# **Supporting Information**

## Bacterial AmpD at the Crossroads of Peptidoglycan Recycling and Manifestation of Antibiotic Resistance

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### **Experimental Procedures**

**Cloning of the** *ampD* **gene from** *Citrobacter freundii*. The *ampD* gene was amplified by PCR from the chromosome of *C. freundii* (ATCC6879) using two custom-synthesized primers AmpDNdeI: 5'-GCGT<u>CATATG</u>TTGTTAGACGAGGGCTGGCTGGCA-3' and AmpDHind: 5'-CGAT<u>AAGCTT</u>TCA TGTCATCTCCTTGTGTGACGAGGGGGT-3' (the Nde I and Hind III sites are underlined). The resulting PCR products were digested by the Nde I and Hind III, and ligated into the polylinker of pET24a(+) vector under the T7 promoter. The vectors were transformed into *Escherichia coli* JM83. The selection of transformants was performed on LB agar supplemented with ampicillin (100  $\mu$ g/mL). The nucleotide sequences of the *ampD* gene from several transformants were verified by sequencing of both DNA strands according to standard procedures. The correct construct was transformed into *E. coli* BL21(DE3) cells for protein expression. In this construct, the *ampD* gene is inducible by isopropyl  $\beta$ -D-thiogalactoside (IPTG).

**Protein expression in** *E. coli* and purification of AmpD. *E. coli* BL21(DE3) cells harboring the above vector pET-24a<sup>+</sup> with the cloned *ampD* gene were grown at 37 °C in 500 mL of LB medium supplemented with kanamycin (50 µg/mL) as the selection agent. The expression of the wild-type AmpD was induced by the addition of IPTG (400 µM, final concentration), when the cell density reached an  $A_{600}$  value of 0.7. After 4 h of induction at 30 °C, the cells were harvested by centrifugation (6,000 g, 15 min, 4 °C), washed with 150 mM NaCl (in water) and then resuspended in 35 mL of 20 mM phosphate buffer containing 1 mM dithiothreitol pH 7.0 (buffer A). Benzonase (5 units/L of culture) and Pefabloc (0.1 mg/mL in suspension) were added to the cell suspension. Cells were lysed at 4 °C by 30 cycles of sonification (30 s of burst and 20 s of rest for each cycle using a Branson sonifier). The debris was removed by centrifugation at 20,000 g for 40 min at 4 °C. The pH of the supernatant was adjusted to 7.0. Then, the supernatant was microfiltered through 0.45 µm Millipore filters and loaded onto a Q-Sepharose\_column (2.5 cm × 30 cm, 150 mL; Sigma) equilibrated in buffer A (supple-

mented with 0.05 mg/mL Pefabloc). The column was eluted with a linear NaCl gradient (720 mL) from 0 to 0.35 M in buffer A containing 0.075 mg/mL Pefabloc. The peak fractions containing AmpD (assessed by SDS-PAGE) were pooled, concentrated to 10 mL by ultrafiltration on a 5,000 Da-cutoff Amicon membrane and applied to a molecular sieve column of Sephacryl S100 HR (2.5  $cm \times 100 cm$ , 500 mL; Sigma) equilibrated in buffer A (supplemented with 0.05 mg/mL Pefabloc). The fractions containing the protein were collected and concentrated to 4 mL. The solution was added to 4 mL of 2.4 M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> to make a final concentration of 1.2 M for  $(NH_4)_2SO_4$ . The enzyme solution (8 mL total) was applied to a Source 15 ISO column (2.5 cm  $\times$  30 cm, 60 mL; GE Healthcare Life Science; hydrophobic chromatography). The desired protein was eluted with a linear gradient of 1.2 to 0 M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> in buffer A. The fractions containing AmpD were collected and dialyzed against 50 mM sodium phosphate buffer, pH 7.0, and concentrated by ultrafiltration to 15~25 mg/mL. After addition of sodium azide (1 mM, final concentration), the enzyme was stored at 4 °C. The protein content from the column fractions was monitored by SDS-PAGE (Figure S1). The AmpD concentration was determined by measuring the absorbance of the solution at 280 nm and using a calculated extinction coefficient of 31,960 M<sup>-1</sup>cm<sup>-1</sup>.<sup>1</sup> Matrix-assisted laser desorption ionization (MALDI) mass spectrometric analysis revealed a molecular mass of  $20.853 \pm 20$ Da for AmpD, in agreement with that value deduced from the gene sequence (20 847 Da) (Figure S2).



**Figure S1**. SDS-PAGE analysis of the purified AmpD, (A) 15 µg and (B) 10 µg, (C) molecular mass standards.

<sup>&</sup>lt;sup>1</sup> Généreux, C.; Dehareng, D.; Devreese, B.; Van Beeumen, J.; Frère, J. M.; Joris, B., *Biochem. J.* 2004, 377, 111-120.

# D:\Data\MVJ\MSF\Mobashery\050409\o\_DHB\_1\0\_J8\1 Comment 1 Comment 2 sample "o" in DHB matrix Intens. [a.u.] 500 220 20852.9 m/z

## Figure S2. MALDI mass spectrum of the purified AmpD.

**Kinetic studies.** The assays were carried out in 20 mM sodium phosphate buffer, pH 7.0, at 25 °C with substrate concentrations ranging from 50  $\mu$ M to 3.0 mM and different enzyme concentrations — 50 nM for AnhMurNAc-tripeptide (**2a**), 100 nM for AnhMurNAc-pentapeptide (**2c**), 1.5  $\mu$ M for GluNAc-AnhMurNAc-pentapeptide (**1**), 500  $\mu$ M for **4a** and **4b**. The reaction mixtures were incubated at 25 °C for 30 min. The reactions were stopped by the addition of 2 volume of 0.075% TFA in water. The internal standard was GluNAc-MurNAc-pentapeptide (**13**). Reaction products were separated and quantified on a C18 reversed-phase HPLC column (Symmetry Shield RP18, 5  $\mu$ m, 3.9 mm × 150 mm; Waters) on a PerkinElmer series 200 System. The column was equilibrated with 0.05% trifluoroacetic acid in water and eluted with a linear acetonitrile gradient from 0 to 15% over 40 min with a flow rate of 1 mL/min. The column effluent was monitored at 205 nm. The catalytic activity of the AmpD was quantified from the rate of substrate disappearance and of tripeptide or pentapeptide appearance. The *t*<sub>R</sub> for **2a** was 30.2 min, for **2c** was 34.5 min, for **1** was 36.2 min, for **4a** was 24.6 min and for **4b** was 29.5 min. HPLC chromatograms of AmpD reaction of **2a** is shown in Figure S3 as a representative example.



**ESI-MS.** Characterization of the reaction products was performed using a Waters Alliance 2695 Separations Module coupled with a Waters 2996 Photodiode Array detector, and Micromass Quattro-LC Triple Quadrupole electrospray ionization (ESI) mass spectrometer (Figure S4). The peaks were initially analyzed using positive ionization mode throughout the m/z of 100 - 1200. The charge states of the major ions were determined as the reciprocal of the spacing between two adjacent isotopic peaks differing in mass by 1 Da.<sup>2</sup> Analysis of the MS data and fragmentation pattern of the reaction products and of compounds **2a**, **3**, and **12a** allowed us to confirm chemical structure of the reaction products.

### Syntheses of Compounds

General Procedures. All organic reagents were purchased from either Sigma-Aldrich Chemical Company or Acros Organics, unless otherwise stated. All reactions were performed under an atmosphere of nitrogen unless noted otherwise. Reactions were monitored by thin-layer chromatography (TLC) carried out on Whatman reagents 0.25 mm silica gel 60-F plates that were visualized using UV light and/or aqueous cerium sulfate staining, followed by heating. Flash chromatography was carried out with silica gel 60, 230-400 mesh (0.040-0.063 mm particle size) purchased from EM Science. NMR spectra, including <sup>1</sup>H, <sup>13</sup>C, DEPT, H-H COSY, and H-C HETCOR experiments, were recorded on a Varian UnityPlus 300, or a Varian INOVA-500, or Varian DirectDrive 600 spectrometer. Proton and Carbon chemical shifts were referenced to residual solvent peaks. NMR signal assignments for synthesized compounds were performed on the basis of H-H COSY, H-C HETCOR, and DEPT experiments. High-resolution mass spectra were obtained at the Department of Chemistry and Biochemistry, University of Notre Dame via FAB ionization, using a JEOL AX505HA mass spectrometer.

Analytical high performance liquid chromatography (HPLC) was performed on Waters 2414 instrument with SunFire C18 reversed-phased column (Waters) or delta-pak C18 reversed-phased column (Waters) using a linear

<sup>&</sup>lt;sup>2</sup> Henry, K. D.; McLafferty, F. W. Org. Mass Spectrom. 1990, 25, 490-492.

gradient of 2-15% acetonitrile in water supplemented with 0.1% TFA over 40 min at 1 mL/min. Detection of the samples was by UV at 205 nm. Preparative HPLC purifications were performed using delta-pak C18 reversed-phased column, 100 Å pore size,  $19 \times 300$  mm.

Crystals were examined under Infineum V8512 oil and placed on a MiTeGen mount, then transferred to the 100 K N<sub>2</sub> stream of a Bruker SMART Apex CCD diffractometer. Unit cell parameters were determined from reflections with I > 10 $\sigma$ (I) harvested from three orthogonal sets of 30 0.5°  $\omega$  scans. Data collection strategy was calculated using COSMO, included in the Apex2 suite of programs<sup>3</sup> to maximize coverage of reciprocal space in a minimum amount of time. Average 4-fold redundancy of measurements was sought. Data were corrected for Lorentz and polarization effects, as well as for absorption. Structure solution and refinement utilized the programs of the SHELXTL software package.<sup>4</sup> Full details of the X-ray structure determinations are in the CIF files included as Supporting Information.



**Figure S3.** The AmpD reaction with compound **2a**. The single peak is compound **2a** at time zero (A). The time course for conversion of compound **2a** by AmpD to the two products (retention times at 3.1 and 21.5 min) were monitored at 10 min (B), 60 min (C), and 90 min (D) of incubation. The two new peaks correspond to product **1** (the tripeptide) and product **2** (anhMurNAc), whose identities were conformed by LC/MS analysis (Figure S4).

<sup>&</sup>lt;sup>3</sup> Apex2. Bruker-AXS: Madison, WI, 2008; Vol. 58.

<sup>&</sup>lt;sup>4</sup> Sheldrick, G. M., Acta Crystallogr. A. 2008, 64, 112-122.



Figure S4. ESI-LC-MS analysis of the AmpD reaction products and comparison to authentic synthetic samples. The spectrum of the synthetic compound 2a (A), of reaction product #1 (B), authentic compound 12a (C), of reaction product #2 (D), and of authentic compound 3 (E).

Compounds 1, 4a, 4b, and 13 were prepared according to the literature methods developed by our laboratory.<sup>5</sup> **Compound 9.** EDCI (0.18 g, 0.94 mmol) was added to a mixture of *N*-hydroxysuccinimde (0.11 g, 0.96 mmol) and 6 (0.28 g, 0.76 mmol) in  $CH_2Cl_2$  (5 mL) in an ice-water bath. The mixture was stirred at room temperature for 20 h. Meanwhile, the Boc-protected tripeptide (0.72 g, 0.91 mmol) in CH<sub>2</sub>Cl<sub>2</sub> (5 mL) was treated with trifluoroacetic acid (2 mL) in an ice-water bath. The temperature was gradually increased to room temperature over 1 h. The reaction mixture was evaporated to dryness under reduced pressure and the residue (7) was dissolved in toluene. This was followed by evaporation to dryness. The residue was dissolved in *i*Pr<sub>2</sub>NEt (0.4 mL, 2.3 mmol) and DMF (5 mL), and the solution was then added to the NHS-ester of the anhydrosugar, prepared above. The resulting mixture was stirred at room temperature for 20 h. The mixture was diluted with CH<sub>2</sub>Cl<sub>2</sub> and water was added. Layers were separated. The organic layer was dried over MgSO<sub>4</sub>, filtered, concentrated and the sample was subjected to column chromatography on silica gel (CH<sub>2</sub>Cl<sub>2</sub>/MeCN/MeOH, 10:3:0.5) to give the title compound (0.57 g, 72%). <sup>1</sup>H NMR (500 MHz, CD<sub>3</sub>OD)  $\delta$  1.29 (d, J = 6.8 Hz, 3H), 1.34 (d, J = 7.0 Hz, 3H), 1.36 - 1.45 (m, 2H), 1.60 - 1.71 (m, 2H), 1.75 - 1.84 (m, 2H), 1.95 - 2.05 (m, 1H), 2.12- 2.21 (m, 1H), 2.29 (t, J = 6.9 Hz, 2H), 3.49 (d, J = 1.2 Hz, 1H, H-4), 3.52 (m, 1H, H-3), 3.68 (dd, J = 7.5, 5.7 Hz, 1H, H-6a), 3.85 (s, 1H, H-2), 4.02 (dd, J = 8.2, 5.2 Hz, 1H, DAP-H-6), 4.17 (g, J = 6.8 Hz, 1H, Lac- $\alpha$ -H), 4.23 (d, J = 7.6 Hz, 1H, H-6b), 4.30 - 4.46 (m, 3H, Ala- $\alpha$ -H, Glu- $\alpha$ -H, DAP-H-2), 4.61, 4.71 (AB, 2H, OCH<sub>2</sub>Ph), 4.67 (m, H-5), 5.08 - 5.22 (m, 6H, OCH<sub>2</sub>Ph), 5.38 (s, 1H, H-1), 7.28 - 7.40 (m, 20H); <sup>13</sup>C NMR (126 MHz, CD<sub>3</sub>OD) δ 18.5, 18.6, 22.7 (3 × q), 23.1, 28.2, 31.8, 32.7 (5 × t), 49.9 (d, C-2), 50.2 (d, Ala-α-C), 53.4 (d, DAP-C-2), 53.7 (d, Glu- $\alpha$ -C), 62.9 (d, DAP-C-6), 66.3 (t, C-6), 68.0, 68.4, 72.6 (4 × t, OCH<sub>2</sub>Ph), 75.4 (d, C-5), 76.9 (d, Lac-α-C), 77.6 (2d, C-3 and C-4), 101.6 (d, C-1), 129.1, 129.2, 129.3, 129.5, 129.6, 129.7, 129.7, 136.8, 137.1, 137.1, 139.2, 164.8, 171.7, 172.6, 172.7, 173.3, 174.7, 174.8, 174.9; HRMS (FAB), calcd for C<sub>54</sub>H<sub>64</sub>N<sub>7</sub>O<sub>14</sub> (M+H<sup>+</sup>), 1034.4511, found 1034.4525.

**1,6-Anhydro-β-D-***N***-acetylmuramyl-L-Ala-γ-D-Glu-***meso***-DAP** (2a). Compound **9** (0.50 g, 0.43 mmol) was dissolved in MeOH (5 mL) and stirred in the presence of 10% Pd/C (0.1 g) under an atmosphere of hydrogen at 50 °C for 3 h. The reaction mixture was filtered through a layer of Celite and the residue was washed with MeOH. The combined filtrate was concentrated to dryness under reduced pressure. The crude product was subjected to HPLC purification to afford compound 2a (0.18 g, 66%). Preparative HPLC purifications were performed on delta-pak C18 reversed-phased column, 100 Å pore size, 19 × 300 mm using a linear gradient of 5-15% acetonitrile in water supplemented with 0.1% TFA over 0.5 h. <sup>1</sup>H NMR (600 MHz, D<sub>2</sub>O) δ 1.30 (d, *J* = 6.1 Hz, 3H), 1.35 (d, *J* = 5.6 Hz, 3H), 1.56 - 2.12 (m, 7H), 1.91 - 1.93 (m, 3H), 1.94 - 1.98 (m, 3H), 2.15 - 2.36 (m, 3H), 3.35 (br.s., 1H, H-3), 3.66 (m, 1H), 3.73 (t, *J* = 6.2 Hz, 1H, H-6a), 3.84 (br.s., 1H, H-2), 3.80 (br.s., 1H, H-4), 4.04 - 4.16 (m, 3H), 4.19 (d, *J* = 7.3 Hz, 1H, H-6b), 4.31 (br.s, 1H), 4.60 (d, *J* = 4.2 Hz, 1H, H-5), 5.40 (s, 1H, H-1); <sup>13</sup>C NMR (151 MHz, D<sub>2</sub>O) δ 17.2, 18.1, 21.9 (3 × q), 21.2, 27.7, 30.2, 31.1, 32.0 (5 × t), 49.5 (d, C-2), 49.5 (d), 65.3 (t, C-6), 68.2 (d, C-4), 76.0 (d, C-5, Lac-α-C), 78.5 (d, C-3), 100.0 (d, C-1); HRMS (FAB), calcd for C<sub>26</sub>H<sub>42</sub>N<sub>5</sub>O<sub>14</sub> (M+H<sup>+</sup>), 648.2728, found 648.2719.

**1,6-Anhydro-β-D-***N***-acetylmuramyl-L-Ala-γ-D-Glu-***meso***-DAP-D-Ala-D-Ala (2c).** This material was prepared in the same manner as described for **2a**, with the exception that pentapeptide **8** was used in place of **7**. **Compound 10**. <sup>1</sup>H NMR (600 MHz, CD<sub>3</sub>CN) δ 1.29 (d, J = 7.0 Hz, 3H), 1.32 (d, J = 6.7 Hz, 3H), 1.34 (d, J = 7.3 Hz, 3H), 1.34 - 2.00 (m, 7H), 1.37 (d, J = 7.3 Hz, 3H), 1.89 (s, 3H), 2.15 - 2.27 (m, 3H), 3.48 (s, 1H, H-4), 3.55 (s, 1H, H-3), 3.71 (dd, J = 7.6, 6.2 Hz, 1H, H-6a), 3.91 (d, J = 8.8 Hz, 1H, H-2), 4.06 (dd, J = 8.7, 4.8 Hz, 1H, DAP-H-6), 4.07 - 4.11 (m, 1H), 4.13 (q, J = 6.9 Hz, 1H, Lac-α-H), 4.16 (d, J = 7.6 Hz, 1H, H-6b), 4.27 - 4.43 (m, 4H), 4.64, 4.68 (AB, J = 12.0 Hz, 2H, OCH<sub>2</sub>Ph), 4.69 (br. s., 1H, H-5), 5.07 - 5.15 (m, 4H, OCH<sub>2</sub>Ph), 5.21 (s, 2H, OCH<sub>2</sub>Ph), 5.39 (s, 1H, H-1), 6.55 (d, J = 8.8 Hz, 1H, NH), 7.31 - 7.44 (m, 20H), 7.52 (t, J = 7.6 Hz, 1H, NH), 7.90 (d, J = 6.5 Hz, 1H, NH); <sup>13</sup>C NMR (151 MHz, CD<sub>3</sub>CN) δ 17.6, 17.9, 18.0, 18.6, 23.1 (5 × q), 22.9, 27.7, 31.7, 32.1 (5 × t), 49.3 (d, C-2), 49.3, 49.8, 50.6 (3 × d, Ala-α-C), 52.1 (d, Glu-α-C)), 55.4 (d, DAP-C-2),

<sup>&</sup>lt;sup>5</sup> Hesek, D.; Lee, M.; Zhang, W.; Noll, B. C.; Mobashery, S., *J. Am. Chem. Soc.* **2009**, *131*, 5187-5193; Hesek, D.; Suvorov, M.; Morio, K.; Lee, M.; Brown, S.; Vakulenko, S. B.; Mobashery, S., *J. Org. Chem.* **2004**, *69*, 778-784.

62.7 (d, DAP-C-6), 66.0 (t, C-6), 67.3, 67.6, 68.1, 72.1 (4 × t, OCH<sub>2</sub>Ph), 75.1 (d, C-5), 76.6 (d, Lac-α-C), 77.0 (d, C-4), 77.4 (d, C-3), 101.4 (d, C-1), 128.8, 128.9, 129.0, 129.1, 129.2, 129.4, 129.5, 129.6, 136.7, 137.0, 137.2, 139.2, 170.7, 171.4, 172.3, 173.2, 173.2, 173.5, 173.8, 174.0, 174.4; HRMS (FAB), calcd for  $C_{60}H_{73}N_9O_{16}$  (M<sup>+</sup>), 1176.5254, found 1176.5288.

**Compound 2c.** <sup>1</sup>H NMR (600 MHz, CD<sub>3</sub>OD)  $\delta$  1.39 (d, J = 6.5 Hz, 3H), 1.39 (d, J = 7.0 Hz, 3H), 1.42 (d, J = 7.3 Hz, 3H), 1.44 (d, J = 7.3 Hz, 3H), 1.51 - 2.03 (m, 7H), 1.99 (s, 3H), 2.22 - 2.39 (m, 3H), 3.42 (s, 1H, H-3), 3.72 (s, 1H, H-4), 3.76 (dd, J = 7.3, 5.6 Hz, 1H, H-6a), 3.88 (s, 1H, H-2), 4.01 (t, J = 6.0 Hz, 1H), 4.21 (q, J = 6.7 Hz, 1H, Lac- $\alpha$ -H), 4.24 - 4.27 (m, 1H), 4.28 (d, J = 7.3 Hz, 1H, H-6b), 4.33 - 4.45 (m, 4H), 4.59 (d, J = 5.0 Hz, 1H, H-5), 5.40 (s, 1H, H-1); <sup>13</sup>C NMR (126 MHz, CD<sub>3</sub>OD)  $\delta$  17.7, 18.0, 18.3, 18.7, 22.8 (5 × q), 22.6, 28.5, 31.2, 32.2, 32.7 (5 × t), 50.0 (d, C-2), 49.5, 50.6, 50.9 (3 × d, Ala- $\alpha$ -C), 52.7 (d, Glu- $\alpha$ -C), 53.9, 55.4 (2 × d, DAP-C-2, DAP-C-6), 66.4 (t, C-6), 70.8 (d, C-4), 77.1 (d, Lac- $\alpha$ -C), 77.7 (d, C-5), 81.0 (d, C-3), 101.9 (d, C-1), 171.9, 173.1, 174.4, 174.6, 174.8, 175.1, 175.3, 175.7, 175.9; HRMS (FAB), calcd for C<sub>32</sub>H<sub>52</sub>N<sub>7</sub>O<sub>16</sub> (M+H<sup>+</sup>), 790.3471, found 790.3455.

**2-Acetamido-1,6-anhydro-4***O***-benzyl-2-deoxy-3***O***-**[(1*R*)**-1**-(methoxycarbonyl)ethyl]-β-D-glucopyranose (11). Compound 3 (0.28 g, 1.0 mmol) in anhydrous MeOH (2 mL) was stirred in the presence of AcOH (2 mL)

at 60 °C for 10 h. The resulting mixture was concentrated to dryness. Crystals were grown from mixed solvents of hexanes and Et<sub>2</sub>O and used for determination of X-ray crystal structure. <sup>1</sup>H NMR (500 MHz, CDCl<sub>3</sub>)  $\delta$  1.42 (d, J = 7.0 Hz, 3H), 2.06 (s, 3H), 3.43 (s, 1H), 3.48 (s, 3H), 3.73 (d, J = 3.2 Hz, 2H), 3.75 (s, 3H), 4.09 (d, J = 8.4 Hz, 1H), 4.19 (d, J = 7.2 Hz, 1H), 4.31 (q, J = 6.9 Hz, 1H), 4.54 (d, J = 5.2 Hz, 1H), 5.36 (s, 1H), 6.91 (d, J = 8.4 Hz, 1H); <sup>13</sup>C NMR (126 MHz, CDCl<sub>3</sub>)  $\delta$  18.3 (q), 22.9 (q), 50.5 (d), 52.2 (q, OCH<sub>3</sub>), 65.4 (t, C-6), 70.1 (d), 74.2 (d), 76.4 (d), 78.1 (d), 95.9 (d), 100.8 (d), 170.6, 173.5.

L-Ala-γ-D-Glu-*meso*-DAP (12a). This material was prepared in the same manner as described for 2a, with the exception that the tripeptide 7 was used in place of 9. <sup>1</sup>H NMR (300 MHz, D<sub>2</sub>O) δ 1.46 - 2.30 (m, 8H), 1.56 (d, J = 7.2 Hz, 3H), 2.38 - 2.49 (m, 2H), 3.90 (t, J = 5.9 Hz, 1H), 4.13 (q, J = 7.0 Hz, 1H), 4.37 (m, 2H); <sup>13</sup>C NMR (126 MHz, D<sub>2</sub>O) δ 17.1, 20.9, 21.4, 27.1, 30.1, 30.6, 31.9, 49.6, 53.2, 53.2, 54.2, 171.3, 173.9, 175.5, 175.8, 176.4, 177.2; HRMS (FAB), calcd for C<sub>15</sub>H<sub>27</sub>N<sub>4</sub>O<sub>8</sub> (M+H<sup>+</sup>), 391.1829, found 391.1839.

**X-ray structures of compounds 11.** Crystals of compound **11** was obtained and their X-ray crystal structure were determined to confirm the structure of 1,6-anhydromuramic acid. Compound **11** keeps a typical anhydropyranose structure, where all substitutens are in axial positions. Two-H bonds were present in compound **11**. The O4 atom engages two H-bonds. One is the intramolecular H-bond between N1–H1N–O4 and the other is the intermolecular H-bond between O4–H4O–O8. Detailed information on H-bonds is given in Table S2. Structural details are given in Figures S5 and S6.

11
C <sub>12</sub> H <sub>19</sub> NO <sub>7</sub>
289.28
$P2_1$
6.3338(1)
15.4559(3)
7.2741(2)
90.00
108.775(1)
90.00
674.20(3)
2
100(2)
1.54178
1.425
1.006
0.0264
0.0684
1.060
$\frac{- F_c  }{ F_o  }; \ GooF = S = \sqrt{\frac{\sum [w(F_o^2 - F_c^2)]}{(n-p)}}$

 Table S1. Crystallographic Details of Compound 11.

 Table S2. Hydrogen-bond geometry of compound 11.

D–H··· $A$	<i>D</i> –H (Å)	H…A (Å)	<i>D</i> … <i>A</i> (Å)	<i>D</i> –Н … <i>А</i> (°)
N1-H1N····O4 <sup>i</sup>	0.83(2)	2.54(2)	3.0638(17)	122.7(10)
O4–H4O…O8 <sup>ii</sup>	0.840	1.914	2.7035(16)	156

\*symmetry codes: (i) x, y, z; (ii) x-1, y, z-1.



**Figure S5**. (A) The molecular structure of compound **11**, showing the atom-numbering scheme. The ORTEP diagram is shown at 50% probability level. Bonds of lactate side chain at C-3 are shown in gray, while other bonds in anhydrosugar backbone are shown in black. Hydrogen atoms are shown as small spheres of arbitrary radii. (B) An alternative view.



**Figure S6**. Two-H bonds in compound **11** are shown in dotted lines. One is the intramolecular H-bond between N1–H1N–O4 (blue) and the other is the intermolecular H-bond between O4–H4O–O8 (pink). A unit cell is shown in dotted lines (dark blue).







- S14 -



- S15 -





- S17 -



#### Pulse Sequence: hetcor

Solvent: cd3od Ambient temperature User: 1-14-87 INOVA-500 "nmr2a.chem.nd.edu" BnO<sub>2</sub>C

Relax. delay 1.500 sec Acq. time 0.111 sec Width 18403.5 Hz 2D Width 3247.3 Hz 8 repetitions 256 increments OBSERVE C13, 125.6905174 MHz DECOUPLE H1, 499.8653292 MHz Power 40 dB on during acquisition off during delay WALTZ-16 modulated DATA PROCESSING Line broadening 1.0 Hz F1 DATA PROCESSING Line broadening 0.3 Hz FT size 4096 x 512 Total time 57 min, 16 sec





70

F2 (ppm)

50

20

30

40

60

80

90

100



exp1 s2pul









- S20 -

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exp5 s2pu1

SAMPL	Ε	DE	C. & VT
date Nov	1 2007	dfrq	599.888
solvent	d20	dn	H1
file	exp	dpwr	36
ACQUISIT	TION	dof	0
sfrq	150.856	dm	ууу
tn	C13	dmm	w
at	0.963	dmf	9708
np	65536	dseq	
sw	34013.6	dres	1.0
fb	18800	homo	n
bs	4		DEC2
tpwr	51	dfrq2	0
pw	8.0	dn2	
d1	2.000	dpwr2	1
tof	1576.9	dof2	0
nt	12000	dm2	'n
ct	9342	dmm 2	с
alock	n	dmf2	15202
gain r	not used	dseq2	
FLAGS	3	dres2	1.0
<b>i</b> 1	n	homo2	n
in	n	PR	DCESSING
dp ·	У	16	1.00
hs	nn	wtfile	
DISPLA	ΑY	proc	ft
sp	1376.1	fn	131072
wp	25833.9	math	f
VS	45		
sc	0	werr	
wc	250	we×p	process p1C
hzmm	103.34	wbs	wft
is	500.00	wnt	
rfl .	1931.1		
rfp	0		
th	6		
ins	100.000		





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exp7 Proton

S	AMPLE		SPECIAL
date .	Jan 15 2008	tem	p 22.0
solvent	cd/3cn	gai	n notused
file	exp	. špi:	n notused
ACQU	ISITION	hst	0.008
sw	9615.4	pw9	0 11.100
at	2.049	alfa	a 10.0 <b>00</b>
np	39396		FLAGS
fb	4000	<b>i</b> 1	n
bs	32	in	n
SS	2	dp	y
d1	1.000	hs	nň
nt	16		PROCESSING
ct	16	fn	65536
TRANS	SMITTER		DISPLAY
tn	H1	sp	652.0
sfrq	599.880	wp	5281.3
tof	599.9	rf1	1208.4
tpwr	61	rfp	0
pw	5.550	r p	-192.9
DECO	DUPLER	1p	2.9
dn	C13	•	PLOT
dof	0	wc	250
dm	nnn	SC	0
dmm	с	vs	328
dpwr	38	th	12
dmf	35088	ai	cdc ph





- S24 -





- S26 -

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exp2 Carbon

SAMP	SPECIAL				
date Jan	18 2008	temp	0		22.0
solvent	CDC13	gaii	n	not	usedi
file	exp	spir	n	not	used
ACOUISI	TION	hst			0.008
sw	36764.7	Dw91	)		7.500
at	1.300	alfa	a	1	0.000
np	95624		FL	AGS	
fb	17000	i1			n
bs	4	in			n
d1	1.000	dp			v
nt	128	hs			nn
ct	128		PROC	ESSIN	G
TRANSMI	TTER	16			0.50
tn	C13	fn		not	used
sfra	150.854		DIS	PLAY	
tof	1542.6	sp		2	303.8
towr	58	wp		24	844.9
pw.	3.750	rf1		3	402.9
DECOUP	LER	rfp			209.7
dn	H1	гр			148.3
dof	0	10			14.4
dm	vvv	•	P	LOT	
dmm	Ŵ	wc			250
dpwr	44	SC			0
dmf	13908	VS			358
		th			6
		ai	cdc	ph	





118.382

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exp1	Proton	ì
	SAMPLE	SPECIAL
date	Feb 16 2008	temp 22.0
solve	nt cd3od	gain not used
file	exp	spin notused
AC	QUISITION	hst 0.008
sw	9615.4	pw90 11.100
at	3.408	alfa 10.000
np	65536	FLAGS
fb	4000	i] n
bs	4	in n
SS	2	dp V
d 1	1.000	hs nn
nt	16	PROCESSING
ct	16	fn 131072
TR	ANSMITTER	DISPLAY
tn	Н1	sp 257.7
sfra	599.879	wp 4455.3
tof	599.8	rfl 1208.5
tpwr	61	rfp 0
<b>D</b> W	11.100	rp -43.9
D	ECOUPLER	1p 3.3
dn	· C13	PLOT
dof	0	wc 250
dm	nnn	sc 0
dom	c	vs 200
dowr	38	th 50
dmf	35088	ai cdc ph
	00000	pi







- S32 -

exp2 Carbon SAMPLE date Feb 16 2008 temp SPECIAL 22.0 gain spin hst pw90 solvent file cd3od exp not used not used ACQUISITION 0.008 36764.7 sw at np fb bs d1 nt ct 1.783 alfa 10.000 131072 FLAGS 17000 **i**1 8 in 1.220 dp 2400 hs 184 PROCESSING 0.50 104 1b C13 fn TRANSMITTER 262144 tn 150.855 DISPLAY sfrq 150.855 1542.6 sp 58 wp 7.500 rfl ER rfp H1 rp 0 lp tof 2091.6 25062.8 tpwr 9730.6 7413.7 pw dn dof dm DECOUPLER 56.**0** 999 w 44 13908 PLOT wc dmm sc vs th dpwr dmf

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n'n

2.7

25**0** 

403

ai cdc ph

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exp2 s2pu1

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					4 4 9 4	α		
		wbs wnt						
		werr wexp						
		math f						
	ai cdc ph	proc ft fn 131072			255			
	rtp 9678.1 th 6	lb 1.00 wtfile			000			
	1\$ 500.00 rfl 11110.6	homo3 n PROCESSING						
	wc 250 hzmm 85.60	dseq3 dres3 1.0						
	vs 304 sc 0	dmm3 c dmf3 10000						
	sp 1225.0 wp 21400.0	dof3 0 dm3 n						
	hs nn DISPLAY	dn3 dpwr3 1						
	in n dp y	DEC3 dfrq30						
	FLAGS 11 n	dres2 1.0 homo2 n						
	alock n gain notused	dmf2 10000 dseq2						
	nt 1200 ct 80	dm2 n dmm2 c				11		
	tof 144.5	dof2 0			Oł	H NHAc		
	pw 10.2	dn2 dpyr2 1				T		
	bs 4 town 52	DEC2			öΖ	-107		
	sw 26963.3 fb 15000	dres 1.0 homo n				ÌO \		
	at 1.215 np 65536	dm f 8787.35 dseq			H <sub>2</sub> CO.	<u> </u>		
	sfrq 125.702 tn C13	dan yyy dana w						
	file exp ACOUISITION	dpwr 40 dof 0						
	date Nov 30 2007 solvent CDC13	dfrq 499.864 dn H1						
	SAMPLE	DEC. & VT						

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18.302

-22.941

11

- - - 1 20 ppm

- S37 -

#### DHL-27\_2

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Pulse Sequence: dept



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DHL - 97

exp2 s2pu1

SAMPLE [ date Oct 10 2008 dfrq DEC. & VT 499.865 solvent D20 dn Η1 file 40 exp dpwr ACQUISITION rq 125.703 C13 1.215 dof dm Ō sfrq ууу dmm 8787.35 tn dmf at 65536 dseq 26963.3 dres 15000 homo np sw 1.0 fb n 4 52 dfrq2 DEC2 bs tpwr 0 pw d1 10.2 dn2 1.800 dpwr2 1 tof 144.5 dof2 ō nt ct 2400 1608 dm2 n dmm2 с alock 1000ŏ n dm f 2 not used FLAGS gain dseq2 dres2 1.0 **i** 1 n homo2 n in DEC3 n y dfrq3 dp hs 0 nn dn3 DISPLAY dpwr3 1 sp wp vs sc 1242.0 21470.7 dof3 0 dm3 n 636 dmm3 с dmf3 10000 0 25 Ŏ wc dseq3 85.88 dres3 1.0 hzmm is rfl rfp th 500.00 homo3 n 500.00 .... 1519.4 PRO 174.7 lb 4 wtfile PROCESSING 1.00 100.000 ft 131072 ins proc fn ai cdc ph math f werr wexp wbs wnt 800 .508 177.250-176.445





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