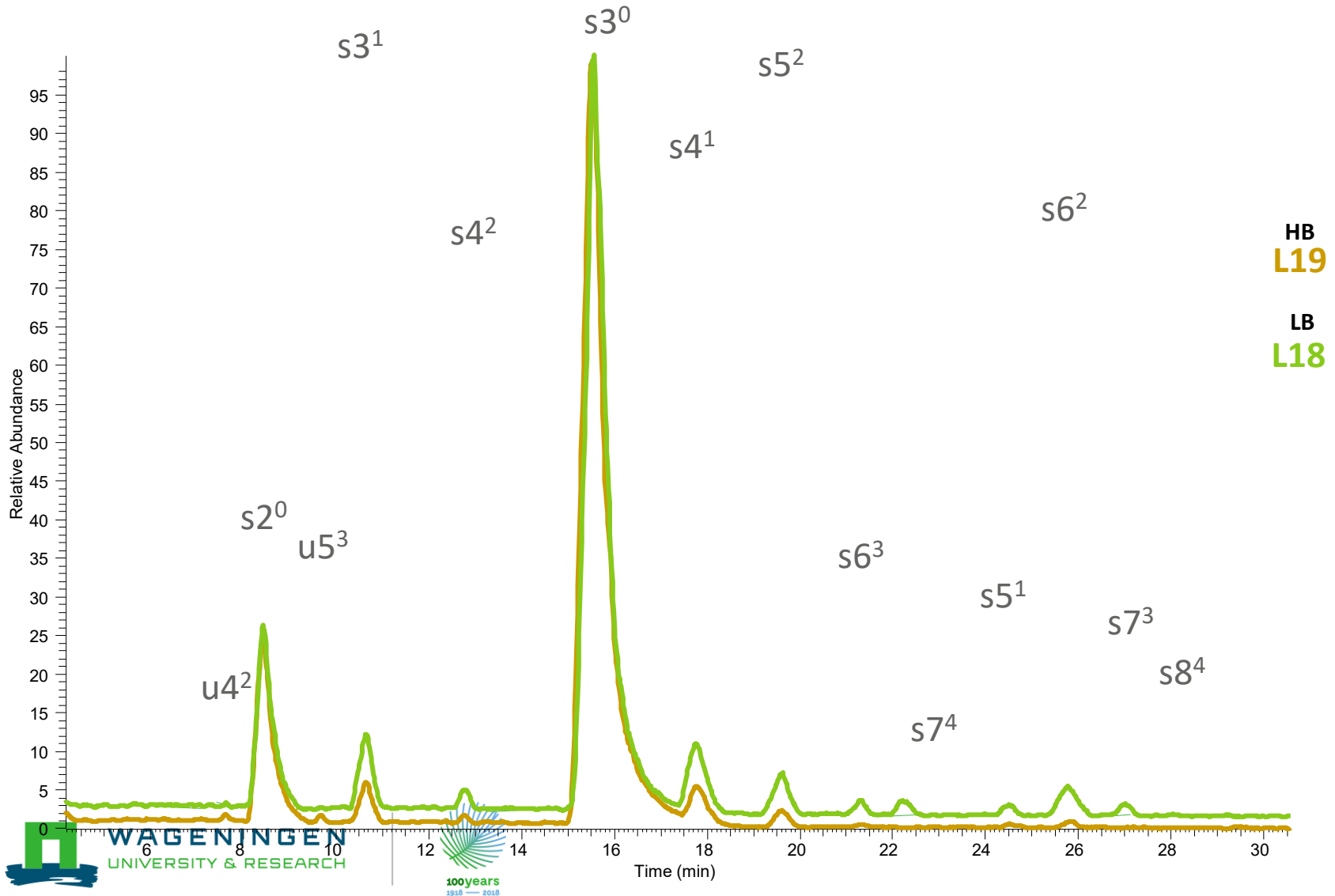
DP = Degree of Polymerisation;  
DP1-n = saturated GalA oligomers  
uDP1-n= unsaturated GalA oligomers

Nice distinction between PG- (saturated) and PL (unsaturated) oligomers  
No information on methyl esters  
Availability of standards is limited

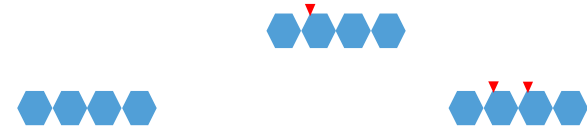
# UPLC-HILIC-MS elution profile of pectins after enzymatic degradation



# UPLC-HILIC-MS elution profile of pectins after enzymatic degradation

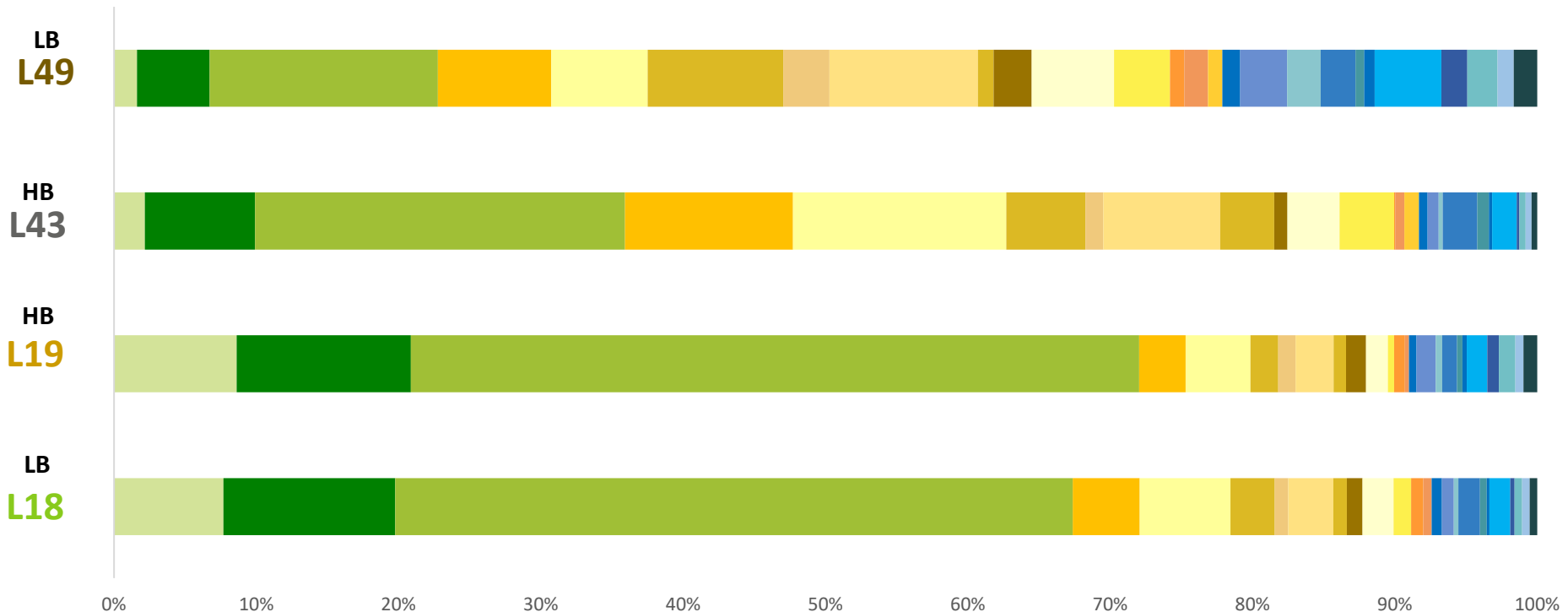
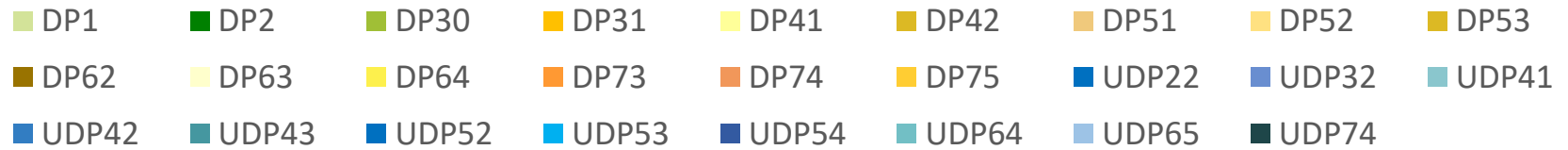


# Pectin descriptive parameters



	Code/DM	Origin	Mw	DB	DB <sub>abs</sub>	DH <sub>PGme</sub>	DH <sub>PLme</sub>
<b>LM Pectin</b>	L19	Lemon	75	93	75	21	10
<b>LM Pectin</b>	L18	Lemon	78	80	66	27	8
<b>MM Pectin</b>	L43	Lemon	74	56	32	73	11
<b>MM Pectin</b>	L49	Lemon	(114)	34	18	65	26

# Relative abundance of oligosaccharides released from the pectins



Oligomers differ in level, size and methyl-ester patterns, highlighting minor and major differences in methyl-ester distribution of pectins having the same overall degree of methyl-esterification.

# Pectin's functionality: Methyl ester level and distribution matters:

- Immune modulation - Pectins in Toll-like receptor activation and inhibition
  - Pectins with blockwise distributed GalA residues strongly induce TLR2-1 signaling in a pectin structure dependent way
- Fermentation characteristics – shaping the human gut microbiome
  - Differently methyl esterified pectins stimulate different gut bacteria and fermentation differs in speed (= location), type and level of metabolites formed.

# Enzymatic fingerprinting of polysaccharides

- Approach successfully applied on:
- Pectins
- Arabinoxylans
- Derivatised starches (Crosslinked, HP-, Ac-, RS3)
- Galactomannans
- Alginates
- Xanthan

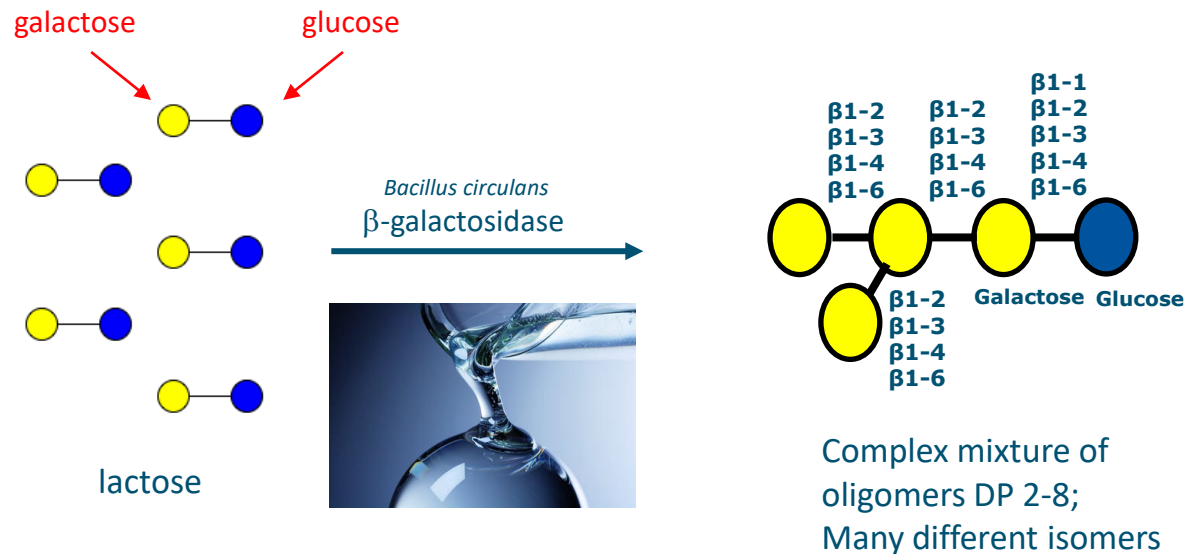


# Oligosaccharide research

# UPLC-HILIC-MS characterisation of oligosaccharides

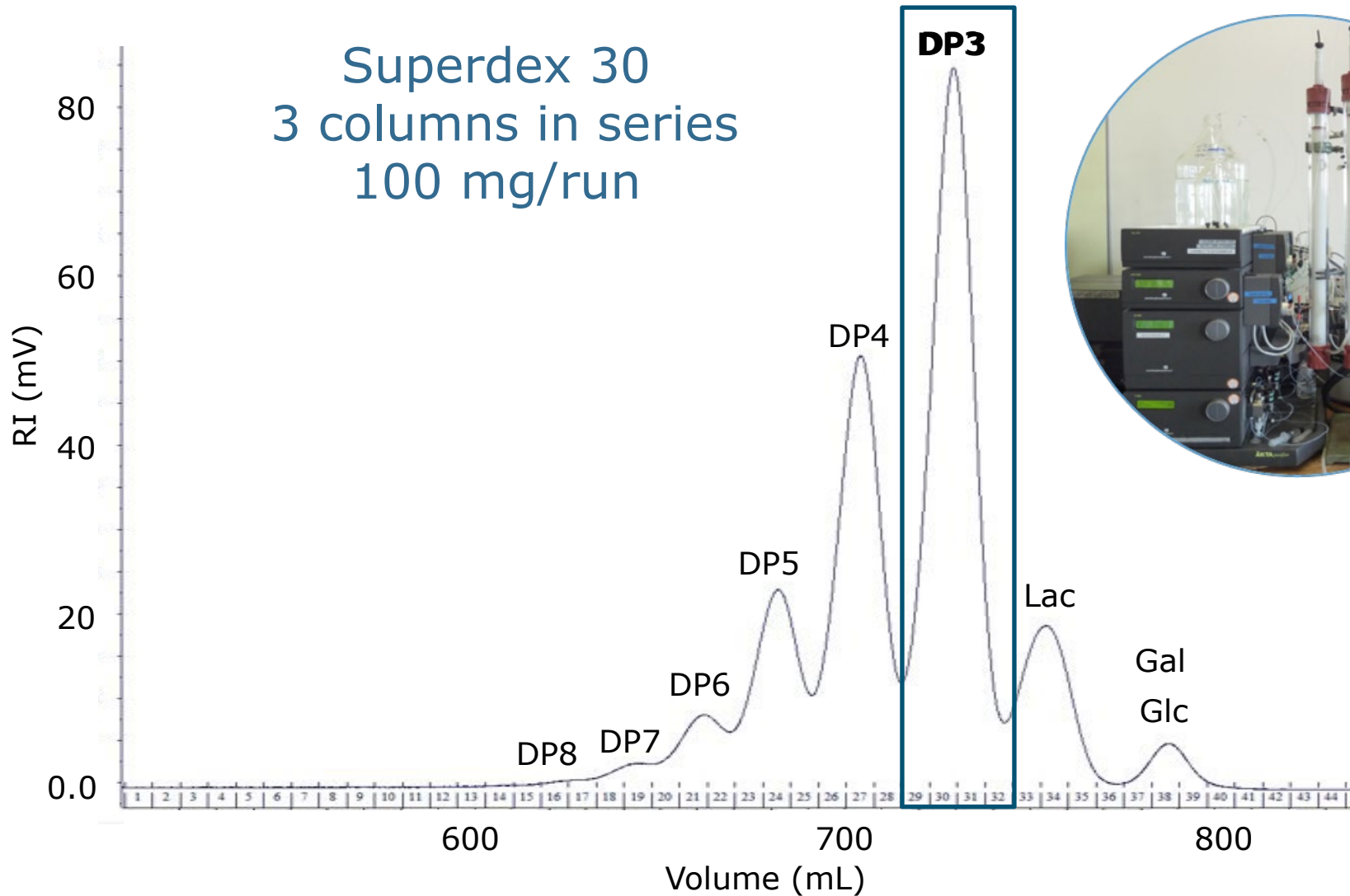
## Prebiotische OS: Galacto-oligosachariden GOS

Enzymatically produced from lactose



# Preparative SEC of GOS

Superdex 30  
3 columns in series  
100 mg/run

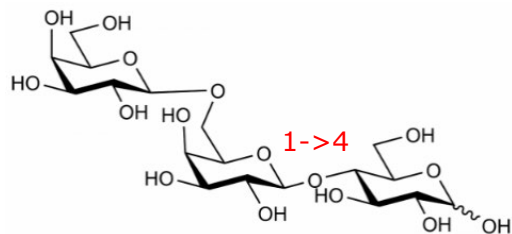


# HPLC-MS analysis of oligomers

- Complex elution pattern and often broad peaks due to (partly) separation of alfa/beta anomers.
- Labelling / reduction of reducing end of oligosaccharide
- Label-enhanced annotation of MS-fragments

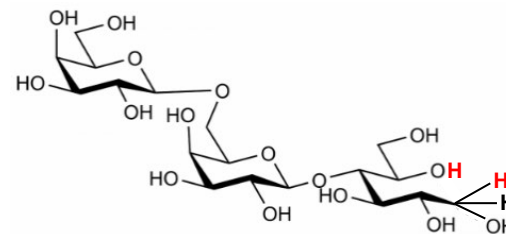
# GOS Pre-treatment before UHPLC-PGC-MS

## Analysis

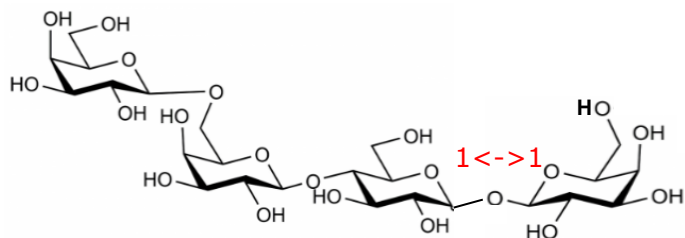


Galactosyl-6-lactose (6'GL)  
*m/z* 504

1. NaBH<sub>4</sub> reduction
2. SPE

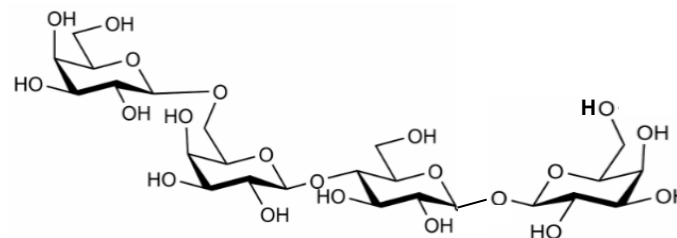


Reduced 6'GL  
*m/z* 504 + 2



DP4 GOS  
*m/z* 666

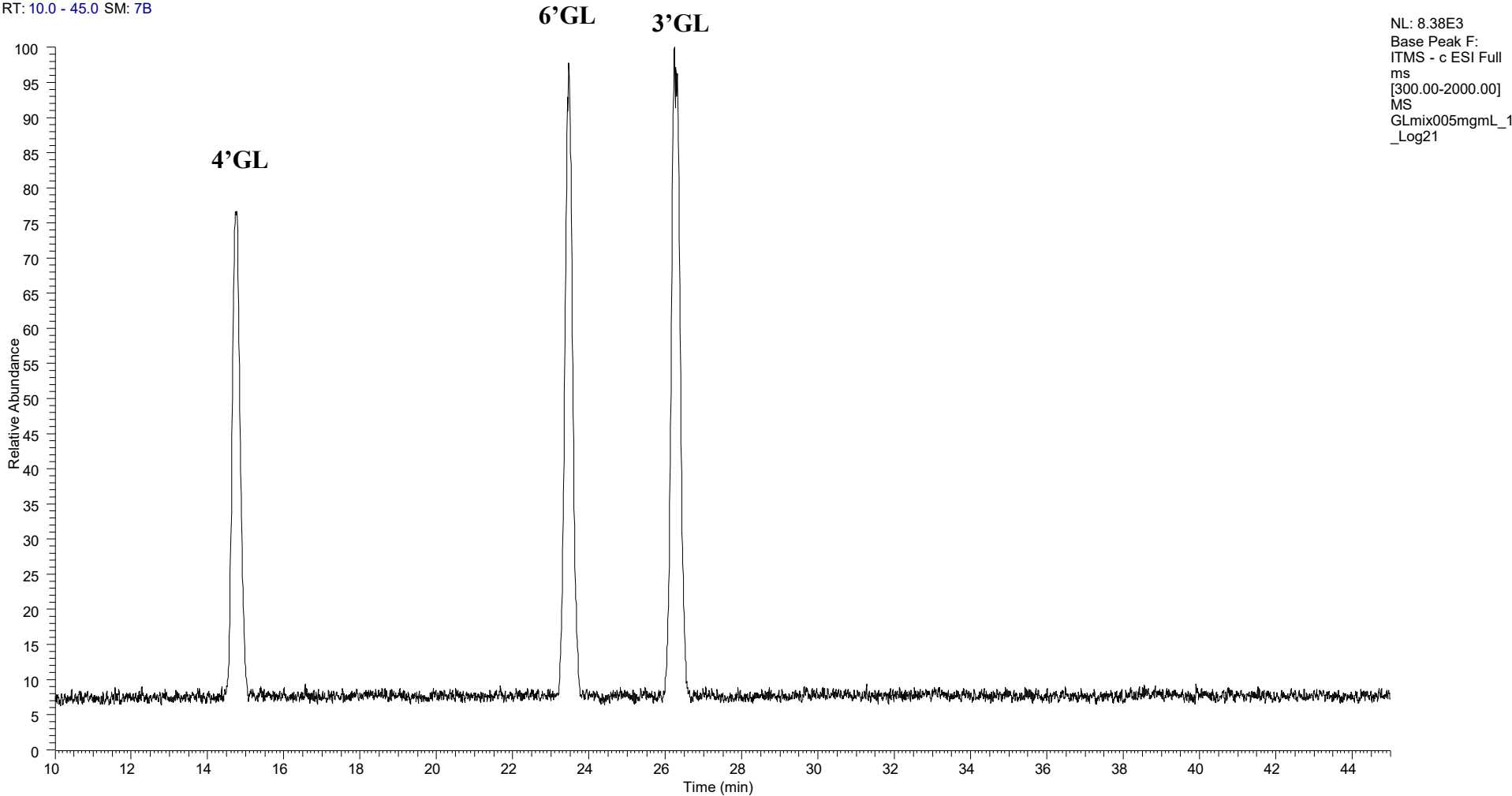
1. NaBH<sub>4</sub> reduction
2. SPE



Non-reduced DP4 GOS  
*m/z* 666

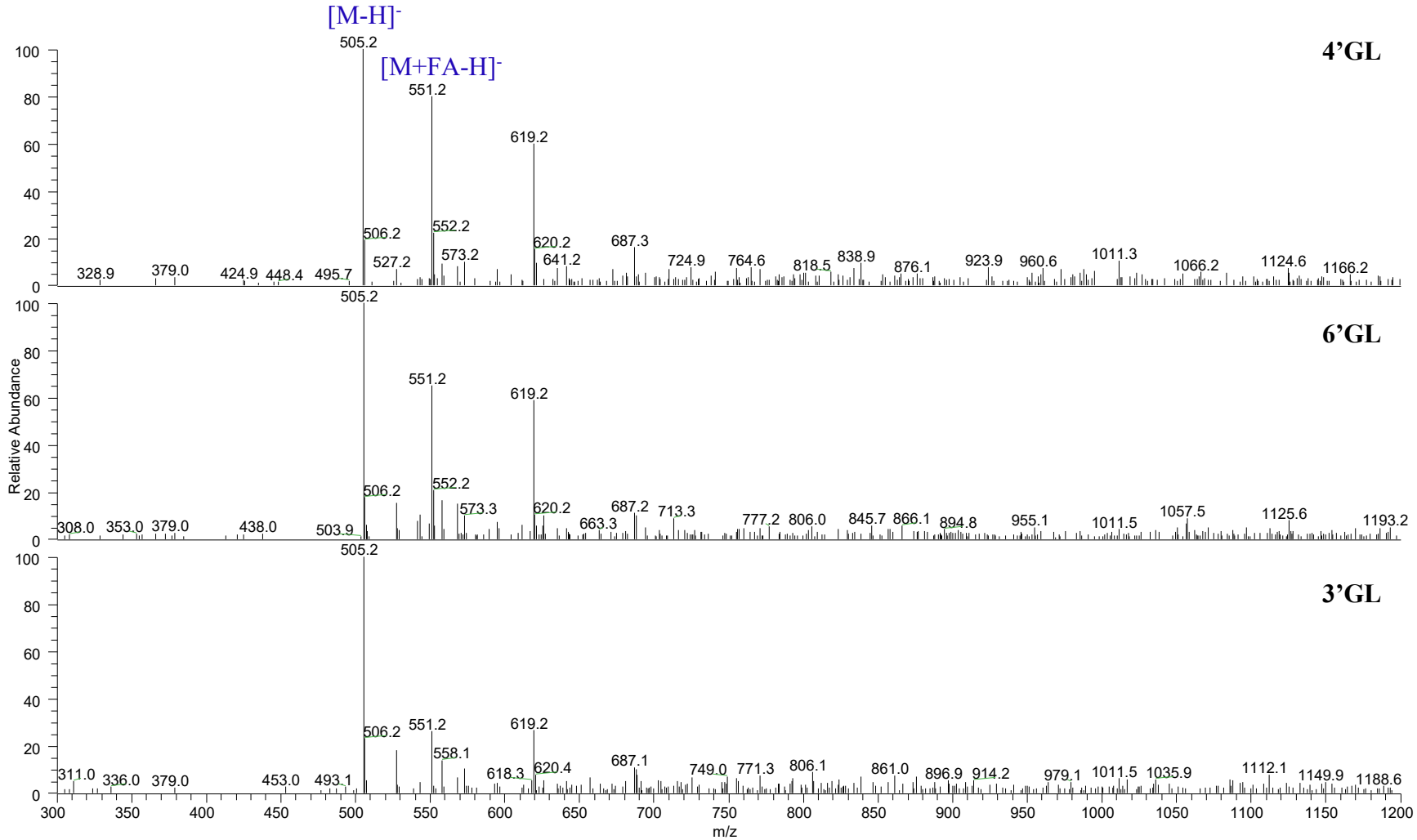
# PGC-MS elution patterns of reduced 3', 4', 6' Galactosyl Lactose standards

RT: 10.0 - 45.0 SM: 7B



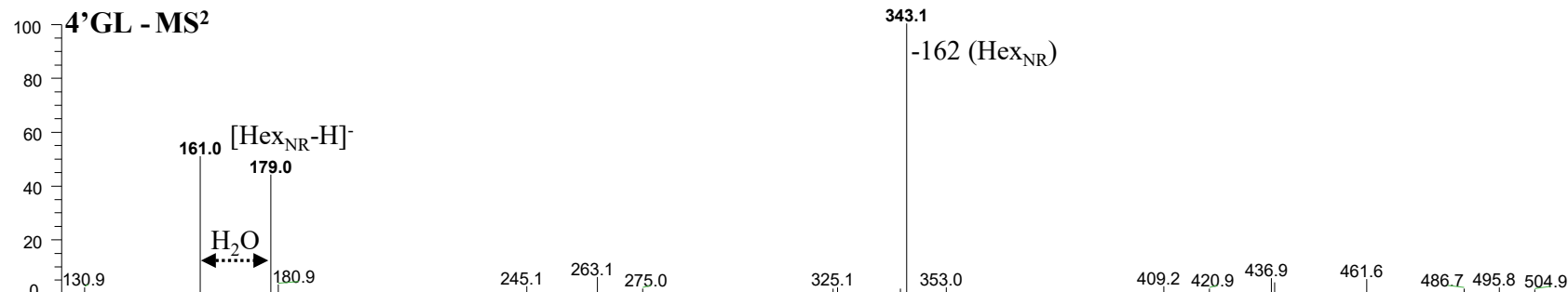
NL: 8.38E3  
Base Peak F:  
ITMS - c ESI Full  
ms  
[300.00-2000.00]  
MS  
GLmix005mgmL\_1  
\_Log21

# Mass spectra of reduced 3', 4', 6' Galactosyl Lactose standards (negative mode)

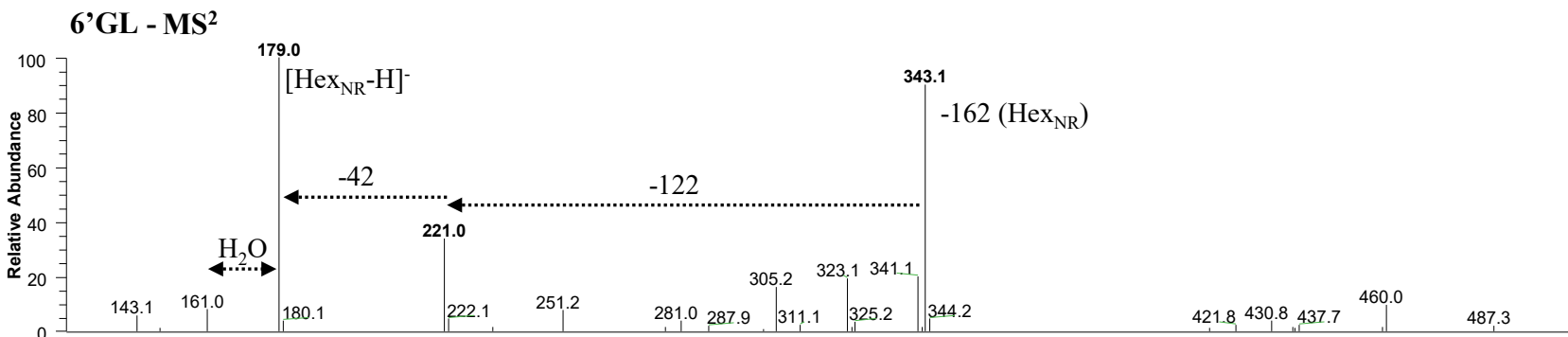


# MS<sup>2</sup> mass spectra of reduced 3', 4', 6' GL

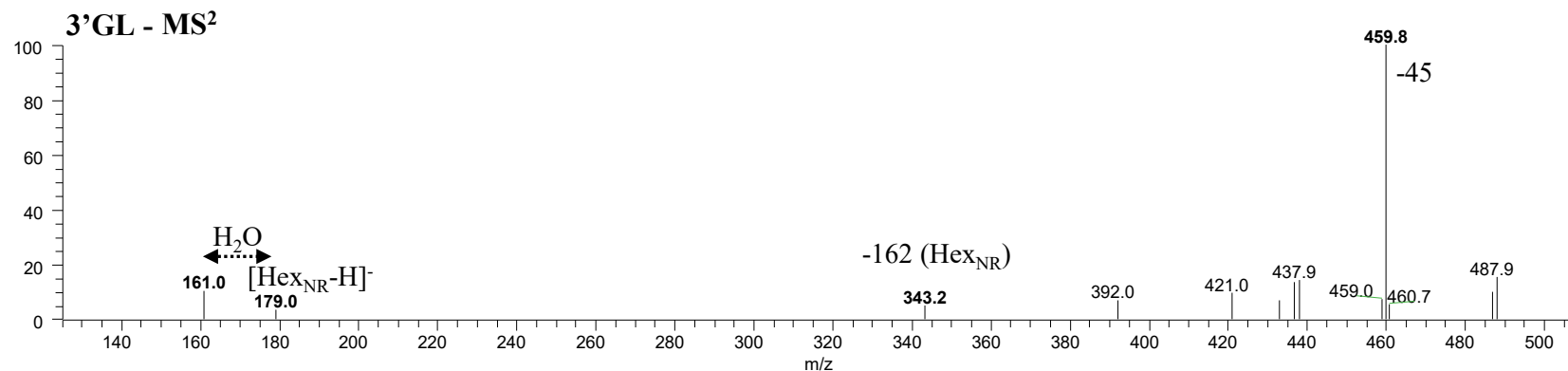
## MS/MS spectra of $m/z$ 505 [M-H]<sup>-</sup>



NL: 2.34E2  
 GLmix005mgmL\_1\_Log21  
 #6100 RT: 14.75 AV: 1 F  
 ITMS - c ESI d Full ms2  
 505.20@cid35.00  
 [125.00-520.00]



NL: 3.66E2  
 GLmix005mgmL\_1\_Log21  
 #9594 RT: 23.45 AV: 1 F  
 ITMS - c ESI d Full ms2  
 505.20@cid35.00  
 [125.00-1025.00]

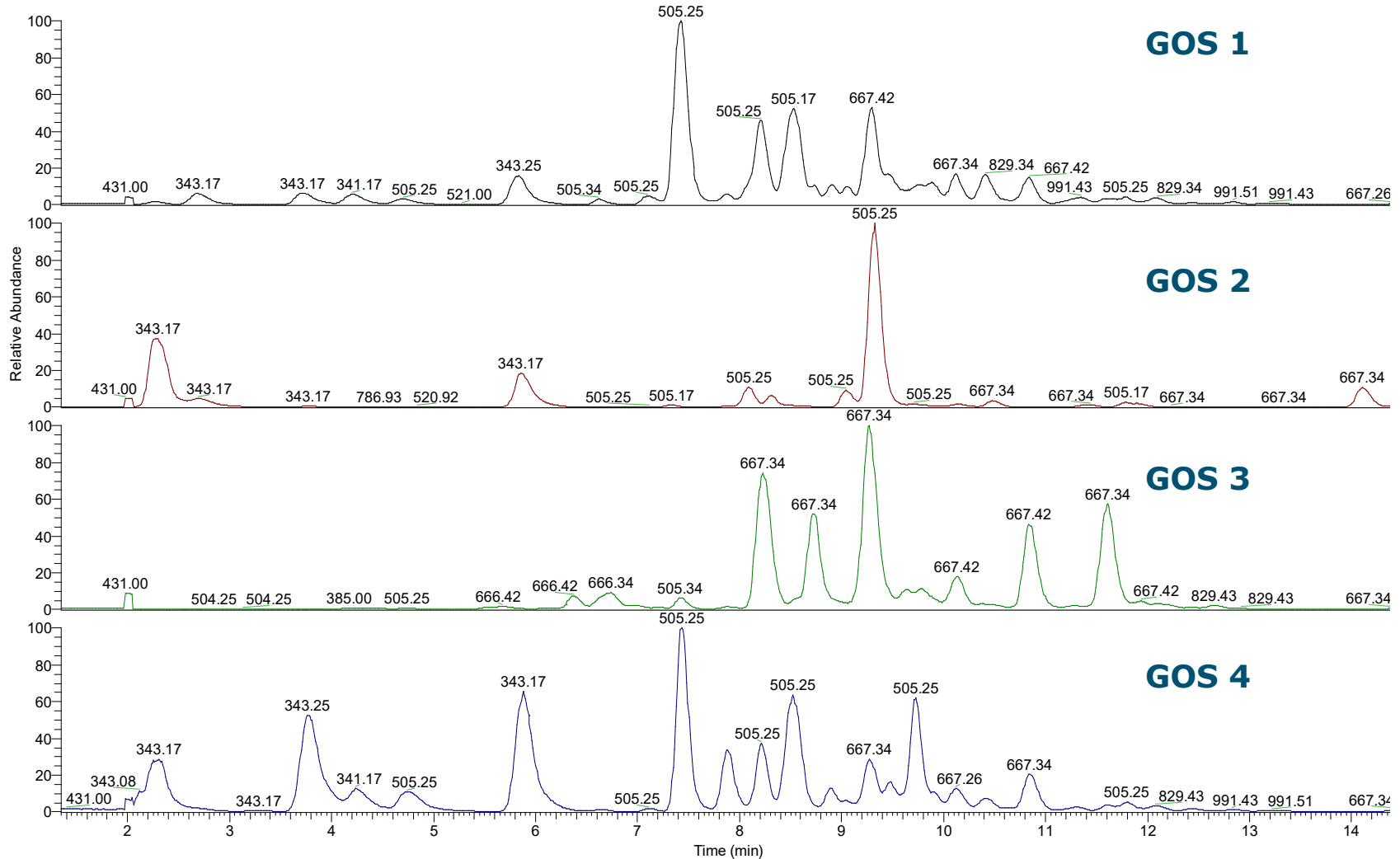


NL: 9.01E1  
 GLmix005mgmL\_1\_Log21  
 #10789 RT: 26.58 AV: 1 F  
 ITMS - c ESI d Full ms2  
 505.20@cid35.00  
 [125.00-1025.00]



# Compositional differences of different GOS samples PGC LC-MS analysis - all oligomers

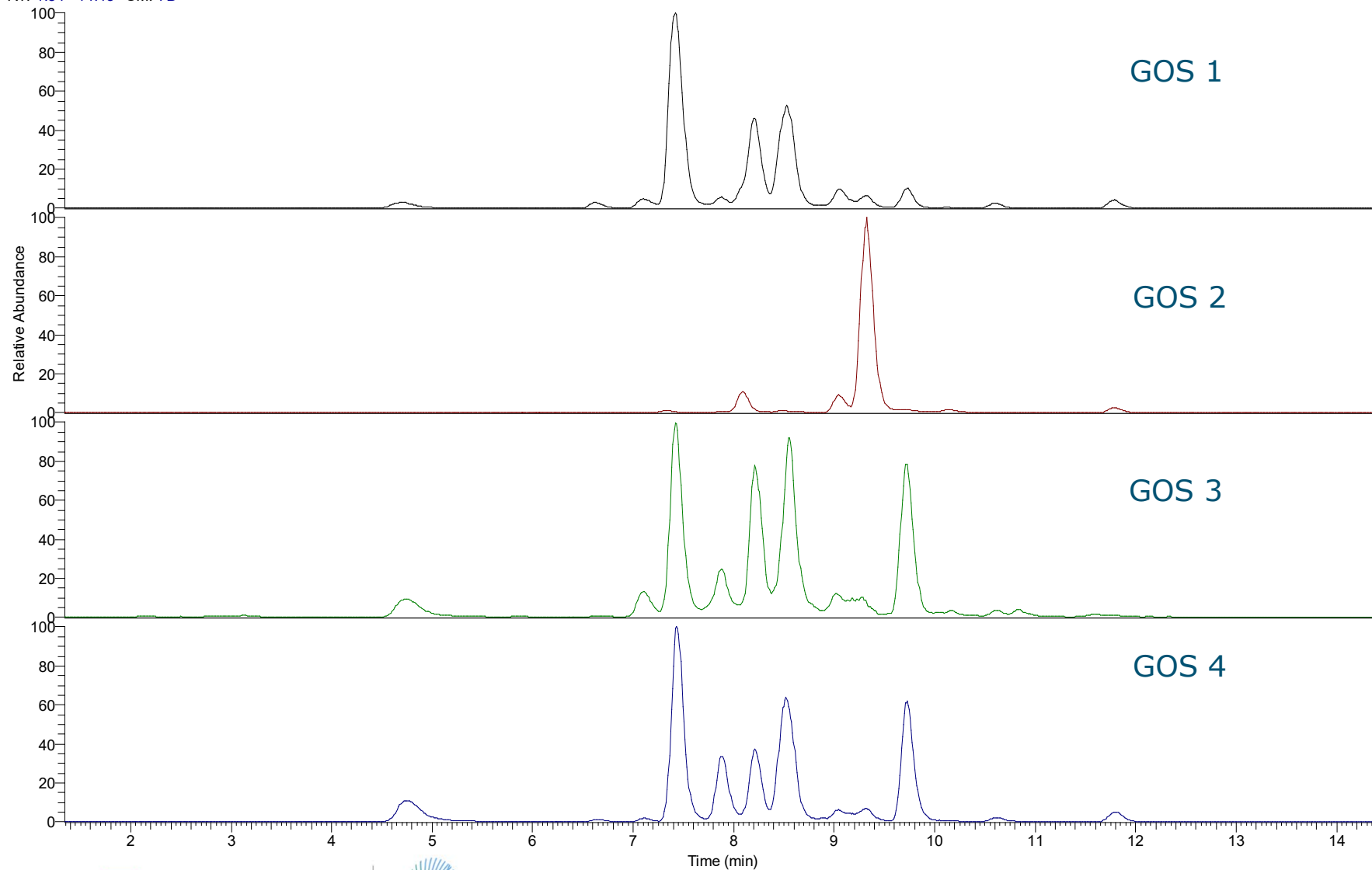
RT: 1.34 - 14.45 SM: 7B



# Compositional differences of GOS

## PGC LC-MS analysis - DP 3 - m/z 505

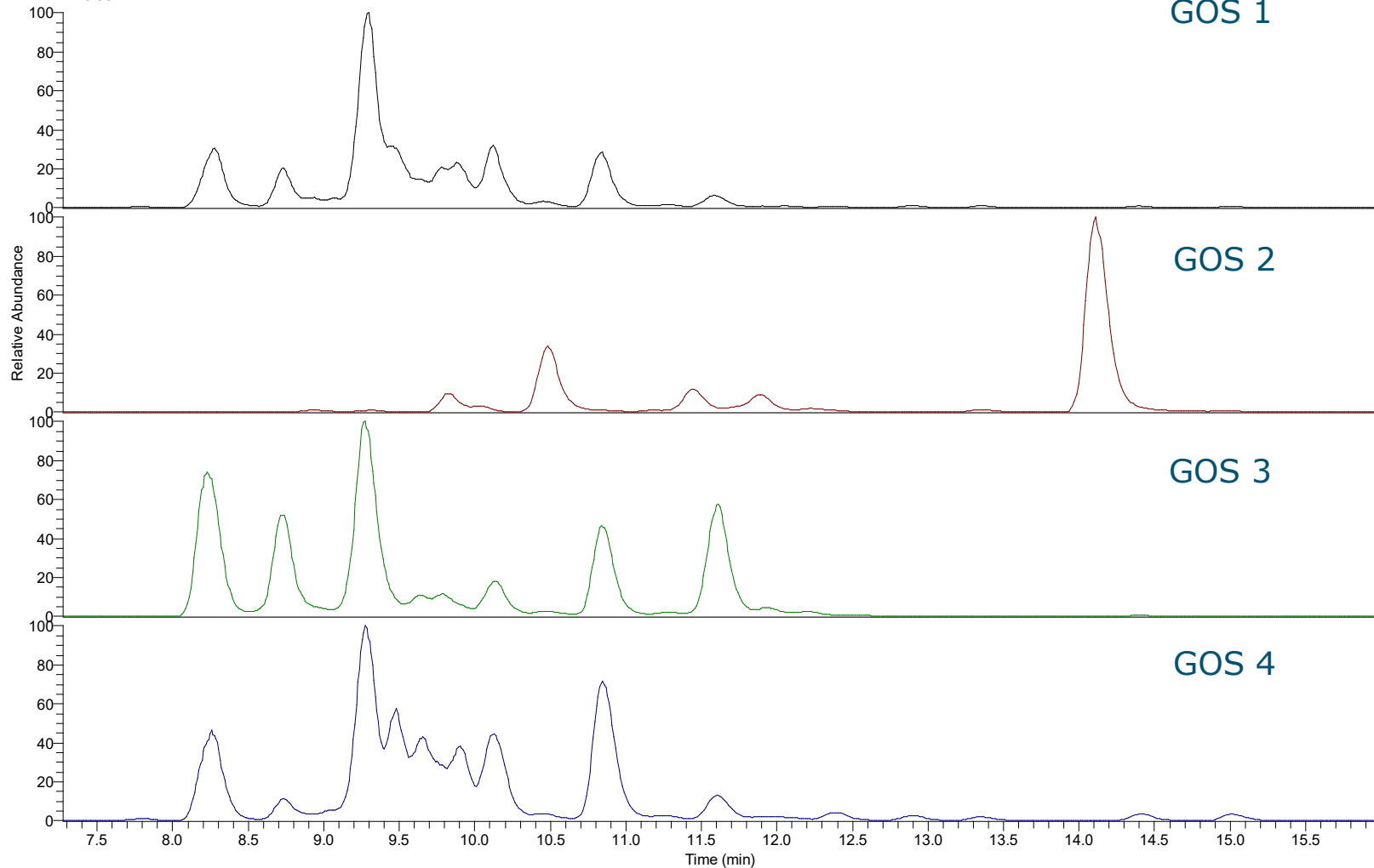
RT: 1.34 - 14.45 SM: 7B



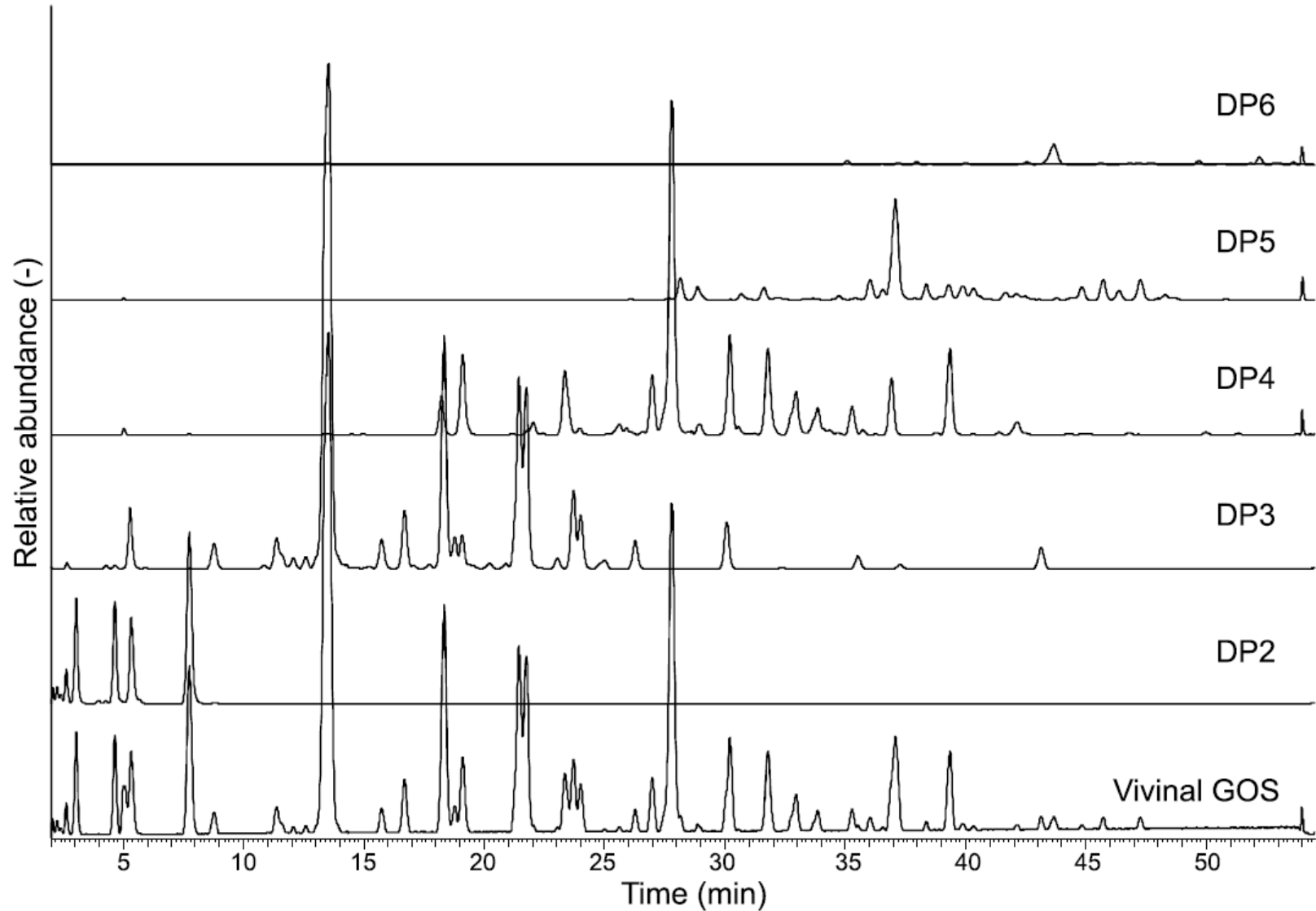
# Compositional differences of GOS

## PGC LC-MS analysis - DP 4 - m/z 667

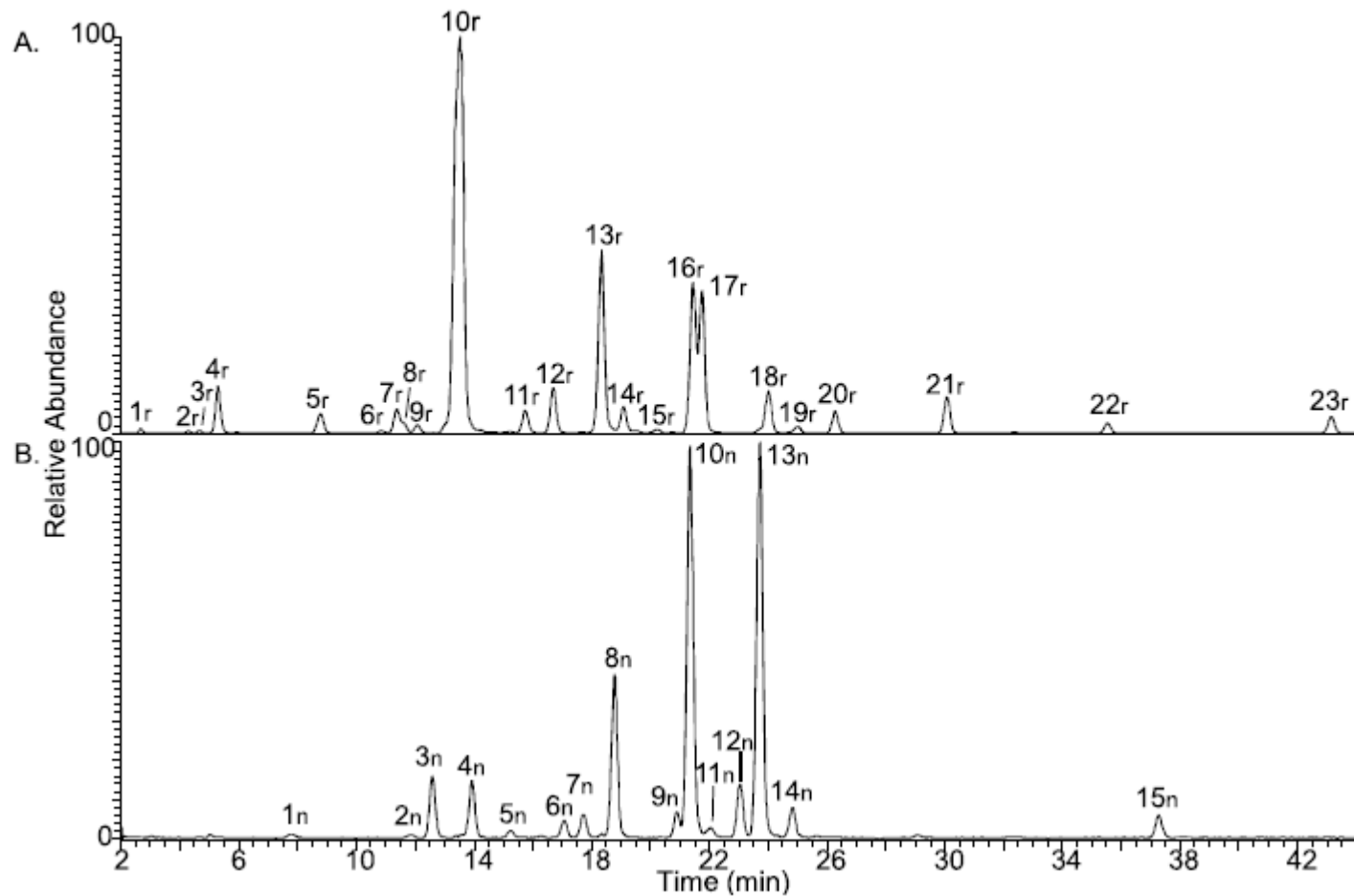
RT: 7.27 - 15.98 SM: 7B



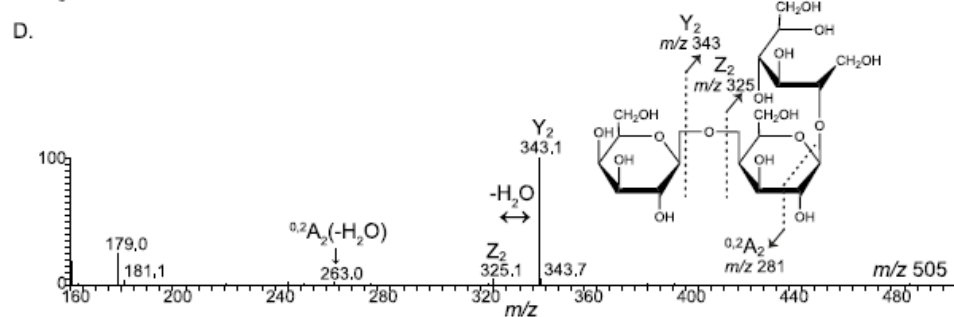
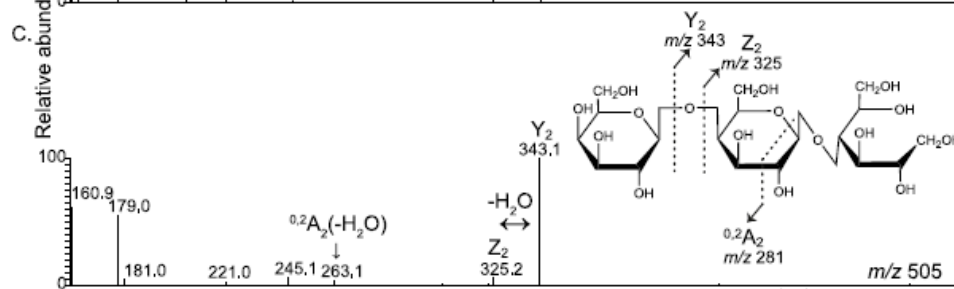
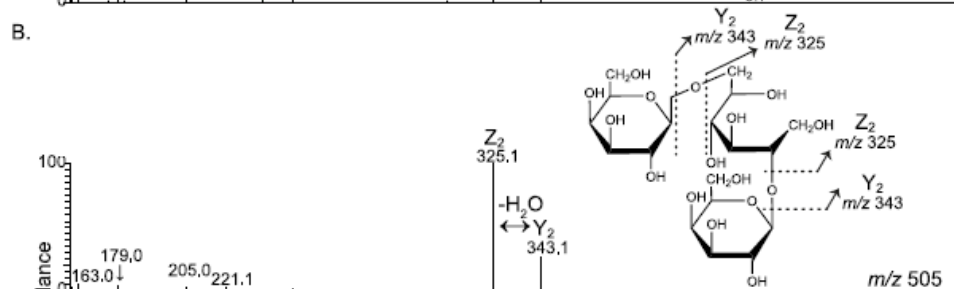
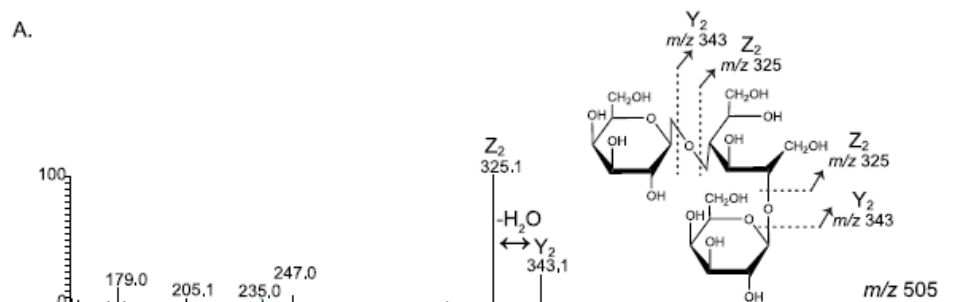
# UHPLC-PGC-MS profile of reducing and non-reducing Vivinal GOS



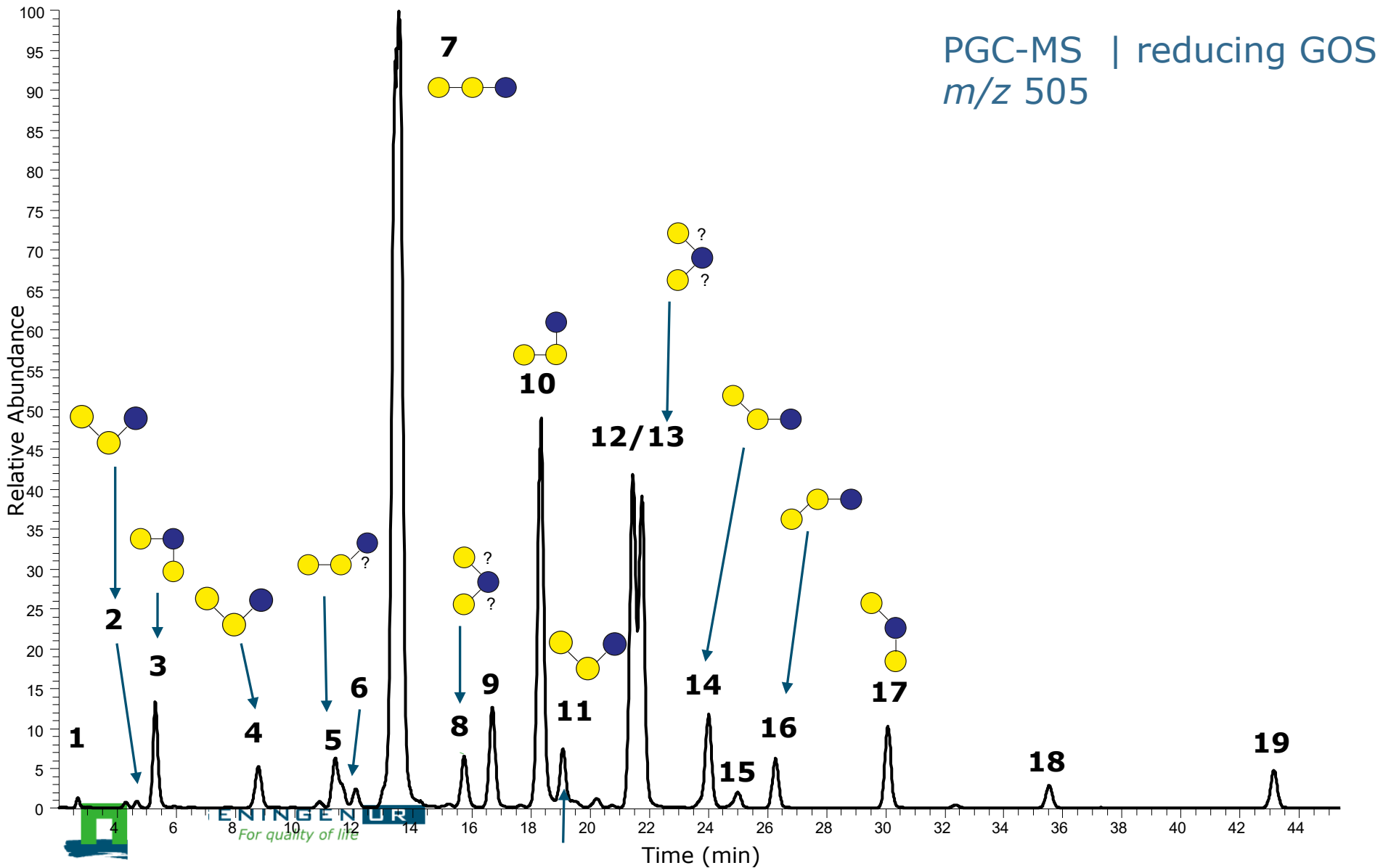
# UHPLC–PGC–MS profile of Vivinal GOS DP3 with the selection of (A) reducing [m/z 505 and 551 (M + FA)] and (B) nonreducing [m/z 503 and 549 (M + FA)] isomers



# Fragmentation spectra (ESI MS<sup>2</sup>) in negative mode of GOS DP3 isomers (A) 4r, (B) 21r, (C) 10r, and (D) 13r

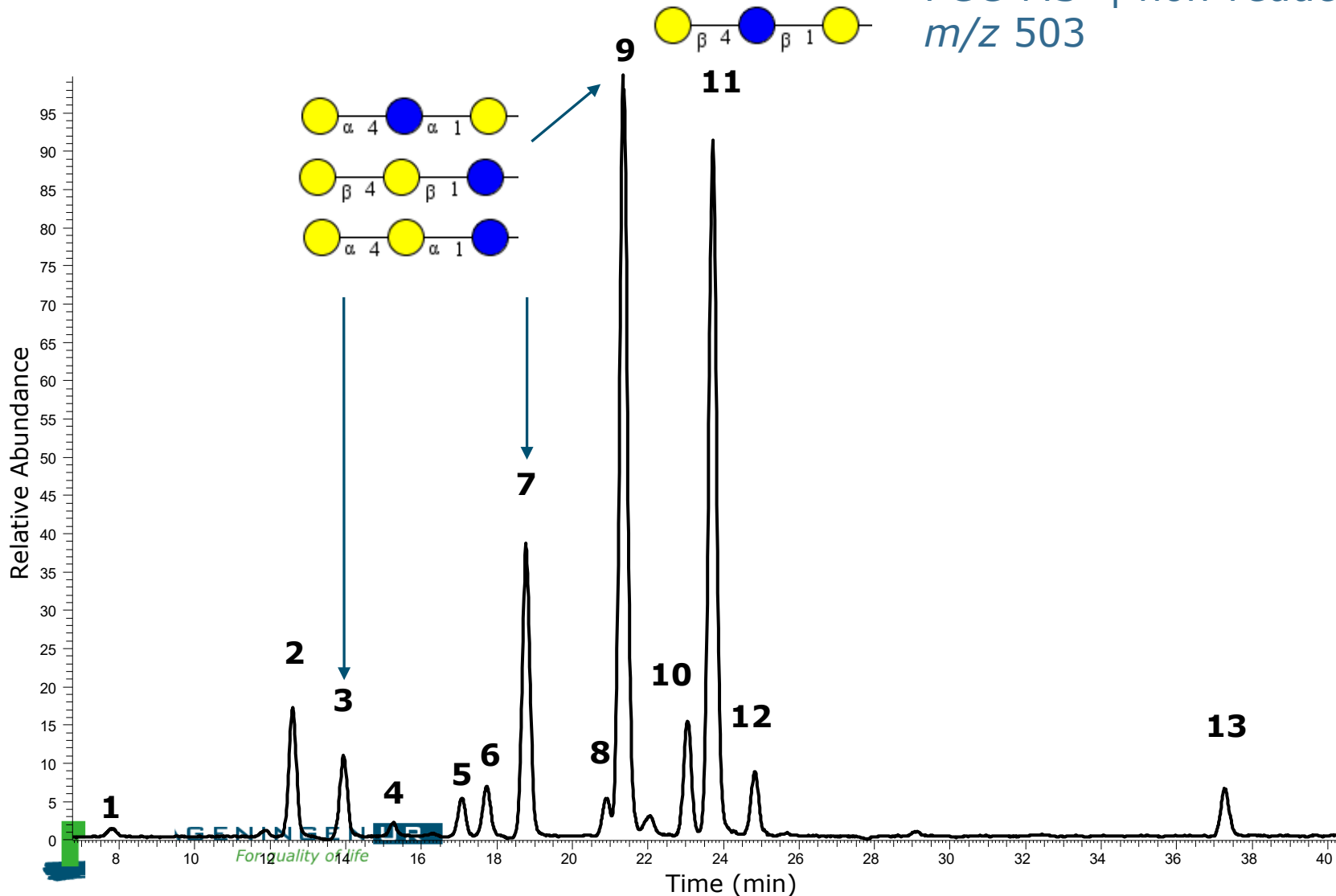


# Characterized GOS DP3 isomers



# GOS DP3 isomers with (1-1)-linkage

PGC-MS | non-reducing GOS  
*m/z* 503





# GOS's functionality: Size and linkages matters

- Fermentation characteristics – shaping the human gut microbiome
  - Differently FOS structures stimulate different gut bacteria and fermentation differs in speed (= location) and in type and level of metabolites formed.
- Immune modulation / strengthening barrier function

# *In vitro* fermentation using human inoculum shows isomer-specific degradation

PGC-MS: Digesta of GOS fermentation using faecal inoculum of 2 weeks old infants

*m/z* DP3 selected

Timepoints:

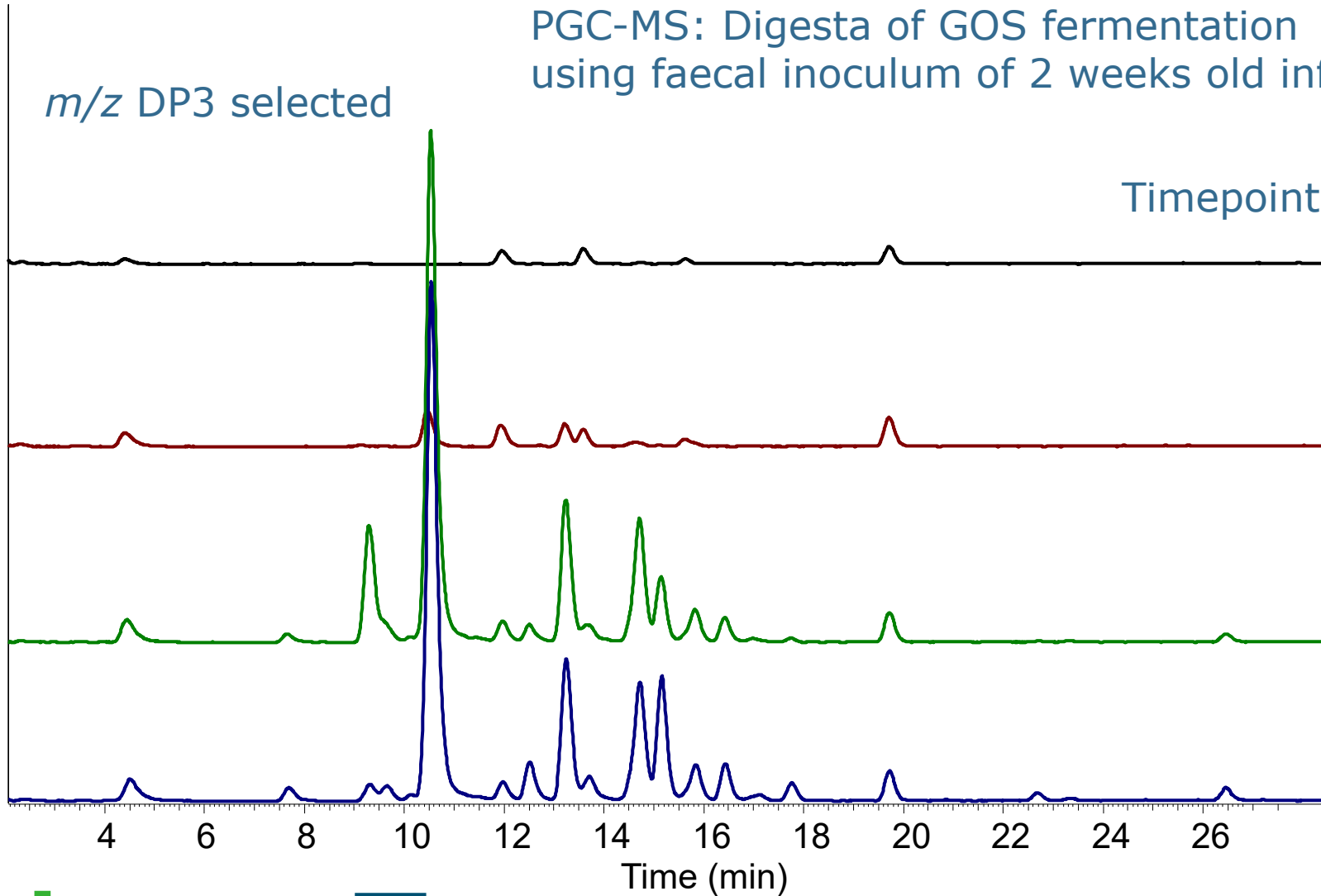
t26

t20

t14

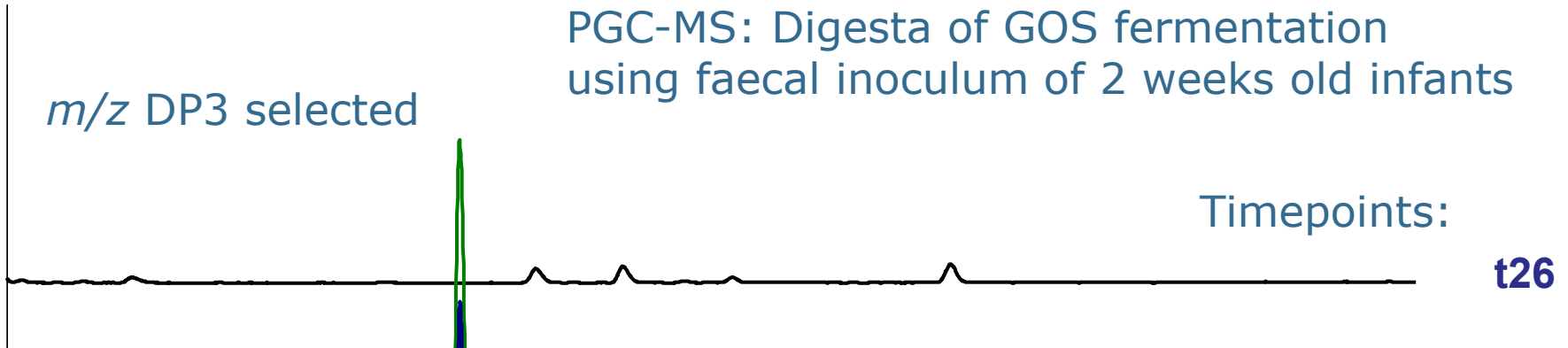
t0

Relative Abundance

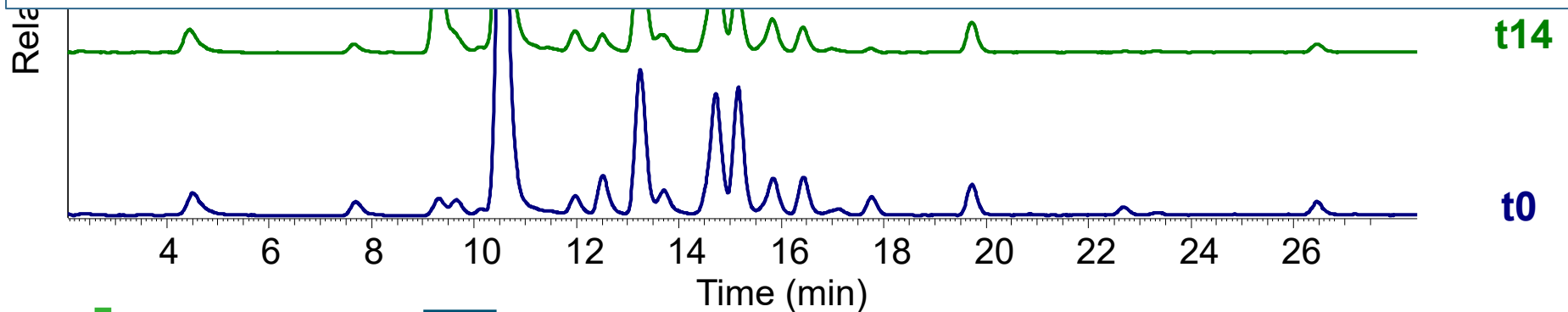


# *In vitro* fermentation using human inoculum shows isomer-specific degradation

PGC-MS: Digesta of GOS fermentation using faecal inoculum of 2 weeks old infants



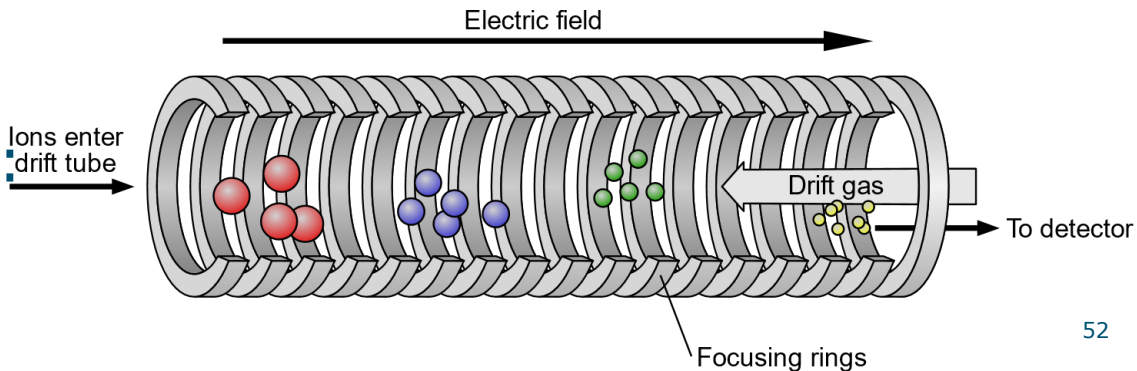
Structure-specific fermentation →  
Structural knowledge of substrates of high importance!



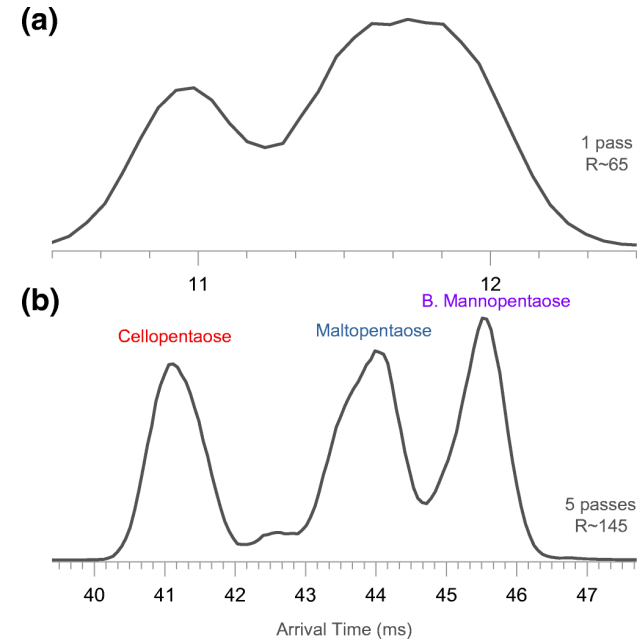
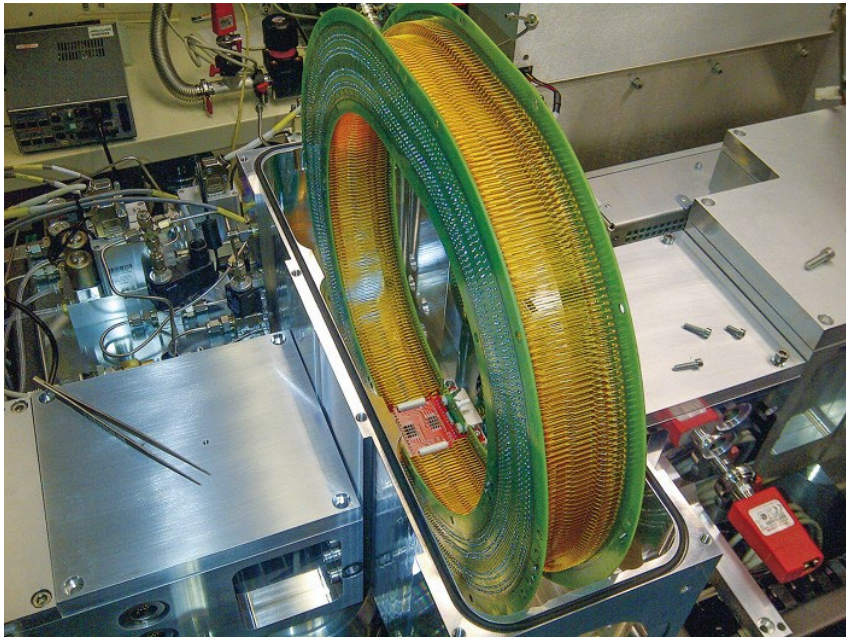
# Ion mobility mass spectrometry

- Ions pushed through tube by electric field
- Drift gas at low pressure/counter flow
- Friction with drift gas slows ions down

- Friction depends on:
  - Size
  - Shape



# Cyclic IMS: multipass separations

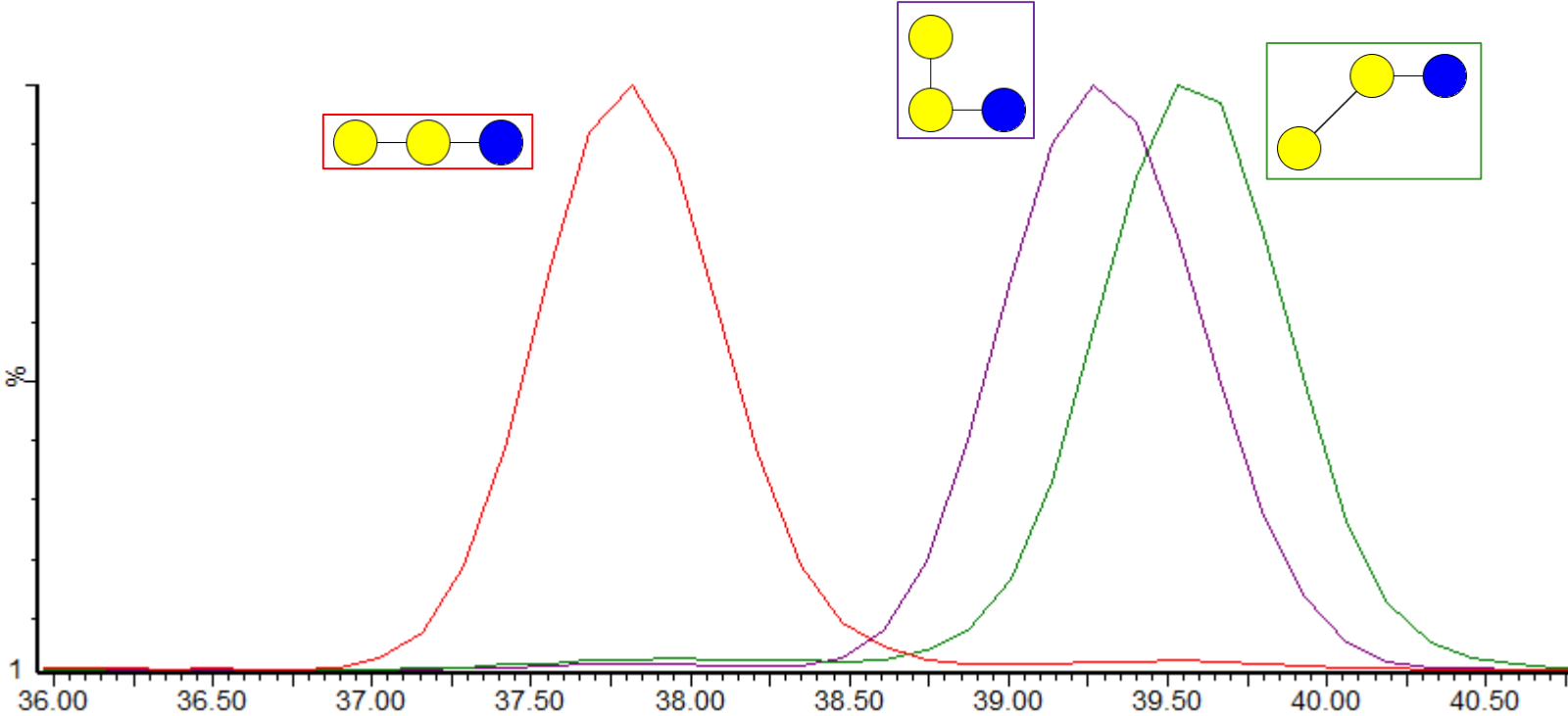


53

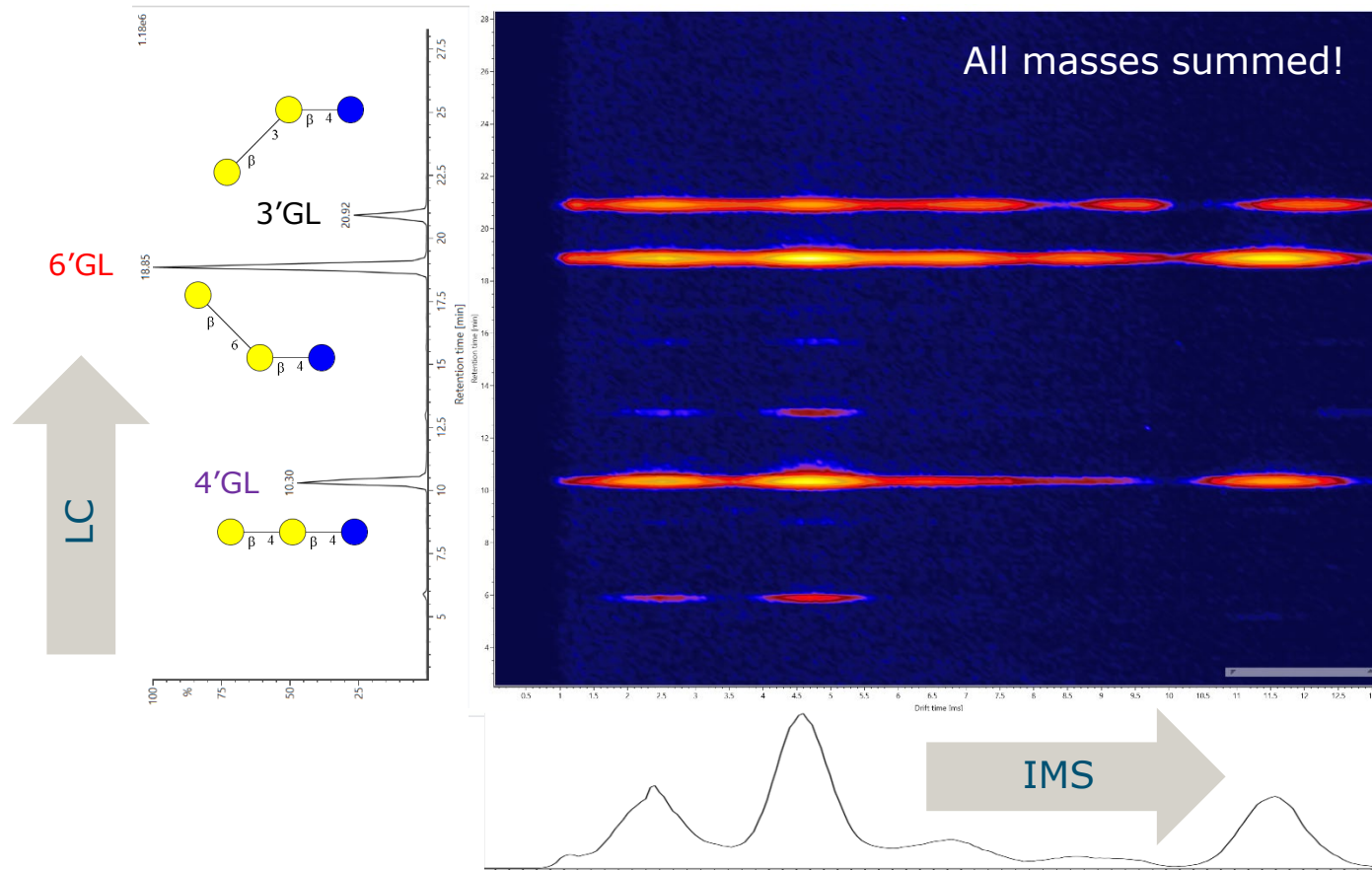
■ Increased resolution

# Cyclic IM MS of Galactosyl Lactose standards

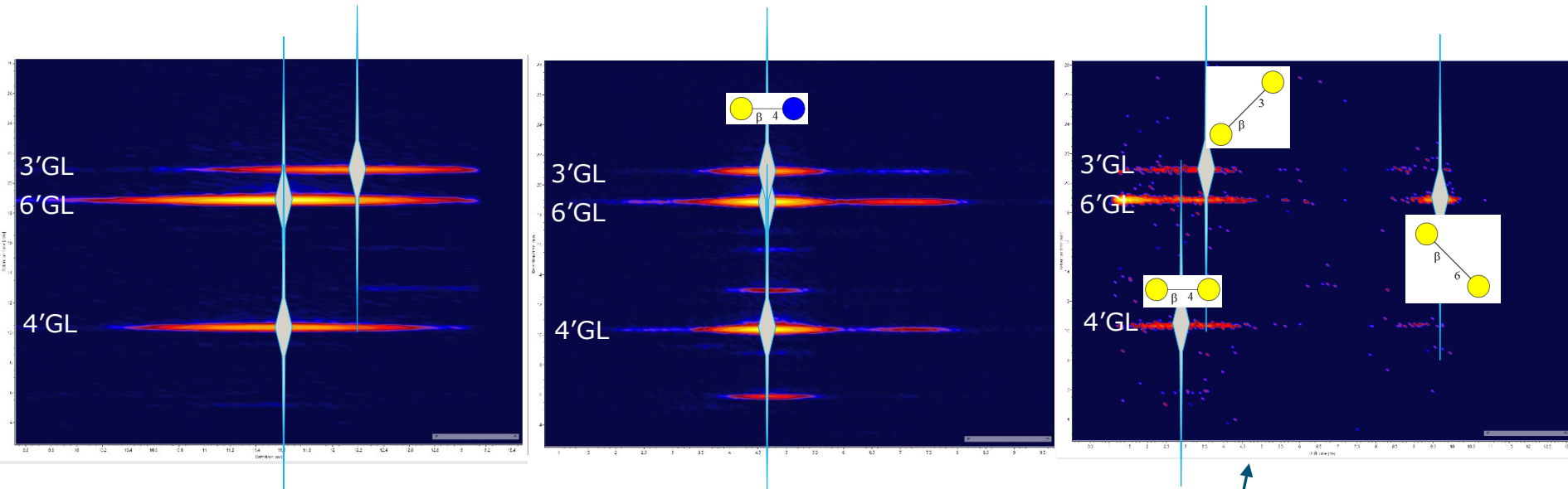
## Influence of linkage type on drift time



# PGC-IM-MS of GL: data structure



# LC-IM-MS: Marker ions



Structural marker ions  
for linkage type



# Conclusions

- Enzymatic fingerprinting and subsequent analysis of diagnostic oligomers is quite powerful in characterising a wide range of polysaccharides.
- UHPLC-MS<sup>n</sup> using a HILIC BEH amide and PGC can be employed to separate a wide variety of oligomeric structures.
- Depending the research question, a whole array of mass spectrometric techniques are available and useful
  - Maldi TOF (TOF) MS
  - Ion trap MS-MS-MS- ..... MS<sup>n</sup>
  - Ion mobility TWIM MS

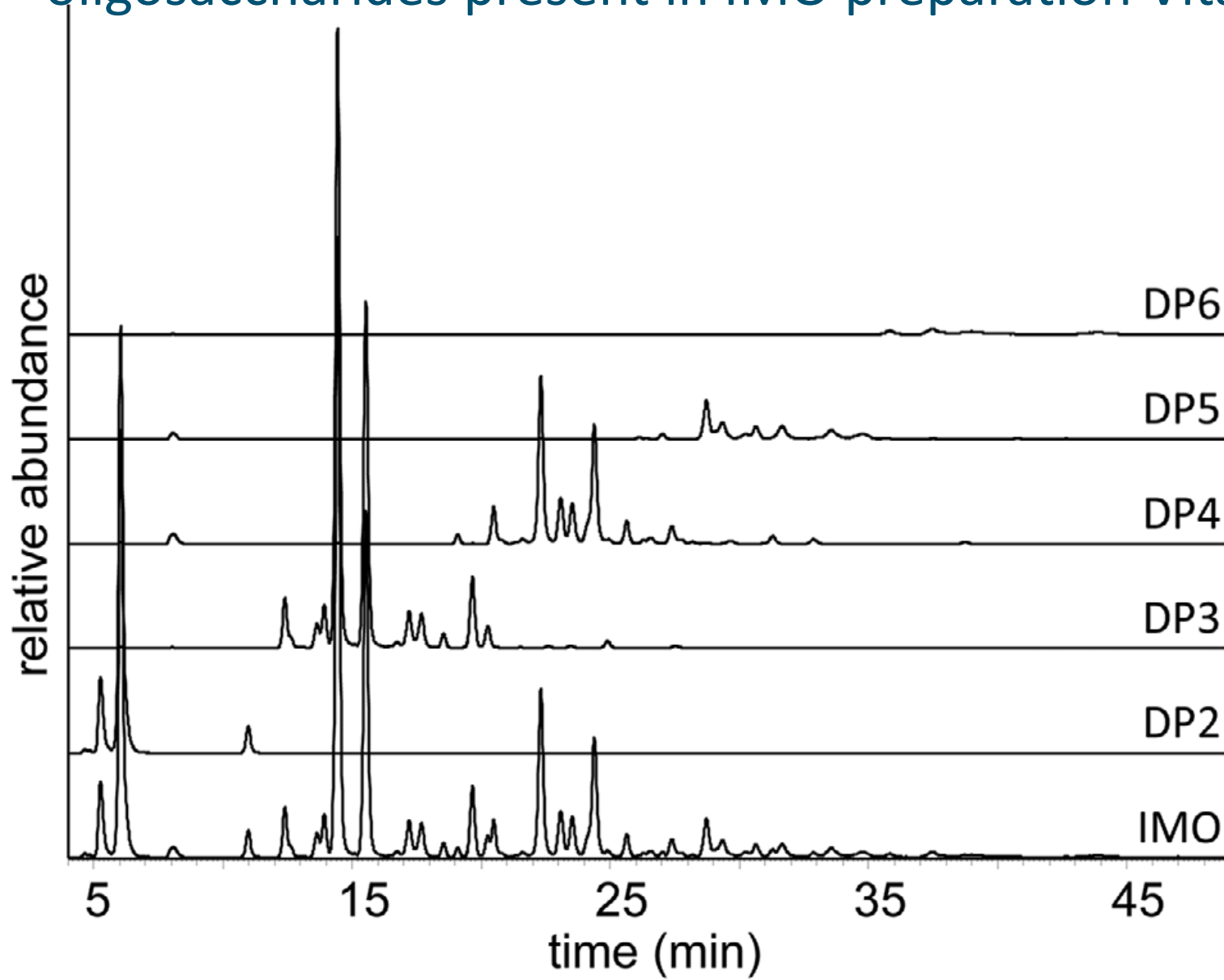
# Thanks for your attention!

## Acknowledgements:

Eva Jermendi  
Madelon Logtenberg  
Carolina Pandeirada  
Bram van de Put



# UHPLC-PGC-MS profile of reducing and non-reducing oligosaccharides present in IMO preparation Vitafiber



# Overview of reducing (A) and non-reducing (B) DP3 isomers present in the IMO preparation Vitafiber.

peak no.	graphical structure <sup>a</sup>	relative abundance (%) <sup>b</sup>	substitution glucitol	chemical structure <sup>c</sup>
A. 1r		4.7	di-substituted	$\alpha$ -D-Glcp-(1 $\rightarrow$ 2)-[ $\alpha$ -D-Glcp-(1 $\rightarrow$ 4)-]D-Glc
2r		2.1	di-substituted	X
3r		3.5	mono-substituted	$\alpha$ -D-Glcp-(1 $\rightarrow$ 6)- $\alpha$ -D-Glcp-(1 $\rightarrow$ 3)-D-Glc
4r		45.3	mono-substituted	$\alpha$ -D-Glcp-(1 $\rightarrow$ 6)- $\alpha$ -D-Glcp-(1 $\rightarrow$ 4)-D-Glc
5r		26.8	mono-substituted	$\alpha$ -D-Glcp-(1 $\rightarrow$ 6)- $\alpha$ -D-Glcp-(1 $\rightarrow$ 6)-D-Glc
6r		3.1	mono-substituted	$\alpha$ -D-Glcp-(1 $\rightarrow$ 4)- $\alpha$ -D-Glcp-(1 $\rightarrow$ 3/6)-D-Glc
7r		3.0	mono-substituted	$\alpha$ -D-Glcp-(1 $\rightarrow$ 4)- $\alpha$ -D-Glcp-(1 $\rightarrow$ 4)-D-Glc
8r		5.7	mono-substituted	$\alpha$ -D-Glcp-(1 $\rightarrow$ 3)- $\alpha$ -D-Glcp-(1 $\rightarrow$ 4)-D-Glc
9r		1.9	mono-substituted	X
B. 1n		1.4	-	$\beta$ -D-Glcp-(1 $\leftrightarrow$ 1)- $\alpha$ -D-Glcp-(6 $\leftarrow$ 1)- $\alpha$ -D-Glcp
2n		1.3	-	$\alpha$ -D-Glcp-(1 $\rightarrow$ 6)- $\beta$ -D-Glcp-(1 $\leftrightarrow$ 1)- $\alpha$ -D-Glcp
3n		0.2	-	$\beta$ -D-Glcp-(1 $\leftrightarrow$ 1)- $\alpha$ -D-Glcp-(4 $\leftarrow$ 1)- $\alpha$ -D-Glcp
4n		0.2	-	$\beta$ -D-Glcp-(1 $\leftrightarrow$ 1)- $\alpha$ -D-Glcp-(2/3 $\leftarrow$ 1)- $\alpha$ -D-Glcp
5n		0.7	-	$\alpha$ -D-Glcp-(1 $\rightarrow$ 4)- $\beta$ -D-Glcp-(1 $\leftrightarrow$ 1)- $\alpha$ -D-Glcp
6n		0.2	-	$\alpha$ -D-Glcp-(1 $\rightarrow$ 2/3)- $\beta$ -D-Glcp-(1 $\leftrightarrow$ 1)- $\alpha$ -D-Glcp

# PGC-MS elution profiles of three IsoMalto OS preparations,

