

Supplementary data

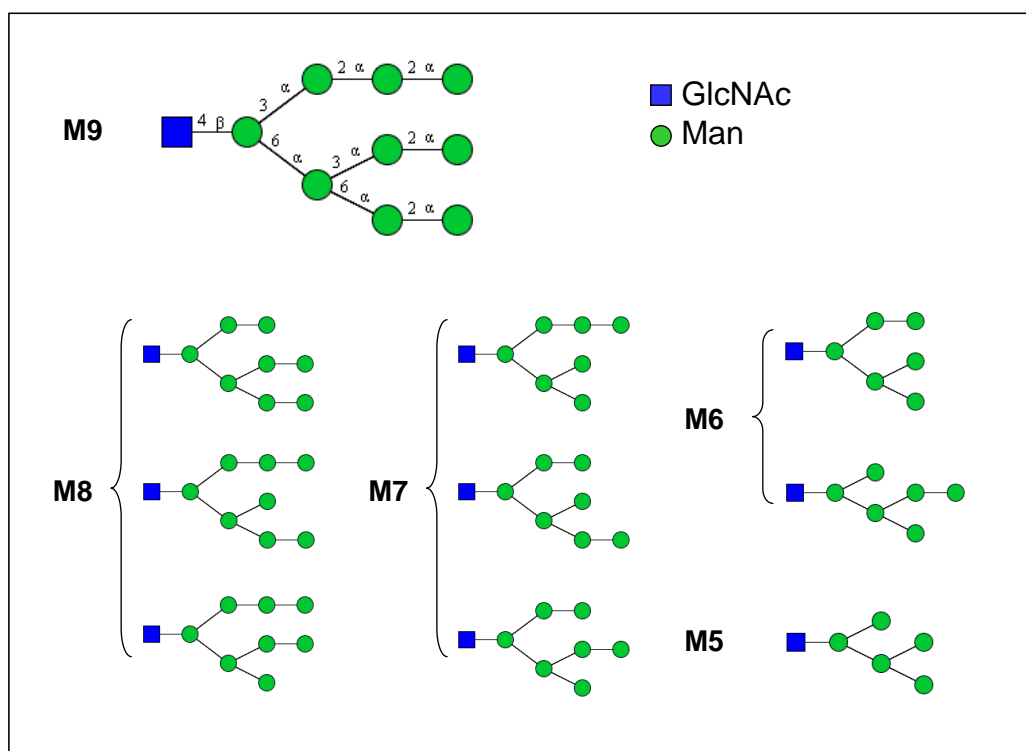


Fig. S-1 Structures of high mannose type *N*-linked glycans $\text{Man}_5\text{GlcNAc}$ (M5) to $\text{Man}_9\text{GlcNAc}$ (M9) and their structural isoforms, adapted from Mikami, K. *et al.*, *Glycobiology*, 20, 310-321, 2010. Structures drawn with GlycoWorkbench v2.1.

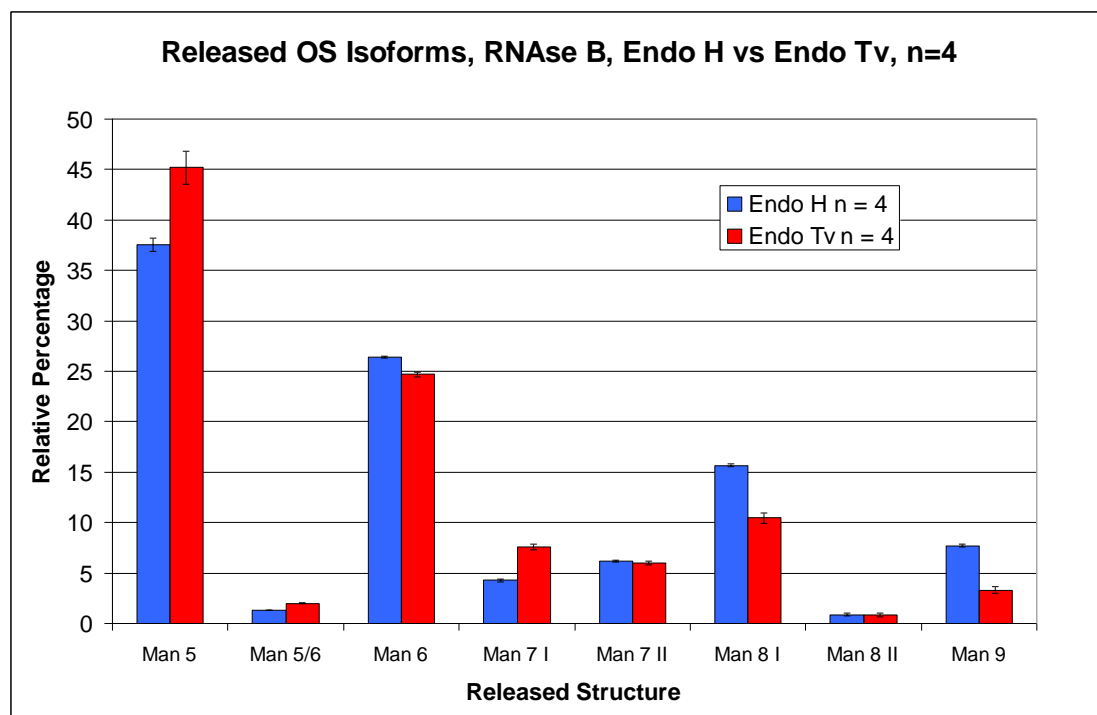


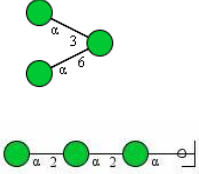
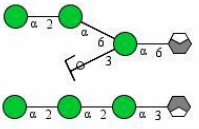
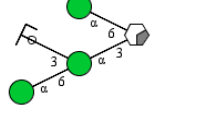
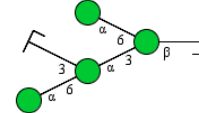
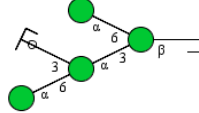
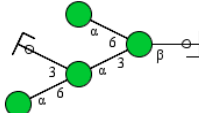
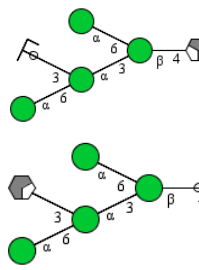
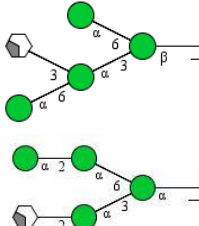
Fig. S-2 Relative percentages of individual high mannose glycoforms (Man₅GlcNAc to Man₉GlcNAc) released by purified Endo Tv and Endo H as quantified by HPAEC-PAD. Data is mean of four replicates, error bars represent standard deviation.

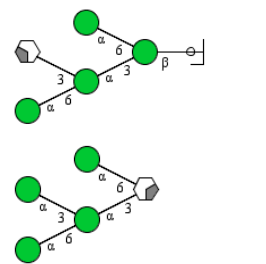
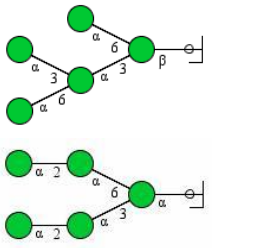
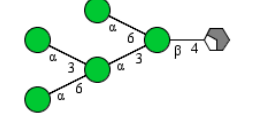
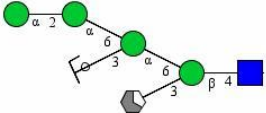
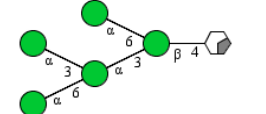
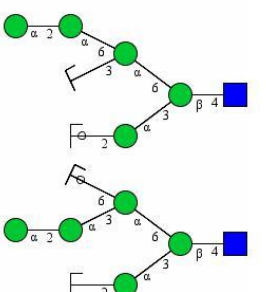
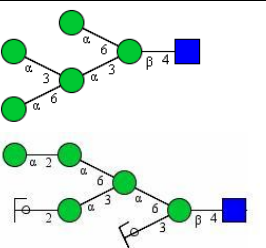
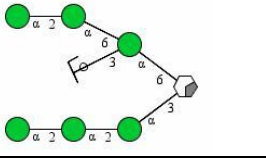
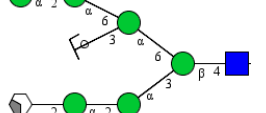
Table S-1 Expected and observed m/z values of PNGase F released structures from RNase B by ESI-MS in negative ion mode (+/- 0.5 Da calibration).

Structures	Expected m/z		Observed m/z	
	[M-H] ⁻	[M-2H] ²⁻	[M-H] ⁻	[M-2H] ²⁻
Man ₅ GlcNAc ₂	1233.43	616.215	1233.6	616.8
Man ₆ GlcNAc ₂	1397.48	698.24	1395.7	698
Man ₇ GlcNAc ₂	1557.53	778.265	-	778.9
Man ₈ GlcNAc ₂	1719.58	859.29	-	859.7
Man ₉ GlcNAc ₂	1881.63	940.315	-	940.5

- not observed.

Table S-2 Deprotonated fragment ions from ESI-LC-MS of bacterial ENGase, Endo F1, and fungal WChTv-released native high mannose structures from RNase B. Fragment structures were made in GlycoWorkbench v2.1 and residues are as in Fig. S-1.

Fragment ion	Type	Expected m/z	Observed m/z	Bacterial	Fungal
	C	503.16	503.0	Y	Y
	$^{0,4}\text{A}_{\text{Man}}\text{Y}$ $^{1,3}\text{A}_{\text{Man}}$	545.17	545.1	Y	Y
	$^{0,2}\text{A}_{\text{Man}}\text{Y}$	605.19	605.1	Y	Y
	BZ	629.19	629.1	Y	Y
	BY	647.2	647.1	Y	Y
	CY	665.21	665.2	Y	Y
	$^{2,4}\text{A}_{\text{GlcNAc}}\text{Y}$ $\text{C}^{0,2}\text{X}_{\text{Man}}$	707.22	707.2	Y	Y
	$\text{B}^{2,4}\text{X}_{\text{Man}}$	749.24	749.2	Y	Y

	$C^{2,4}X_{Man}$ ${}^{0,2}A_{Man}$	767.25	767.2	Y	Y
	C	827.27	827.2	Y	Y
	${}^{2,4}A_{GlcNAc}$	869.28	869.3	Y	Y
	${}^{1,5}X_{Man}Y$	896.29	896.3	N	Y
	${}^{0,2}A_{GlcNAc}$	929.3	929.3	Y	Y
	YZ ZY	1012.34	1012.3	Y	Y
	[M-H] ⁻ YY	1030.35	1030.4	Y	Y
	${}^{0,2}A_{Man}Y$	1091.35	1091.4	Y	N
	${}^{2,4}X_{Man}Y$	1294.43	1294.6	Y	Y

	$Y^{1,3}X_{Man}$				
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Table S-3. Glycoproteins tested with WChTv and their *N*-linked oligosaccharide structures.

Glycoprotein	Source Organism	Most Prevalent <i>N</i>-linked Oligosaccharides
Fetuin	<i>B. taurus</i>	Bi-, tri- and tetra-antennary complex
RNase B	<i>B. taurus</i>	High mannose
Ovalbumin	<i>G. gallus</i>	High mannose, hybrid, bisecting GlcNAc
IgG	<i>B. taurus</i>	Biantennary complex, bisecting GlcNAc, $\alpha(1,6)$ -linked fucose
Invertase	<i>S. cerevisiae</i>	High mannose, yeast-type oligomannose