

The SPASIBA Force Field for Chondroitin Sulfate: Vibrational Analysis of D-Glucuronic and N-acetyl-D-Galactosamine 4-Sulfate Sodium Salts

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Normal-mode analyses were carried out on the two components of the chondroitin 4-sulfate linear glycosaminoglycan, a copolymer implying alternate D-glucuronate β -(1 \rightarrow 3) and N-acetyl-D-galactosamine 4-sulfate β -(1 \rightarrow 4) (hereafter named D-galactosamine 4-sulfate) residues. Scaled quantum mechanical calculations (SQM) using the density functional theory approach at different levels of theory (B3LYP/6-31G** and B3LYP/6-31++G**) were performed to obtain correct vibrational assignments. The SPASIBA empirical force field parameters were then obtained from both theoretical predictions and observed IR and Raman data. It is shown that calculations including diffuse functions at the B3LYP/6-31++G** level and the introduction of the Na⁺ counterion are necessary to give correct assignments of the CO₂⁻ symmetric (ν_s) and antisymmetric (ν_a) stretching modes for the glucuronic carboxylate residue.

I. Introduction

Glycosaminoglycans (GAG) form an important part of cartilage, displaying large swellings in aqueous solutions containing Na⁺ or Ca²⁺ cations and conformational properties originating from their interactions with the carboxylate and sulfate groups present all along the polymeric chain and between neighboring molecules. Chondroitin sulfate (CS) and hyaluronic acid (HA) have been the center of a large number of conformational studies involving vibrational (infrared and Raman, infrared dichroism) spectroscopies¹ or molecular dynamics studies to measure effects of water and counterions on the overall dynamics properties of cartilage.^{2,3} Chondroitin 4-sulfate (CS4) exhibits alternating dimers of pyranose rings containing carboxylate (β 1 \rightarrow 3 D-glucuronic) or sulfate (N-acetyl D-galactosamine β 1 \rightarrow 4) groups. The crystalline conformations of chondroitin sulfate in the presence of counterions were derived by Winter et al.⁴ and by Cael et al.⁵

As a consequence of the local environments of carboxylate and sulfate groups upon the presence of Na⁺ or Ca²⁺ ions, this copolymer can adopt different molecular conformations such as helical structures.^{6–8} The conformational dependence of this polymer versus the degree of hydration was also largely investigated.⁹

The present purpose was to get derived empirical force field parameters for further conformational studies, such as molecular dynamics in the natural environment (water and counterions). The empirical SPASIBA force field allows these parameters to be obtained from spectroscopic vibrational data and applied to the D-glucuronate and D-galactosamine 4-sulfate anions treated first as isolated species and then in the presence of Na⁺ counterions.

II. Methodology

II.a. Vibrational Spectra. Due to the instability of D-galactosamine 4-sulfate sodium salt at room temperature, no experimental data could be obtained for this compound.

The infrared spectrum of the D-glucuronate sodium salt in the solid-state form was recorded using an IR Avatar 360 Nicolet apparatus. Raman spectra were obtained using a Raman TF Bruker FS 100/s apparatus and the 1064-nm line of a Nd:YAG continuous laser with 140-mW power for a spectral resolution of 4 cm⁻¹.

II.b. Scaled Quantum Mechanical Calculations. The geometry optimizations and normal-mode analyses have been performed using the density functional theory (DFT) at different levels, B3LYP/6-31G** for the isolated anion species and B3LYP/6-31++G** when in the presence of a sodium counterion using the *Jaguar* program¹⁰ (see Supporting Information for data). The optimized Hessian matrix was then translated to the internal coordinate space, leading to the possibility of applying scaling factors to the internal force constants in fitting the theoretical wavenumbers to the experimental ones using least-squares methods. This part was done using the *Redong* program of Allouche and Pourcin.¹¹

At this level of DFT calculations, a general scaling factor of 0.96–0.98 is usually recommended to simulate correctly the experimental vibrational frequencies and to obtain an adequate potential energy distribution (PED) among internal coordinates.¹²

II.c. Empirical Force Field. The SPASIBA force field is a spectroscopic molecular-mechanics-derived empirical potential function first devoted to proteins¹³ and extended to a large variety of chemical groups such as alkanes, alkenes, amino acids, ethers, esters, thiols, alcohols, saccharides, and phospholipids.^{14–20} Not only does this force field appear to be an adequate tool for molecular mechanics studies of monosaccharides, but it has also been extended to force constant determination related to various glycosidic linkages along the establishment of Ramachandran's ϕ , ψ maps.^{14,15}

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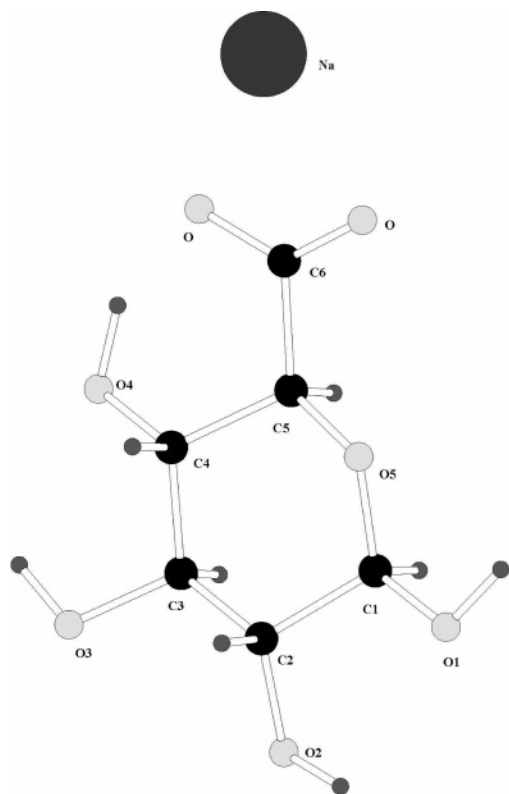


Figure 1. D-Glucuronic acid sodium salt (ball-and-stick representation).

The SPASIBA force field has been developed in our group for many years. It is able to reproduce at the same time structures energies and vibrational spectra with a much higher precision on the latter than commonly available force fields. This is the main reason it has recently been introduced into the *CHARMM* package.¹⁵ Therefore, the SPASIBA force field is a molecular force field which can be used with high confidence, particularly in molecular dynamics simulations where it has to be reliable over the whole potential energy surface rather than in the vicinity of the minima, since the parameters deduced from spectra reflect the curvature of the potential surface. The philosophy of SPASIBA and all the procedures for parameter determination have been given in detail in a series of papers corresponding to thermally excited modes (see refs 13–15 and references therein). In particular, in addition to the classical quadratic parameters K (bond stretching coordinate) and H (bond angle bending coordinate), SPASIBA introduces the Urey–Bradley F quadratic force constant related to the 1–3 nonbonded distance in a bond angle, solves the redundancy problem among internal coordinates, and adds specific parameters to correctly fit spectra (see ref 14 and Table 7). Special interest has been devoted to the low-wavenumber spectral range (10–200 cm^{-1}) corresponding to thermally excited modes. These modes are of large amplitude and reflect molecular flexibility. In this spectral range, coupled modes are found mainly corresponding to torsional coordinates and/or eventually mixed with in-plane and out-of-plane angular bending coordinates and sometimes even more stretching coordinates (longitudinal and transverse acoustical vibrations of long-chain molecules.^{21,22} Assuming a functional form for the internal rotation potential (a Fourier series), the various barriers to internal rotation V_n (Table 7) may be deduced from the experimental and/or theoretical spectra. This was particularly done for carbohydrates and the glycosidic linkages.^{23–26}

TABLE 1: Geometry Parameters Derived from DFT and Semiempirical Geometry Optimizations for the Sodium Salt Form of Glucuronic Acid Taken as an Isolated Anion^a or in Presence of Its Counterion^b

internal coordinates ^c	DFT(6-31G**) ^a	DFT(6-31++G**) ^b	SPASIBA
C1–O5	1.402	1.416	1.412
C5–O5	1.438	1.422	1.44
C1–C2	1.531	1.537	1.529
C2–C3	1.525	1.529	1.521
C3–C4	1.526	1.535	1.54
C4–C5	1.537	1.535	1.552
C5–C6	1.566	1.532	1.516
C1–O1	1.411	1.399	1.434
C2–O2	1.423	1.418	1.433
C3–O3	1.423	1.420	1.434
C4–O4	1.408	1.418	1.449
C6–O1	1.236	1.257	1.245
C6–O2	1.278	1.284	1.249
C5C6O1	118.6	116.5	119.9
C5C6O2	112.2	120.1	119.8
O1–C6–O2	129.2	123.4	120.1
C1–O5–C5	111.7	112.1	113.9
H1,C1–O1,HO1	80.9	64.6	131.1
H2,C2–O2,HO2	–67.0	–60.4	–92.1
H3,C3–O3,HO3	–79.3	–68.9	–85.5
H4,C4–O4,HO4	81.0	71.3	86.4
C4,C5–C6,O1	141.3	146.2	91.1
O5,C5–C6,O1	19.5	24.2	–24.1
C4,C5–C6,O2	–40.9	–35.3	–94.0
O5,C5–C6,O2	–162.7	–157.4	150.85
HO4⋯O2	1.602	1.861	1.96
C4–O4–HO4	100.5	105.1	107.4
O4–HO4⋯O2	153.1	140.2	136.9
C4,O4–HO4,O2	10.7	19.8	3.7
O1⋯Na		2.19	
O2⋯Na		2.20	
C6O1–O2Na		180.	

^c Distances are given in angstroms and angles in degrees.

III. Results and Discussion

III.a. D-Glucuronic Acid Sodium Salt. The sodium salt of glucuronic acid was first investigated as an anionic moiety without participation of the Na^+ counterion (Figure 1). A B3LYP geometry optimization was performed using the 6-31G** basis set, and final geometrical parameters can be examined in Table 1. As ab initio or DFT-derived vibrational wavenumbers currently display overestimated values than experimental ones, the Cartesian F_X matrix was transformed into the internal coordinate space before scaling of the force constants via the *Redong* program.¹¹ A general scaling factor of 0.962 was first applied to every internal coordinate force constant, as, generally, such a value leads to correct vibrational wavenumbers and assignments of the normal modes. However, in the present case, the localization of the symmetric stretching mode of the carboxylate group appears quite appalling. As can be noted from examination of the optimized geometry parameters, one of the carboxylate oxygens undergoes a hydrogen bond with the O4 hydroxyl hydrogen atom ($\text{H}\cdots\text{O}_{\text{CO}_2} = 1.602 \text{ \AA}$; $\text{O4–H}\cdots\text{O}_{\text{CO}_2} = 153^\circ$) leading to a longer length value for the implied C–O carboxylate bond, 1.27 \AA , as compared to the free C–O one (1.236 \AA).

A surprisingly low scaling factor of 0.89 had to be applied to the force constants related to the internal C–O stretching coordinates to correctly locate the antisymmetric stretching mode (ν_a) of the CO_2^- group (calculated here at 1584 cm^{-1}), while an anomalously low wavenumber (1195 cm^{-1}) was theoretically obtained here for the symmetric $\nu_s(\text{CO}_2)$ mode in place of the experimental value, generally expected in the 1320–1390 cm^{-1}

TABLE 2: Vibrational Wavenumbers as Obtained from DFT Calculations at the B3LYP/6-31++G Level for the D-Glucuronic Sodium Salt in Presence of the Na⁺ Counterion^a**

Raman	IR	6-31G**	6-31++G**	potential energy distribution
		64.9	94.7	0.82 τ CTCT + 0.20 τ C5O5 + 0.08 τ C5C6
		77.6	108.7	0.70 τ CTCT + 0.17 τ C5O5 + 0.13 τ C5C6
		112.7	118.9	0.91 τ CTCT + 0.09 τ CTO5
146 vw		139.8	159.1	0.30 τ CTO5 + 0.25 τ C5O5 + 0.25 τ CTCT + 0.08 δ CTO5CT + 0.07 δ CTCTC6 + 0.05 δ C5H
170 vw		169.6		0.62 τ C1O1 + 0.27 τ CTCT + 0.26 τ CTO5
187 vw				
222 vw		239.1	241.4	0.40 δ C3O + 0.25 δ C2O + 0.13 δ O5C5C6 + 0.12 δ CTCTC6
246 vw		259.8	252.1	0.24 δ C1O1 + 0.20 δ C2O + 0.19 δ C2O + 0.10 δ C3O + 0.09 δ O5C5C6 + 0.09 δ C4O
			259.4	0.23 δ O5C5C6 + 0.16 δ C2O + 0.14 δ C3O + 0.13 τ C1O1 + 0.12 δ C1O1 + 0.12 δ CTCTC6
298 w		298.2	297.2	0.25 τ CTCT + 0.18 δ C2O + 0.14 δ C3O + 0.13 τ C1O1 + 0.11 δ C4O + 0.10 τ CTCT + 0.08 δ C3H
314 w		306.6	315.0	0.50 δ C4O + 0.17 τ C1O1 + 0.17 δ C4O + 0.08 δ CTCTC6 + 0.08 δ CTCTO5
			335.6	0.41 τ C1O1 + 0.15 δ C4O + 0.13 δ CTCTC6 + 0.10 ν C5C6 + 0.08 δ C1O1 + 0.08 δ O5C5C6
356.		342.3	359.7	0.48 τ C1O1 + 0.14 ν C5C6 + 0.13 δ CTO5CT + 0.11 ν CTCT + 0.07 δ CTCTCT
381 S			387.3	0.26 τ C2O + 0.20 δ CTCTO5 + 0.18 τ CTO5 + 0.18 δ C3O.10 τ CTCT + 0.09 δ C3O
		380.4		0.52 δ CTH + 0.18 δ CTCTCT + 0.16 δ CTCTCT + 0.16 δ CTH
			399.3	0.64 τ C2O + 0.34 δ CTCTCT + 0.12 δ CTO5CT
423 S		417.2	417.8	0.62 τ C2O + 0.12 δ C1O1 + 0.10 δ C2O + 0.09 δ CTCTCT + 0.07 ν CTCT
		383.5	418.5	0.63 δ (CCO) + 0.17 ν CTCT + 0.08 δ C4O + 0.07 δ C2O + 0.05 δ CTCTCT
452 S		485.0	447.9	1.00 τ C3O
470		399.9	454.7	0.31 δ (CCO) + 0.23 τ C3O + 0.14 ν C5O5 + 0.12 ν CTCT + 0.10 δ CTCTCT + 0.10 ν C1O1
538			520.7	0.33 δ C3O + 0.21 γ (CO2) + 0.13 δ C1O1 + 0.12 τ C5O5 + 0.11 δ C3H + 0.10 δ C2H
	569	559.0	573.8	0.34 δ CTCTO5 + 0.20 ν C2O + 0.16 ν C5C6 + 0.10 δ CTO5CT + 0.10 ν CTCT + 0.10 δ C2O
581	582	570.0	583.7	0.30 δ C4O + 0.26 δ C1O1 + 0.14 δ C2O + 0.11 δ C3O + 0.07 δ C2H + 0.06 δ C3H + 0.06 δ (CCO)
615 sh	617	632.9	644.3	0.28 δ C1O1 + 0.21 δ (CCO) + 0.17 γ (CO2) + 0.16 δ C4O + 0.12 δ O5C5C6 + 0.06 δ C3O
681 w	677 S	664.8	687.1	0.86 τ C4O + 0.14 γ (CO2)
740 w	733 VS	754.1	694.0	0.57 τ C4O + 0.16 γ (CO2) + 0.11 δ (CO2) + 0.08 δ (CCO) + 0.08 ν C5C6
827 vw	834 m		800.8	0.36 δ (CO2) + 0.33 γ (CO2) + 0.25 δ (CCO) + 0.07 δ O5C5C6 + 0.06 ν (CO2)
903 vw	901 m	897.3	939.9	0.37 ν C5C6 + 0.25 ν (CO2) + 0.12 γ (CO2) + 0.09 ν CTCT + 0.08 δ (CO2) + 0.08 ν C3O
957 w	960 m	976.3	990.8	0.49 ν CTCT + 0.12 ν C2O + 0.11 ν C4O + 0.11 ν C3O + 0.10 ν C1O1 + 0.08 δ C2OH
		981.0	996.9	0.31 ν CTCT + 0.14 ν C3O + 0.14 ν C2O + 0.12 ν C4O + 0.12 ν CTCT + 0.09 δ CTCTO5
1016 w	1019 VS	1005.1	1023.5	0.32 ν CTCT + 0.30 ν CTO5 + 0.18 δ C1OH + 0.09 ν C4O + 0.06 δ C2H + 0.05 δ CTO5CT
1035 w	1039 VS	1033.5	1048.3	0.38 ν CTO5 + 0.22 ν CTCT + 0.16 ν C5O5 + 0.09 δ C2O + 0.07 δ CTCTO5 + 0.07 δ CTO5CT
1054 w		1055.5	1069.9	.64 ν CTCT + 0.12 ν C4O + 0.08 δ CTCTO5 + 0.07 ν C2O + 0.07 δ C5H
1079 w	1068 VS	1071.1	1081.4	.27 ν C2O + 0.21 ν CTCT + 0.16 ν CTO5 + 0.16 ν C4O + 0.11 ν C5O5 + 0.08 ν C1O1
		1085.4	1086.8	.51 ν C3O + 0.12 ν C1O1 + 0.10 ν CTCT + 0.07 δ C2H + 0.07 ν CTCT + 0.07 ν C2O
	1113 S	1105.5	1106.5	0.39 ν C2O + 0.28 ν C4O + 0.26 ν C5O5 + 0.08 ν CTO5
1108 VS	1128 m	1112.8	1119.3	0.52 ν CTO5 + 0.28 ν C4O + 0.20 ν CTCT
1165	1163 S		1136.7	0.60 ν C1O1 + 0.32 ν C3O + 0.07 δ CTCTCT
1197 w	1192 w		1171.2	0.19 ν C1O1 + 0.17 δ C3H + 0.15 δ C3H + 0.13 δ C2H + 0.13 δ C2OH + 0.13 δ C3OH + 0.10 δ C1H
		1195.7		0.45 ν S(CO2 + .36 δ C5H + 0.18 δ C2H
		1213.1		0.42 ν s(CO2) + 0.39 δ CH + 0.19 δ C1O1H
		1222.8	1222.6	0.38 δ C1OH + 0.23 δ C1H + 0.09 δ C4H + 0.09 δ C1H + 0.09 δ C3H + 0.06 δ C2OH + 0.06 δ C2H
	1237	1239.7	1238.7	0.26 δ C5H + 0.22 δ C2OH + 0.12 δ C4H + 0.11 δ C4H + 0.11 δ C5H + 0.10 δ C2H + 0.07 δ C5H
1247	1254		1269.5	0.26 δ C3OH + 0.25 δ C3H + 0.18 δ C2H + 0.12 δ C3H + 0.10 δ C2OH + 0.09 δ C2H
			1273.6	0.39 δ C4H + 0.29 δ C5H + 0.19 δ C4O4H + 0.07 δ C1O1H + 0.06 δ C2H
1296.6	1297	1295.3	1293.2	0.72 δ C5H + 0.16 δ C1H + 0.11 ν (CO2)
1316 m		1315.8	1309.2	0.33 δ C2H + 0.27 δ C2H + 0.22 δ C1OH + 0.18 δ C2OH
1332 m	1337 m	1337.9	1334.1	0.21 δ C4H + 0.20 δ C4OH + 0.16 ν C1H6 + 0.15 δ C3H + 0.11 δ C3OH
		1349.2	1351.7	0.61 δ C1H + 0.16 δ C2OH + 0.16 δ C2H + 0.07 δ C3OH
			1357.1	0.44 δ C3H + 0.34 δ C4H + 0.14 δ C5H + 0.08 δ C4OH
1365 w sh	1364 (sh)	1366.4	1365.4	0.20 δ C3OH + 0.17 δ C2H + 0.15 ν (CO2) + 0.14 δ C1H + 0.14 ν C1H6 + 0.11 δ C2OH
1365 m	1380 S		1391.4	0.36 ν s(CO2) + 0.21 δ C4OH + 0.10 δ C4H + 0.10 ν C5C6 + 0.10 δ C5H + 0.07 δ C1H + 0.07 δ C2H
		1403.7	1418.7	0.30 δ C1H + 0.25 δ C1H + 0.16 δ C1OH + 0.09 ν CTCT + 0.07 δ C2H + 0.07 δ C2H + 0.06 ν (CO2)
1426	1424 S	1424.5	1430.7	0.18 δ C1H + 0.15 δ C1H + 0.15 δ C1OH + 0.15 ν (CO2) + 0.14 δ C4OH + 0.12 ν C5C6

TABLE 2: Continued.

Raman	IR	6-31G**	6-31++G**	potential energy distribution
	1457 w		1439.4	0.33 δ C4OH + 0.15 δ C3H + 0.11 δ C3H + 0.11 δ C2H + 0.10 δ C2H + 0.10 δ C3OH + 0.09 δ C2OH
1457	1473 w 1520(sh)	1468.2		0.48 ν (CO2) + 0.42 ν CTCT + 0.15 δ C4H
1569	1581 S	1584.8	1582.4	0.80 ν a(CO2) + 0.10 ν CTCT + 0.05 ν C5C6 + 0.05 δ (CCO)
1611 w				
1642 w				
	2736	2839	2888.3	1.00 ν C1H
	2795	2893	2901.1	1.00 ν C5H
2927	2847	2910	2925.9	0.74 ν C3H + 0.26 ν C4H
2903	2905	2870	2939.6	0.76 ν C4H + 0.24 ν C3H
2927	2930	2953	2969.0	1.00 ν C2H
	3139	2943	3507.3	1.00 ν O4H
3330	3333	3604	3620.6	1.00 ν O3H
	3472	3651.9	3641.3	1.00 ν O2H
	3597	3660.3	3647.6	1.00 ν O1H

^a Corresponding predicted B3LYP/6-31G** wavenumbers are given when comparable potential energy distribution was found. Scaling factors for internal force constants: ν C–O (scf = 0.97); ν O–H (scf = 0.962); and all others (scf = 0.98). ν : stretching. δ : in-plane bending. γ : out-of-plane bending. τ : torsion. ν_s and ν_a : antisymmetric and symmetric stretching modes of the CO2 group. w: weak. m: medium. S: strong. VS: very strong. sh: shoulder.

range (Table 2). The low difference in bond lengths between the two C–O groups does not, in our minds, justify the use of a different scaling factor for each of them. However, this apparent large shift between the ν_a (CO2) and ν_s (CO2) normal modes will lead us to use diffuse functions and to examine the effects of the presence of a counterion in the neighborhood of the carboxylate group. This will be discussed below.

Several contributions to the out-of-plane wagging mode of the carboxylate group are predicted to occur at 665 and 883 cm^{-1} , and the δ (OCO) in-plane bending mode is mainly predicted at 754 cm^{-1} when keeping a general scaling factor of 0.962 for the B3LYP/6-3G** type of calculations. These values have to be related to those obtained for the calcium malonate dihydrate as given by Brusau et al.,²⁷ i.e., 785 cm^{-1} δ (OCO), 605 cm^{-1} δ (CCO) predicted here at 632 cm^{-1} . These authors identified the ν_a and ν_s (CO2) modes to occur at 1565 and 1365 (and 1430) cm^{-1} , respectively.

III.a.1. Endocyclic Ring and Exocyclic Hydroxyl modes. The 1500–1200 cm^{-1} range appears as a region of complex coupled modes of vibrations involving hydrogen atoms (i.e., COH, HCO, CCH). In this range, the quantum mechanically derived δ CH and δ C–O in-plane deformations take place predominantly. These results support quite well the work of Dauchez et al.^{23,25,26} performed on normal-mode investigations for mono- and disaccharides in the crystal forms.

The 1200–1000 cm^{-1} domain was confirmed by the last authors to imply principally ν C–O and ν C–C stretching modes. The present DFT calculations extend these assignments to a lower boundary of 900 cm^{-1} .

The 1000–600 cm^{-1} vibrational range is well-known to contain two distinct domains implying the so-called fingerprint and crystalline regions for monosaccharides in the crystal state. They exhibit vibrations originating from the hemiacetal group (C5O5C1O1), generally involving endocyclic in-plane bending modes, as calculated here at 559–570 cm^{-1} (δ C2C1O5, δ C2C1O1, and δ CO).²³

The theoretical DFT exocyclic δ CCO modes are predicted in the range 260–380 cm^{-1} and correspond to the empirical force field determinations performed by Dauchez and co-workers.

The high-frequency modes including the O–H stretching modes are correctly predicted to occur in the 3400–3600 cm^{-1} range, apart from the O4–H stretching motion calculated at

2943 cm^{-1} when using the general scaling factor of 0.962. This mode is expected to appear at approximately 3130 cm^{-1} corresponding to a Raman and IR experimental value. This mode frequency certainly corresponds in the present model to a strong hydrogen bond taking place between one of the carboxylate oxygen atoms and the O4 hydroxyl hydrogen atom.

III.a.2. Use of Diffuse Functions. Implication of a Na⁺ Counterion. Addition of diffuse functions to the basis sets has been shown to be essential for accurate analyses of compounds containing lone pairs or anions or when dealing with transition structures, but it produces only a few changes when applied to molecules such as sugars.²⁸

Recently, Keresztury et al.²⁹ have shown that SQMFF-type calculations on the acetate ion at the B3LYP/6-31G* level were unable to explain the frequency splitting between the ν_a and ν_s modes of the carboxylate group. Furthermore, these authors pointed out the necessity to introduce a Na⁺ counterion as a bidentate complex or as a water complex to obtain adequate vibrational descriptions of the antisymmetric and symmetric C–O stretching modes. They also used a polarizable continuum model (PCM) and were able to reproduce the experimental shift between these two modes.

In the present work, a B3LYP calculation using the 6-31++G** basis set involving diffuse functions was performed on the sodium salt form of D-glucuronic acid. The carboxylate anion now forms a bidentate complex with the sodium ion in the OCO plane at a distance of 2.2–2.4 Å from each carboxyl oxygen atom. Similar values in bond lengths, valence angles, and torsion structural parameters obtained after geometry optimization by both DFT methods can be noted in Table 1.

As for the isolated anionic moiety, a transformation from the Cartesian to the internal coordinate space allowed scaling of the internal force constants. A high general scaling factor of 0.98 was appropriate to fit most of the theoretical wavenumbers to the experimental vibrational data. Table 2 displays the potential energy distribution (PED) among internal coordinates corresponding to DFT calculations at the B3LYP/6-31++G** level.

A root-mean-square deviation (RMSD) of 17.4 cm^{-1} between the theoretical DFT and experimental vibrational frequencies was presently calculated when using only this single scaling factor.

In a first attempt, we did not try to determine specific scaling

TABLE 3: D-Glucuronic Acid Sodium Salt^a

ν (cm ⁻¹)	assignments
76.9	0.66 τ C4O4 + 0.14 τ O5C5 + 0.11 δ O5C5C4 + 0.10 τ C4C5
112.3	0.30 τ C1O5 + 0.26 δ O5C5C6 + 0.15 τ C5C6 + 0.14 δ C1O5C5 + 0.14 δ C3C4C5
133.7	0.42 τ C5C6 + 0.25 τ C2C3 + 0.20 τ C3C4 + 0.11C3O3
158.6	0.59 τ C1O1 + 0.17 τ O2C2 + 0.13 δ C1C2C3 + 0.13 δ O5C1O1
221.9	0.93 τ C1O1 + 0.04 τ C2O2 + 0.02 δ O1C1C2
238.9	0.90 τ C1O1 + 0.09 τ C2O2
289.1	0.81 τ C2O2 + 0.11 δ O2C2C3 + 0.05 τ C3O3 + 0.03 δ O3C3C4
293.9	0.81 τ C2O2 + 0.07 δ O1C1C2 + 0.06 τ C1O1 + 0.06 τ C4O4
319.6	0.36 δ O2C2C3 + 0.22 δ C2C3O3 + 0.20 δ O5C1C2 + 0.11 τ C3O3 + 0.11 τ C2O2
327.9	0.64 τ C4O4 + 0.19 δ O5C1O1 + 0.11 τ O1C1 + 0.07 τ O2C2
336.2	0.82 τ C4O4 + 0.09 δ C1C2O2 + 0.05 δ O5C5C4 + 0.04 δ O5C1O1
352.0	0.51 τ C3O3 + 0.49 τ O4C4
380.5	0.72 τ C2O2 + 0.28 τ C4O4
397.3	0.21 ν C2C3 + 0.21 ν C1O1 + 0.19 ν O5C5 + 0.13 ν C4O4 + 0.13 δ C1O5C5 + 0.13 τ C4O4
425.9	0.34 τ C3O3 + 0.13 τ O2C2 + 0.09 τ C1O1 + 0.08 δ CTCTCT + 0.08 δ CTCTOH
435.6	0.73 τ C3O3 + 0.27 τ C4O4
450.0	0.56 τ C3O3 + 0.43 τ C4O4
467.1	0.43 τ C1O1 + 0.33 τ C2O2 + 0.13 δ O5C1C2 + 0.11 δ O4C4C5
518.8	0.33 ν C2O2 + 0.20 δ C1C2O2 + 0.18 ν O5C1 + 0.10 δ O5C1C2 + 0.10 δ (CO2-) + 0.09 δ O5C1O1
535.2	0.34 ν C4C5 + 0.26 δ O4C4C5 + 0.12 δ O5C1O1 + 0.10 δ O3C3C4 + 0.09 ν C4O4 + 0.09 ν C3O3
608.7	0.30 δ C1O1 + 0.27 δ (CCO) + 0.30 δ C1O1 + 0.16 δ O5C5C6 + 0.15 δ C2C3O3 + 0.13 ν O5C5
619.5	0.25 δ O2C2C3 + 0.22 δ C3C4O4 + 0.17 δ C2C3O3 + 0.14 δ (CCO) + 0.14 γ (CO2-) + 0.09 δ (CO2-)
648.9	0.30 ν C1O1 + 0.24 δ C1O5C5 + 0.14 ν C5C6 + 0.14 δ (CCO) + 0.10 ν C4O4 + 0.08 δ O5C5C4
734.6	0.89 γ (CO2-) + 0.07 δ C4C5C6 + 0.04 δ C3O3
906.6	0.36 ν C5C6 + 0.27 ν C1O1 + 0.13 ν O5C1 + 0.13 ν (CO2-) + 0.08 ν O5C5 + 0.04 δ C1O5C5
959.0	0.35 ν C2C3 + 0.23 ν C3O3 + 0.15 ν C1C2 + 0.13 ν C2O2 + 0.10 ν C4O4 + 0.04 ν C4C5
979.6	0.30 ν C3C4 + 0.21 ν C3O3 + 0.19 ν C4O4 + 0.11 ν C4C5 + 0.10 ν O5C1 + 0.09 ν C2O2
999.6	0.57 ν C1C2 + 0.22 ν C2O2 + 0.06 δ C1C2O2 + 0.06 ν C2C3 + 0.05 δ C1H + 0.05 ν O5C1
1055.3	0.30 ν C4C5 + 0.20 ν C3O3 + 0.19 ν C4O4 + 0.16 ν O5C5 + 0.08 ν C1O1 + 0.07 ν C2C3
1061.8	0.51 ν O5C1 + 0.21 ν C3C4 + 0.10 ν O5C5 + 0.07 ν C1C2 + 0.06 ν C2O2 + 0.06 δ C1O1H
1069.3	0.30 ν C1O1 + 0.21 ν C4C5 + 0.20 ν C2O2 + 0.12 ν C1C2 + 0.12 ν O5C1 + 0.06 ν C3C4
1090.1	0.55 ν C4O4 + 0.16 δ C4C5HC + 0.13 ν C3C4 + 0.11 ν O5C5 + 0.05 ν C1C2
1129.4	0.34 ν C3O3 + 0.24 ν O5C5 + 0.18 ν C3C4 + 0.15 ν C2C3 + 0.04 ν C2O2 + 0.04 ν C5C6
1139.9	0.56 ν C2O2 + 0.20 ν C2C3 + 0.11 ν O5C1 + 0.05 δ C1O1H + 0.04 ν C3C4 + 0.04 ν C1C2
1162.5	0.27 ν C4O4 + 0.23 ν O5C5 + 0.20 ν C4C5 + 0.18 ν C3O3 + 0.06 δ C4H + 0.05 ν C6-O
1187.3	0.35 δ C1H + 0.23 δ C1O1H + 0.17 ν C1O1 + 0.15 δ C2H + 0.11 ν C3O3
1208.0	0.29 ν C1O1 + 0.22 δ C1H + 0.13 ν O5C5 + 0.12 δ C2H + 0.12 δ C1O5C5 + 0.11 δ C1O1H
1242.7	0.51 δ C1O1H + 0.20 δ C1H + 0.13 δ C1O5C5.08 ν O5C5 + 0.07 δ C2O2H
1264.9	0.55 δ HCC3C4 + 0.23 δ C2H + 0.13 δ C3O3H + 0.09 δ C4H
1302.2	0.61 δ C2O2H + 0.14 δ C1O1H + 0.12 ν s(CO2-) + 0.04 ν O5C1 + 0.04 δ C1H
1318.0	0.52 ν s(CO2-) + 0.17 ν C5C6 + 0.04 δ C3O3H + 0.03 δ C2O2H + 0.01 δ (OCO)
1321.9	0.67 δ C3O3H + 0.12 δ C4H + 0.06 ν s(CO2-) + 0.05 δ C2O2H + 0.05 ν C3O3 + 0.05 ν C4O4
1338.2	0.33 δ O5C1HC + 0.23 δ C1O1H + 0.23 ν O5C1 + 0.11 δ HCC3O3 + 0.10 ν C1O1
1362.6	0.46 δ C5H + 0.24 δ C4H + 0.20 δ C3O3H + 0.11 ν O5C5
1386.1	0.35 δ C2H + 0.26 δ C3H + 0.16 ν C2O2 + 0.12 ν C3O3 + 0.11 ν O5C1
1404.4	0.43 δ C5H + 0.25 δ C4H + 0.18 ν C4O4 + 0.15 ν O5C5
1408.5	0.23 δ C1O1 + 0.20 ν C1O1 + 0.17 δ C1H + 0.12 ν C1C2 + 0.09 δ C2H + 0.08 δ C1O5C5
1443.1	0.44 δ C3H + 0.34 δ HCC2 + 0.14 ν C2C3 + 0.08 ν C2O2
1449.4	0.90 δ C4O4H + 0.05 ν a(CO2-) + 0.05 ν CTCT
1543.3	0.61 δ C4H + 0.20 ν a(CO2-)
1587.9	0.91 ν a(CO2-)
2922.3	0.43 ν C3H + 0.24 ν C2H + 0.17 ν C4H + 0.10 ν C1H + 0.06 ν C5H
2927.3	0.39 ν C1H + 0.24 ν C5H + 0.20 ν C4H + 0.15 ν C2H
2933.4	0.38 ν C5H + 0.31 ν C3H + 0.27 ν C1H
2944.2	0.38 ν C2H + 0.24 ν C4H + 0.20 ν C5H + 0.17 ν C1H
2949.7	0.35 ν C4H + 0.23 ν C2H + 0.22 ν C3H + 0.13 ν C5H + 0.06 ν C1H
3504.7	0.62 ν O2H + 0.32 ν O1H + 0.06 ν O3H
3511.9	0.61 ν O1H + 0.21 ν O3H + 0.17 ν O2H
3513.5	0.72 ν O3H + 0.21 ν O2H
3547.5	1.00 ν O4H

^a Vibrational wavenumbers (in cm⁻¹) and potential energy distribution among internal coordinates as obtained from the SPASIBA empirical force field. ν : stretching. ν_a and ν_s : antisymmetric and symmetric stretching modes. δ : in-plane valence bending. γ : out-of-plane wagging. τ : torsion.

factors attached to each internal coordinate type, this being principally due to the complexity of the normal modes. With this in mind, DFT calculations using only one general scaling factor offer an approximative general description of the vibrational potential energy distribution among internal coordinates. This could explain the rather large RMSD obtained between experimental data and theoretical wavenumber values.

No internal hydrogen bond could now be detected between

the O4 hydroxyl hydrogen and a carboxylate oxygen atom as observed above for the isolated anionic form. The antisymmetric ν_a (CO2) mode is always predicted to occur in the 1580–1590 cm⁻¹ range, while a considerable change occurs for the symmetric mode. This mode is now quite well predicted to occur between 1360 and 1400 cm⁻¹.

The out-of-plane wagging mode of the carboxylate group shows numerous contributions to several modes between 520

and 700 cm^{-1} . The $\delta(\text{CCO})$ in-plane bending is rather well located in the 410–460 cm^{-1} range, while the corresponding in-plane bending $\delta(\text{OCO})$ contribution appears near 800 cm^{-1} . One can note the large mixing of the in- and out-of-plane motions with the endocyclic νCC , νCO and δCCO5 , δCCC vibrational motions with participation of bending modes of the exocyclic hydroxyl groups. The in-plane vibrations remain defined in the same wavenumber range than those obtained in the previous calculation with the 6-31G** basis set.

Different scaling values were applied to the $\gamma(\text{CO2})$ out-of-plane mode, but only small shifts in frequencies could be detected. This mode can then be considered as being “frozen” by the presence of the counterion.

The local group motions of the exocyclic δCH and $\delta\text{C-O}$ groups are well-defined in the 1500–1200 cm^{-1} domain, and $\nu\text{C-OH}$ motions occurring in the range 1200–1000 cm^{-1} have comparable corresponding wavenumbers and potential energy distribution among internal coordinates than those predicted for the pure anionic form. The 1000–600 cm^{-1} region corresponds to the $\delta(\text{CCOH})$ and $\delta(\text{CCO})$, $\delta(\text{COC})$ ring-bending modes.

It can be easily observed that the use of diffuse functions and inclusion of a counterion only operate on the normal modes of the anionic part of the molecule. The present general scaling factor is close to unity for the major part of the internal force constants. In our mind, this offers a good example of the necessity to add a counterion and to use an adapted basis set including diffuse functions when dealing with charged species in quantum mechanical studies.

III.a.3. Normal-Mode Analysis Using the Empirical SPASIBA Force Field. As could be asserted from the former arguments, DFT calculations using adequate basis functions and addition of counterions can be of great help to obtain reliable vibrational assignments when no experimental assignments could be obtained.

The SPASIBA force field is a spectroscopically derived force field and was applied in previous normal-mode analyses on mono- and disaccharides by our group.^{23,26} Here, we used the existing SPASIBA force constant database with very few modifications. Torsional potentials related to ring bonds and exocyclic hydroxyl groups were deduced from spectroscopic data on crystal forms of monosaccharides and extended to a variety of glycosidic linkages appearing in disaccharides.^{14,15}

Examination of the low-frequency region (76–300 cm^{-1}) reveals a good agreement with the DFT predictions, in particular, for the monosaccharide ring normal modes involving CT-CT, CT-O5, and exocyclic hydroxyl group torsional librations and ring deformations.

Comparison between the DFT and SPASIBA-derived geometry parameters (Table 1) leads to some important remarks regarding mainly the carboxylate group. The two C6–O bonds remain on the same order of length when using molecular mechanics but are predicted to have different values in both DFT calculations; this fact implies unequal electronic properties between the two bonds. The SPASIBA torsional C5–C6 equilibrium value displays a large difference (about 50°) from the corresponding ones obtained from DFT calculations. The corresponding SPASIBA torsional parameter was derived from vibrational analyses using pure C_{2v} symmetry which, in fact, does not seem to correspond presently to the case predicted by DFT methods.

Table 3 displays the potential energy distribution (PED) obtained for the D-glucuronate isolated anion. A RMSD of 34.5 cm^{-1} is obtained between the experimental and SPASIBA-derived vibrational wavenumbers. The largest discrepancies

TABLE 4: Geometry Parameters for D-Galactosamine 4-Sulfate as Derived from Theoretical DFT Calculations and the Empirical SPASIBA Force Field^a

	DFT B3LYP /6-31G** (1)	DFT B3LYP /6-31++G** (2)	SPASIBA
C5–O5	1.440	1.442	1.442
C1–O5	1.426	1.396	1.430
C4–OT	1.423	1.422	1.477
OT–S	1.718	1.708	1.712
S–O	1.493 ^b	1.490	1.465
	1.476	1.498	1.462
	1.465	1.461	1.463
C4–OT–S	115.7	118.9	115.9
OT–S–O	102.7 ^b	99.8	105.2
	104.0	106.4	105.5
	101.3	103.1	104.9
O–S–O	114.2 ^b	117.8	113.4
	115.0 ^b	110.6	113.2
	116.7	116.5	113.5
C3,C4–OT,S	–98.8	–122.0	–113.3
C5,C4–OT,S	141.0	115.6	125.7
H1,C1–O1,HO	64.9	64.8	44.3
H3,C3–O3,HO	–148.0	65.5	–102.6
O5,C5–C6,O6	58.0	52.3	59.0
C4,C5–C6,O6	–179.1	173.5	–175.1
C1,C2–N,C	92.5	–153.9	97.3
C3,C2–N,C	–150.0	–34.3	–141.9
C2,N–C,CT	163.6	–173.0	–179.5
H,N–C,O	–156.9	175.9	179.2
HO3···O–S	1.71		2.02
O3,HO3···O–S	167.7		158.4
C3,O3–HO3···O–S	62.9		–78.5
O3,HO3···O–S	–50.6		42.1
HO3···O(C=O)		1.557	
HO3···O=C		115.6	
O3–HO3···O(C=O)		163.7	
O3–HO3···O=C		23.5	

^a Distances are given in angstroms and bond valence angles in degrees. (1) isolated anionic form; (2) diffuse functions added in the presence of the Na⁺ counterion. ^b Refer to the O atom displaying a hydrogen-bonded character with the C4 hydroxyl hydrogen.

between molecular mechanics predictions and experimental data stand in the 510–540 and 620–740 cm^{-1} spectral ranges, both implying the participation of valence angles and out-of-plane motions attached to the carboxylate group. This is mainly responsible for the relative large deviations from experimental data.

On the contrary, the empirical force field constants associated with the carboxylate group, being deduced from experimental data assuming a C_{2v} symmetry type, lead to correct assignments of the antisymmetric stretching mode, which is well-reproduced at 1570–1600 cm^{-1} , while the corresponding symmetric mode is predicted to occur at about 1320 cm^{-1} .

Along empirical minimization without distance constraints of the D-glucuronate anion in the presence of its counterion primitively spreading in the OCO plane, the Na atom moves out of the OCO plane at a C–O distance of 3.47 Å from the O4 oxygen atom. A new strong contribution to the $\nu_s(\text{CO2})$ mode is then calculated at 1361 cm^{-1} .

III.b. D-Galactosamine 4-Sulfate Sodium Salt. Due to the large instability at room temperature of the sodium salt form of D-galactosamine 4-sulfate, we did not achieve success in recording the infrared and/or Raman spectra. We shall thus use the IR linear dichroism data reports of Servaty et al.¹ on hyaluronic acid and chondroitin sulfate and IR measurements of Matsuhiro et al.³⁰ to support our theoretical predictions on some vibrational wavenumbers and assignments.

Two types of quantum mechanical treatments have been carried out in the present work.

TABLE 5: DFT/B3LYP Derived Vibrational Wavenumbers (in cm^{-1}) on D-Galactosamine 4-Sulfate in Its Isolated Anionic Form^a and in the Presence of Its Sodium Counter Ion^{b,c}

6-31G** ^a	6-31++G** ^b	potential energy distribution (in the presence of the sodium counterion)
48.5	63.0	0.62 τ CTCT + 0.18 τ CTN + 0.13 τ CN + 0.06 τ OT-S
58.1	78.6	0.29 τ CTO5 + 0.28 τ CTCT + 0.16 δ CT-N + 0.15 γ NH + 0.10 τ CN
99.5	86.9	0.38 τ OT-S + 0.32 τ CTCT + 0.12 τ CN + 0.09 τ CTN + 0.04 γ NH
55.1	105.5	0.81 τ C4-OT + 0.19 τ OT-S
	113.7	0.55 τ OT-S + 0.36 τ C5C6 + 0.08 δ C4-OT-S
99.5	114.9	0.36 τ OT-S + 0.18 τ C5C6 + 0.12 δ CTCTOT + 0.08 δ (SO3) + 0.08 τ C1O1 + 0.006 τ C4OT + 0.06 γ NH
123.3	127.3	0.29 τ CTCT + 0.12 τ CN + 0.11 δ C5C6 + 0.11 γ NH + 0.11 τ CTN + 0.08 τ C5O5 + 0.06 δ CTCTCT
110.1	137.8	0.46 τ C-CT + 0.16 δ CT-N + 0.23 δ C5C6 + 0.15 τ CTCT
150.2	159.0	0.23 τ CN + 0.22 τ C-CT + 0.21 γ NH + 0.16 τ CTCT + 0.09 δ CTN
168.6	176.2	0.34 τ CTCT + 0.33 τ CT-O5 + 0.1 δ C1O5C5 + 0.10 δ C1O1 + 0.07 δ CT-OT + 0.06 δ C4O5
190.4	188.7	0.36 τ CTO5 + 0.27 δ C5C6 + 0.21 δ CT-OT + 0.10 δ C1O5C5 + 0.07 δ C5C6O6
177.4	201.3	0.67 δ C4-OT-S + 0.20 δ (OT-S-O) + 0.12 τ OT-S
214.3	214.4	0.25 τ CTCT + 0.21 τ CTO5 + 0.15 τ C5C6 + 0.11 δ C2O2 + 0.11 δ C5C6 + 0.09 ν OT-S
227.0	238.5	0.29 τ OT-S + 0.19 τ CTO5 + 0.18 δ C1O1 + 0.18 δ C5C6 + 0.11 δ (O-S-O) + 0.10 τ OTCT + 0.08 δ C5C6O6
273.8	264.8	0.44 δ CT-N-C + 0.19 δ NH + 0.13 δ C=O + 0.09 δ C2O2 + 0.07 δ N-C-CT + 0.07 τ NC
273.8	295.5	0.26 δ CT-N + 0.21 δ N-C-CT + 0.15 δ CTCTO5 + 0.12 δ C=O + 0.10 ν CTCT + 0.08 ν C5C6 + 0.06 ν CTN
348.4	337.8	0.26 δ (OT-S-O) + 0.25 τ CN + 0.18 τ CTO5 + 0.12 δ C3O3 + 0.11 δ CTCTCT + 0.06 δ (O-S-O)
410.0	341.3	0.72 τ C1O1 + 0.15 δ C1O1 + 0.12 τ C-CT
361.4	364.5	0.40 δ (OT-S-O) + 0.13 δ (O-S-O) + 0.21 τ OT-S + 0.12 δ CT-OT + 0.08 τ C1O1 + 0.06 τ CT-OT
392.8	373.8	0.45 δ (OT-S-O) + 0.12 δ (O-S-O) + 0.12 τ C6O6 + 0.12 δ CTN + 0.10 τ C1O1 + 0.07 δ C5C6O6
429.5	396.6	0.31 δ C3O3 + 0.27 τ C6O6 + 0.20 δ CTOT + 0.16 δ (OT-S-O) + 0.05 δ (O-S-O)
410.0	398.5	0.31 τ C6O6 + 0.17 τ C1O1 + 0.11 δ CT-N + 0.05 δ C3O3
429.5	420.6	0.23 τ C-CT + 0.22 δ CTCTCT + 0.17 ν CTCT + 0.14 δ C1O1 + 0.12 δ CT-N + 0.09 δ CTCTO5
429.5	432.5	0.26 δ CTCTO5 + 0.21 δ C5C6O6 + 0.16 τ C6O6 + 0.14 δ NH + 0.11 δ (O-S-O) + 0.10 δ CTO5CT
478.1	476.0	0.45 δ (O-S-O) + 0.30 ν OT-S + 0.17 δ (OT-S-O) + 0.07 τ CTCT
488.5	486.0	0.26 δ C=O + 0.20 δ CTOT + 0.15 δ CTC5C6 + 0.12 δ (OT-S-O) + 0.09 ν OT-S + 0.09 δ CTN + 0.07 δ (O-S-O)
519.1	510.4	0.47 δ (O-S-O) + 0.18 δ C1O1 + 0.15 δ CTOT + 0.11 δ (OT-S-O) + 0.09 ν CT-OT
534.2	534.5	0.38 δ C3O3 + 0.25 δ C1O1 + 0.14 δ C=O + 0.13 δ C5C6 + 0.09 δ C5C6O6
520.5	541.5	0.81 δ (O-S-O) + 0.19 δ (OT-S-O)
561.2	552.3	0.41 δ (O-S-O) + 0.34 δ (OT-S-O) + 0.13 δ (CT-OT-S) + 0.11 τ OT-S
581.7	579.7	0.30 δ C=O + 0.21 δ C1O1 + 0.18 δ C1H + 0.16 δ C5C6 + 0.14 γ C=O
609.6	586.6	0.77 γ C=O + 0.23 γ NH
621.8	607.8	0.26 δ (CT-OT-S) + 0.22 ν OT-S + 0.20 δ C=O + 0.14 δ (O-S-O) + 0.10 δ C3O3 + 0.08 ν C-CT
656.2	669.0	0.27 δ C4-OT + 0.22 ν OT-S + 0.16 δ CTCTO5 + 0.13 δ C3H + 0.08 δ C=O + 0.07 ν N-CT + 0.06 τ CTN
	679.3	0.37 τ CN + 0.34 τ CTN + 0.15 γ C=O + 0.14 γ NH
699.5	700.3	0.46 δ C4-OT + 0.33 δ C=O + 0.20 ν CTCT
812.5	789.5	0.22 δ CTCTO5 + 0.16 δ C4H + 0.15 δ C4-OT + 0.15 ν OT-S + 0.15 ν CTCT + 0.11 ν CTN + 0.05 ν C4OT
864.8	859.3	0.32 ν C5O5 + 0.16 ρ CH2 + 0.14 δ C1O5C5 + 0.11 δ C1O1 + 0.09 ν CTCT + 0.09 ν C5C6 + 0.08 δ CTCTCT
875.8	868.6	0.38 ν C4-OT + 0.16 ν CTCT + 0.11 δ C3H + 0.10 δ CTN + 0.09 ν C-CT + 0.08 ν CN + 0.08 ν OT-S
691.3	893.3	0.99 τ C3O3
917.6	907.2	0.30 ρ CH2 + 0.24 τ C3O3 + 0.18 ν C5C6 + 0.14 ν C4-OT + 0.07 δ C5H + 0.06 ν CN
917.6	936.9	0.58 τ CTCT + 0.12 ρ CH2 + 0.10 ν CN + 0.09 δ C5H + 0.06 δ C1H + 0.05 δ CTCTCT
956.6	951.6	1.0 ν (SO3)
1010.6	979.5	0.38 ρ CH2 + 0.21 ν C-CT + 0.13 ν CTN + 0.1 ν CTCT + 0.06 ν C3O3 + 0.05 ν C5C6 + 0.04 ν C4-OT
1010.6	1001.4	0.35 ρ CH2 + 0.17 ν C5C6 + 0.15 ν CTCT + 0.13 ν C6O6 + 0.11 ν C4-OT + 0.08 ν CT-O5
1001.8	1018.2	0.34 ν CTCT + 0.21 ν C3O3 + 0.16 ν C1O1 + 0.11 ν C-CT + 0.10 δ C=O + 0.07 δ C1O1H
974.4	1030.0	0.81 ρ CH3 + 0.19 γ C=O
1010.6	1033.6	0.68 ν C6O6 + 0.17 ν C5C6 + 0.14 ρ CH2
1097.3	1041.8	0.35 ν C3O3 + 0.21 ν C6O6 + 0.12 δ C1O1H + 0.11 ν C1O1 + 0.10 δ C3H + 0.09 δ C2H
1119.6	1057.8	0.21 ν CTN + 0.18 ν C1O5 + 0.16 δ CTCTCT + 0.15 ν CTCT + 0.12 ν C5C6 + 0.08 ρ CH3 + 0.08 ν C3O3
1087.0	1070.5	0.34 ρ CH2 + 0.31 ν C6O6 + 0.18 ν CTO5 + 0.08 ν C5C6 + 0.08 δ C6O6H
	1084.6	0.30 ρ CH2 + 0.27 ν C6O6 + 0.21 ν CTN + 0.15 ν CTCT + 0.06 δ C6O6H
1097.3	1096.1	0.39 ν C1O5 + 0.25 ν C4OT + 0.18 ν CTN + 0.17 δ CTCTCT
1060.1	1120.1	0.76 ν CTO5 + 0.14 ν CTCT + 0.09 ν C4-OT
1148.6	1123.1	1.0 ν (SO3)
1163.4	1126.4	0.55 ν C1O1 + 0.20 ν (SO3) + 0.17 ν C3O3 + 0.06 δ CTCTCT
1204.2	1197.9	0.36 twi CH2 + 0.21 δ C6O6H + 0.15 δ C2H + 0.15 δ C1H + 0.12 δ C1O1H
1221.8	1215.5	0.29 twi CH2 + 0.25 δ C1H + 0.19 δ C2H + 0.17 δ C6O6H + 0.09 δ C1O1H
1258.3	1244.6	0.32 δ C5H + 0.30 δ C4H + 0.27 ν (SO3) + 0.11 δ C1H
1232.3	1247.7	0.68 ν (SO3) + 0.18 δ C1O1H + 0.13 δ C1H
1251.1	1249.1	0.28 ν (SO3) + 0.19 δ C1O1H + 0.19 δ C4H + 0.12 δ C5H + 0.10 δ C1H + 0.10 δ C2H
1258.3	1265.4	0.51 δ C2H + 0.39 δ C3H + 0.10 ν CN
1303.7	1290.7	0.46 δ C3H + 0.22 ν CN + 0.18 δ NH + 0.07 ν CT-N + 0.06 ν C-CT
1258.3	1296.6	0.32 δ C4H + 0.31 δ C5H + 0.14 δ C3H + 0.14 way CH2 + 0.07 ν CTCT
1317.3	1306.4	0.37 δ C5H + 0.33 δ C1O1 + 0.30 δ C2H
1341.5	1327.7	0.32 δ C5H + 0.30 δ C2H + 0.15 δ C1H + 0.15 δ C4H + 0.08 δ C3H
1341.5	1347.6	0.55 δ C4H + 0.35 δ C3H + 0.10 δ C1H

TABLE 5: Continued

6-31G** ^a	6-31++G** ^b	potential energy distribution (in the presence of the sodium counterion)		potential energy distribution (in the presence of the sodium counterion)	
		6-31G** ^a	6-31++G** ^b	6-31G** ^a	6-31++G** ^b
1353.3	1352.6	0.47wagCH ₂ + 0.42δC6O6H + 0.10δC3H	2904.5	2888.3	0.81νC5-H + 0.19νC3-H
1365.9	1362.1	0.42δC4H + 0.37δC3H + 0.10δC2H + 0.10δC5H	2881.6	2900.2	0.81νC3-H + 0.19νC5-H
1370.1	1372.2	1.0δsCH ₃	2921.6	2906.2	1.0νsCH ₃
1383.0	1374.7	0.65δC1H + 0.29δC5H + 0.06δC6O6H	2947.6	2933.1	1.0νsCH ₂
1407.7	1391.6	0.82wagCH ₂ + 0.10δC6O6H + 0.07δC5H	3043.6	2973.5	1.0νC2-H
1435.5	1407.4	0.65δC1H + 0.21δC1O1H + 0.08δC2H + 0.06νCTCT	2988.9	2977.3	1.0νaCH ₃
1448.2	1433.4	1.0δaCH ₃	2984.6	2979.0	1.0νC4-H
1464.0	1449.7	1.0δaCH ₃	3002.0	2985.8	1.0νaCH ₂
1481.6	1459.2	1.0sciCH ₂	3010.3	2987.0	1.0νaCH ₃
1472.0	1510.4	1.0δC4O4H	3241.0	3296.0	1.0νO3-H
1509.7	1528.0	0.67δNH + 0.32νCN	3520.9	3461.0	1.0νN-H
1644.6	1648.4	0.82νC=O + 0.09δNH + 0.09νCN	3702.3	3664.7	1.0νO1-H
2839.9	2837.4	1.0νC1-H	3695.7	3681.2	1.0νO6-H

^c ν: stretching, δ: in-plane bending, τ: torsion, γ: out-of-plane wagging, ρ: rocking mode for methyl and methylene groups. ν_{as}, ν_s: antisymmetric and symmetric stretching modes. δ_{as}, δ_s: in-plane bending antisymmetric and symmetric modes. Force constants scaling factors: 0.95 for the C-H stretching modes of the CH₂ and CH₃ groups, 1.00 for the O3-H stretching mode, and 0.97 for all others.

(i) The D-galactosamine 4-sulfate moiety was first investigated in the isolated anionic form. The related optimized DFT/B3LYP/6-31G** geometry displays a chair conformation, and one can note the presence of a hydrogen-bond-like structure between the HO3 hydrogen atom and an oxygen atom of the SO₃ group. The amide hydrogen atom spreads toward this last atom with, however, no hydrogen bond setting up. Table 4 displays the current structural values obtained from DFT optimizations for this structure.

(ii) The second molecular model includes a Na⁺ counterion placed primitively as a bidentate structure in the OSO plane neighboring the O3 hydroxyl oxygen atom. The geometry optimization was performed via the DFT/B3LYP/6-31++G** method implying diffuse functions to take into account the particular electronic effects related to the anionic structure. After geometry optimization, the bidentate structure displays a mean Na⁺...O (SO₃) distance of 2.34 Å, while the sugar ring is still in a chair conformation. The carbonyl oxygen atom of the acetyl amide group lying at the C2 ring position undergoes one hydrogen bond with the hydroxyl hydrogen of the hydroxyl O3 group. Such a hydrogen bond changes the relative orientation of the C3O3H hydroxyl group (65.5°), which is to compare to the calculated DFT dihedral angle (-148°) when no internal hydrogen bond exists (Table 4). The DFT-optimized C2-N torsional parameter is predicted to take very different values when a Na⁺ counterion (and hydrogen bond) is present (-154°, -34°) or not (92°, -150°).

The sulfate group displays an approximate C_{3v} geometry, while the exocyclic hydroxyl groups display gauche conformations (at C1 and C3) and a gauche-trans conformation for the hydroxymethylene group as can be also noted in the isolated anionic form.

The potential energy distribution among internal coordinates and theoretical wavenumbers have both been deduced from DFT calculations using the force constant scaling method of Allouche et al.¹¹ A general scaling factor of 0.98 was used for the isolated anion, and a corresponding factor of 0.97 for the bidentate complex. Only a few scaling factors have to be modified to fit the experimental data (see footnotes in Table 5).

III.b.1. DFT-Derived Normal Modes Implying the Sulfate Group. Table 5 displays the DFT vibrational wavenumbers obtained at the B3LYP/6-31G** level for the isolated anionic form of this compound and the corresponding ones for the bidentate complex using diffuse functions and its associated counterion (B3LYP/6-31++G**).

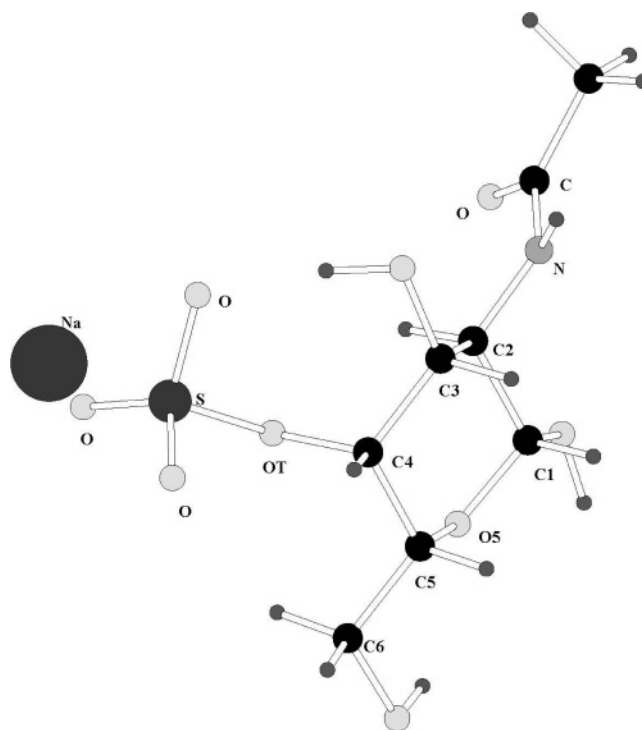


Figure 2. D-Galactosamine 4-sulfate sodium salt (ball-and-stick representation).

Matsuhiro³⁰ attributed a band observed at 1261 cm⁻¹ to a νS=O-type vibration, while Servaty reported two bands at 1226 and 1063 cm⁻¹ as originating from the ν_{as} antisymmetric stretching modes of the SO₃⁻ group.¹ From examination of the internal parameters obtained after geometry optimization (Table 4), one can observe that one of the S-O bonds is longer than the other two in the isolated anionic form of D-galactosamine 4-sulfate, as it undergoes formation of an internal hydrogen bond between the oxygen and the hydrogen O4 hydroxyl atom (Figure 2). We will assume here a practically regular tetrahedral conformation for the charged OSO₃⁻ moiety, as we obtained the two corresponding ν_{as} (SO₃) modes at 1233 and 1148 cm⁻¹ for the isolated anionic form and at 1247 and 1123 cm⁻¹ for the bidentate complex. Boggs et al.³¹ identified this mode to occur in the 1216–1223 cm⁻¹ range using FTIR measurements on sulfate cerebroside (CBS) and could observe only very small frequency changes upon Ca²⁺ complexation.

TABLE 6: Calculated Wavenumbers and Potential Energy Distribution of D-Galactosamine 4-Sulfate as Obtained from the Empirical SPASIBA Force Field^a

ν (cm ⁻¹)	assignments
36.3	0.60 τ C1O1 + 0.30 τ C3O3 + 0.10 τ C2N
38.3	0.74 τ OT-S + 0.15 τ C1O1 + 0.08 τ C3O3
46.4	1.0 τ C1O1
55.6	0.95 τ C1O1
67.5	0.96 τ C1O1
70.4	0.90 τ C1O1 + 0.06 τ C3O3
81.7	0.90 τ C-CT + 0.08 τ C1O1
82.0	0.73C1O1 + 0.15 τ C-CT + 0.12 τ CN
102.6	0.61 τ C5C6 + 0.32C1O1 + 0.06 τ C6O6
140.5	0.96 τ C3O3
158.7	0.55 τ C3O3 + 0.45 τ C6O6
164.3	0.98 τ C3O3
183.0	0.65 τ C3O3 + 0.15 τ C6O6 + 0.10 δ CTNC + 0.09 δ CTCTCT
195.4	0.70 τ C3O3 + 0.22 δ CT-OT-S + 0.08 δ OT-S-O
218.4	0.34 δ C3C4OT + 0.18 δ OT-S-O + 0.18 τ C1O5 + 0.17 ν C4OT + 0.13 ν OT-S
231.0	0.30 δ O5C5C4 + 0.21 δ OTC4C5 + 0.16 δ C1O5C5 + 0.11 δ OT-S-O + 0.11 ν C3C4 + 0.11 ν O5C5
243.6	0.37 τ C1O1 + 0.31 δ C1O1 + 0.23 δ O5C5C6 + 0.10 τ C6O6
252.7	0.23 δ OTC4C5 + 0.22 ν C2N + 0.15 δ C5C6O6 + 0.14 δ C3O3 + 0.14 ν NC + 0.12 δ O5C1C2
292.8	0.42 δ C1O1 + 0.20 δ C3O3 + 0.15 ν C4C5 + 0.12 ν C3C4 + 0.11 ν C1C2
296.8	0.60 τ CN + 0.14 δ CTN + 0.09 γ C=O + 0.09 δ C3O3 + 0.06 τ C3O3
348.7	0.26 δ C5C6O6 + 0.24 δ C1O1 + 0.15 δ C3O3 + 0.13 ν C4C5 + 0.10 δ CTN + 0.10 ν C3O3
381.0	0.37 δ (OT-S-O) + 0.20 δ CTCTO5 + 0.20 ν CTOT + 0.17 δ C=O + 0.05 ν OT-S
426.6	0.32 δ (OT-S-O) + 0.25 δ (O-S-O) + 0.15 ν C3O3 + 0.15 ν CTCT + 0.11 δ CTCTCT
450.0	0.36 δ (OT-S-O) + 0.20 δ C1O1 + 0.14 ν C1O1 + 0.10 δ CTCTCT + 0.09 ν C3O3 + 0.09 ν O5CT
480.0	0.43 δ (OT-S-O) + 0.18 δ (O-S-O) + 0.14 δ CTCTO5 + 0.12 ν C1O1 + 0.11 ν OT-S
500.1	0.39 δ (OT-S-O) + 0.14 δ CTO5CT + 0.14 ν C1O1 + 0.10 δ C3O3 + 0.08 ν C1O5 + 0.08 ν C5C6
513.2	0.53 δ (OT-S-O) + 0.22 δ (O-S-O) + 0.08 δ C=O + 0.08 ν C1O5 + 0.06 δ NCCT
524.9	0.82 δ (O-S-O) + 0.10 δ (OT-S-O) + 0.07 ν OT-S
541.7	0.76 δ (O-S-O) + 0.14 ν S-O + 0.05 δ (OT-S-O) δ a(SO3)
545.7	0.77 δ (O-S-O) + 0.14 ν S-O + 0.08 δ (OT-S-O) δ a(SO3)
561.9	0.26 δ C3O3 + 0.24 γ C=O + 0.24 δ C1O1 + 0.15 δ (O-S-O) + 0.11 δ (OT-S-O)
580.4	0.56 γ C=O + 0.39 τ NC
600.9	0.25 δ C1O5C5 + 0.17 ν C5C6 + 0.16 δ OTSOOS + 0.15 δ O5C1O1 + 0.13 δ O5C5C6 + 0.13 ν O5C5
623.5	0.48 δ C=O + 0.35 ν CCT + 0.08 ν NCT + 0.08 δ NH
664.7	0.46 δ CTCTOT + 0.18 δ C3O3 + 0.12 δ (OT-S-O) + 0.10 ν C6O6 + 0.07 δ C5C6O6 + 0.07 ν C3O3
704.5	0.32 τ NC + 0.17 ν C4OT + 0.13 γ NH + 0.09 δ CTCTCT + 0.07 ν OT-S + 0.07 δ O5C5C4 + 0.06 γ C=O
759.7	0.50 τ NC + 0.30 γ NH + 0.12 γ C=O
878.0	0.28 ν O5C5 + 0.25 ρ CH2 + 0.21 ν CTCT + 0.16 ν C1O1 + 0.09 ν CN
882.0	0.37 ν S-O + 0.23 ν OT-S + 0.18 ν C4OT + 0.10 ν CCT + 0.06 δ CT-OT-S + 0.04 ν NC
902.6	0.55 ν S-O + 0.19 ν OT-S + 0.11 ν CCT + 0.08 ν NC + 0.06 ν C=O ν s(SO3)
932.7	0.38 ν C4OT + 0.40 ν S-O + 0.11 ν NC + 0.10 ν C=O
944.0	0.82 ρ CH3 + 0.08 ν C=O + 0.05 ν NC + 0.04 ν CCT
963.9	0.48 ν C1C2 + 0.18 ν C1O1 + 0.13 ν C3O3 + 0.08 ν O5C1 + 0.07 ν C5C6 + 0.07 δ C1O1H
977.6	0.47 ρ CH3 + 0.35 γ C=O + 0.12 τ NC + 0.05 γ NH
984.4	0.30 ν C3O3 + 0.23 ν C4C5 + 0.22 ν C3C4 + 0.09 ν C1C2 + 0.09 ν C2C3 + 0.07 ν O5C5
1036.4	0.66 ν C6O6 + 0.09 ν C4C5 + 0.09 ν C3C4 + 0.06 ν C2C3 + 0.06 ν C1C2 + 0.05 ν C1O1
1039.9	0.30 ν C4OT + 0.23 ν C1C2 + 0.17 ν C1O1 + 0.11 ν C6O6 + 0.11 ν C2C3 + 0.08 ν O5C1
1065.3	0.28 ν C1O5 + 0.25 ν C2C3 + 0.20 ν C3C4 + 0.14 ν C4C5 + 0.06 ν C5O5 + 0.05 δ C3O3H
1069.7	0.28 ν O5C1 + 0.27 ν C6O6 + 0.17 ν C5C6 + 0.12 ν C4C5 + 0.08 ν C4OT + 0.08 ν OT-S
1091.0	0.41 ν OT-S + 0.22 ν S-O + 0.14 ν C3OH + 0.09 ν O5C5
1099.0	0.39 ν C3O3 + 0.31 ν OT-S + 0.08 ν C3C4 + 0.08 ν C4-OT + 0.10 ν S-O
1113.5	0.37 ν C1O1 + 0.35 ν O5C1 + 0.10 ν C4C5 + 0.07 ν C1C2 + 0.06 ν C5C6 + 0.06 ν C2N
1154.1	0.38 ν O5C5 + 0.16 ν C5C6 + 0.15 ν C4C5 + 0.14 ν C3OH + 0.09 δ C6O6H + 0.09 ν C4OT
1173.1	0.59 ν C2N + 0.14 δ C1O1H + 0.10 ν CCT + 0.08 ν NC + 0.05 ν C2C3 + 0.04 δ C2H
1210.8	0.42 δ C1O1H + 0.26 δ C6O6H + 0.20 δ C1H + 0.12 δ C1O5C5
1216.9	0.37 δ C6O6H + 0.19 ν C5C6 + 0.16 ν C1OH + 0.13 δ C1O5C5 + 0.09 ν C2N + 0.07 ν NC
1220.5	0.96 ν S-O + 0.02 δ O-S-O ν a(SO3)
1225.5	0.86 ν S-O + 0.07 δ C6O6H + 0.04 δ C1O1H ν a(SO3)
1226.9	0.62 δ C6O6H + 0.16 δ C5H + 0.10 ν O5C1 + 0.07 δ C1O5C5 + 0.06 δ C1O1H
1245.9	0.61 δ C3O3H + 0.16 δ C3H + 0.11 δ C1O1H + 0.07 δ C1H + 0.06 ν C3OH
1262.2	0.35 δ C1H + 0.29 ν CN + 0.17 ν C-CT + 0.0 δ C1O1H
1275.3	0.53 δ C3O3H + 0.34 δ C4H + 0.23 ν C3C4
1281.9	0.39 τ twiCH2 + 0.18 δ C6O6H + 0.16 δ C4H + 0.11 ν O5C1 + 0.11 δ C1O1H
1293.9	0.33 τ twiCH2 + 0.20 δ C1O1H + 0.20 δ C1H + 0.13 ν O5C1 + 0.12 ν C1O1
1296.2	0.86 τ twiCH2 + 0.07 δ C1O1H + 0.07 δ C2C1O5
1309.2	0.70 δ C2H + 0.19 δ C3O3H + 0.10 δ C4H
1323.8	0.45 δ sCH3 + 0.14 δ C1H + 0.10 ν C2N + 0.09 ν O5C1

TABLE 6: Continued

ν (cm ⁻¹)	assignments
1330.9	0.54 δ sCH3 + 0.15 ν NC + 0.11 ν C2N
1344.3	0.38 δ C1H + 0.25 δ C3H + 0.23 δ C3O3H + 0.12 δ C5H
1363.5	0.64 δ C3H + 0.14 ν C3O3 + 0.12 δ C4H + 0.09 ν C3C4
1379.7	0.38 δ C1H + 0.18 δ C3H + 0.18 δ C4H + 0.10 ν C1O1 + 0.07 ν C1C2 + 0.07 ν C2N
1396.7	0.31 ν O5C5 + 0.31 δ C4H + 0.17 δ C5H + 0.10 ν C1O1 + 0.10 δ C1O1
1424.3	0.37 δ C5H + 0.22 δ C4H + 0.19 δ aCH3 + 0.11 ν C1O1 + 0.08 ν wagCH2
1427.2	0.97 δ aCH3
1437.0	0.97 δ aCH3
1444.9	0.75 δ C2H + 0.11 δ NH + 0.10 δ CT-N + 0.04 ν C=O
1455.8	0.95 ν sciCH2
1541.1	0.45 δ NH + 0.22 ν CN + 0.16 ν C2N + 0.09 ν C=O
1648.8	0.80 ν CO + 0.10 δ NH + 0.07 ν CN
2873.1	1.0 ν sCH2
2903.4	1.0 ν aCH2
2914.6	1.0 ν sCH3
2970.2	1.00 ν C5H
2972.6	1.0 ν aCH3
2975.3	1.0 ν aCH3
2983.7	0.52 ν C2H + 0.25 ν C1H + 0.22 ν C3H
2990.8	0.98 ν C4H
2995.5	0.51 ν C3H + 0.47 ν C1H
3006.4	0.47 ν C2H + 0.27 ν C3H + 0.26 ν C1H
3445.1	1.00 ν NH
3681.1	1.0 ν O1H
3681.2	1.0 ν O6H
3688.8	1.0 ν O3H

^a ν : stretching. δ : in-plane bending. τ : torsion. γ : out-of-plane wagging. ρ : rocking. ν_s, ν_a : symmetric and antisymmetric stretching modes. δ_s, δ_a : symmetric and antisymmetric in-plane bending modes.

The ν C–O–S stretching modes of the sulfate groups have been identified by Grant et al.³² using IR studies on heparins to occur in the 750–950 cm⁻¹ range. According to these authors, the 890 and 937 cm⁻¹ bands have to be related to C–O–S and ring deformations. The present work predicts the occurrence of ν (S–O) stretching modes at 956 and 961 cm⁻¹ for the isolated anionic form and only one band at 952 cm⁻¹ for the bidentate complex. A strong contribution to the ν C4–OT vibrational mode is reported here at 869 cm⁻¹ for the bidentate complex, while a corresponding ν OT–S vibrational mode is obtained at 917 cm⁻¹ for the isolated anionic form.

In-plane bending deformations involving the sulfate group, δ (OT–S–O) and δ (O–S–O) vibrations are predicted to occur in two distinct regions (340–520 cm⁻¹) and (480–560 cm⁻¹) for both models of D-galactosamine 4-sulfate. The number of DFT-derived normal modes devoted to the bending deformations of the O–SO₃ group, however, does not correspond to the number expected for a C_{3v} symmetry when their numerous participations to the potential energy distribution (i.e., 622, 561, 520, 410, 393, 361, and 348 cm⁻¹ for the isolated anionic form and 552, 541, 510, 476, 374, 364, and 338 cm⁻¹ for the bidentate complex) are considered.

III.b.2. Hydroxyl Groups and Ring Modes. The hydroxymethylene group adopts a *gt* orientation in both calculations, while the C1 and C3 hydroxyl group have *gauche* (*g*, *g'*) orientations in the bidentate complex and approximately *gauche*–*trans* (*t*–*g*) conformations in the isolated anionic form, with this *trans* form being related to the presence of the hydrogen-bond-like structure involving the O3H hydroxyl group.

In the 1500–1200 cm⁻¹ range, most of the vibrational modes are due to the δ CH and δ CT–OH groups for both types of structures. This is in agreement with corresponding normal modes found for the D-glucuronic acid sodium salt. The 1200–1000 cm⁻¹ region reflects principally the internal ring ν CTCT, ν CT–O5, and exocyclic stretching modes for both the isolated anionic and bidentate conformations. The 1000–600 cm⁻¹ range

implies in both cases the participation of the hemiacetal moiety, involving particularly endocyclic stretching and bending modes.

III.b.3. Empirically Determined Vibrational Frequencies Using the SPASIBA Force Field. A few empirical force constants, particularly those devoted to the sulfate group, had to be adapted to fit the DFT-predicted wavenumbers. Table 6 displays the calculated wavenumbers and related assignments for D-galactosamine 4-sulfate. The SPASIBA-derived potential energy distribution gives coherent results for ring and exocyclic hydroxyl group motions when compared to the present DFT predictions or to previous empirical calculations on sugars. A RMSD of 36.3 cm⁻¹ is obtained here between the SPASIBA- and DFT-derived wavenumbers (as no experimental data are available) when using diffuse functions in the presence of the Na⁺ counterion. As for D-glucuronic acid sodium salt, the DFT calculations were performed using only one general scaling factor. Further work has to be done to obtain a complete set of DFT-derived scaling factors corresponding to each type of internal coordinates leading to a better empirical force field determination.

In the present work, the same set of parameters (as obtained for D-glucuronic acid sodium salt) related to the ring CT–CT, CT–O5 torsional librations was used. For the sulfate group, the torsional motions appear less well localized than they are from DFT predictions; however, the optimized torsional CT–OT parameter agrees fairly well with the DFT value when using diffuse functions.

Moreover, the largest deviations between wavenumbers would originate principally from normal modes involving the in-plane bending δ (OT–S–O) and δ (O–S–O) motions leading to an increase of the RMSD values obtained between the DFT and empirical methods. The OTSO₃ group stretching vibrations are predicted to occur in the 381–513 cm⁻¹ range (with contribution of δ (OT–S–O) vibrational motions) and in the 524–546 cm⁻¹ range for motions involving mainly the participation of the δ –(O–S–O) bending modes. Both regions remain, however, in

TABLE 7: SPASIBA Parameters Related to the Internal Coordinates of D-Glucuronic and D-Galactosamine 4-Sulfate Sodium Salts^a

bond	K (kcal mol ⁻¹ Å ⁻²)	R_0 (Å)
CT-CT	165.0	1.53
CT-HC	320.0	1.10
CT-C6	160.6	1.506
CT-C9	165.0	1.53
C9-HM	291.3	1.11
CT-O5	255.0	1.426
CT-OH	263.0	1.43
OH-HO	486.0	0.95
C-O(CO2 ⁻)	515.0	1.24
C-N	365.2	1.32
N-H	439.0	1.00
C=O	615.0	1.236
C-CT	160.65	1.506
S-O	550.0	1.465
OT-S	400.0	1.712

valence angle	H (kcal mol ⁻¹ rad ⁻²)	Θ_0 (deg)	F (kcal mol ⁻¹ Å ⁻²)
CT-CT-CT	18.70	111.8	47.47
CT-CT-OH	26.40	109.2	50.0
CT-O5-CT	85.0	112.8	70.0
CT-CT-O5	21.0	110.0	55.0
O5-CT-OH	28.45	108.0	41.0
O5-CT-HC	16.0	109.3	60.1
HC-CT-OH	15.0	107.2	80.0
CT-N-H	17.23	114.5	51.0
CT-N-C	26.25	119.0	40.28
C-N-H	25.15	119.5	66.18
N-C-CT	9.0	100.8	57.54
N-C=O	36.0	123.0	115.10
CT-C=O	14.0	123.6	35.0
CT-OH-HO	28.40	108.2	41.40
HC-CT-HC	29.6	108.5	10.07
OH-CT-HC	20.55	109.5	50.0
C-CT-HC	11.65	109.5	73.37
O-S-O	55.0	112.2	10.0
OT-S-O	50.0	104.0	10.0
CT-CT-HC	15.89	109.5	69.43
N-CT-HC	20.85	109.5	69.05

torsion	$Vn/2$ (kcal mol ⁻¹)	n	γ
X-CT-CT-X	0.15	3	0
X-CT-O5-X	0.20	3	0
X-CT-OT-X	0.01	3	0
X-CT-C-X	0.25	2	180
X-OT-SO-X	0.20	3	0
X-CT-N-X	0.015	3	0
X-CT-O5-X	0.2	3	0
X-C-N-X	8.65	2	180
X-CT-OH-X	0.05	-3	0
	0.02	-2	0
	0.70	1	0

improper	$Vn/2$ (kcal mol ⁻¹)	n	γ
CT-N-C=O	11.0	2	180
CT-N-C-H	1.85	2	180
O-CT-C-O	11.0	2	180

^a The specific Urey-Bradley-Shimanouchi force constants K , LCH_2 , and $trans-gauche$ used in this work originate directly from ref 13 and were not given here. R_0 : equilibrium distance. Θ_0 : equilibrium value of the valence angle bending. Vn : torsional barrier. n : order. γ : phase.

accordance with the DFT predictions, spreading over the 348–478 cm⁻¹ and 519–562 cm⁻¹ ranges for the isolated anionic form on one hand and the 338–374 cm⁻¹ and 476–552 cm⁻¹ ranges predicted for the sodium salt form on the other hand. The empirically derived stretching $\nu S-O$ modes show contributions at 882, 903, and 933 cm⁻¹ and at 1220 and 1225 cm⁻¹. These values have to be related to the 956, 960, 1148, and 1232

cm⁻¹ DFT values obtained for the isolated anionic form and to the 952, 1247, and 1249 cm⁻¹ values obtained in the presence of the sodium counterion using diffuse functions in the basis set.

The in-plane $\delta C=O$ and out-of-plane $\gamma C=O$ modes originating from the acetamide group have been predicted to occur in the 570–600 cm⁻¹ range by both DFT and empirical methods. The amide II vibration obtained from the SPASIBA force field at 1548 cm⁻¹ is in agreement with the DFT values (1510 and 1528 cm⁻¹). The amide I ($\nu C=O$) stretching mode is predicted at 1649 cm⁻¹ (SPASIBA) and at 1644 or 1648 cm⁻¹ (DFT). The out-of-plane bending vibration of the NH group (amide V) is in the present case badly defined by both DFT methods (760 cm⁻¹ for SPASIBA).

The final empirical set of SPASIBA parameters deduced from the vibrational analysis are displayed in Table 7 and would have to be considered as a starting database for further molecular dynamics studies.

As no experimental vibrational data could be obtained for D-galactosamine 4-sulfate, it appears difficult to compare theoretical methods between them in more expanded detail.

Conclusion

In the present work, empirical parameters were obtained from DFT calculations performed on the two constituents of chondroitin sulfate, i.e., D-glucuronic acid and D-galactosamine 4-sulfate. For D-glucuronate, it has been shown that a sodium counterion and basis sets with diffuse functions along DFT calculations are necessary to correctly fit the CO₂ group stretching vibrations to the experimental data. For D-galactosamine 4-sulfate, the use of diffuse functions and introduction of the counterion does not show such a marked effect. An empirical set of force constants has been obtained after comparison of DFT and experimental data when available, which will be used for further dynamical studies on copolymers of these two residues.

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Supporting Information Available: Two files containing data obtained with *Jaguar* 4.0 program. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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