Carbohydrate Research, 239 (1993) 51–60
Elsevier Science Publishers B.V., Amsterdam

Overlapping anomeric effects in a sucrose analogue

Alfred D. French [a], Lothar Schäfer [b] and Susan Q. Newton [b]

[a] *Southern Regional Research Center, U.S. Department of Agriculture, P.O. Box 19687, New Orleans, Louisiana 70179 (USA)*
[b] *Department of Chemistry, University of Arkansas, Fayetteville, Arkansas 72701 (USA)*

(Received May 4th, 1992; accepted July 30th, 1992)

ABSTRACT

Previous calculations with the molecular mechanics program MM3 gave unusually high energies (as much as 5.5 kcal/mol) for sucrosyl geometries found in single-crystal diffraction studies of oligosaccharides. Comparable MM3 energies for observed interresidue linkage conformations of disaccharides such as maltose and cellobiose are all within 2.8 kcal/mol. These results suggest that some energies calculated by MM3 for the linkage between anomeric centers of a pyranose ring and a furanose ring are too high. In the present paper, *ab initio* calculations at the 4-21G level and MM3 were used to study the conformational energies and geometry of a sucrose analogue, tetrahydro-2-[(tetrahydro-2-furanyl)oxy]-2*H*-pyran. The range of energies of the observed structures was substantially reduced (to 2.4 kcal/mol) with the 4-21G calculations for the analogue despite an increase for the analogue (to 7.5 kcal/mol) based on new MM3 calculations. Besides the improved energy values, the 4-21G calculations also reproduced the observed variations in the endocyclic C–O bond lengths better than did MM3.

INTRODUCTION

Recently, the conformations of all of the two-bond linked disaccharides of glucose were investigated with a thorough, relaxed-residue molecular mechanics treatment[1–3]. The α and β anomers of each disaccharide were treated separately, and as many as 24 combinations of side-group orientations were used in making starting models for each of these 15 different disaccharides. Each of the starting models was optimized with MM3[4,5]. For each increment of the interresidue torsional angles, the lowest energy obtained from the set of starting models was used to prepare an energy surface for each compound. Then, the conformations from available crystal structures were plotted on the energy maps. The energies corresponding to the observed geometries were all within 2.8 kcal/mol of the lowest calculated value. This was true even of the maltosyl linkages for which there are hundreds of examples with interresidue torsional angles ranging over 90°. Even

Correspondence to: Dr. A.D. French, Southern Regional Research Center, U.S. Department of Agriculture, P.O. Box 19687, New Orleans, Louisiana 70179, USA.

when there was little or no crystallographic data available, the calculated energy values were in reasonable agreement with other information such as ratios of the anomeric forms in solution. The worst apparent deficiency in those studies was overestimation (by as much as 0.05 Å) of the C-1–O-1 bond lengths on the reducing end of the disaccharides. Because that bond is not directly involved in the disaccharide linkage, the discrepancy was deemed unimportant for that work. One small discrepancy[2] was noted regarding the relative average energy of (1 ↔ 1) linked α,β-trehalose, a disaccharide of glucose having both anomeric centers joined through a common oxygen linkage.

A clearer sign of trouble regarding the molecular mechanics treatment of disaccharides arose during similar MM3 studies of the linkage between the glucopyranose and fructofuranose rings of the disaccharide sucrose[6,7]. That work found that the geometry of the sucrosyl linkage in the crystalline trisaccharide raffinose[8] (α-D-Gal*p*-(1 → 6)-α-D-Glc*p*-(1 ↔ 2)-β-D-Fru*f*) corresponds to a calculated energy of 5.5 kcal/mol. Corresponding energies for the planteose[9] and nystose[7] crystals were 4.0 and 3.5 kcal/mol.

Even though other available crystalline sucrosyl linkage geometries fell near the minimum in the MM3 energy, the overall distribution of the 12 available experimental geometries did not fit the predicted zone of low energy very well. Only four geometries were within the 1 kcal/mol contour. Inspection suggests that the position of the calculated minimum was in error. By subtracting 35° from the observed rotations about the C-2′–O-1 bond and 15° from the rotations about the C-1–O-1 bond, 11 of the 12 would fall within the 1 kcal/mol contour. Even though other workers' relaxed-residue results showed the sucrosyl geometry in raffinose to have an energy as high as 8 kcal/mol[10], it appears that the results for the sucrose linkage derived with MM3 may not be calculated as accurately as for the other disaccharides.

Using Lii and Allinger's CRSTL program[11], the intermolecular, or lattice, energy of crystalline glucose is −38 kcal/mol (unpublished data). Relative to a lattice energy per residue of this magnitude, a value of 5.5 kcal/mol for the geometry of the sucrosyl linkage in raffinose might not seem to be a serious discrepancy. However, it can be argued that the conformation of a molecule in the crystal must be likely in solution or the crystal might never nucleate and grow, despite eventual thermodynamic advantages to the crystalline form. In any case, a realistic understanding of the energies and geometric changes involved in crystallization from solution is central to the ability to study experimentally intractable problems with carbohydrates. Therefore, we decided to investigate further the apparent discrepancies associated with such linkings of anomeric centers.

Some of the phenomena that fall under the heading of anomeric effects[12] can be reproduced, at least in part, by simple molecular mechanics. However, the results with molecular mechanics can be improved by taking special account of the atomic sequence, C–O–C–O–C. The atoms affected by anomeric effects are recognized explicitly either by the modeler or automatically by the program and

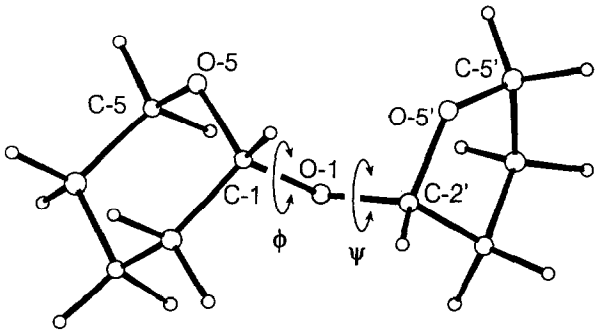

Fig. 1. The sucrose analogue used, with numbering corresponding to sucrose numbering. The unmarked large atoms are carbon, and the small unmarked atoms are hydrogen. The circular arrows indicate the bonds about which the pyranoid and furanoid rings were rotated.

additional parameterization is employed to reproduce results obtained by experiment or *ab initio* calculations[5,13–15]. Initial *ab initio* studies were necessarily confined to simple analogues, such as methane diol[16], but a few years ago anomeric effects were studied on the glucose analogue, 2-methoxytetrahydropyran, with 3-21G calculations[17]. (We note here that, while our tetrahydropyran–furan analogue (**I**) was named with "organic nomenclature", atom labeling will be consistent with atom names for sucrose using "carbohydrate nomenclature" as shown in Fig. 1.) Other *ab initio* work, on furanose rings, has been published by Serianni and Chipman[18]. In those studies, C–O and other bond lengths were predicted to depend on the torsional angle for the anomeric sequences. Also, preferred conformations place the hydroxymethyl group attached to the anomeric carbon gauche to the ring oxygen.

The predicted anomeric effects on torsional angles are relatively easy to detect experimentally. In another effect, the interior C–O bond lengths of the dimethoxymethane moiety are shortened relative to the external bonds. This is also often observed in crystal structures. Rohrer[9] mentioned that the difference between the O-5–C-5 and C-2–O-5 bond lengths of fructofuranose rings is greater than the corresponding difference for glucopyranose rings.

Because quantum mechanical studies are so time-consuming, it is usual practice to employ a smaller but otherwise analogous molecule. This practice seems to work well. In the MM3 work on the trehaloses, kojibiose, nigerose, maltose, sophorose, laminaribiose and cellobiose, the tetrahydropyran analogues were also studied[1–3]. The analogue maps had much in common with the disaccharide maps.

As far as we know, the present paper is the first use of quantum mechanics to attempt to unravel the mysteries of "overlapping" anomeric effects between a pyranoid ring and a furanoid ring. The same analogue (Fig. 1) was earlier studied by Du Bois et al., who proposed an ideal linkage conformation, after searching the Cambridge Crystallographic Data Base[19]. Our calculations, at the 4-21G level, are perhaps the largest practical for a molecule of this size. Work by Garrett and

Serianni[20,21] has shown that the 3-21G level is the first from which results suited for our purposes can be obtained.

METHODS OF CALCULATION

The *ab initio* calculations were performed with program BRABO[22] on an IBM RS/6000 workstation. The 4-21G basis set[23] was used. Five of the structures were optimized by constraining the torsional angle C-1–O-1–C-2′–O-5′ (Ψ) at 10, −10, −30, −50 and −70°, covering the range of values crystallographically observed in sucrosyl linkages for this parameter. A sixth structure was fully optimized without any constraint. For all unconstrained coordinates, the largest residual forces in the optimized geometries are < 0.0001 aJ/Å for bond stretches and < 0.0001 aJ/rad for angle bends, except for the model having $\Psi = -30°$. Its optimization was stopped at values of < 0.0003 aJ/Å and < 0.0003 aJ/rad. Each cycle of optimization required about one hour, and approximately 30 cycles were required to reach termination.

The five starting models for the structures to be optimized with the 4-21G method were first optimized with MM3[4,5], holding the O-5–C-1–O-1–C-2′ (Φ) torsional angle at 120°. The sixth model to be fully optimized by the 4-21G method corresponded to the structure at the MM3 minimum (shown in Fig. 2). The 4-21G model with Ψ of −70° optimized to give a Φ torsional angle of 129° (see Fig. 2), a model that gave the lowest calculated energy. However, that conformation was substantially different from the observed structures containing the sucrosyl moiety and may be an artifact of the use of an analogue rather than the entire sucrose molecule. In our comparisons of structure, therefore, we used instead the sixth structure, the one that resulted from freely optimizing the structure that had minimal MM3 energy. That structure had 0.5 kcal/mol higher energy than the 129, −70° structure but is surrounded by three of the 12 observed sucrose structures. The structure freely optimized with the 4-21G method had a linkage conformation very similar to the MM3 minimum-energy structure. The failure of the free optimization to find the lower-energy structure is probably due to an energy barrier between the two points.

After the 4-21G calculations, models having the same Φ and Ψ torsional angles were optimized with MM3 for comparisons of the energy, C–O bond lengths and puckering. The MM3 energy surface (Fig. 2) was generated with 20° increments of the two torsional angles.

MM3 calculations were done on a VAX computer with the standard January 1990 version of the program incorporating the corrections of April, 1991. Unlike the work on glucose disaccharides[1–3,6], the calculations herein used the standard −1 dihedral driver. That was feasible in this case because of the limited torsional range covered and the lack of rotating side groups. In all cases, the energy optimization routine was used, with the standard termination. Dielectric constants, to which MM3 is usually quite sensitive for carbohydrates[24], were either 1.5 (the

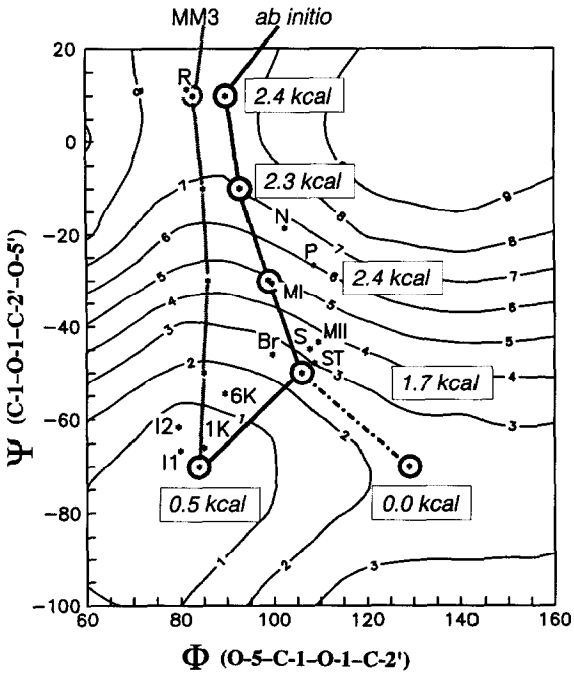

Fig. 2. The MM3 energy surface for the sucrose analogue shown in Fig. 1. The contours are at 1 kcal/mol, and the geometries observed in single crystals containing sucrosyl moieties are indicated by R (raffinose[8]), N (nystose[7]), P (planteose[9]), MI (melizitose I[29]), S (sucrose[30]), MII (melizitose II[31]), ST (stachyose[32]), Br (sucrose NaBr[33]), 6K (6-kestose[34]), 1K (1-kestose[35]), I1 (sucrose NaI-1[36]) and I2 (sucrose NaI-2[36]). The solid black line links the conformations optimized with the 4-21G calculations. Except for the conformation with $\Psi = -70°$, the 4-21G structures linked by the black line were optimized with the Ψ torsion angle held at values of 10, −10, −30 and −50°. All of those structures moved (left) to values of the Ψ torsion angle lower than the 120° starting value. The point at −70° was fully optimized, starting from a structure at the MM3 minimum. The −70° point at the end of the dashed line was held at −70° during optimization but has a Φ value of 129°. Although it had a lower 4-21G energy than the other −70° point, it was not used in the structure comparisons because it was distant from any observed structures (see text). The gray line connects points optimized in the same manner, but with MM3. The increment of rotation of the two torsion angles was 20°. If the contouring were perfect and the increment of rotation fine enough, the gray line would cross the contours at right angles.

default) for comparisons with *ab initio* results, or 4, for comparison with crystal structures. Because there are no hydroxyl groups in the analogue, there was little difference in the results for the two dielectric constants and only the results for a dielectric of 1.5 are presented.

Recently, RHF (restricted Hartree–Fock) energies and MP2 energies were calculated for some organic compounds containing C, H, O, and N (various conformations of glycine and *N*-formylalanine amide)[25,26]. They showed that simple double-zeta RHF energies (e.g., HF–4-21G) can agree better with both experimental results and MP2 calculations than RHF calculations that include

TABLE I

Energies for the 4-21G and MM3 models

Torsion angle O-5′–C-2′–O-1–C-1 (°)	Torsion angle C-2′–O-1–C-1–O-5 (°)	Relative energy (kcal/mol)	
		4-21G	MM3
10	90.3	2.4	7.7
−10	92.8	2.3	7.0
−30	99.6	2.4	4.9
−50	106.2	1.7	2.5
−70	129.3	0.0	2.2
−69.2 (optimized)	84.2	0.5	0.0

polarization functions. In the investigated cases[25,26] the errors in the HF–4-21G calculated energies were about 1 kcal/mol.

Comparisons of HF–4-21G and MP2–6-31G** structures show[25,26] that the former contain the essential structural trends found in organic molecules, in agreement with the latter. That is, relative structural parameters, such as differences among C–O bond lengths and C–C–O angles for different conformers are determined rather accurately by RHF calculations. This claim is corroborated by an extensive comparison RHF geometries of organic compounds, obtained at various levels, with experimental gas-phase structures[27] and by the quantitative utility of 4-21G parameters found in many earlier experimental studies[28]. Thus the 4-21G calculations establish structural trends that are often more accurate than corresponding trends from experimental work such as X-ray crystallography.

RESULTS AND DISCUSSION

The MM3 energy surface for **I** is shown in Fig. 2. On this surface are plotted the observed crystal structure conformations of sucrose and related oligomers. Also plotted are the points derived by the 4-21G studies. Table I contains the results of the 4-21G and MM3 determinations of energy and Table II gives the bond lengths of the overlapped anomeric sequence C-5–O-5–C-1–O-1–C-2′–O-5′–C-5′.

The relative MM3 energy values on this surface for the analogue are similar to those obtained in the MM3 study of sucrose, but the values for the analogue increase at a higher rate moving away from the minimum-energy conformation. The range of MM3 energy values plotted beneath the observed structures is more than 7 kcal/mol, corresponding to a range of 5.5 kcal/mol on the MM3 sucrose map. On the other hand, the *ab initio* energies span only 1.9 kcal (or 2.4 kcal/mol if the 129, −70° point is included). This much smaller range of energy values is closer to what we expected for crystalline conformations, and it confirms our suspicions of possible error in the MM3 calculations.

TABLE II

C–O Bond lengths or the 4-21G and MM3 models

Torsion angle (°) Φ O-5′-C-2′-O-1-C-1 Ψ	Torsion angle (°) Ψ C-2′-O-1-C-1-O-5 Φ	Method	Bond lengths (Å)					
			C-5	O-5	C-1	O-1	C-2′	O-5′	C-5′
10	90.3	4-21G	1.457	1.436	1.431	1.444	1.430	1.471	
		MM3	1.422	1.421	1.417	1.430	1.417	1.432	
−10	92.8	4-21G	1.456	1.435	1.433	1.446	1.425	1.473	
		MM3	1.422	1.422	1.417	1.431	1.415	1.434	
−30	99.6	4-21G	1.456	1.432	1.437	1.441	1.423	1.471	
		MM3	1.422	1.422	1.418	1.427	1.417	1.435	
−50	106.2	4-21G	1.456	1.429	1.439	1.435	1.423	1467	
		MM3	1.421	1.421	1.419	1.422	1.422	1.435	
−70	129.3	4-21G	1.456	1.423	1.444	1.430	1.426	1.466	
		MM3	1.422	1.416	1.423	1.418	1.426	1.434	
−69.2 (optimized)	84.2	4-21G	1.454	1.424	1.435	1.431	1.425	1.465	
−70	82.2	MM3	1.422	1.416	1.423	1.418	1.426	1.434	
Experimental average			1.441	1.420	1.413	1.431	1.418	1.455	
4-21G Average (corrected by 0.99142)			1.443	1.419	1.422	1.427	1.413	1.455	
MM3 Average			1.422	1.422	1.418	1.426	1.419	1.434	
Neutron diffraction of sucrose			1.439	1.411	1.422	1.429	1.408	1.445	
High-accuracy X-ray diffraction of sucrose			1.443	1.413	1.428	1.433	1.408	1.449	
HF4-21G (corrected by 0.99142) (at −50, 106)			1.444	1.417	1.427	1.423	1.411	1.454	
MM3 (at −5-, 106)			1.421	1.421	1.419	1.422	1.422	1.435	

TABLE III

Cremer–Pople ring puckering parameters for the 4-21G and MM3 models

Torsion angle (°) O-5′–C-2′–O-1–C-1 Ψ	Torsion angle (°) C-2′–O-1–C-1–O-5 Φ	Modeling method	Furanose		Pyranose		
			q	ϕ	q	ϕ [a]	θ
10	90.3	4-21G	0.361	262.7	0.566	198.4	2.46
		MM3	0.357	273.1	0.558	289.5	1.76
−10	92.8	4-21G	0.354	243.5	0.564	207.0	3.13
		MM3	0.369	260.0	0.557	278.6	2.24
−30	99.6	4-21G	0.364	231.9	0.567	202.8	2.33
		MM3	0.380	253.3	0.557	283.3	2.02
−50	106.2	4-21G	0.383	224.9	0.567	193.6	1.85
		MM3	0.383	251.3	0.557	289.3	1.92
−70	129.3	4-21G	0.386	237.1	0.571	164.0	0.87
		MM3	0.383	254.0	0.555	278.9	2.08
−69.2 (optimized)	84.2	4-21G	0.380	246.8	0.569	173.6	1.04
		MM3	0.386	257.1	0.561	310.8	1.88

[a] When θ is close to 0 or 180°, values of ϕ do not indicate different structures.

Table II also presents averages of the experimental anomeric bond lengths, taken from the crystal structures listed in Fig. 2. Because the experimental bond lengths occur over a range of conformations similar to the *ab initio* values, they are reasonably suitable for comparison with the calculated values. As noted previously, there are orientational dependencies of the C-1–O-1 and O-1–C-2′ (and other) bond lengths for the calculated values. Because the size of these variations is similar to the uncertainties in the experimental values, no comparison is offered here. Only the larger variations are discussed below. Besides the average values in Table II, bond lengths from the neutron diffraction[30] and especially accurate X-ray diffraction[37] determinations of sucrose are given and compared with the nearest calculated point. In the latter comparisons, the *ab initio* values are scaled as described below.

Typically, the relative values of bond lengths from adequate-basis set *ab initio* studies are better than the absolute values. The present calculated values seem to be uniformly large, and a scaling factor of 0.99142 was derived by the ratio of the sum of all six of the averaged experimental bond lengths to the sum of the six averaged 4-21G lengths. The scaled, averaged 4-21G bond lengths are also given in Table II. The scaling brings the 4-21G values and the experimental values to a standard deviation of 0.005 Å. The MM3 values do not profit from a similar scaling; their standard deviation with the experimental values is 0.010 Å.

The MM3 C-5–O-5 and C-5′–O-5′ bond lengths are less than the experimental values by nearly 0.02 Å. The ring-bond disproportionations are predicted much better with the *ab initio* calculations. The average experimental bond length

difference ($d_{C\text{-}5\text{-}O\text{-}5} - d_{O\text{-}5\text{-}C\text{-}1}$) for the pyranose ring is 0.021 Å, with a 4-21G value of 0.024 Å. For the furanose ring, the mean experimental disproportionation ($d_{C\text{-}5'\text{-}O\text{-}5'} - d_{O\text{-}5'\text{-}C\text{-}2'}$) is 0.038 Å, while the 4-21G value is 0.043 Å. The corresponding MM3 values are 0.0002 and 0.0146 Å.

Table III gives the puckering parameters[38] for both the pyranose and furanose rings. Both methods predict structures of **I** that are very similar to the observed values[7,39]. This was not expected, because the side groups (missing in the present work) are thought to be a major influence on puckering energies for furanose rings[20,40,41]. Also, by analogy with cyclopentane, almost facile pseudorotation among the various furanose forms might be expected for the tetrahydrofuran residue because of the lack of any side groups (except for O-1 and the tetrahydropyran residue).

Based on the above results concerning both energy and bond lengths, it seems that the overlapping anomeric effects in sucrose and the sucrose analogue have to a certain extent defeated the anomeric effects mechanisms built into MM3. Acceptance of the 4-21G results as more realistic suggests that the anomeric compensation in MM3 can be improved, given a more thorough study of this particular sucrose analogue. That work is underway. However, Allinger et al.[42] recently reported that the estimation of heats of formation with 6-31G* quantum mechanical calculations is somewhat less reliable (SD 0.78 kcal/mol) for compounds with anomeric sequences than for alcohols and ethers not having such sequences (SD 0.52 kcal/mol).

REFERENCES

1 M.K. Dowd, A.D. French, and P.J. Reilly, *J. Comput. Chem.*, 13 (1992) 102–114.
2 M.K. Dowd, J. Zeng, A.D. French, and P.J. Reilly, *Carbohydr. Res.*, 230 (1992) 223–244.
3 M.K. Dowd, A.D. French, and P.J. Reilly, *Carbohydr. Res.*, 233 (1992) 15–34.
4 N.L. Allinger, Y.H. Yuh, and J.-H. Lii, *J. Am. Chem. Soc.*, 111 (1989) 8551–8566.
5 N.L. Allinger, M. Rahman, and J.-H. Lii, *J. Am. Chem. Soc.*, 112 (1990) 8293–8307.
6 S. Pérez, C. Meyer, A. Imberty, and A.D. French, in G. Birch and M. Mathlouthi (Eds.), *Sweet Taste Chemoreception*, Elsevier, Amsterdam, in press.
7 A.D. French, N. Mohous-Riou, and S. Pérez, unpublished results.
8 G.A. Jeffrey and D.-B. Huang, *Carbohydr. Res.*, 206 (1990) 173–182.
9 D.C. Rohrer, *Acta Crystallogr., Sect. B*, 28 (1972) 425–433.
10 V.H. Tran and J. Brady, *Biopolymers*, 29 (1990) 961–976.
11 J.-H. Lii and N.L. Allinger, *J. Am. Chem. Soc.*, 111 (1989) 8576–8582.
12 I. Tvaroska and T. Bleha, *Adv. Carbohydr. Chem. Biochem.*, 47 (1989) 45–123.
13 G.A. Jeffrey and R. Taylor, *J. Comp. Chem.*, 1 (1980) 99–109.
14 L. Norskov-Lauritsen and N.L. Allinger, *J. Comp. Chem.*, 5 (1984) 326–335.
15 S.W. Homans, *Biochemistry*, 29 (1990) 9110–9118.
16 G.A. Jeffrey, J.A. Pople, and L. Radom, *Carbohydr. Res.*, 25 (1972) 117–131.
17 K.B. Wiberg and M.A. Murcko, *J. Am. Chem. Soc.*, 111 (1989) 4821–4828.
18 A.S. Serianni and D.M. Chipman, *J. Am. Chem. Soc.*, 109 (1987) 5297–5303.
19 J.E. Du Bois, A. Cossé-Barbi, and D.G. Watson, *Tetrahedron Lett.*, 30 (1989) 167–170.
20 E.C. Garrett and A.S. Serianni, *ACS Symp. Ser.*, 430 (1990) 90–119.
21 E.C. Garrett and A.S. Serianni, *Carbohydr. Res.*, 206 (1990) 183–191.
22 C. Van Alsenoy, *J. Comput. Chem.*, 9 (1988) 620–626.

23 P. Pulay, G. Fogarasi, F. Pang, and J.E. Boggs, *J. Am. Chem. Soc.*, 101 (1979) 2550.
24 A.D. French and M.K. Dowd, *Proceedings of Cellulose '91*, Elllis Horwood, London, 1992, in press.
25 R.F. Frey, J. Coffin, S.Q. Newton, M. Ramek, V.K.W. Cheng, F.A. Momany, and L. Schäfer, *J. Am. Chem. Soc.*, 114 (1992) 5369–5377.
26 M. Ramek, V.K.W. Cheng, R.F. Frey, S.Q. Newton, and L. Schäfer, *J. Mol. Struct.*, 235 (1991) 1–10.
27 J. De Smedt, F. Vanhouteghem, C. Van Alsenoy, H.J. Geise, and L. Schäfer, *J. Mol. Struct.*, (1992) in press.
28 L. Schäfer, *J. Mol. Struct.*, 230 (1991) 5–11.
29 D. Avenel, A. Neuman, and H. Gillier-Pandraud, *Acta Crystallogr., Sect. B*, 32 (1976) 2598–2605.
30 G.M. Brown and H.A. Levy, *Acta Crystallogr., Sect. B*, 29 (1973) 790–797.
31 J. Becquart, A. Neuman, and H. Gillier-Pandraud, *Carbohydr. Res.*, 111 (1982) 9–21.
32 G.A. Jeffrey and D.-B. Huang, *Carbohydr. Res.*, 210 (1991) 89–104.
33 C.A. Accorsi, F. Bellucci, B. Bertolasi, B. Ferretti, and G. Gilli, *Carbohydr. Res.*, 191 (1989) 105–116.
34 V. Ferretti, V. Bertolasi, and G. Gilli, *Acta Crystallogr., Sect C*, 40 (1984) 531–535.
35 G.A. Jeffrey and Y.J. Park, *Acta Crystallogr. Sect B*, 28 (1972) 257–267.
36 C.A. Accorsi, V. Bertolasi, B. Ferretti, and G. Gilli, *Carbohydr. Res.*, 191 (1989) 91–104.
37 J.C. Hanson, S.C. Sieker, and L.H. Jensen, *Acta Crystallogr., Sect. B*, 29 (1973) 797–808.
38 D. Cremer and J.A. Pople, *J. Am. Chem. Soc.*, 97 (1976) 1354–1358.
39 A.D. French, R.S. Rowland, and N.L. Allinger, *ACS Symp. Ser.* 430 (1990) 120–140.
40 B. Lesyng and W. Saenger, *Carbohydr. Res.*, 133 (1984) 187–197.
41 A.D. French and V. Tran, *Biopolymers*, 27 (1990) 1599–1611.
42 N.L. Allinger, L.R. Schmitz, I. Motoc, C. Bender, and J.K. Labanowski, *J. Am. Chem. Soc.*, 114 (1992) 2880–2883.