

# A 500-MHz $^1\text{H-NMR}$ Study on the N-Linked Carbohydrate Chain of Bromelain

## $^1\text{H-NMR}$ Structural-reporter-groups of Fucose $\alpha(1-3)$ -Linked to Asparagine-bound N-Acetylglucosamine

J A VAN KUIK, R A HOFFMANN, J H G M MUTSAERS, H VAN HALBEEK, J P KAMERLING and J F G Vliegenthart\*

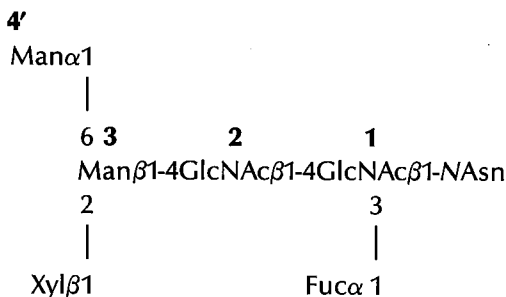
Department of Bio-Organic Chemistry, State University of Utrecht, Transitorium III, Padualaan 8, NL-3584 CH Utrecht, The Netherlands

Received February 23, 1986.

Key words: bromelain, 500-MHz  $^1\text{H-NMR}$  spectroscopy, N-glycosidic glycan

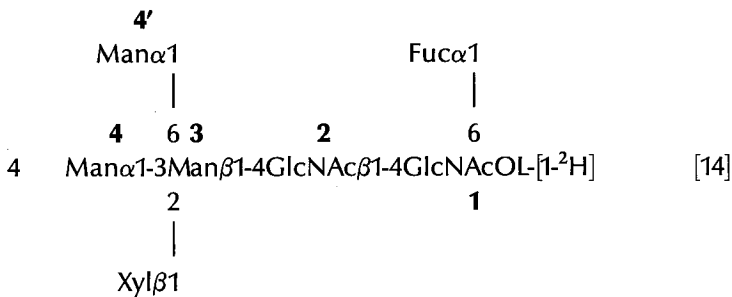
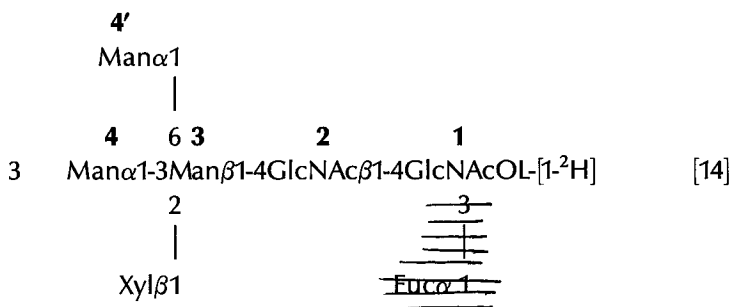
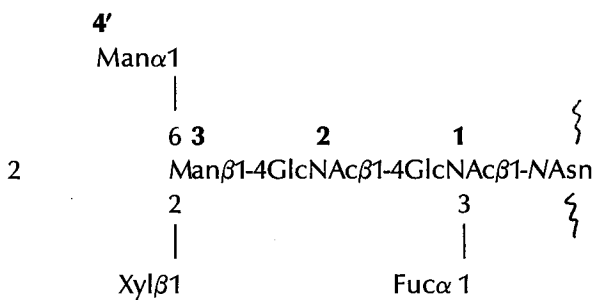
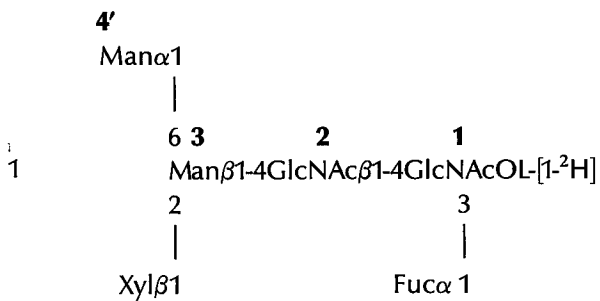
The 500-MHz  $^1\text{H-NMR}$  characteristics of the N-linked carbohydrate chain  $\text{Man}\alpha 1-6[\text{Xyl}\beta 1-2]\text{Man}\beta 1-4\text{GlcNAc}\beta 1-4[\text{Fuc}\alpha 1-3]\text{GlcNAc}\beta 1-\text{NAsn}$  of the proteolytic enzyme bromelain (EC 3.4.22.4) from pineapple stem were determined for the oligosaccharide-alditol and the glycopeptide, obtained by hydrazinolysis and Pronase digestion, respectively. The  $^1\text{H-NMR}$  structural-reporter-groups of the  $\alpha(1-3)$ -linked fucose residue form unique sets of data for the alditol as well as for the glycopeptide.

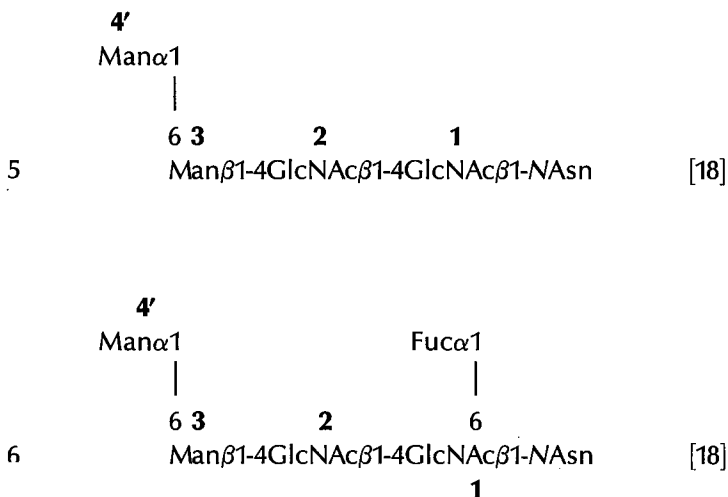
The structural characterization of the N-linked carbohydrate chain(s) of the proteolytic enzyme bromelain (EC 3.4.22.4) from pineapple stem has been the subject of several investigations [1-11]. Finally, Ishihara *et al.* [11] reported the structure



in which all the sugars have the D-configuration except fucose. This structure can be extended with an additional mannose,  $\alpha(1-6)$ -linked to Man-4'. In view of the unusual

\*Author for correspondence.





**Figure 1.** Carbohydrate structures discussed in this study.

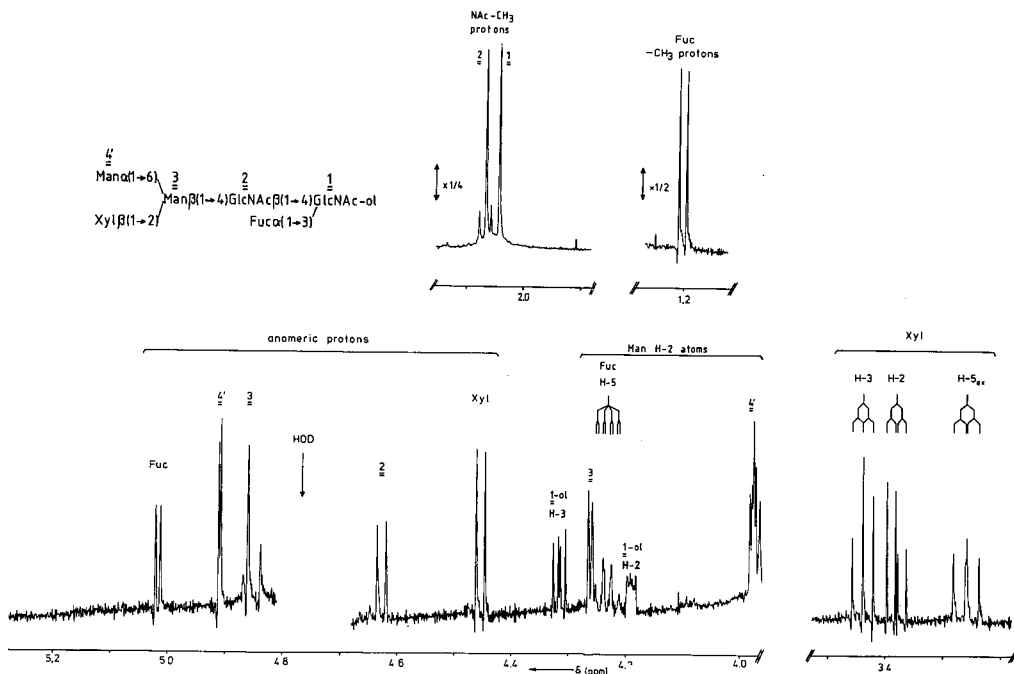
features of the structure, namely, the occurrence of xylose  $\beta(1-2)$ -linked to the  $\beta$ -mannose, and in particular, the presence of fucose  $\alpha(1-3)$ -linked to the asparagine-bound *N*-acetylglucosamine, the isolation of substantial amounts of this carbohydrate chain as an oligosaccharide-alditol and as a glycopeptide was carried out in order to establish the  $^1\text{H-NMR}$  chemical shift values of structural-reporter-groups typical for these compounds.

## Materials and Methods

Commercially available bromelain preparations (Boehringer, Mannheim, W. Germany; suspension in ammonium sulfate solution/ Sigma Chemical Co., St Louis, MO, USA; approx. 50% protein) were purified using Sephadex G-100 gel filtration and SE- or SP-Sephadex C-50 cation-exchange chromatography [5].

For the preparation of neutral hexasaccharide-alditol-[1- $^2\text{H}$ ], compound 1 in Fig. 1, the thoroughly dried, purified (Boehringer) bromelain (200 mg) was subjected to the hydrazinolysis procedure, including high-voltage paper electrophoresis and Bio-Gel P-4 fractionation [12-14]. Sugar analysis [15] of compound 1 indicated Fuc:Xyl:Man:GlcNAc:GlcNAcOL in the molar proportions 0.7 : 0.9 : 2.2 : 1.0 : 0.5.

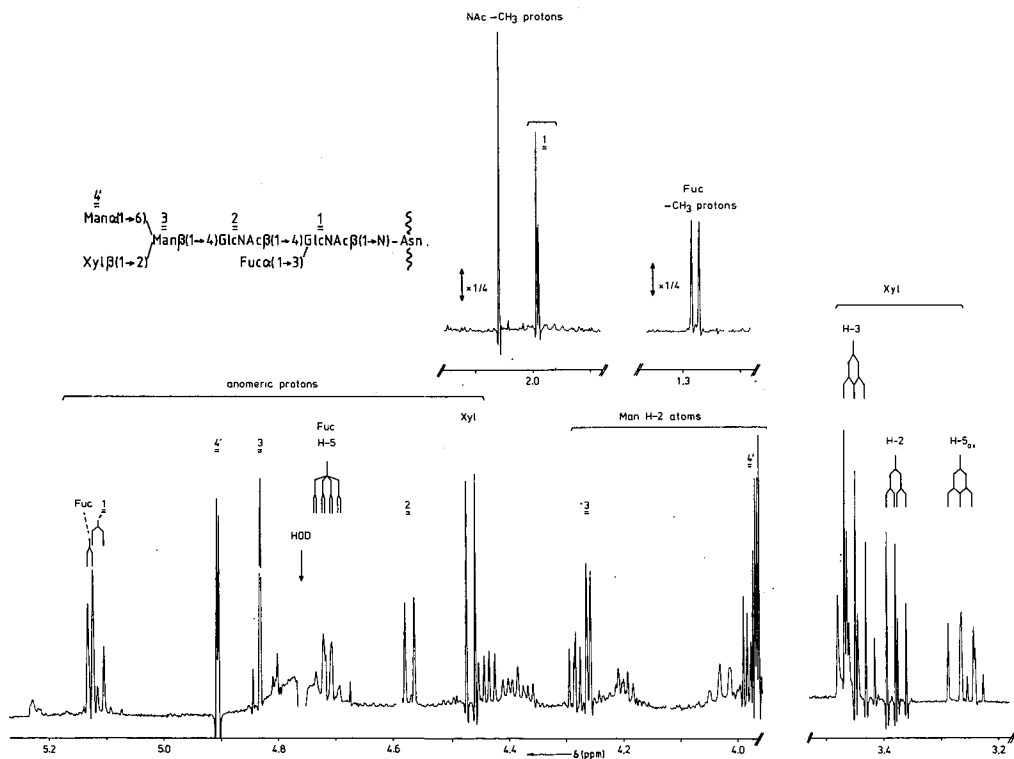
For the preparation of glycopeptide 2, 500 mg of the denatured purified glycoprotein material (Sigma) were subjected to exhaustive Pronase digestion [14]. After fractionation on Bio-Gel P-6 [14], the main glycopeptide fraction was lyophilized. Sugar analysis indicated Fuc:Xyl:Man:GlcNAc in the molar proportions 1.1 : 1.1 : 2.4 : 2.0 (the *N*-acetylglucosamine value has been corrected for non-cleaved GlcNAc-Asn [15]). Methylation analysis [16] gave rise to the partially methylated alditol acetates indicative for terminal



**Figure 2.** Structural-reporter-group regions of the 500-MHz <sup>1</sup>H-NMR spectrum (<sup>2</sup>H<sub>2</sub>O; p<sup>2</sup>H 7; 27°C) of oligosaccharide-alditol-[1-<sup>2</sup>H] (obtained from bromelain). The numbers in the spectrum refer to the corresponding residues in the structure. The relative-intensity scale of the *N*-acetyl and Fuc-CH<sub>3</sub> proton regions differs from that for other parts of the spectrum, as indicated.

mannose, xylose and fucose; 2,6-substituted mannose; 4-substituted *N*-acetylglucosamine; and 3,4-substituted *N*-acetylglucosamine residues, in the molar ratios 1.1 : 1.1 : 1.2 : 1.0 : 1.0 : 0.5. Amino acid analysis showed Asp:Glu:Ser:Pro:Gly:GlcNAc in the molar proportions 2.0 : 1.9 : 0.9 : 1.1 : 0.7 : 2.0, which can accommodate the presence of the reported peptide sequence Asn-Asn(carbohydrate)-Glu-Ser [17] in the glycopeptide fraction. Additional amino acids were detected in molar ratios of less than 0.4. Further purifications were not carried out.

For <sup>1</sup>H-NMR analysis, the carbohydrate samples were repeatedly treated with <sup>2</sup>H<sub>2</sub>O at room temperature, with intermediate lyophilization, finally using 99.96% <sup>2</sup>H<sub>2</sub>O (Aldrich, Milwaukee, WI, USA). 500-MHz <sup>1</sup>H-NMR spectra were obtained using a Bruker WM-500 spectrometer (SON hf-NMR facility, Department of Biophysical Chemistry, University of Nijmegen, The Netherlands) operating in the Fourier transform mode at a probe temperature of 27°C [18]. Resolution-enhancement of the spectra was achieved by Lorentzian-to-Gaussian transformation [19]. Chemical shifts ( $\delta$ ) are expressed in ppm downfield from the signal for internal sodium 4,4-dimethyl-4-silapentane-1-sulfonate (DSS), and measured by reference to internal acetone ( $\delta$  2.225).



**Figure 3.** Structural-reporter-group regions of the 500-MHz <sup>1</sup>H-NMR spectrum (<sup>2</sup>H<sub>2</sub>O; p<sup>2</sup>H 7; 27°C) of glycopeptide 2 obtained from bromelain. The numbers in the spectrum refer to the corresponding residues in the structure. The relative-intensity scale of the *N*-acetyl and Fuc-CH<sub>3</sub> proton regions differs from that for other parts of the spectrum, as indicated. For GlcNAc-1 H-1 only the main signal has been indicated.

## Results and Discussion

The sugar analysis and methylation analysis data of oligosaccharide-alditol 1 and glycopeptide 2 (see Fig. 1) indicated that only the reported hexasaccharide was present [11]. In none of the bromelain preparations was there any indication of the occurrence of a carbohydrate chain extended at Man-4' with an α(1-6)-linked mannose residue. Although not discussed here, we have evidence that the hydrazinolysis procedure as used for the preparation of compound 1 results in the removal of the (1-3)-linked fucose and degradation of the reducing terminal *N*-acetylglucosamine residue (see also [9]).

The 500-MHz <sup>1</sup>H-NMR spectra of compounds 1 and 2, recorded in <sup>2</sup>H<sub>2</sub>O, are depicted in Figs. 2 and 3, respectively. Relevant NMR parameters of these compounds together with NMR data of the reference compounds 3-6 (see Fig. 1) [14, 18] are compiled in Table 1.

**Table 1.** Relevant  $^1\text{H-NMR}$  characteristics of constituent monosaccharides for the oligosaccharide-alditol-[1- $^2\text{H}$ ] **1** and the glycopeptide **2** derived from bromelain, together with those of reference substances **3-6**.

Residue <sup>a</sup>	Reporter group	Chemical shift (ppm) <sup>b</sup>					
		3	4	1	5	6	2
GlcNAc-1-(O1)	H-1				5.071	5.076	5.121 <sup>d</sup>
	H-2	4.239	4.219	4.189	n.d. <sup>c</sup>	n.d.	n.d.
	H-3	n.d.	n.d.	4.315	n.d.	n.d.	n.d.
	NAc	2.057	2.058	2.043	2.014	2.017	2.000 <sup>d</sup>
GlcNAc-2	H-1	4.634	4.718	4.625	4.618	4.690	4.579
	NAc	2.073	2.081	2.066	2.076	2.095	2.066
Man-3	H-1	4.883	4.884	4.859	4.767	4.770	4.839
	H-2	4.270	4.270	4.262	4.080	4.083	4.268
Man-4	H-1	5.122	5.124				
	H-2	4.039	4.040				
Man-4'	H-1	4.913	4.914	4.909	4.915	4.916	4.913
	H-2	3.983	3.982	3.976	3.968	3.967	3.988
Fuc <sup>6</sup>	H-1		4.898			4.877	
	H-5		4.077			4.125	
	CH <sub>3</sub>		1.225			1.209	
Fuc <sup>3</sup>	H-1			5.017			5.136
	H-5			4.232			4.722
	CH <sub>3</sub>			1.202			1.285
Xyl	H-1	4.449	4.449	4.453			4.474
	H-2	3.377	3.379	3.379			3.385
	H-3	3.437	3.453	3.439			3.456
	H-5ax	3.250	3.253	3.258			3.273

<sup>a</sup> For numbering of monosaccharide residues and complete structures, see Fig. 1. A superscript at the Fuc residue indicates to which position of the adjacent monosaccharide it is linked.

<sup>b</sup> Chemical shifts are given in ppm downfield from internal sodium 4, 4-dimethyl-4-silapentane-1-sulfonate in  $^2\text{H}_2\text{O}$  ( $27^\circ\text{C}$ ). Compounds are represented by shorthand symbolic notation [14,18]: ●, GlcNAc; ◆, Man; □, Fuc; ⊠, Xyl.

<sup>c</sup> n.d., not detected.

<sup>d</sup> Chemical shift values of the main glycopeptide(s).

Comparison of the structural-reporter-groups of oligosaccharide-alditol **1** (Fig. 1) with those of the reference alditols **3** and **4** leads to the following comments. The set of structural-reporter-group signals of xylose in compound **1** namely, H-1 ( $\delta$  4.453), H-2 ( $\delta$  3.379), H-3 ( $\delta$  3.439) and H-5ax ( $\delta$  3.258), show essentially the same chemical shift values

as those observed for compounds 3 and 4 (Table 1). Apparently, the presence of the mannose residue (Man-4)  $\alpha(1-3)$ -linked to Man-3 essentially does not influence the NMR parameters of the xylose. As was demonstrated earlier [14], the attachment of a xylose residue in the presence of both Man-4' and Man-4 has a distinct influence on the position of the Man-3 H-1 signal (Man $\alpha$ 1-6[Man $\alpha$ 1-3]Man $\beta$ 1-4GlcNAc $\beta$ 1-4GlcNAcOL,  $\delta$  4.78 [14]; compared to the values  $\delta$  4.883 and 4.884 for compounds 3 and 4, respectively). Compared with 3 and 4, the absence of Man-4 in compound 1 causes an upfield chemical shift effect on Man-3 H-1 of  $\Delta\delta$ -0.024 ppm relative to the positions in 3 and 4 (compound 1,  $\delta$  4.859). Finally, the position of the Man-4' H-1 and H-2 signals, being typical for a terminal Man $\alpha$ (1-6) residue [18], are not influenced by the presence of Man-4 (compare compound 1 with 3 and 4).

The structural-reporter-group signals of the fucose  $\alpha(1-3)$ -linked to GlcNAcOL-1 (H-1,  $\delta$  5.017; H-5,  $\delta$  4.232; CH<sub>3</sub>,  $\delta$  1.202) differ drastically from those reported for fucose  $\alpha(1-6)$ -linked to GlcNAcOL-1 (H-1,  $\delta$  4.898; H-5,  $\delta$  4.077; CH<sub>3</sub>,  $\delta$  1.225). The chemical shift effects on the chitobiosyl unit caused by the  $\alpha(1-3)$ - and  $\alpha(1-6)$ -linked fucose residues are also different. This is most pronounced for the *N*-acetyl signals of GlcNAcOL-1 and GlcNAc-2. The presence of  $\alpha(1-3)$ -linked fucose in compound 1 leads to upfield shifts of both resonances, as compared with their positions in compound 3 ( $\Delta\delta$ -0.014 and -0.007 ppm, respectively). In the case of the  $\alpha(1-6)$ -linked fucose residue in compound 4 the *N*-acetyl signal of GlcNAcOL-1 is hardly affected, whereas the *N*-acetyl signal of GlcNAc-2 is shifted downfield 0.008 ppm, when compared to compound 3. The position of H-2 of GlcNAcOL-1 is influenced much more in compound 1 than in 4. Compared with compound 3, in 1 an upfield shift of 0.050 ppm is observed. In the latter case also GlcNAcOL-1 H-3 resonates away from the bulk of skeleton protons. The assignment of this signal was made by selective irradiation of GlcNAcOL-1 H-2.

Comparison of the structural-reporter-groups of glycopeptide 2 (Fig. 3) with those of the glycopeptides 5 and 6 shows the following features. The set of structural-reporter-group signals of  $\alpha(1-3)$ -linked fucose in 2, namely, H-1 ( $\delta$  5.136), H-5 ( $\delta$  4.722) and CH<sub>3</sub> ( $\delta$  1.285) differ enormously, when compared to the set observed for the  $\alpha(1-6)$ -linked fucose in 6 (see Table 1). It has to be noted that due to the heterogeneity in the peptide backbone, the GlcNAc-1 H-1 and NAc signals show heterogeneity. The rather downfield position of the GlcNAc-1 H-1 signal for glycopeptide 2 at  $\delta$  5.121 cannot be attributed merely to the influence of the type of fucose linkage, because the peptide moiety can considerably influence this chemical shift value [18]. The attachment of fucose at C-3 instead of C-6 of GlcNAc-1 has also a clear effect on the  $\delta$ -values of GlcNAc-2 H-1 and NAc. Compared to compound 5, these values are shifted upfield ( $\Delta\delta$  -0.039 and -0.010 ppm, respectively) when fucose is (1-3)-linked to GlcNAc-1, while they are found at downfield positions for (1-6)-linked fucose ( $\Delta\delta$  0.072 and 0.019 ppm, respectively).

The structural-reporter-groups of xylose (H-1, H-2, H-3, H-5ax) are found at more downfield positions for glycopeptide 2, compared to oligosaccharide-alditol 1. The chemical shift value of Xyl H-3 was assigned by selective irradiation of H-2. The sensitivity of the Man-3 H-1 and H-2 structural-reporter-groups to the attachment of xylose through a  $\beta(1-2)$ -linkage mentioned above was also found in glycopeptide 2. These signals ( $\delta$  4.839 and 4.268, respectively) are observed at rather downfield positions when compared with those in glycopeptides 5 and 6.

When comparing oligosaccharide-alditol 1 with glycopeptide 2, it appears that in 2 the chemical shift values of the structural-reporter-groups of fucose occur at well-

pronounced more downfield positions: H-1,  $\Delta\delta$  0.119 ppm; H-5,  $\Delta\delta$  0.490 ppm; and CH<sub>3</sub>,  $\Delta\delta$  0.083 ppm. It is evident that the alditol chain (GlcNAcOL-1) and the ring structure (GlcNAc-1) influence the NMR parameters of fucose quite differently.

## Acknowledgements

The authors thank Prof. Dr. J.J. Beintema (State University of Groningen, The Netherlands) for assistance with the amino acid analyses.

This investigation was supported by the Netherlands Foundation for Chemical Research (SON) with financial aid from the Netherlands Organization for the Advancement of Pure Research (ZWO), and by the Netherlands Foundation for Cancer Research (KWF, Grant UUKC 83-13).

## References

- 1 Murachi T, Yasui M, Yasuda Y (1964) *Biochemistry* 3:48-55.
- 2 Ota S, Moore S, Stein WH (1964) *Biochemistry* 3:180-85.
- 3 Feinstein G, Whitaker JR (1964) *Biochemistry* 3:1050-54.
- 4 Murachi T, Suzuki A, Takahashi N (1967) *Biochemistry* 6:3730-36.
- 5 Scocca J, Lee YC (1969) *J Biol Chem* 244:4852-63.
- 6 Yasuda Y, Takahashi N, Murachi T (1970) *Biochemistry* 9:25-32.
- 7 Lee YC, Scocca JR (1972) *J Biol Chem* 247:5753-58.
- 8 Takahashi N, Murachi T (1976) *Methods Carbohydr Chem* 7:175-84.
- 9 Fukuda M, Kondo T, Osawa T (1976) *J Biochem (Tokyo)* 80:1223-32.
- 10 Lee RT, Lee YC (1978) *Carbohydr Res* 67:389-402.
- 11 Ishihara H, Takahashi N, Oguri S, Tejima S (1979) *J Biol Chem* 254:10715-19.
- 12 Takasaki S, Mizuochi T, Kobata A (1982) *Methods Enzymol* 83:263-68.
- 13 Yamashita K, Mizuochi T, Kobata A (1982) *Methods Enzymol* 83:105-27.
- 14 van Kuik JA, van Halbeek H, Kamerling JP, Vliegthart JFG (1985) *J Biol Chem* 260:13984-88.
- 15 Kamerling JP, Vliegthart JFG (1982) *Cell Biol Monogr* 10:95-125.
- 16 Waeghe TJ, Darvill AG, McNeil M, Albersheim P (1983) *Carbohydr Res* 123:281-304.
- 17 Takahashi N, Yasuda Y, Kuzuya M, Murachi T (1969) *J Biochem (Tokyo)* 66:659-67.
- 18 Vliegthart JFG, Dorland L, van Halbeek H (1983) *Adv Carbohydr Chem Biochem* 41:209-374.
- 19 Ernst RR (1966) *Adv Magn Res* 2:1-135.