

## Electronic Supplementary Information

### Polymorphism of chitosan-based networks stabilized by phytate

#### investigated by molecular dynamics simulations

Raluca M. Visan, Anca R. Leonties, Ludmila Aricov, Viorel Chihaiia, Daniel G. Angelescu\*

**Table S1.** The atom charges in the united atom representation for the chitosan and phytate

Chitosan			Phytate		
Atom type	Atom Name	Charge( <i>e</i> unit)	Atom type	Atom Name	Charge( <i>e</i> unit)
CH1R	C1	0.464	C	C	-0.015
	C2	0.197		C2	0.142
CH2	C3 C4 C5	0.232		C3	0.016
	C6	0.232		C4	-0.040
OA	O1 O3 O4 O6	-0.642	Cpos	C1	0.198
				C5	0.258
OR	O5	-0.464	OAlc	O18	-0.406
				O19	-0.457
				O20	-0.437
				O21	-0.443
				O22	-0.421
			OM	O23	-0.464
				O	-0.766
				O1	-0.749
				O2	-0.762
				O3	-0.756
				O4	-0.771
OEOp	O5	-0.753			
	O6	-0.759			
	O8	-0.718			
	O11	-0.765			
	O12	-0.721			
	O14	-0.797			
	O16	-0.754			
NT (CHT0, CHTN)	N2	-0.845	O7	-0.705	
			O9	-0.701	
			O10	-0.697	
			O13	-0.701	
			O15	-0.709	
			O17	-0.690	

NL (CHTP)	N2		-0.448	P	P	1.013
					P1	1.018
					P2	0.975
					P3	1.038
					P4	1.022
					P5	1.007
H	HO1	HO3	0.410	HC	H	0.097
	HO4	HO6			H1	0.097
	H21	H22	0.324		H2	0.125
		H23	0.407 – CHTP		H3	0.114
					H4	0.091
					H5	0.078
				HS14	H7	0.435
					H9	0.459
					H10	0.436
					H13	0.460
					H15	0.444
					H17	0.434

**Table S2.** Lennard-Jones interaction parameters for the atom types

Atom type	$C_6$ (kJ mol <sup>-1</sup> nm <sup>6</sup> )	$C_{12}$ (kJ mol <sup>-1</sup> nm <sup>12</sup> )
CH1R	0.00606841	9.70225e-05
CH2	0.0074684164	3.3965584e-05
CPos	0.002025	1e-06
OA	0.0022619536	1.505529e-06
OR	0.0022619536	1.21e-06
OM	0.0022619536	7.4149321e-07
OEOp	0.00308914	4.77422e-06
OAlc	0.00177494	1.21e-06
NT	0.0024364096	5.0625e-06
NL	0.0024364096	2.319529e-06
P	0.01473796	2.2193521e-05
H	0	0
HC	8.464e-05	1.5129e-08
HS14	0	0

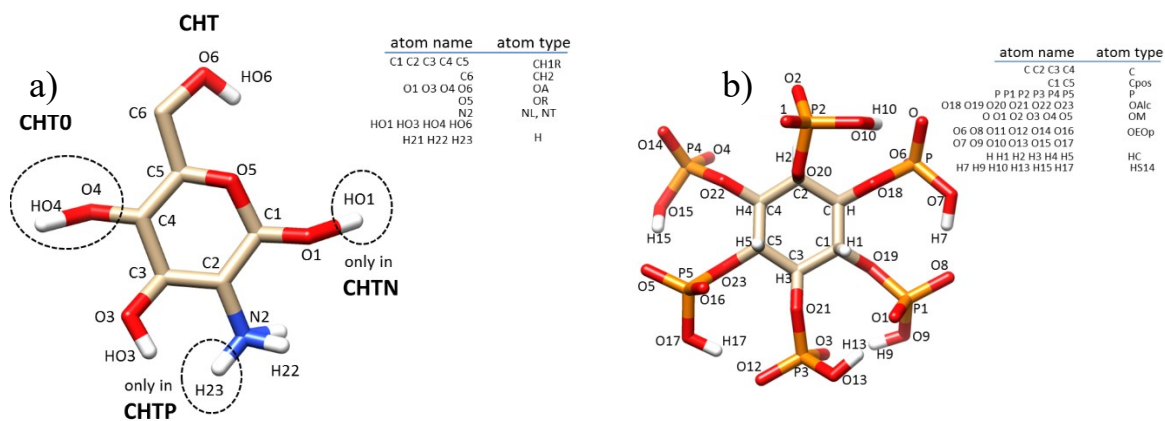
\* other parameters for special intramolecular Lennard-Jones interactions can be found in Table 10 of ref. (Naumov & Ignatov, 2017)

**Table S3.** Parameters for the bond interactions.

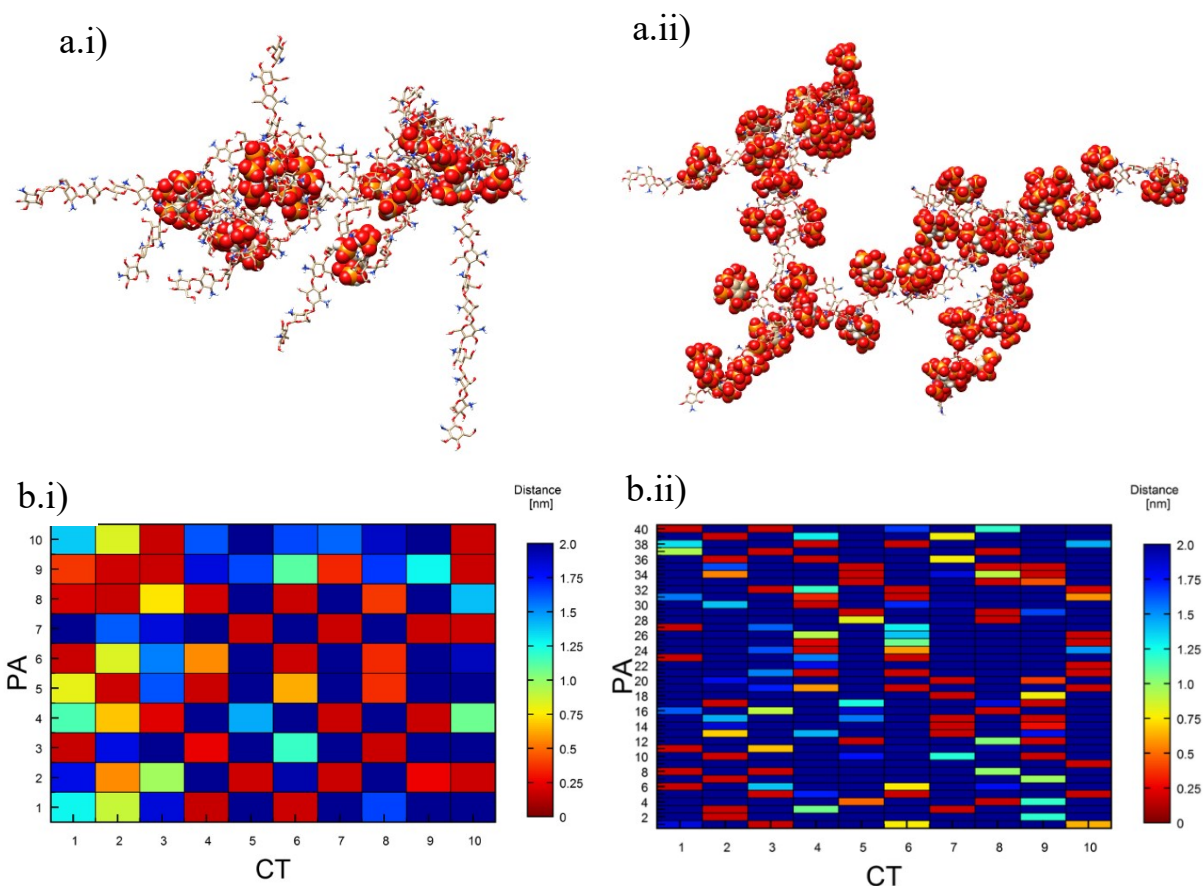
Bond type	$b_0$ (nm)	$K_b$ ( $10^6$ kJmol $^{-1}$ nm $^{-4}$ )
<b>Chitosan</b>		
CH1R-OA, CH1R-OR, CH2-OA	0.1435	6.1000e+06
CH1R-CH1R, CH1R-CH2	0.1520	5.4300e+06
OA-H	0.1000	1.5700e+07
CH1R-NT,NL	0.1470	8.7100e+06
NT,NL-H	0.1000	1.8700e+07
NT,NL-C	0.1340	1.0500e+07
<b>Phytic acid</b>		
C-C	0.1540	4.2166e+06
C-Cpos	0.1560	3.0819e+06
Cpos-OAlc	0.1420	3.2236e+06
C-OAlc	0.1410	6.5389e+06
	0.1430	8.1800e+06
C-HC	0.1090	1.2300e+07
OEOp-HS14	0.1010	1.5700e+07
	0.1000	2.1076e+07
OEOp-P	0.1630	4.7200e+06
OM-P	0.1530	7.1500e+06
	0.1500	8.3700e+06
	0.1510	3.7279e+06
OAlc-P	0.1660	2.9032e+06
	0.1670	3.0478e+06

**Table S4.** Number of H-bonds between the CT residues and PA averaged over the last 50 ns simulation time.

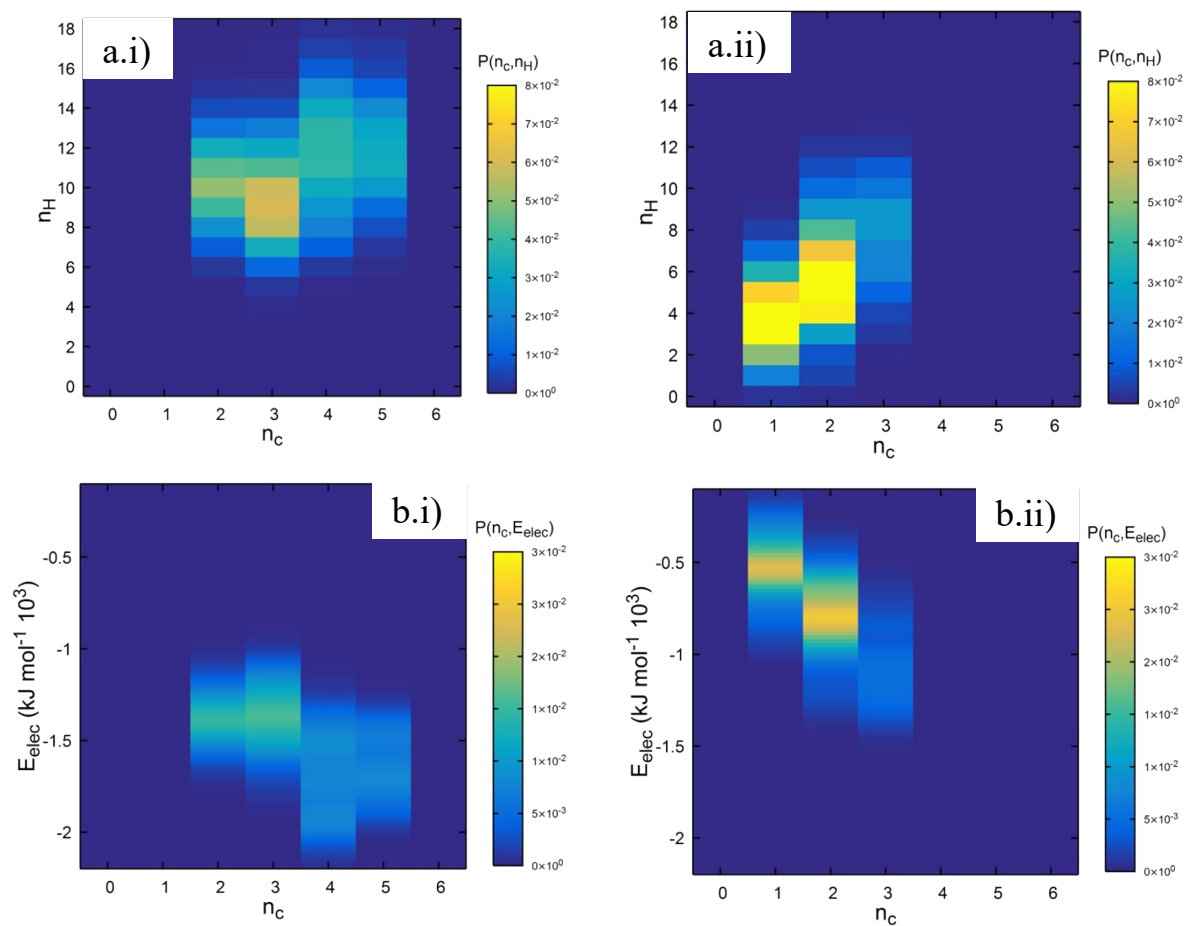
System	Residue type	
	CHTP (charged)	CHT0, CHTN, CHT (uncharged)
CT-083-10	98±4.9	8.7±2.2
CT-050-10	75±4.6	36.6±3.1
CT-033-10	56±4.1	48.2±4.4



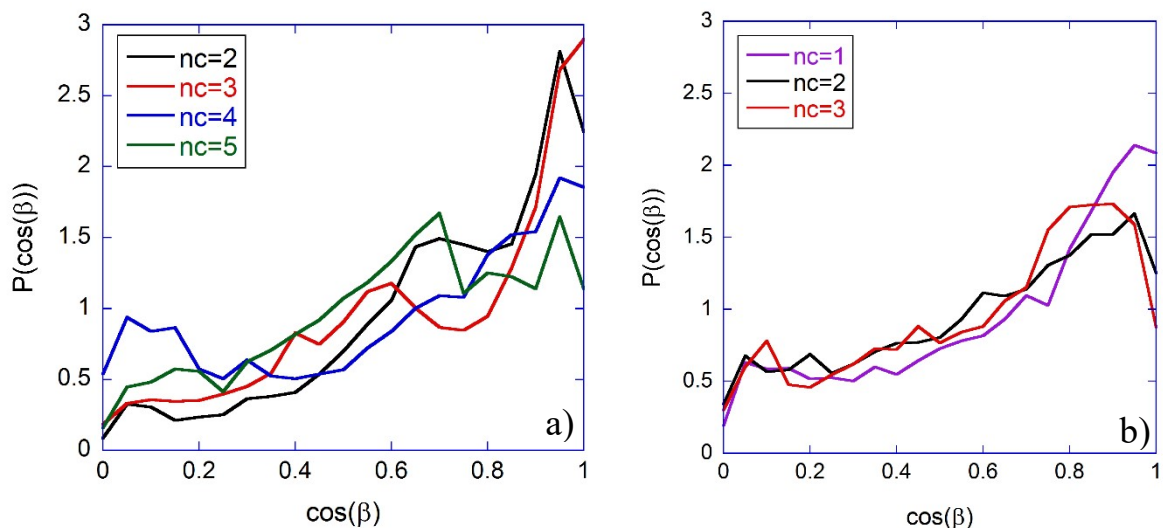
**Figure S1.** a) Types of monomers for the chitosan chain description and names and types of atoms according to the implemented force field; b) atom names and types for the atomistic representation of the phytate ion(cis-1,2,3,5-trans-4,6-cyclohexanehexol hexakisphosphate); the myo-isomer with five equatorial phosphate substituents at C, C1, C3, C5 and C4 and one axial phosphate substituent at C2 is shown in b).



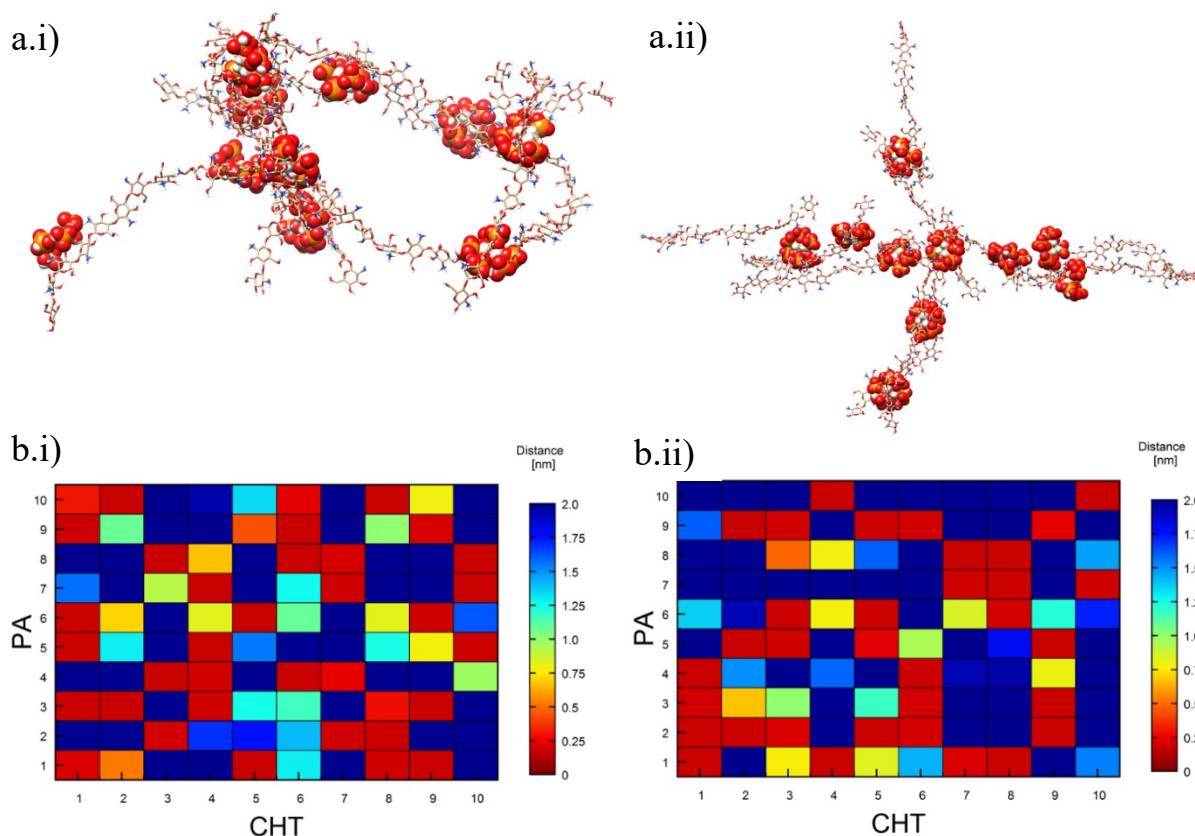
**Figure S2.** a) Snapshot of the final configuration and b) and minimum distance between CT and PA averaged over the last 50 ns simulation time interval for i) CT-083-10 and ii) CT-083-40; the water and counterions were omitted in a) for clarity sake.



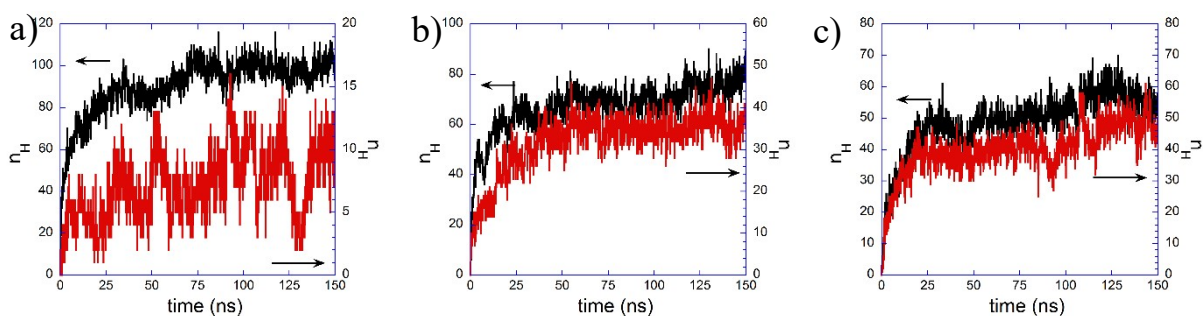
**Figure S3.** Probability distribution of the number of crosslinked chitosan chains by a PA  $n_c$  and a) H bond number  $n_H$  and b) electrostatic energy  $E_{elec}$  between anion and chitosan for i) CT-083-10, ii) CT-083-40



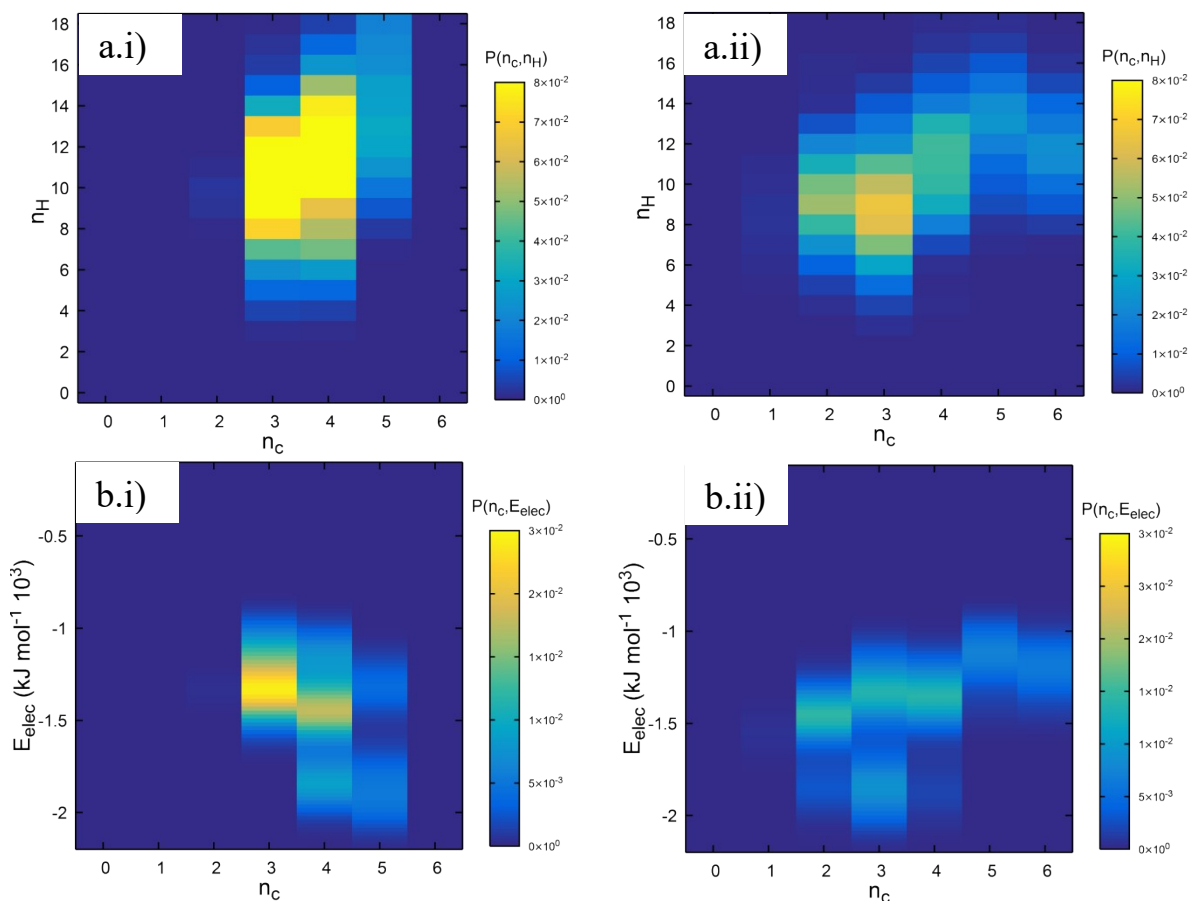
**Figure S4.** Probability distribution of the angle made by the inositol with the closest glucopyranose rings at the indicated number of crosslinked chains for a) CT-083-10, b) CT-083-40.



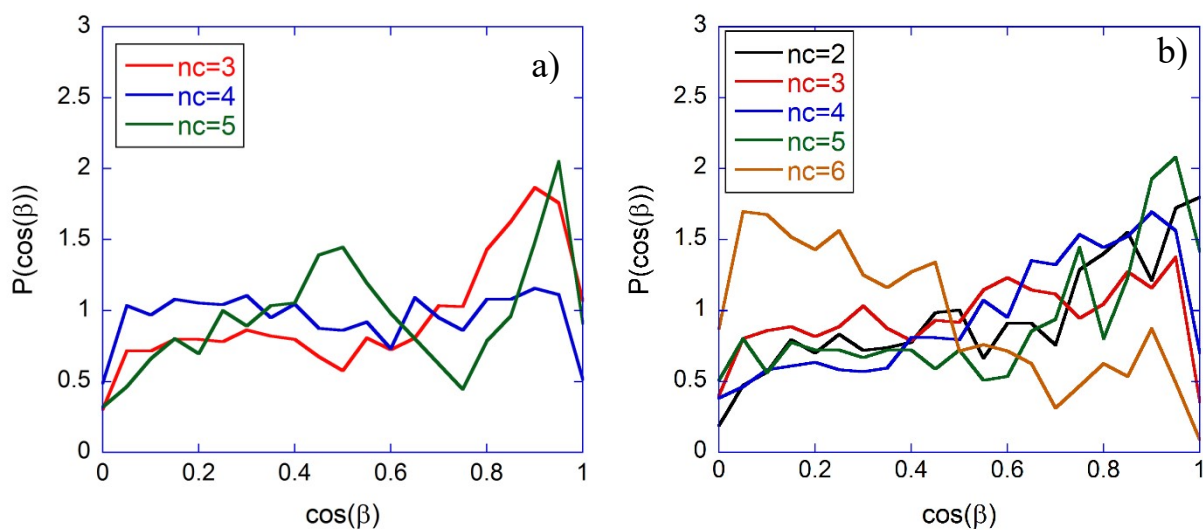
**Figure S5.** a) Snapshot of the final configuration and b) and minimum distance between CT and PA averaged over the last 50 ns simulation time interval for i) CT-050-10 and ii) CT-033-10.



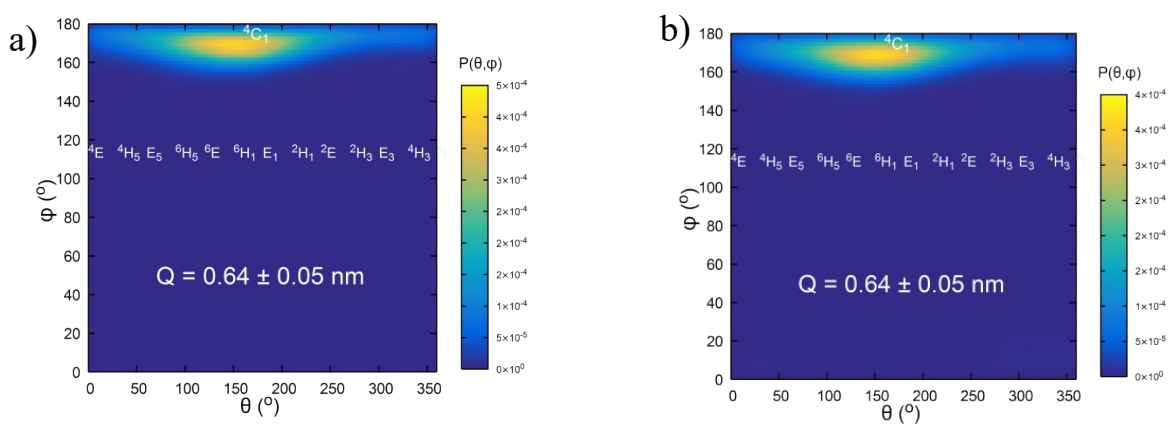
**Figure S6.** The time evolution of H bond number made by PA with charged (black curves) and uncharged (red curves) CT monomers for i) CT-83-10, ii) CT-50-10 and iii) CT-33-10.



**Figure S7.** Probability distribution of the number of crosslinked chitosan chains by a PA  $n_c$  and a) H bond number  $n_H$  and b) electrostatic energy  $E_{elec}$  between the anion and chitosan chains for i) CT-050-10 and ii) CT-033-10.

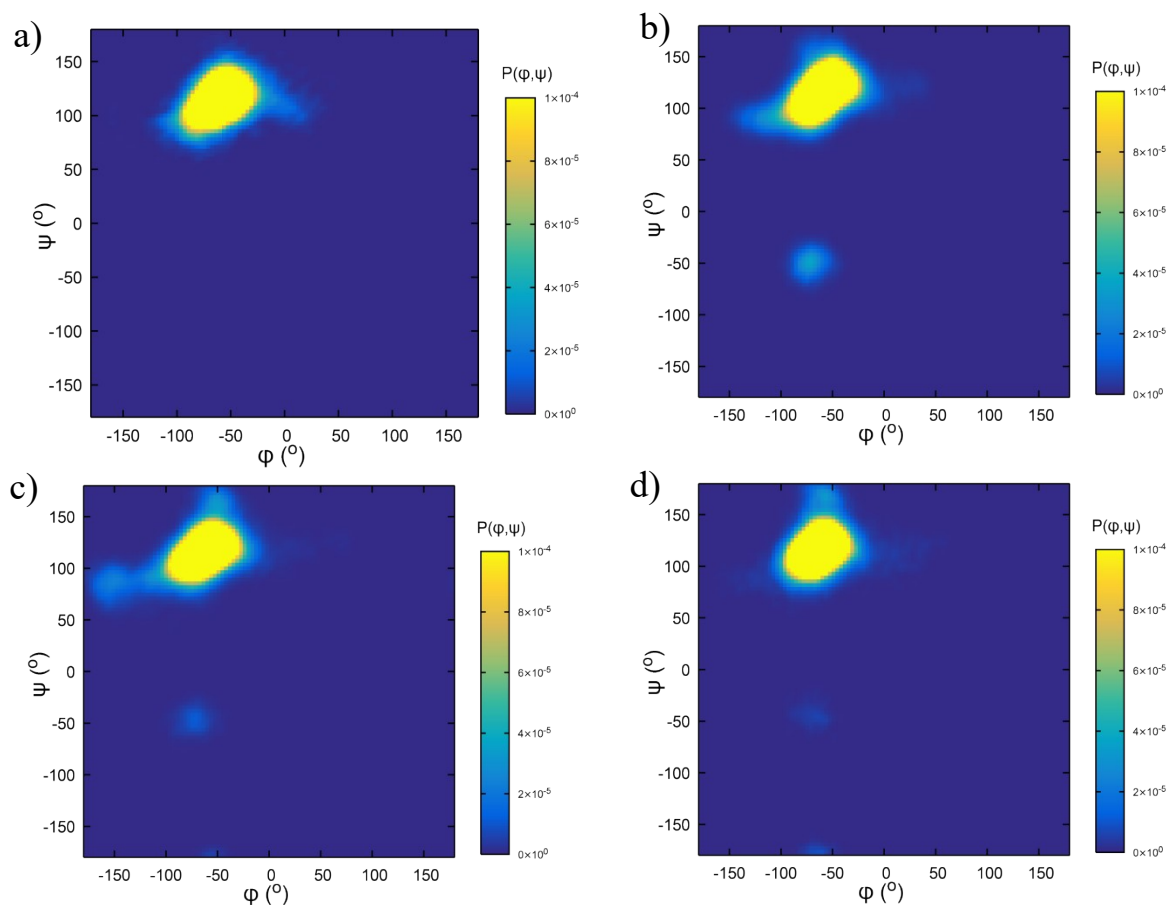


**Figure S8.** Probability distribution of the angle made by the inositol with the closest glucopyranose rings at the indicated number of crosslinked chains for a) CT-050-10, b) CT-033-10.

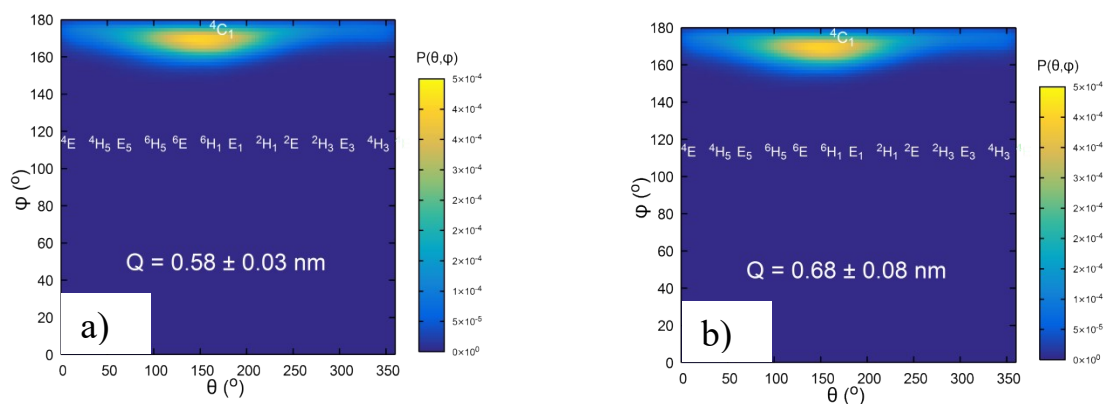


**Figure S9.** Probability distribution of puckering phase angles,  $\theta$  and  $\varphi$  for pyranose in a) CT-water system and b) CT-083-5. The puckering amplitude  $Q$  and location of the closest characteristic ring conformers ( ${}^4E \dots {}^4H_3$ ) are also given.

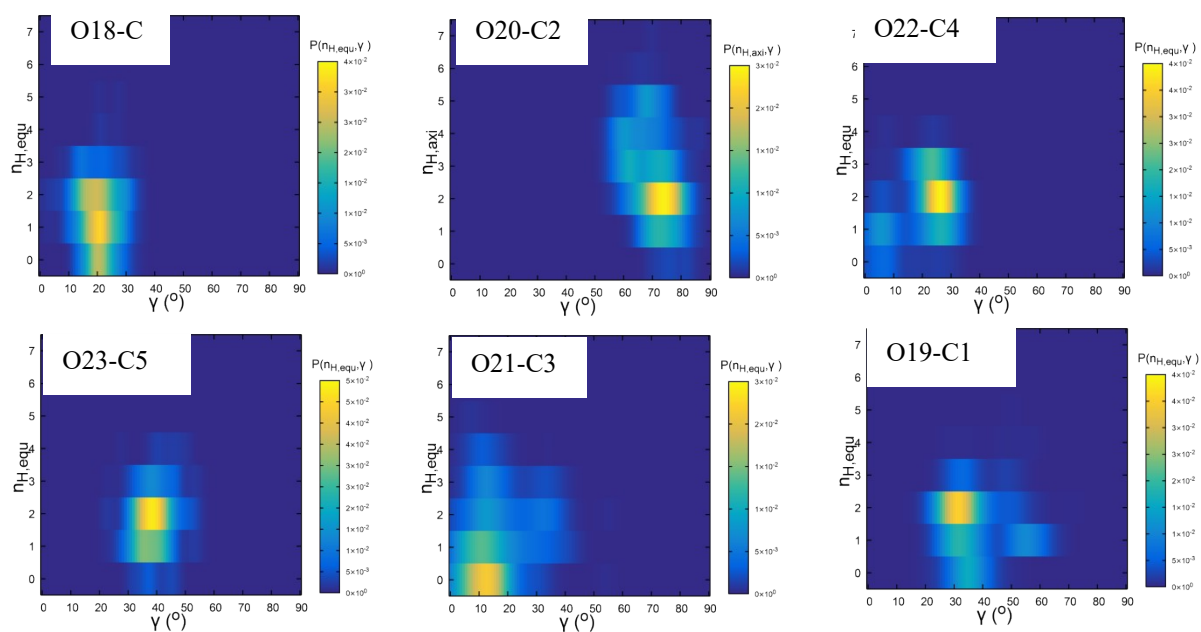




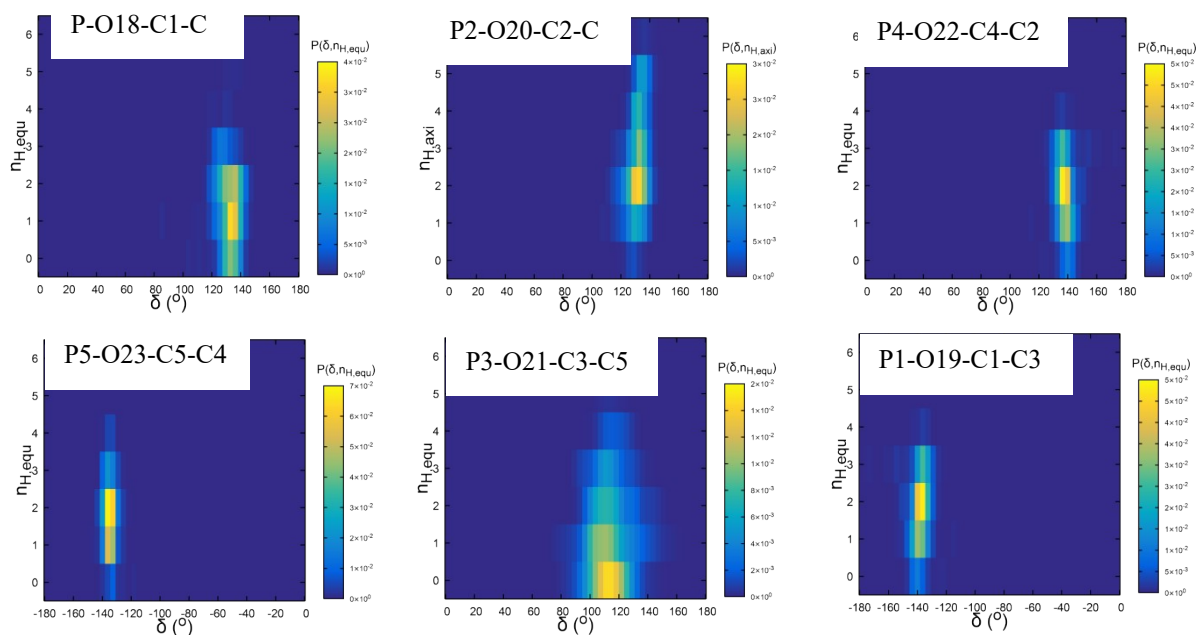
**Figure S10.** Probability distribution of the torsional angles of the chitosan chains  $\varphi$  and  $\psi$  for a) CT-083-10, b) CT-083-40, c) CT-050-10, d) CT-033-10.



**Figure S11.** Probability distribution of puckering phase angles,  $\theta$  and  $\varphi$  of the inositol ring in a) phytate-water system and b) CT-083-5. The puckering amplitude  $Q$  and location of the closest characteristic ring conformers ( ${}^4E \dots {}^4H_3$ ) are also given.



**Figure S12.** Pair probability distribution  $P(\gamma, n_H)$  of the angle  $\gamma$  made by C-O bonds with main plane of inositol and H bond number  $n_H$  of the phosphates substituted at the indicated inositol positions for CT-083-5.



**Figure S13.** Pair probability distribution  $P(\delta, n_H)$  of dihedral angle along the six phosphoester bonds  $\delta$  and the H bond number  $n_H$  of the phosphates substituted at the indicated inositol positions in CT-083-5.