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Crystal Structures of Methyl (Methyl 3-azido-2,3-dideoxy- β -L-*lyxo*- and - β -D-*arabino*-hexopyranosid)uronates

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Crystal Structures of Methyl (Methyl 3-azido-2,3-dideoxy- β -L-*lyxo*- and - β -D-arabino-hexopyranosid)uronates

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Single-crystal x-ray diffraction data for methyl (methyl 3-azido-2,3-dideoxy- β -L-lyxoand β -D-arabino-hexopyranosid)uronates are presented. Three independent molecules in the asymmetric part of the unit cell of the β -D-arabino stereoisomer were found. These differ slightly in the geometry of the groups bound to the pyranose rings. Conformations and the geometry parameters of all the molecules as well as the planarity of the carbomethoxy group, the linearity of the azido group, and the orientation of the aglycone in the crystal lattice are discussed. Influence of the hybridization, resonance, and crystal packing on the geometry parameters is shown.

Keywords Sugar amino acid; Geometry parameters; Conformation; Hybridization; Resonance; *Exo*-anomeric effect.

INTRODUCTION

Sugar amino acids (SAAs) are carbohydrates bearing both an amino group and a carboxyl group. Syntheses and applications of SAAs have recently been widely reviewed.^[1-5] Applications of SAAs, especially as the polyfunctional scaffolds or isosters, requires the sugar ring to be rigid with a well-defined spatial orientation. X-ray crystallography is still the best method for characterizing the atomic structure of new compounds. It provides geometric parameters needed for visualization of a conformational space of the molecule. An agreement of the crystallographic and NMR data allows a conclusion on the geometry of sugar ring in a solution to be made.^[6,7]

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Previously we reported on the synthesis of methyl 3-amino-2,3-dideoxyhexopyranosiduronic acids, new sugar amino acids, and their diglycotides.^[8] It began with the addition of hydrazoic acid to the α,β -unsaturated aldehyde derived from methyl 3,4-di-O-acetyl-2,6-anhydro-5-deoxy-D-lyxo-hex-5enopyranonate (commercial name-methyl 3,4-di-O-acetyl-D-glucuronal) (1) followed by methyl glycosylation. The methyl (methyl 4-O-acetyl-3-azido-2,3-dideoxy- α/β -D-arabino- and $-\alpha/\beta$ -D-ribo-hexopyranosid)uronates (2–5) obtained were then O-deacetylated to yield the corresponding methyl (methyl 3azido-2,3-dideoxyhexopyranosid)uronates (6-11). As reported, under the basic conditions of the O-deacetylation reaction, small amounts of the D-ribo substrates (3 and 4) altered their configuration at the C-5 carbon atom (α relative to the 5-carbomethoxy group). In this way the unexpected products 8 and 10 were obtained. Specifically, it was only the D-ribo compounds that epimerized in the basic environment of the reaction; the configuration of the D-arabino compounds remained unchanged. This happened because the D-ribo structures are conformationally less stable (${}^{4}C_{1} = {}^{1}C_{4}$ conformational equilibrium) than the D-arabino structures (${}^{4}C_{1}$ form). C-5 epimerization of **3** and **4** provided the conformationally stable products 8 and 10 (${}^{1}C_{4}$ form). Possible C-5 epimerization of 2 and 5 did not occur because this would have led from the conformationally stable D-arabino structure to the conformationally unstable L-xylo^[9,10] structure. This is an example of how conformation may influence the chemical properties of sugars.



a: 1. HgSO₄, H₂SO₄, H₂O, dioxane; 2. NaN₃, CH₃COOH; 3. MsCl, MeOH, s-collidine; b: MeONa / MeOH

The structure of *O*-deacetylation products **6–11** were established by NMR spectroscopy.^[8] This paper reports on single-crystal x-ray diffraction data for methyl (methyl 3-azido-2,3-dideoxy- β -L-*lyxo*- (**10**) and β -D-*arabino*hexopyranosid)uronates (**11**), which were recently obtained in their crystal forms. Presented data complete the discussion on the configuration and conformation of the previously reported sugar amino acids. These also demonstrate how hybridization, resonance, and crystal packing affect the geometry parameters of presented molecules. The application of SAAs as polyfunctional scaffolds or isosters requires the pyranose ring to be rigid with a well-defined spatial orientation. The presentation of the crystal structures of **10** and **11** provides concrete geometric parameters, which are useful in the study of the SAA geometry.

RESULTS AND DISCUSSION

The Crystal Structure of 10

The crystal structure of **10** undoubtedly corroborates our earlier statements that this compound is the β -L-*lyxo* stereoisomer of methyl (methyl 3azido-2,3-dideoxyhexopyranosid)uronate. In the crystal **10** adopts the ${}^{1}C_{4}$ conformation^[11,12] (Fig. 1) with ring puckering parameters^[13,14] Q = 0.563(3) Å, $\theta = 175.2(3)^{\circ}$, and $\varphi = 176(4)^{\circ}$. This conformation is the same as established for **10** in methanol solution on the basis of NMR data.^[8] This finding also confirms the geometry of the 3-amino analog of **10** (**10a**), which was previously established on the basis of NMR data only.^[8] Recorded for **10** and **10a**, $J_{H,H}$ coupling constants are indicative for the same configuration and conformation of 3-azido and 3-amino analogs (Table 1).

X-ray analysis of **10** revealed that the 5-COOCH₃ group is almost planar in the region of the C5, C10, O3, O4, and C11 atoms (Fig. 1). This is demonstrated by the C5-C10-O3-C11 torsion angle of 178.1° as well as the O4-C10-O3-C11 torsion angle of -1.4° (Table 4). This planarity is due to the resonance that causes the O3 oxygen lone pair of electrons to delocalize onto the O4 carbonyl oxygen atom. Such delocalization stabilizes the compound and increases the O3-C10 rotational barrier. On the other hand, this resonance requires the O3



Figure 1: Structure of 10 showing 25% probability displacements for ellipsoids. The hydrogen atoms are shown as small spheres of arbitrary radius.

Table 1: The ¹H-¹H coupling constants (Hz) for 10, 10a, 11, 11a, and 11b

| Comp. | Structure | $J_{1,2a}$ | $J_{1,2e}$ | $J_{2a,2e}$ | $J_{2a,3}$ | $J_{2e,3}$ | $J_{3,4}$ | J _{4,5} |
|--|---|---------------------|---------------------|------------------------|------------------------|---------------------|----------------------------|---------------------|
| R'OOC O OMe HO | | | | | | | | |
| 10 ^{a.c.e} 10a ^{a.d} HO | β -L-lyxo $R = N_3, R' = Me$ $R = NH_2, R' = Me$ COOR' O | 6.84 9.6 Me | 2.0 | 12.8 | 8.79 12.4 | 4.4 | 2.93 3.2 | < 1 1.2 |
| 11ª,c 11 a ª,c 11 b ^{b,d} | β -D-arabino $R = N_3, R' = Me$ $R = NH_2, R' = Me$ $R = NH_2, R' = H$ | 9.28 9.28 9.2 | 1.95 1.96 2.0 | 12.70 12.70 12.4 | 12.21 12.21 12.4 | 4.40 4.40 4.8 | n.d. 9.77 9.6 | 9.28 9.27 9.6 |

n.d., not determined. ^aCD₃OD. ^bD₂O. ^c500 MHz. ^d400 MHz. ^eThe H-2 protons are chemically and magnetically equivalent.

oxygen atom to be sp² hybridized. Indeed, the C10-O3-C11 valence angle of 115.3° (Table 4) is suited to a hybridization intermediate between sp² and sp³.

The carbonyl O4 oxygen atom in the crystal lattice of **10** is oriented opposite to the O5 ring oxygen atom with the O5-C5-C10-O4 torsion angle of 175.4° (Table 4). Such an orientation is in agreement with findings, according to which repulsion of the carbonyl oxygen and ring oxygen lone pairs of electrons strongly determine the rotational preferences of the carboxyl group in the glucuronic acid.^[15]

As required by the respective resonance structures, the azido group is almost linear with the C3-N7-N8-N9 torsion angle of 159° and the N7-N8-N9 valence angle of 172.7° (Table 4). These data are indicative of the sp hybridization of the N8 nitrogen atom. The hybridization of the N7 nitrogen atom seems to be between sp³ and sp², which is manifested by the C3-N7-N8 valence angle of 115.4° (Table 4).

The nearly antiperiplanar orientation of the methyl C6 carbon atom to the C2 carbon atom, resulting from the rotation around the C1-O1 bond, with the C2-C1-O1-C6 torsion angle of -173.9° (Table 4) is typical of glycosides and is due to the *exo*-anomeric effect.

Both C–H \cdots O close contacts and O–H \cdots O intermolecular hydrogen bonds are observed in the crystal structure of **10** (Table 5).

The Crystal Structure of 11

X-ray analysis shows that there are three independent molecules in the asymmetric part of the unit cell of the methyl (methyl 3-azido-2,3-dideoxy- β -D-arabino-hexopyranosid)uronate (11). All these molecules adopt the ${}^{4}C_{1}$ conformation^[11, 12] (Fig. 2) with ring puckering parameters^[13,14] Q = 0.572(3) Å, $\theta = 5.1(3)^{\circ}$, and $\varphi = 335(3)^{\circ}$ for ring A; Q = 0.587(3) Å, $\theta = 4.6(3)^{\circ}$, and $\varphi = 1(4)^{\circ}$ for ring B; and Q = 0.583(3) Å, $\theta = 3.9(3)^{\circ}$, and $\varphi = 14(4)^{\circ}$ for ring C. This conformation is the same as established for 11 in methanol solution on the basis of NMR spectra.^[8] This finding also confirms the geometry of the 3-amino analog of 11 (11a) and geometry of SAA 11b, which were previously established on the basis of NMR data only.^[8] Recorded for 11, 11a, and 11b, $J_{H,H}$ coupling constants are indicative for the same configuration and conformation of all these analogs (Table 1).

Although there are three molecules in the asymmetric part of the unit cell of **11**, the geometry of these molecules does not differ substantially. In particular, the geometry parameters of the pyranose rings are almost the same in these three molecules (Fig. 3). Small differences are found in the geometry of the groups bound to the pyranose rings. As far as the respective bond lengths—hard geometry parameters—are concerned, the biggest difference is found for the C3-N7 bond lengths, which range from 1.468 Å to 1.493 Å (Table 4). The difference of 0.025 Å is small enough for all measured C3-N7



Figure 2: Structures of three molecules of 11 showing 25% probability displacements for ellipsoids. The hydrogen atoms have been omitted for clarity.

bond lengths to be classified as single bonds. The three molecules of **11** likewise do not differ significantly in their valence angles. The largest difference is found for the C4-C5-C10 valence angles, which range from 110.0° to 112.1° . Such a difference is small and yet still indicative of the sp³ hybridization of the C5 carbon atom. The biggest differences in the geometry of the three molecules of **11** refer to the torsion angle, the softest geometry parameter. However, these differences are still small and they do not disturb the ${}^{4}C_{1}$ conformation of the rigid pyranose ring, because they refer not to the pyranose ring but to the ring substituents (Fig. 3).

The 5-COOCH₃ group in all molecules of **11** is planar in the region of the C5, C10, O3, O4, and C11 atoms, as is the 5-COOCH₃ group in **10**. This is



Figure 3: Overlapping of the A (black), B (gray), and C (light gray) molecules of 11.

demonstrated by the C5-C10-O3-C11 torsion angles of -177.3° , -179.0° , and -175.6° in molecules A, B, and C, respectively, as well as the O4-C10-O3-C11 torsion angles of 2.1° , 0.0° , and 3.3° in molecules A, B, and C, respectively (Table 4). This planar group rotates around the C5-C10 bond, and the torsion angles related to this rotation seem to be relatively flexible. They differ by 6.6° (the C4-C5-C10-O3 torsion angle), 6.7° (the C4-C5-C10-O4 and O5-C5-C10-O3 torsion angles), and 6.8° (the O5-C5-C10-O4 torsion angle). Typically, the azido group is linear with C3-N7-N8-N9 torsion angles of 171° , 176° , and 179° in molecules A, B, and C, respectively, and with N7-N8-N9 valence angles of 173.6°, 172.2°, and 173.0° in molecules A, B, and C, respectively. These data are indicative of the sp hybridization of the N8 nitrogen atom, as in the case of **10**. The hybridization of the N7 nitrogen atom seems to be between sp³ and sp^2 , which is manifested by the C3-N7-N8 valence angles of 115.6° , 115.6° , and 115.1° in molecules A, B, and C, respectively, and which is in agreement with the resonance structures of the azido group. Rotation around the C3-N7 bond also slightly differentiates the geometries of the molecules in **11**. The C4-C3-N7-N8 torsion angles of molecules A, B, and C differ by 4.5° . With regard to the aglycone, it is clear that the rotation around the C1-O1 bond also contributes to the geometric diversity of **11**. The measured difference in the C2-C1-O1-C6 torsion angles of molecules A, B, and C is 6.6°, whereas in the O5-C1-O1-C6 torsion angles it is 5.8°.

The observed differences in the geometries of the three molecules of 11 emerge from the properties of the crystal lattice of 11. There is only one molecule in the asymmetric part of the unit cell of 10, which is a stereoisomer of 11, and in the 4-O-acetyl derivative of 11.^[16] It is probably the advantageous crystal packing that gives rise to the slight changes in the geometry of 11, which results in three molecules being in the asymmetric part of the unit cell.

In contrast to compound **10**, the carbonyl O4 oxygen atom in all molecules of **11** is not oriented opposite to the O5 ring oxygen atom—this is demonstrated by the O5-C5-C10-O4 torsion angles of -40.6° , -39.3° , and -46.1° in molecules A, B, and C, respectively (Table 4). In **11**, the O3 oxygen atom seems to be repulsed more strongly than the O4 oxygen atom by the O5 ring oxygen atom, because the respective O5-C5-C10-O3 torsion angles are 140.0° , 141.7° , and 135.0° in molecules A, B, and C. These results may indicate that the considerable repulsion between the carbonyl O4 oxygen atom and the ring O5 oxygen atom lone pairs is not as significant as theoretical calculations suggest.^[15]

Typically, the methyl C6 carbon atom in all the molecules of **11** is oriented nearly antiperiplanarly to the C2 carbon with the C2-C1-O1-C6 torsion angles of 159.1° , 165.7° , and 162.7° in molecules A, B, and C, respectively (Table 4); this is due to the *exo*-anomeric effect.

Both C-H \cdots O close contacts and O-H \cdots O intermolecular hydrogen bonds are present in the crystal structure of **11** (Table 6).

| Table 2: | Crystal | data | and | structure | refinem | ent for | 10 | and | 11 |
|----------|---------|------|-----|-----------|---------|---------|----|-----|----|
| | | | | | | | | | |

| | 10 | 11 |
|--|---|--|
| Empirical formula Formula weight Temperature (K) Wavelength (Å) Crystal system Space group Unit cell dimensions | $C_8H_{13}N_3O_5$ 231.21 295(2) 0.71073 Orthorhombic $P2_12_12_1$ | $C_8H_{13}N_3O_5$ 231.21 295(2) 0.71073 Monoclinic $P2_1$ |
| a (Å) b (Å) c (Å) α (°) β (°) γ (°) V (Å ³) Z D _{calcd} (mg/m ⁻³) Absorption | 4.5430(6) 12.5027(18) 19.764(4) 90 90 90 1122.6(3) 4 1.368 0.115 | 11.0505(10) 12.7980(8) 12.7647(10) 90 106.948(9) 90 1726.8(2) 6 1.334 0.112 |
| coefficient (mm ⁻¹) F(000) Crystal size (mm) Θ Range for data | 488 0.35 × 0.25 × 0.12 3.26–24.98 | 732 0.30 × 0.15 × 0.10 3.18–25.00 |
| Collection (*) Limiting indices Reflections collected/unique Completeness 20 = | $\begin{array}{l} -5 \leq h \leq 5, -14 \leq k \leq \\ 14, -3 \leq l \leq 23 \\ 21854/1193 \ (R_{int} = \\ 0.1412) \\ 99.7 \end{array}$ | $-13 \le h \le 11, -15 \le k$ $\le 14, -15 \le l \le 15$ $12891/3162 (R_{int} = 0.0464)$ 99.2 |
| 50.00° (%) Refinement method Data/restraints/parameters Goodness of fit on F^2 Final R indices ($l > 2\sigma(l)$) | Full-matrix least-squares on F^2 1193/0/162 0.771 $R_1 = 0.0369$ | Full-matrix least-squares on F^2 3162/1/462 0.806 $R_1 = 0.0300$ |
| R indices (all data) Largest diff. peak and hole (e Å ⁻³) | $wR_2 = 0.0735$ $R_1 = 0.0834$ $wR_2 = 0.0794$ 0.106 and -0.143 | $wR_2 = 0.0575$ $R_1 = 0.0675$ $wR_2 = 0.0624$ 0.092 and -0.109 |

| 10 | | | | | | | 11 | | |
|------|----------|----------|---------|--------|-------------------------|---|-------------------------------|-------------------------------|---------------------------|
| Atom | x | У | Ζ | U(eq)ª | Atom | x | У | Ζ | U(eq)ª |
| C-1 | 7087(9) | 9462(2) | 1915(2) | 49(1) | C-1A C-1B | 3491(3) -24(3) | 8793(2) 5441(2) | 4228(2) 3301(2) | 55(1) 55(1) |
| O-1 | 8586(6) | 10377(2) | 1683(1) | 59(1) | 0-1A 0-1B | -1535(3) 3867(2) -1138(2) | 7105(3) 8194(2) 4903(2) | 5182(2) 2784(2) | 54(1) 71(1) 63(1) |
| C-2 | 7792(9) | 9285(3) | 2646(2) | 47(1) | C-2A C-2B | -2302(2) 391(3) 417(3) | 6642(2) 8591(2) 5132(2) | 9337(2) 3567(2) 4492(2) | 64(1) 59(1) 56(1) |
| O-2 | 10276(5) | 7080(2) | 2454(1) | 56(1) | O-2C O-2A O-2B | -170(3) 2083(2) 3819(2) | 6888(2) 9325(2) 5878(2) | 9361(2) 859(2) 4868(2) | 58(1) 69(1) 72(1) |
| C-3 | 6427(10) | 8248(3) | 2891(2) | 50(1) | O-2C C-3A C-3B | | 7624(2) 9099(2) 5631(2) | 6905(2) 2460(3) 5041(2) | 66(1) 56(1) 58(1) |
| O-3 | 9011(7) | 7007(2) | 717(1) | 71(1) | C-3C O-3A O-3B | $\begin{array}{r} 657(3) \\ -343(2) \\ 3572(2) \end{array}$ | 7391(2) 9453(2) 6134(2) | 8/35(2) 1743(2) 2331(2) | 57(1) 73(1) 75(1) |
| C-4 | 7198(8) | 7315(3) | 2424(2) | 46(1) | O-3C C-4A C-4B | -1946(2) 2562(3) 2625(3) | 7723(2) 8812(2) 5385(2) | 5193(2) 1890(2) 4408(2) | 70(1) 52(1) 56(1) |
| O-4 | 6444(7) | 5830(2) | 1318(1) | 93(1) | C-4C O-4A O-4B | $ 192(3) \\ 75(2) \\ 2956(3) $ | /114(2) 7794(2) 4489(2) | 7529(2) 2159(2) 2192(3) | 52(1) 91(1) 112(1) |
| C-5 | 6517(9) | 7633(3) | 1699(2) | 46(1) | O-4C C-5A C-5B | -1888(3) 1769(3) 2059(3) | 6065(2) 9034(2) 5679(2) | 5672(2) 2661(2) 3202(2) | 84(1) 48(1) 51(1) |
| O-5 | 8024(5) | 8586(2) | 1509(1) | 49(1) | C-5C O-5A O-5B | -1229(3) 2248(2) 893(2) | 7357(2) 8460(1) 5129(1) | 7074(2) 3652(2) 2769(2) | 49(1) 52(1) 52(1) |
| C-6 | 7841(12) | 10687(3) | 1009(2) | 82(2) | O-5C C-6A C-6B | -1904(2) 3402(5) -1793(4) | 6817(1) 8561(3) 5335(3) | 7702(2) 6048(3) 1722(3) | 51(1) 103(2) 81(1) |
| N-7 | 7479(8) | 7960(3) | 3574(2) | 74(1) | C-6C N-7A N-7B | -3556(4) 4783(3) 2120(3) | 7079(3) 8740(3) 5196(2) | 9100(3) 1816(3) 6152(2) | 87(1) 80(1) 79(1) |
| N-8 | 6006(12) | 8295(3) | 4037(2) | 90(1) | N-7C N-8A N-8B | $1951(3) \\ 4861(3) \\ 2937(3)$ | 6985(3) 9322(3) 5700(2) | 9237(3) 1083(3) 6810(3) | 80(1) 79(1) 73(1) |
| N-9 | 4737(15) | 8530(4) | 4517(2) | 156(3) | N-8C N-9A N-9B | $2807(4) \\ 5024(4) \\ 3682(4)$ | 7533(3) 9808(3) 6086(3) | 9103(2) 389(3) 7504(3) | 78(1) 110(1) 107(1) |
| C-10 | 7318(9) | 6721(3) | 1227(2) | 57(1) | N-9C C-10A C-10B | $\begin{array}{r} 3684(4) \\ 424(3) \\ 2888(3) \end{array}$ | 7967(3) 8674(2) 5346(3) | 9041(3) 2173(2) 2519(3) | 113(1) 55(1) 63(1) |
| C-11 | 9745(13) | 6153(3) | 242(2) | 101(2) | C-10C C-11A C-11B | -1723(3) -1649(4) 4425(5) | 6964(2) 9197(3) 5904(4) | 5925(3) 1205(3) 1696(5) | 52(1) 92(1) 97(1) |
| H-1 | 4961 | 9566 | 1862 | 58 | C-11C H-1A H-1B | -2336(4) 3490 -166 | 7425(3) 9537 6197 | 4057(3) 4411 3230 | 98(1) 66 66 |

Table 3: Atomic coordinates (\times 104) and equivalent isotropic displacement parameters (Ų \times 103) for 10 and 11

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(Continued on next page)

Table 3: Atomic coordinates (\times 10⁴) and equivalent isotropic displacement parameters (Å² \times 10³) for 10 and 11 (*Continued*)

| 10 | | | | | | | 11 | | |
|-------|-----------|-----------|----------|--------|-------------------------|----------------------------|------------------------------|-------------------------|--------------------------|
| Atom | X | У | Ζ | U(eq)ª | Atom | x | Y | Ζ | U(eq)ª |
| H-2A | 7130(70) | 9850(20) |)2944(1 | 4)57 | H-1C H-2A H-2D | -1690(30) 4471 492 | 7940(30) 7844 4378 | 8830(20 3478 4553 |) 64 71 67 |
| H-2B | 10010(80) |)9300(20) |)2718(1 | 4)57 | H-2G H-2B H-2E | -65 5220 -198 | 6136 8864 5357 7126 | 9371 3954 4854 | 69 71 67 |
| H-2C | 10350(90) |)6490(30) |)2778(1 | 7)84 | H-2H H-2C H-2F | o∠ 2130(40) 3740(40) | 9980(30) 6580(30) | 940(30) 4830(30 |) 104) 108 |
| H-3 | 4240(80) | 8310(30) |)2897(1 | 5)60 | H-3A H-3B H-3C | 3998 1585 652 | 9860 6390 8152 | 2548 5080 8822 | 67 70 69 |
| H-4 | 6053 | 6681 | 2550 | 56 | H-4A H-4B H-4C | 2530 2766 301 | 8058 4629 6360 | 1752 4445 7463 | 62 68 62 |
| H-5 | 4410(80) | 7720(20) |) 1655(1 | 4)56 | H-5A H-5B H-5C | 1760(30) 1911 -1374 | 9810(20) 6434 8111 | 2850(20 3132 7097 |) 57 61 59 |
| H-6A | 8662 | 11379 | 915 | 123 | H-6A H-6D H-6G | 3833 -2580 -4015 | 8206 4973 6726 | 6714 1426 9528 | 154 121 131 |
| H-6B | 5739 | 10717 | 964 | 123 | H-6B H-6E H-6H | 2511 -1278 -3990 | 8425 5254 6993 | 5870 1238 8336 | 154 121 131 |
| H-6C | 8621 | 10174 | 695 | 123 | H-6C H-6F H-6I | 3550 -1955 -3497 | 9299 6064 7810 | 6141 1798 9280 | 154 121 131 |
| H-11A | 11031 | 6428 | -102 | 152 | H-11A H-11D | -2067 4910(50) -2571 | 9792 6550(40) 8037 | 800 1620(40 3609 | 138 1) 145 147 |
| H-11B | 7974 | 5888 | 36 | 152 | H-11B H-11E | -2061 3850(50) -3047 | 9008 5630(40) | 1744 940(40) | 138 145 |
| H-11C | :10711 | 5582 | 479 | 152 | H-11C H-11F H-11I | -1689 4870(50) -1649 | 8622 5350(40) 7078 | 714 1950(40 3881 | 138 138 145 147 |

 $^{\alpha}U_{eq}$ is defined as one-third of the trace of the orthogonalized U_{ij} tensor.

| 10 | Bond length | (Å) | 11 Bond length | (Å) | Difference ^a (Å) |
|-------|--------------|-----------|---|---|--------------------------------|
| C-3- | —N-7 | 1.476(4) | C-3A—N-7A C-3B—N-7B C-3C—N-7C | $\begin{array}{c} 1.493(5) \\ 1.468(4) \\ 1.481(4) \end{array}$ | 0.025 |
| Vale | ence angles | (°) | Valence angles | (°) | Difference ^a (°) |
| C-3- | —N-7—N-8 | 115.4(3) | C-3A—N-7A—N-8A C-3B—N-7B—N-8B | $115.6(3) \\ 115.6(3)$ | 0.5 |
| C-4- | C-5C-10 | 109.7(3) | C-3C—N-7C—N-8C C-4A—C-5A—C-10A C-4B—C-5B—C-10B C-4C—C-5C—C-10C | $115.1(3) \\111.1(2) \\112.1(3) \\110.0(2)$ | 2.1 |
| N-7- | N-8N-9 | 172.7(5) | N-7A—N-8A—N-9A N-7B—N-8B—N-9B | 173.6(4) 172.2(4) | 1.4 |
| C-10 |)—O-3—C-11 | 115.3(3) | N-7C—N-8C—N-7C C-10A—O-3A—C-11A C-10B—O-3B—C-11B C-10C—O-3C—C-11C | $173.0(4) \\117.3(3) \\116.7(3) \\117.3(2)$ | 0.6 |
| Torsi | ion angles | (°) | Torsion angles | (°) | Difference ^a (°) |
| C-2- | C-1C-6 | -173.9(3) | C-2A—C-1A—O-1A—C-6A C-2B—C-1B—O-1B—C-6B | 159.1(3) 165.7(3) | 6.6 |
| C-3- | —N-7—N-8—N-9 | 159(4) | C-2C-C-1C-O-1C-C-6C C-3A-N-7A-N-8A-N-9A C-3B-N-7B-N-8B-N-9B | $162.7(3) \\ 171(3) \\ 176(3) \\ 176(3)$ | _ |
| C-4- | C-5C-10O-3 | -128.7(3) | C-3C—N-7C—N-8C—N-9C C-4A—C-5A—C-10A—O-3A C-4B—C-5B—C-10B—O-3B | 179(3) -100.4(3) -99.6(3) | 6.6 |
| C-4- | C-5C-10O-4 | 51.8(5) | C-4C—C-5C—C-10C—O-3C C-4A—C-5A—C-10A—O-4A C-4B—C-5B—C-10B—O-4B | -106.2(3) 78.9(4) 79.3(4) | 6.7 |
| C-4- | —C-3—N-7—N-8 | -146.9(4) | C-4C—C-5C—C-10C—O-4C C-4A—C-3A—N-7A—N-8A C-4B—C-3B—N-7B—N-8B | $72.6(4) \\83.6(4) \\79.1(4) \\82.4(4)$ | 4.5 |
| 0-4- | | -1.4(6) | 0-4A—C-10A—O-3A—C11A 0-4B—C-10B—O-3B—C11B | $\begin{array}{c} 82.4(4) \\ 2.1(5) \\ 0.0(5) \\ \end{array}$ | 3.3 |
| C-5- | | 178.1(4) | O-4C—C-10C—O-3C—C11C C-5A—C-10A—O-3A—C11A C-5B—C-10B—O-3B—C11B | 3.3(5) -177.3(3) -179.0(3) | 3.4 |
| O-5- | C-5C-10O-3 | -5.1(4) | C-5C-C-10C-O-3C-C11C O-5AC-5AC-10AO-3A O-5BC-5BC-10BO-3B | -175.6(3) 140.0(2) 141.7(2) | 6.7 |
| 0-5- | C-5C-10O-4 | 175.4(4) | O-5CC-5CC-10CO-3C O-5AC-5AC-10AO-4A O-5BC-5BC-10BO-4B | $135.0(2) \\ -40.6(4) \\ -39.3(4)$ | 6.8 |
| O-5- | C-1C-6 | 65.1(4) | U-5C—C-5C—C-10C—O-4C O-5A—C-1A—O-1A—C-6A O-5B—C-1B—O-1B—C-6B O-5C—C-1C—O-1C—C-6C | $\begin{array}{r} -46.1(4) \\ -81.5(3) \\ -75.7(3) \\ -78.3(3) \end{array}$ | 5.8 |

Table 4: Selected geometry parameters for methyl (methyl3-azido-2,3-dideoxy- β -L-lyxo- (10) and β -D-arabino-hexopyranosid)uronates (11)

 $^{\alpha}\mbox{The biggest}$ difference between the same geometry parameter for three molecules in an asymmetric part of the unit cell of 11.

To recapitulate, two crystal structures of new precursors of sugar amino acids are presented to provide geometric parameters for these compounds. The respective valence and torsion angles indicate that the methoxycarbonyl group is planar and that the azido group is linear as a consequence of their resonance structures. The aglycone methyl group is oriented in accordance with the *exo*anomeric effect.

EXPERIMENTAL

Diffraction data were collected at rt (295 K) on a Gemini R-Ultra diffractometer^[17] with MoK α radiation ($\lambda = 0.71073$ Å). The initial phase angle determination was performed using SHELXS.^[18] All H atoms that participate in the hydrogen bonds were located on a Fourier difference map and refined using a riding model with U_{iso}(H) = $1.5U_{eq}(O)$ and U_{iso}(H) = $1.2U_{eq}(C(alkyl))$, and U_{iso}(H) = $1.2U_{eq}(C(methyl))$. All other H atoms were located geometrically and refined using a riding model with C-H = 0.97-0.98 Å, and U_{iso}(H) = $1.2U_{eq}(C)$ (C-H = 0.96 Å and U_{iso}(H) = $1.5U_{eq}(C)$ for the methyl H atoms). Table 2 summarizes the crystallographic data, data collection, and structure refinement; Table 3 sets out the coordinates of the atoms and their isotropic temperature factors; Table 4 gives selected crystals' geometric parameters; and Tables 5 and 6 summarize the hydrogen interactions.

The crystal structure of **10** was refined to $R_1 = 0.0834$ (21,854 reflections—all unique) and $R_1 = 0.0369$ (1193 reflections with $F_0 > 2\sigma(F_0)$) using the full-matrix least-squares method and the SHELXL-97 program^[19] based on 162 parameters. The crystal structure of **11** was refined to $R_1 = 0.0675$ (12,891 reflections—all unique) and $R_1 = 0.0300$ (3162 reflections with $F_0 > 2\sigma(F_0)$) using the full-matrix least-squares method and the SHELXL-97 program based on 462 parameters. The structures of the compounds showing the conformations and atom numbering system are illustrated in Figures 1 (**10**) and 2 (**11**).^[20] The molecular packing in the crystals, illustrated in Figures 4 (**10**) and 5 (**11**), was prepared with the aid of PLUTO-78.^[21] The computational material for this publication was prepared using the PLA-TON program.^[14]

SUPPLEMENTARY MATERIALS

Full crystallographic details, excluding structures features, have been deposited (deposition No. CCDC 756578 and 756579) with the Cambridge Crystallographic Data Center. These data may be obtained, on request, from the Director, CCDC, 12 Union Road, Cambridge, CB2 1EZ, UK (tel.: +44-1223-336408; fax: +44-1223-336033; e-mail: deposit@ccdc.cam.ac.uk or www: http://www.ccdc.cam.ac.uk).



Figure 4: Molecular packing of 10 (view along *a*-axis).

Table 5: Intermolecular hydrogen interactions for **10** with distances (d): d(D...A) < R(D)+R(A)+0.50Å; d(H...A) < R(H)+R(A)-0.12Å and angle (<) $<D-H...A > 100.0^{\circ}$

| D-H | А | d(D-H) | d(HA) | d(DA) | < D-H A |
|----------|--------------------|---------|---------|----------|---------|
| 0-2-H-2C | O-1 ⁱ | 0.98(4) | 1.82(4) | 2.777(3) | 166(4) |
| C-2-H-2A | O-4 ⁱⁱ | 0.97(3) | 2.50(3) | 3.410(5) | 156(2) |
| C-3-H-3 | O-2 ⁱⁱⁱ | 1.99(4) | 2.52(4) | 3.269(5) | 131(3) |
| C-5-H-5 | O-2 ⁱⁱⁱ | 0.97(4) | 2.58(3) | 3.278(5) | 129(2) |

Symmetry codes: (i) -x + 2, y-1/2, -z + 1/2; (ii) -x + 1, y + 1/2, -z + 1/2; (iii) x-1, y, z.

Table 6: Intermolecular hydrogen interactions for 11 with distances (d): $d(D \dots A) < R(D) + R(A) + 0.50$ Å; $d(H \dots A) < R(H) + R(A) - 0.12$ Å and angle (<) < D-H \ldots A > 100.0°

| D-H | А | d(D-H) | d(HA) | d(DA) | < D-H A |
|---|--|---|---|--|---|
| O-2A-H-2C O-2C-H-2I C-1C-H-1C C-11B-H-11E C-5A-H-5A | 0-1C ¹ 0-1B ¹ 0-4B ¹ N-9A ¹¹ 0-4C ¹ | 0.85(4) 0.95(4) 1.01(4) 1.02(3) 1.02(3) | 2.17(4) 2.02(4) 2.55(3) 2.60(5) 2.45(3) | 2.992(3) 2.946(3) 3.434(5) 3.220(7) 3.337(3) | 165.0(3) 164(3) 146(2) 117(4) 144.7(19) |

Symmetry codes: (i) -x, y + 1/2, -z + 1; (ii) -x + 1, y-1/2, -z.



Figure 5: Molecular packing of 11 (view along *b*-axis).

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